28th IPVS Congress Viet Nam 2026

THE 28TH INTERNATIONAL PIG VETERINAR SOCIETY CONGRESS

16-19 June 2026

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WELCOME MESSAGE

Dear colleagues and friends in Viet Nam and around the world working in swine production and veterinary medicine,

With great honor and pleasure, I am delighted to announce that the 28th International Pig Veterinary Society (IPVS) Congress will be held in Ho Chi Minh City, Viet Nam, from **June 16-19, 2026,** hosted by Nong Lam University Ho Chi Minh City, which has been selected by the IPVS Board as the official host institution. This congress represents one of the world's largest and most prestigious scientific gatherings for the global pig production and veterinary community. It will provide an exceptional platform for researchers, veterinarians, industry professionals, and stakeholders to exchange knowledge, share experiences, and discuss the latest advances in swine health and production. The congress will feature presentations and discussions on cutting-edge scientific topics in pig health and production, alongside exhibitions showcasing innovative technologies, products, and achievements in the swine industry.

We warmly invite you to join us in Ho Chi Minh City for this important scientific event and to experience the rich culture, hospitality, and vibrant atmosphere of Viet Nam. Additional information and updates regarding congress activities will be continuously provided in the coming months.

We look forward to welcoming you to IPVS 2026.



Associate Professor, Dr. Nguyen Tat Toan
President of the 28th IPVS congress
President of Nong Lam University HCMC

ABOUT CONGRESS LOCAL HOST

NONG LAM UNIVERSITY HO CHI MINH CITY



With nearly 70 years of establishment and development, Nong Lam University Ho Chi Minh City (NLU) has earned a strong reputation as one of Viet Nam's leading institutions in agriculture, veterinary medicine, animal science, and rural development. Over the years, the university has evolved into a multidisciplinary institution offering more than 50 academic programs spanning diverse fields of science and technology, while continuously advancing its educational quality toward international standards.

In addition to education and research, NLU plays an important role in promoting scientific innovation, technology transfer, and collaboration with industries and communities. The university has established extensive partnerships with international institutions and has successfully organized numerous national and international conferences, workshops, and scientific events. These activities have strengthened

NLU's capacity in research and academic exchange while creating opportunities for global collaboration.

As the host institution of the 28th International Pig Veterinary Society (IPVS) Congress, NLU is well positioned to provide an excellent environment for one of the world's most prestigious events in swine health and production. The university's long-standing strengths in veterinary and animal sciences, its international experience, modern facilities, and strong organizational capabilities make it an ideal host for bringing together scientists, veterinarians, researchers, and industry professionals from around the world.

Hosting IPVS 2026 represents not only an important milestone for NLU but also a valuable opportunity to strengthen global scientific exchange and further advance swine health and production for the international community.

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PLENARY SESSION 1

"A New Paradigm for Biosecurity: Building a Foundation for Long-Term Animal Health and Disease Prevention"

June 16, 2026; from 15:15 to 16:00

Prof. Dr. Derald Holtkamp
Iowa State University, Ames, Iowa, USA

Biography

Dr. Derald Holtkamp is a Professor in the Department of Veterinary Diagnostic and Production Animal Medicine at Iowa State University. A leading authority on swine health management, he specializes in the economics of disease, biosecurity, and infectious disease risk assessment. He is internationally recognized for his pivotal role in developing herd classification systems for PRRSV and *Mycoplasma hyopneumoniae*, work that has standardized industry approaches to disease monitoring, and for his research into the costs of PRRSV and other diseases. A prolific speaker and researcher, he has authored over 75 peer-reviewed publications and delivered more than 300 invited presentations globally. Additionally, he has mentored more than 400 professional and graduate students, playing a pivotal role in shaping the next generation of production animal medicine veterinarians and scholars.

ABSTRACT

Introduction and Objectives

Despite advances in knowledge and the application of biosecurity control measures, sustained progress toward the intended biosecurity outcomes has been elusive. In the United States, the incidence of outbreaks caused by porcine reproductive and respiratory syndrome virus (PRRSV) and porcine epidemic diarrhea virus (PEDV) in sow farms remains persistently high (MSHMP, 2023). Lateral introductions of PRRSV and other pathogens into groups of growing pigs continue to occur at a high frequency (Dion et al., 2021; Osemeke et al., 2025). Furthermore, the spread of African swine fever virus (ASFV) worldwide (WOAH, 2026) does not suggest that progress on biosecurity is being made. The lack of improvement in the intended biosecurity outcomes suggests that significant gaps remain unaddressed. The aim of this article is to describe why progress in the intended outcomes of biosecurity has been so elusive and what is needed to make progress.

Why progress has been elusive

Over the past 40 years, revolutionary changes in pig production have increased biosecurity risks. Geographic segregation of the breed-to-wean and wean-to-market phases of production means that

growing pigs are transported two or more times from birth to market, sometimes for long distances, facilitating the rapid spread of endemic disease and new transboundary and emerging diseases when they arise.

Industry consolidation has resulted in fewer, but larger, herds managed by increasingly large and more complex companies. As companies grew larger, organization charts became more complex, and specialized departments formed, making coordinated decision-making more challenging. Veterinarians are increasingly sidelined as decisions that impact biosecurity and animal health are made without their input.

As companies grew in size, their ability to use fixed assets more efficiently, such as livestock trailers, feed trucks, and manure removal equipment, increased. Instead of having equipment dedicated to a single farm, fleets of equipment can be used more efficiently with little time sitting idle. The fixed assets are used on multiple farms, increasing the likelihood of transmitting pathogens from one herd to another. Owner provided labor has been replaced by employees and the development of specialized boar studs, feed mills, and service centers, such as manure management and maintenance, has led to a significant increase in the frequency of entry events where pathogen-carrying agents, such as semen, feed, vehicles, people, and equipment, enter farms.

At the same time, the approach to biosecurity has not kept pace with the increasing challenges. The modern production system, characterized by large populations of animals raised in total confinement, is geographically separated but highly interconnected**.** Given all the changes over the last 40 years in how pigs are raised, the level of interconnectedness has increased substantially, and the production processes that form the links have become increasingly complex. The production processes that form the links are the source of biosecurity hazards that increase the likelihood of pathogen transmission between herds.

What needs to be done to make progress?

To rise to the challenge created by the revolutionary changes in pig production, biosecurity needs to be approached in an equally revolutionary way. The methodology used by the food industry to ensure food safety provides an excellent model. The Hazard Analysis and Critical Control Point (HACCP) methodology takes a proactive, preventive approach to identify, evaluate, and control hazards (Motarjemi et al., 2023). HACCP originated in the US National Aeronautics and Space Administration (NASA) in the 1960s as a systematic method to identify food safety hazards in the food production processes to ensure that food carried by astronauts on missions was not contaminated. The emphasis on analyzing and monitoring the production process for hazards makes the HACCP approach and terminology, with some adaptations, well-suited for assessing biosecurity hazards in livestock production.

A critical adaptation is defining a biosecurity hazard. A key concept for defining a biosecurity hazard is the three failures. The three failures describe the circumstances that must occur for a pathogen-carrying agent to successfully transmit a pathogen to a herd. Pathogen-carrying agents

are any agents, such as people, vehicles, and pigs, that can be infected or contaminated with a pathogen and can carry it from one herd to another. The three failures are 1) failure to prevent the pathogen-carrying agent from being contaminated or infected with an infectious pathogen, 2) failure to mitigate the contamination or infection of the pathogen-carrying agent, and 3) failure to prevent pig(s) in the herd from being infected with the pathogen from the pathogen-carrying agent after it arrives at the farm.

All three failures are necessary for transmission to occur. Using the three-failure concept, a biosecurity hazard is any aspect of the production process that increases the probability of one or more failures.

Adaptation of HACCP for biosecurity includes the following principles

Principle 1. Identify biosecurity hazards through a biosecurity hazard analysis. Because biosecurity hazards are embedded within production processes, a biosecurity hazard analysis consists of a review of the entire production process. To assess biosecurity hazards, every detail of the production processes linked to an entry event must be thoroughly investigated. The relevant details include the operational aspects (how procedures are carried out, by whom, and when); structural aspects (the building design and site layout where the procedures occur); and resource aspects (what physical and non-physical resources, such as training, are available to carry out the procedures).

The Standardized Outbreak Investigation Program (SOIP) is a standardized, systematic, and comprehensive approach to conducting biosecurity hazard analyses (Holtkamp et al., 2025a) following an outbreak. A web-based application for the standardized instrument was launched in 2024. The application makes it easy for veterinarians to use and capture data from investigations in a secure database. While each investigation provides valuable insights, a centralized database facilitates identifying patterns and learning from multiple investigations over time. The SOIP investigation database offers a unique opportunity to leverage the collective experience of the entire industry.

As of October 2025, the SOIP database contained data for 87 completed investigations on sow farms across 24 different companies. Most investigations were conducted for PRRSV (65) and PEDV (19). The results presented here reflect all 87 investigations, regardless of pathogen. While biosecurity hazards vary by producer and farm, analyzing data at the industry level reveals where time and resources should be prioritized to strengthen biosecurity.

Each entry event creates an opportunity for pathogens to enter the herd. Some entry events occur continuously, such as air and water entry, while others occur periodically but are frequently unobserved, like rodents, wild animals, insects, and non-swine domestic animals. All other entry events on sow farms occur periodically and are generally observable. Among these, employee entry is by far the most frequent. On average, 118.43 employee entries occurred per 1,000 sows over a 4-week period. For a typical 4,000-sow farm, this equals about 6,158 events annually (Table 1).

A key component of the investigation is a subjective evaluation of the likelihood that each entry event may be associated with an outbreak. This evaluation is based on information collected in the SOIP investigation form. The investigator(s) is responsible for making this determination and assigning a hazard rating of high, medium, or low to each entry event.

Although an objective scoring system could offer advantages, a subjective approach allows investigators to weigh the biosecurity hazards identified within the broader context, including site location, season, weather conditions, and other factors that may influence the assigned hazard ratings.

The entry events most frequently rated high were swine movement events. Specifically, cull sows hauled from the farm received a high rating in 38 of 80 investigations where a rating was assigned, and weaned pigs hauled from the farm were rated high in 36 of 84 investigations (Table 1). The total number of ratings does not equal 87 for all entry events because ratings were not assigned when an event did not occur during the investigation period, and in a few cases, investigators omitted ratings even when the event did occur.

Table 1. Frequency of entry events on sow farms, and the frequency with which entry events were rated high for 87 investigations in the SOIP database

Entry event	Entry events / 1,000 sows (28 days)	Entry events for a 4,000-sow farm annually	Frequency rated high (n = 87 investigations)
On-farm employees enter farm	118.43	6,158	17
Feed or feed ingredients delivered to farm	5.29	275	13
Semen delivered to farm	2.73	142	2
Weaned pigs hauled from farm	2.34	122	36
Veterinarians, vendors, other visitors and off-farm personnel enter the farm	2.20	115	4
New tools and supplies delivered to farm	1.84	96	10
Garbage collection from farm	1.41	73	1
Cull sows hauled from farm	1.17	61	38
Repair/service personnel working outside barns	1.04	54	6
Repair/service personnel working inside barns	0.98	51	15
Mortalities removed from farm	0.94	49	17
Breeding replacements entered into herd	0.76	40	8
Manure removed from farm	0.24	12	8
Transferred tools and supplies delivered to farm	0.21	11	4
Propane, fuel and CO2 delivered to farm	0.18	9	1
Air entry			7
Water entry			5

Entry event	Entry events / 1,000 sows (28 days)	Entry events for a 4,000-sow farm annually	Frequency rated high (n = 87 investigations)
Other animals outside of barns			3
Pork and other food entered into farm			2
Other animals inside of barns			2
Insects inside of barns			0

Principle 2. Identify the critical control points, establish critical limits and monitor the process. Critical control points are steps in the production process where biosecurity hazards arise and are important for preventing the transmission of pathogens between herds. Critical limits are observable, measurable metrics that can be established to determine whether the critical control points in the production process are being performed correctly. For example, if trailers that enter a farm to haul cull sows also deliver them to cull markets or haul culls from other farms known to be positive for PRRSV or PEDV, then washing, disinfecting, and thoroughly drying those trailers between loads may be considered critical control points.

We need to get them right nearly every time. A critical limit for disinfection, for example, may be that the chemical disinfectant is applied at a desired concentration (e.g., 1:64). Finally, monitoring must be done to assure that the critical limits are being met at the critical control points. Too often, these are left to chance.

If monitoring is absent, there is no control

A study of 18 truck washes, located in the US and Canada, evaluated the effectiveness and consistency with which critical limits were achieved for several critical control points for trailer sanitation and decontamination (Dion et al., 2026). The wash, disinfection, and drying of one or more trailers were evaluated at each of the 18 washes. Key finding from the study were that the water temperature used to wash the trailers ranged from 17 to 77°C and the measured temperature was lower than the critical limit communicated by truck wash personnel at all truck washes except one. The concentration of chemical disinfectants was applied at the critical limit, defined as the label concentration, on 17 trailers and above the critical limit on 10 trailers, none of the trailers were disinfected at a concentration below the critical limit.

Principle 3. Establish record-keeping and validation procedures. Validation is the final step to ensure that the critical control points are being done correctly nearly every time (it is probably unreasonable to expect perfection). Veterinarians or specially trained experts need to conduct periodic audits by reviewing records, independently observing and measuring critical limits at the critical control points.

Conclusions and Recommendations

Over the past several decades, structural and operational changes in the swine industry have fundamentally altered the biosecurity risk landscape. Although important advancements in the knowledge and application of biosecurity practices have been made, these advancements have not translated into sustained improvements in the intended biosecurity outcomes.

Adapting concepts and terminology from HACCP provides a practical and effective approach to making sustainable progress in the intended outcomes of biosecurity. By identifying biosecurity hazards through the lens of the three failures, producers and veterinarians can more effectively target the steps in the production process that create the greatest risk for pathogen introduction. Meaningful progress will depend on consistent execution of critical control points, clearly defined critical limits, and independent monitoring and validation to ensure that controls are functioning as intended. Without monitoring and verification, biosecurity remains aspirational rather than controlled.

The establishment of standardized investigation methods, centralized data collection, and periodic validation audits creates an opportunity for continuous learning at both the farm and industry levels. Leveraging these tools and adopting a process-based, preventive mindset are essential steps if the swine industry is to reduce the biological and economic burden of disease and build a biosecurity system capable of meeting current and future threats.

Keywords: Biosecurity, Biosecurity hazards, Biosecurity hazard analysis, HACCP.

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PLENARY SESSION 1

"From Legacy to Innovation:
Applying Mechanism-Based Immunology to PRRSV Control"

June 16, 2026; from 16:00 to 16:45

Professor Dr. Sanipa Suradhat
Faculty of Veterinary Science, Chulalongkorn University
Bangkok, Thailand

Biography

Dr. Sanipa Suradhat is a professor in immunology at the Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand. Her career is marked by significant contributions to the field of veterinary immunology, with a focus on the immunobiology of porcine viral diseases, particularly classical swine fever (CSF) and porcine reproductive and respiratory syndrome (PRRS) viruses. Her research emphasizes porcine cellular immunity, regulatory T lymphocytes, and vaccine development and evaluation. She graduated Doctor of Veterinary Medicine (D.V.M.) from Chulalongkorn University and Ph.D. from Western College of Veterinary Medicine (WCVM), University of Saskatchewan, Canada, in 1999. She is a well-recognized expert in veterinary vaccinology and immunology. Over the years, she has served on several national committees and as a resource person, providing numerous lectures and consultations to veterinary and biomedical professionals at both national and international levels. From 2012 to 2014, she served as the Regional Laboratory Network Coordinator at the Food and Agriculture Organization Regional Office for Asia and the Pacific (FAO-RAP) of the United Nations (UN). She also served as the Dean of the Faculty of Veterinary Science, Chulalongkorn University during October 2021 to September 2025.

ABSTRACT - Tom Alexander Memorial Lecture

The evolution of modern swine health management is inseparable from the legacy of Tom Alexander whose scientific leadership and practical insight profoundly shaped modern swine health management, and veterinary education. His career exemplified the integration of rigorous research, field application, and international collaboration principles that continue to guide the global swine veterinary community.

Dr. Alexander's work on swine dysentery, herd health modelling, and structured pig flow systems demonstrated that sustainable control strategies must be grounded in a clear understanding of pathogenesis, transmission dynamics, and host response. Beyond his research contributions, his founding role in the International Pig Veterinary Society (IPVS) created a global forum where science and practice converge to improve herd health worldwide. His guiding principle *"understanding the mechanism before designing the intervention"* remains highly relevant to contemporary challenges in swine medicine.

One of the most persistent challenges facing swine practitioners today is porcine reproductive and respiratory syndrome virus (PRRSV). Despite decades of vaccination and intensive management efforts, PRRSV continues to cause significant economic losses worldwide. The difficulty in controlling PRRSV lies largely in its ability to manipulate the pig's immune system, resulting in delayed viral clearance and inconsistent vaccine performance under field conditions.

Recent research has focused on clarifying the immunological mechanisms underlying PRRSV persistence. Evidence demonstrates that PRRSV actively induces immunoregulatory cytokines, creating an immunosuppressive environment that dampens effective antiviral responses.

The viral nucleocapsid (N) protein has been identified as a key driver of IL-10 production and, subsequently, induction of PRRSV-specific regulatory T lymphocytes (Tregs). This immunomodulatory activity helps explain why protective cellular immunity is often suboptimal following natural infection or conventional vaccination. For practitioners, these findings provide mechanistic insight into common field observations, including incomplete protection, and variability in vaccine outcomes.

The implications from the presented work are practical and forward-looking. First, recognition of PRRSV's immunomodulatory capacity underscores the importance of minimizing co-infections, environmental stressors, and management factors that may further compromise immune function. Second, cellular immune biomarkers, such as IFN-γ producing cells and regulatory T cell dynamics, may serve as valuable tools for evaluating vaccine performances. Third, future vaccine evaluation and selection should incorporate assessment of cellular immune balance and immunoregulation.

In summary, applying mechanistic immunological insight to PRRSV control reflects the enduring legacy of Tom Alexander guiding principles. By linking pathogenesis, immune modulation, and rational vaccine design, the approach provides swine practitioners with a forward-looking, science-driven framework for improving disease prevention. Advancing PRRSV control will require continued integration of immunology, epidemiology, and herd management, ensuring that innovation remains firmly anchored in biological understanding and field relevance.

ABSTRACT - Outsmarting PRRSV: Immune Lessons for the Next Generation of Swine Vaccines

Porcine reproductive and respiratory syndrome virus (PRRSV) remains one of the most economically devastating pathogens in global swine production. Despite the widespread use of modified-live and inactivated vaccines, field protection remains variable, cross-protection against heterologous strains is inconsistent, and viral persistence continues to challenge eradication efforts. Increasing evidence suggests that the limited efficacy of current vaccination strategies is not solely attributable to viral genetic diversity, but also to the virus's intrinsic capacity to modulate and suppress host immune responses. A comprehensive understanding of PRRSV immunopathogenesis is therefore critical for the rational development of next-generation vaccines.

Over the past two decades, our laboratory has systematically characterized the immunomodulatory mechanisms employed by PRRSV in the porcine host. Early during infection, PRRSV induces a regulatory cytokine milieu characterized by elevated production of interleukin-10 (IL-10) and interleukin-1 receptor antagonist (IL-1Ra). These mediators suppress pro-inflammatory signaling, attenuate antigen presentation, and impair the development of effective antiviral responses. Concurrently, PRRSV infection alters macrophage polarization and functional phenotype. A central finding from our work is the identification of the PRRSV nucleocapsid (N) protein as a key driver of immune dysregulation. Beyond its structural role in viral assembly, the N protein actively induces IL-10 production in porcine immune cells. Mechanistic studies demonstrate that N protein-mediated signaling promotes the expansion of PRRSV-specific regulatory T cells ($CD4^+CD25^+Foxp3^+$ Tregs), which suppress effector T-cell proliferation and IFN-γ production. This virus-induced regulatory network delays the development of protective cellular immunity and contributes to prolonged viremia, viral persistence and complications from viral induced immunodeficiency. These immunomodulatory mechanisms provide a biological explanation for several well-recognized clinical and field observations: delayed and poor neutralizing antibody development and cell-mediated immune responses, prolonged viral infection, and inconsistent vaccine-mediated protection. Importantly, they suggest that vaccine design strategies focusing solely on antigenic matching or humoral immunity may be insufficient to achieve robust and durable protection.

Building on these insights, we pursued a rational vaccine design approach aimed at mitigating PRRSV-induced immune suppression while enhancing protective cellular immunity. Specifically, we constructed a "proof-of-concept" DNA vaccine expressing a linearized form of the N protein, engineered to reduce immunosuppressive activities and B cell signaling while preserving relevant T-cell epitopes. In controlled experimental studies, pigs immunized with this construct demonstrated enhanced PRRSV-specific IFN-γ producing T-cell responses, reduced frequencies of PRRSV-specific Tregs, and accelerated viral clearance following homologous challenge. These findings indicate that modulation of viral immune evasion pathways can significantly influence the quality and kinetics of antiviral immunity.

Collectively, our data support a paradigm shift in PRRSV vaccine development: from empirical attenuation strategies toward mechanism-based immunological design. Effective next-generation vaccines should aim not only to induce neutralizing antibodies but also to promote strong, balanced cellular immunity while minimizing virus-induced regulatory pathways. Integration of immune biomarkers, such as IFN-γ–secreting T cells and Treg dynamics, may further enhance the predictive assessment of vaccine efficacy in both experimental and field settings.

Beyond PRRSV, the principles elucidated through these studies highlight the broader importance of understanding virus-host immune interactions in veterinary vaccinology. Targeting immune dysregulation mechanisms represents a promising avenue for improving vaccine performance against complex, immune-evasive pathogens in swine and other livestock species.

Keywords: Immunomodulation, Nucleocapsid, PRRSV, Treg, Vaccine.



PLENARY SESSION 2

"Active Surveillance Based on Environmental Sampling: Opportunities and Challenges"

June 19, 2026, from 8:30 to 9:15

Prof. Jeffrey James Zimmerman
(J Zimmerman, B Armenta-Leyva, & B Munguía-Ramírez)
Iowa State University, Ames, Iowa, USA

Biography

Jeff Zimmerman (DVM, PhD, DACVPM) is a professor in the College of Veterinary Medicine at Iowa State University (Ames Iowa USA) working in the area of swine infectious disease diagnostics, epidemiology, and economics. His recent research has focused on aspects of diagnostic medicine related to assay development and applications in surveillance. Dr. Zimmerman has collaborated with colleagues and students to produce 261 refereed publications, book chapters, and books, as has co-edited 4 editions of Diseases of Swine (9th, 10th, 11th and 12th editions).

ABSTRACT

Recent years have seen dramatic improvements in the effectiveness, efficiency, and practicality of on-farm surveillance. In particular, the shift from individual samples collected from restrained animals to easily collected samples, e.g., oral fluids and processing fluids, has produced surveillance designs that are less expensive to implement, more sustainable, and more diagnostically sensitive. In this presentation, we discuss a possible future direction in surveillance. Specifically, we consider the question: *Is environmental sampling the next step in better, easier, and cheaper surveillance of swine populations?*.

The logic behind environmental sampling is simple and compelling: Infected animals shed pathogens into the environment via secretions and excretions. It follows that PCR-positive samples from the environment represent the presence of the pathogen of interest in the population occupying the environment.

There are numerous examples of the successful application of environmental sampling to human and animal pathogens. Highlighting examples relevant to swine, Vilalta et al. (2019) reported continuous PRRSV detection by RT-qPCR in surface wipes and airborne particle deposition samples collected from a 6,000-sow farrow-to-wean herd for up to 14 weeks post-outbreak. Similarly, Melini et al. (2024) reported PRRSV detection by RT-qPCR from environmental surface wipes collected from breeding and growing pig production sites. In the aggregate, examples of the detection of pathogens via environmental sampling include most swine pathogens:

Influenza A virus (Anderson et al., 2016; Garrido-Mantilla et al., 2019; Lauterbach et al., 2018; Neira et al., 2018; Neira et al., 2016; Prost et al., 2018), PCV (López-Lorenzo et al.,2021), PEDV (Alonso et al., 2017), PRRSV (Firnstahl et al., 2025), *Lawsonia intracellularis* (López-Lorenzo et al., 2026), *Salmonella* spp. (Dorr et al., 2009; O'Connor et al., 2006; Rao et al., 2010), and others.

These results are highly encouraging, but there are both technical and statistical sampling issues that need to be addressed before environmental sampling can become reliable.

The technical aspects of environmental sampling are critical but manageable. Accuracy, precision, reproducibility, and repeatability (the hallmarks of quality data) - are based on optimized, standardized methods. In contrast, a variety of sampling protocols have been described for collecting air, water or slurry (Luo et al., 2014), and surface (floors, walls, equipment, animals) samples. No optimized method for the recovery and detection of specific pathogens in environmental samples has been clearly identified for any of these approaches.

We can illustrate this point using air sampling as an example. A variety of samplers have been described in refereed publications, including the SKC BioSampler (Anderson et al., 2016), Midwest Micro-Tek cyclonic collector (Lauterbach et al., 2018; Neira et al., 2018), MD8 Airport (López-Lorenzo et al., 2026), Andersen cascade impactor (Alonso et al., 2017), Tisch cascade impactor (Alonso et al., 2017), and the Coriolis cyclone sampler (Bonifait et al., 2014). However, in a comparative study of 9 air samplers, Dybwad et al. (2014) concluded that air samplers differed in sampling efficiency and that "*in all likelihood no single air sampler will be universally optimal*". Differences in performance among air samplers is just one variable. Researching airborne PRRSV and influenza A virus, Hermann et al. (2006) showed that collection medium and sampling time also affected the recovery of airborne virus.

Standard methods for environmental sampling can and will be established in future research. More challenging will be answering the simple questions that define surveillance: *Where should I sample on my farm? How many samples should I collect? What probability of detection will that provide? What does a positive result mean for my pigs?* The difficulty in answering these questions is that we have little data on pathogen distribution in swine facilities. A common belief is that microorganisms are widely and homogenously distributed in the air and on surfaces. This may be true for certain pathogens. Specifically, those that are highly prevalent in the population, extensively shed by infected pigs, and resistant to degradation in the environment. For example, Lachapelle et al. (2017) reported that "*the majority of environmental samples were positive for group A rotavirus and/or porcine astrovirus RNA*" in a study of a network of 10 finishing farms and an abattoir.

More commonly, the distribution of pathogens in production facilities is spatiotemporally heterogenous, i.e., dynamic and variable in space and over time. Even in abattoir lairage pens where hundreds of pigs moved through the facility, O'Connor et al. (2006) found that the distribution of *Salmonella* on floor surfaces was spatially heterogeneous. In a study on PRRSV, Melini et al. (2024) detected PRRSV RNA in just 19 (13%) of 143 environmental samples collected from 7 farms undergoing PRRSV outbreaks. Spatiotemporal heterogeneity in the

environmental distribution of pathogens is the result of: 1) differences in the rate, duration, and route of pathogen shedding by infected pigs; 2) differences in farm size, design, and management affecting the diffusion of pathogens via air, people, animals, and fomites; 3) differences among pathogens in their ability to persist in the environment; and 4) differences in farm location and their climatic settings.

Nevertheless, just as the technical aspects of how to sample will be established through careful research, the simple, pragmatic, statistically-based questions of "*where to sample?*" and "*how many samples to collect?*" will be answered by the collection of sufficient field data and careful analyses.

Keywords: Environmental sampling, Surveillance.

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PLENARY SESSION 2

"Understanding the Epidemiology of Swine Diseases Through Voluntary Programs"

June 19, 2026, from 9:15 to 10:00

Prof. Cesar A. Corzo
University of Minnesota, St. Paul-MN, United States of America

Biography

Dr. Cesar A Corzo is an Associate Professor and the Allen D. Leman Chair in Swine Health and Productivity at the University of Minnesota's College of Veterinary Medicine. Dr. Corzo focuses on the occurrence, transmission dynamics and control of infectious diseases in swine populations. His research integrates real-world production system challenges with epidemiological modeling to develop sustainable strategies for pathogen prevention, control, and elimination. Dr. Corzo is the director of the Morrison Swine Health Monitoring Project (MSHMP), a nationally collaborative initiative funded in part by the Swine Health Information Center (SHIC) that monitors disease trends in more than half of the U.S. breeding herd and provides timely, science-based intelligence on high-impact pathogens such as PRRSV, PEDV, PDCoV and SVA. Under his leadership, MSHMP has evolved into a cornerstone of voluntary swine health surveillance and industry benchmarking, facilitating early detection and coordinated response efforts across commercial systems.

ABSTRACT

Introduction and Objectives

The swine industry continues its fight against infectious diseases globally, whether these are endemic, emerging or foreign animal diseases, veterinarians and producers are always seeking answers and solution that can help them prevent or eliminate diseases. While important advancements in herd health and biosecurity have been made, recurrent herd infections continue to exist in specific areas of the world. These recurrent infections have led to important levels of frustration for producers and veterinarians as every time there is an infectious disease outbreak, efforts to mitigate the impact of the outbreak are costly and in some cases the effectiveness of these may not be the one the industry expected. In addition, producers and veterinarians are left with multiple unanswered questions regarding the outbreak. One example is the question related to how the pathogen was introduced into the herd. While transmission characteristics have been understood for some pathogens, there are still facets of this process that need to be further understood. Bridging this knowledge gap is needed to implement procedures to reduce the probability of transmission. Therefore, by assembling voluntary programs in which producers are willing to share their herd status on a regular basis, multiple studies can be conducted to bridge this knowledge gap.

In the United States of America, the progressive nature of both veterinarians and producers has allowed to make major progress in the understanding of the epidemiology of swine diseases. An example is the collaborative effort led by the University of Minnesota initiative known as the Morrison Swine Health Monitoring Project (MSHMP) (mshmp.umn.edu) which was created by Dr. Bob Morrison who played an important role in shaping collaborative approaches to eliminate swine diseases such as Aujeszky's Disease and Porcine reproductive and respiratory syndrome (PRRS). This project is based on a collaborative and non-blaming philosophy with the overarching goal of helping the industry prevent and eliminate diseases.

Establishment and growth of voluntary swine health projects

Throughout the last few decades, the U.S swine industry has been able to work together to eliminate different diseases, one of them being Aujeszky and more recently, attempts to eliminate PRRS. These efforts mostly began with producer and practitioners' leadership which provided enough momentum to bring these initiatives to a level in which regional projects became national programs. While all these companies were and continue to be natural competitors, they understood early in the process that cooperation was needed to improve industry wide outcomes which ultimately became the foundation for voluntary programs that would monitor health and reduce disease incidence. In the early 2000's, PRRS was generating important levels of frustration which led to the creation of regional control programs in the U.S. In Minnesota, a project known as the "Stevens Country PRRS Project" became an important proof of concept as producers and veterinarians were successful at reducing incidence and prevalence. Trust, willingness to collaborate and communication were key ingredients for these types of projects to be successful.

Given the yearly frustration PRRS generated to the U.S. swine industry, the industry recognized rapidly that larger dataset was needed to better characterize the epidemiological trends of this disease at the national level. This need led to the conception of the MSHMP in which companies provided data voluntarily and the through data analysis and aggregate visualizations, the yearly cumulative incidence of this virus was estimated and allowed for benchmarking year after year.

As the project became known by the industry, production companies joined the effort increasing the representativeness of the dataset. Today, the project accounts for 3.9 million sows across 38 production companies.

Understanding the epidemiology of infectious diseases

The level of granularity of the database built within MSHMP enabled different levels of research for PRRS but also other diseases such as PED and SVA. In the case of PRRS, the cumulative incidence was estimated to vary between 20 - 30% annually and the prevalence of unstable farms was estimated to be approximately 30%. Furthermore, the onset of the epidemic was identified to begin between October and November with the lowest incidence occurring in the summer months.

Other characteristics of PRRS were elucidated including the identification of areas of higher or lower risk throughout the year together with factors such as herd size (e.g., > 2,500 sows), density as well as how air filtration system would decrease the risk of outbreaks when density and pressure system (e.g., positive vs negative) are considered.

In addition, PRRS viral diversity was another piece of the puzzle that was better understood as sequences were linked to sow farm outbreaks and thus frequency of specific viruses was characterized and complementary projects such as Variants Under Monitoring (VUM) were developed.

Conclusions and Recommendations

Voluntary projects can be successful and provide actionable information for industry stakeholders, academia and regulatory agencies. While the process of assembling these projects may need important amounts of time, dedication and persistence, the rewards from these projects will contribute to the advancement of animal health and the collaborative nature of any industry.

Keywords: Collaboration, Diseases, Epidemiology, Program, Voluntary.

Acknowledgements: We would like to acknowledge all MSHMP participating producers and veterinarians for their willingness to share their data and for their constructive feedback to continue to make this project relevant for them and the industry. We would also like to thank the Swine Health Information Center (SHIC) for their financial support and guidance.

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PARALLEL SESSION 1: NUTRITION AND GUT MICROBIOTA I

"Functional Nutrition to drive Productivity"

June 17, 2026; from 8:30 to 9:00

Dr. Hagen Schulze

ADM International Sarl, Rolle, Switzerland

Biography

Dr Hagen Schulze, Global Director CD&D at ADM Animal Nutrition brings over 30 years of experience across animal nutrition, feed additives, biotechnology, and functional ingredients, including senior innovation and technical leadership roles across the global feed industry. His background includes driving novel solutions development, leading cross-functional and matrix teams, and commercializing highly technical products across species and geographies. He has held positions such as Innovation & Technical Director at AB Agri – Agilia/Livalta, VP Business Development at ERBER Future Business, and senior technical and product leadership positions at Danisco/DuPont, DSM, Provimi, and Finnfeeds International. He has a deep technical expertise and experience with high-value, high-technical-input solution portfolios that is scientifically grounded by his PhD in pig nutrition from Wageningen University. Throughout his career he (co)-authored >40 peer-reviewed scientific articles and publications, mainly swine but also poultry and dairy nutrition focused. Initiating and supervising research projects at universities across Europe and America he facilitated the successful conclusion of numerous PhD and MSc students in animal nutrition.

ABSTRACT

Functional nutrition is the strategic use of nutrients, feed ingredients, and feeding practices to support not only growth and feed efficiency, but also gut health, immunity, resilience, and environmental performance. In swine production, it links nutrition with animal health, welfare, productivity, and sustainability outcomes. In practical terms, it shifts formulation from meeting requirements on paper to managing biological risk across the production cycle.

A broader systems perspective is required

Meaningful progress in sustainable swine production requires movement beyond isolated multidisciplinary efforts toward more integrated approaches that connect animal health, environmental stewardship, and management decisions. Within that framework, functional nutrition becomes a practical route for translating "One Health" and sustainability concepts into on-farm action through precise formulation, precision feeding, and targeted use of functional ingredients and feed additives.

Precision feeding and productivity

At the core of this interaction is nutrient precision: matching amino acids, energy, minerals, water, and feed intake to the animal's biological stage, genetic potential, sanitary status, and environment. Precision diet formulation avoids systematic overfeeding above the pig's requirement, while precision feeding aims to align nutrient supply more closely with the needs of groups or individual pigs under specific production and environmental conditions.

Modern least-cost formulation should therefore be interpreted more broadly than ingredient price optimization. It also depends on the use of biosecure ingredients with high nutrient availability, low anti-nutritional pressure, and acceptable environmental footprints. Accurate nutritional characterization of feedstuffs, including digestible nutrient content, starch and protein digestion kinetics, physicochemical properties of fiber, fermentation potential, and interactions with the gut microbiome, further improves the biological value of formulation decisions.

Accurate nutritional characterization of feedstuffs, including digestible nutrient content, starch and protein digestion kinetics, physicochemical properties of fiber, fermentation potential, and interactions with the gut microbiome, further improves the biological value of formulation decisions.

Precision levers	Implications for productivity and sustainability
Raw material characterization	Reduces variability in digestible nutrient supply and improves formulation accuracy.
Protein and amino acid precision	Improves nitrogen efficiency, lowers hindgut protein overflow, and supports lean growth.
Precision feeding by stage or individual	Matches supply to requirement more closely and reduces overfeeding of nutrients.
Fiber and fermentation design	Supports satiety, gut function, and environmental outcomes through more efficient nutrient use.

Why functional nutrition matters more in post-AGP, low-Cu/low-Zn systems

With bans on antimicrobial growth promoters and tighter restrictions on pharmacological use of copper and zinc oxide, nutritional strategy must shift from pharmacological compensation to biological resilience**.** In these systems, productivity depends less on suppressing microbial challenge through high-dose interventions and more on developing and preserving gut integrity, moderating immune cost, and sustaining intake during periods of transition stress, especially around weaning.

The biological rationale is now well aligned across recent reviews**:** the most reproducible nutritional mechanisms are reduced protein overflow to the hindgut, improved gastric acidification, greater butyrate availability, more favorable fermentation patterns, and tighter control of inflammatory and oxidative burden. In practice, this means that resilient performance is achieved by designing diets that reduce the opportunity for enteric disruption rather than by depending on a single replacement additive.

Functional nutrition toolbox

• Digestibility-first formulation: High digestibility supports early feed intake and lowers nutrient overflow to the distal gut.

• Reduced crude protein with SID amino acid precision: Lower crude protein can reduce proteolytic substrate while preserving amino acid supply for growth, mucosal repair, and immune competence.

• Organic acids and butyrate: These support gastric function, epithelial energy supply, barrier integrity, and the post-weaning transition.

• Probiotics, postbiotics, and functional fiber: These can shape fermentation and microbial resilience, support gut development and modulate the immune system.

• Phytobiotics: These are best positioned as anti-inflammatory, digestive, antimicrobial-modulating, and antioxidant support tools in solution offerings to replacement AGPs.

Organic trace minerals: Organic sources of Zn, Cu, Mn, and especially Se may improve mineral efficiency at legal nutritional levels while reducing excretion pressure.

• Antioxidant and immunity support: Selenium and vitamin E remain a defensible antioxidant core, while threonine, sulfur amino acids, and tryptophan are important for mucosal and immune functions.

Resilience and longevity across production stages

Nursery pigs

The first 10 to 14 days after weaning remain the highest-priority nutritional window. Diets should maximize intake, lower acid-binding capacity, control excess crude protein, and deploy acids, butyrate and selected (post)biotic, phytobiotic, or antioxidant tools to reduce the severity of post-weaning dysbiosis.

Grow-finish pigs

The focus shifts toward maintaining digestive efficiency and limiting compensatory inflammation. Enzyme use, fiber structure, mineral source, and continued control of nutrient variability can reduce performance variance and improve feed efficiency while also lowering nitrogen and mineral losses.

Gilt and sow herd

Longevity depends on body-condition control, skeletal soundness, oxidative balance, and recovery between parities. Gestation fiber, appropriate mineral nutrition, and periparturient antioxidant support should be treated as core design features, not secondary refinements, because the sow herd is the starting point for whole-system resilience.

Resilience should therefore be interpreted as lower performance variance and lower treatment pressure under challenge, not only as higher average daily gain. Relevant outcomes include diarrhea incidence, therapeutic intervention rate, mortality, fallback pig percentage, and sow retention across parities.

This interpretation is especially important in systems where pharmaceutical ZnO withdrawal could otherwise be followed by greater therapeutic antibiotic use if nutrition and management are not redesigned together.

Implications for scientific and applied discussion

From a scientific perspective, functional nutrition is best understood as an integrated systems approach rather than a collection of discrete feed additives. Its biological effect emerges from the interaction among diet formulation, ingredient quality, stage-specific feeding programs, gut function, immune activation, the microbiome and oxidative status, together with management variables such as water quality, feed form, hygiene, stocking density, and transition management. This systems view is essential for interpreting inconsistent responses to individual additives and for designing studies that capture both mechanistic and production-level outcomes.

Within this framework, applied discussion can focus on practical examples that connect mechanism with measurable farm outcomes. These include managing raw-material variability, improving dietary protein utilization efficiency, controlling post-weaning crude protein and acid-binding capacity, optimizing trace-mineral source and inclusion strategy in AGP-free and nutritional Cu and Zn programs, and quantifying how precision feeding affects both productivity and environmental emissions. Presented this way, functional nutrition becomes not only a health-support strategy, but also a platform for more resilient and sustainable swine production.

Keywords: AGP-free, Functional Nutrition, Precision Feeding, Productivity, Resilience, Swine.

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PLENARY SESSION 2: HERD HEALTH MANAGEMENT I



Herd Health Management in Pigs: Ten Things to Look at!

June 17, 2026; from 8:30 to 9:00

Dr. John Carr

Melbourne and Adelaide Universities. Howells Veterinary Services, UK

Biography

John started learning the ropes about pigs at the age of 11.

A Leverhulme residency in pigs and the PhD in urinary tract problems of pigs at Liverpool specialising in microbiology and pathology. He has a Diploma in Pig Medicine and is a Diplomate of the European College of Pig Health Management. His is recognised by the Royal College of Veterinary Surgeons as a pig specialist and by the Australasian Veterinary College Board.

ABSTRACT

There have been nine things the veterinarian should examine when looking at the farm.

Biosecurity, Pig Flow, Medicine, Water, Food, Floor, Air, Stock and Stockpeople. But there is a tenth aspect.

Slaughterhouse.

The veterinarian should care for the pig cradle to grave, and the nine aspects considered the live animal, but the dead are just as important. The veterinarian must consider all the way to the fork and table. It is important to consider the dead animal not just the wholesome food but the postmortem finings. What does the slaughterhouse tell you about the remaining live pigs at the farm.

Introduction

Biosecurity; pig flow; medicine; water, food, floor, air; stock and stockpeople has been the mantra of the nine areas a veterinarian that is required to be examined on each and every farm.

There is the tenth which has been staring us in the face all along - the slaughterhouse. From cradle to grave.

The Slaughterhouse

From cradle to grave. The responsibility of the veterinarian has to also include the slaughterhouse. This paper considers European Legislation, other countries maybe less (or more) strict but the role of the veterinary surgeon is the same all over the world.

Loading

The design of the loading area is essential. The aim is to prevent pathogen entry onto the unit. This has proven particularly problematic with Africa Swine Fever virus where if you cheat and rush the best biosecurity can be broken and the unit succumb.

The loading area must be efficient and safely and cleanly separates the farm staff from the truck driver. The animals are not to move back through the loading area. Many farms today will have two loading areas from the farm area, the grey zone and then the off-farm area. This is essential for African Swine Fever control.

The movement for animals on to a farm, should be through an isolation area.

Semen is a difficult but essential to many farms

Transport

How the pigs get to the slaughterhouse. There should be very few losses. The truck and driver should be well versed in this task. It is essential that the veterinarian trains the drivers in which animals can go. Who needs a separate area. The "fit to arrive" guides are an essential part of this training.

The slaughterhouse report

Pre-mortem: Pigs which die in transit or are condemned at the plant before slaughter.

Dead on arrival

Unable to walk into the slaughterhouse. The animal may have been injured in transport and s unable to rise.

Condition diagnosed pre-mortem. This may include a hernia which should not touch the ground, have no injury and be less than 30cm in circumference.

Conditions of the skin such as *Erysipelothrix rhusiopathiae.*

Post-mortem: After the pig has been killed

The whole pig

Colour changes

Neoplasma

Odd smell

Poly-arthritis

Poly-abscess

Tail bite

Partial of the pig

Abscess

Fracture of a limb. Generally associated with mechanical injury

Kidney defects – nephritis; hydronephritis and infarct for example

Milk spot – marks on the liver - *Ascaris suum*

Pericarditis

Peritonitis

Pleurisy

Pneumonia

Skin lesions

Tail bite

Mechanical contamination from slaughterhouse equipment.

Conclusion

Animals appear to be rejected in the slaughterhouse and are given a blanket diagnosis. Such as poly-arthritis. Poly means more than one. Poly-arthritis means more than one joint is affected but when the veterinary surgeon requests further information it is vague or none-existent and may include a single picture of a single joint and shows nothing. This loss is approaching 2% of animals presented (more on individual loads) which is very wasteful and expressive.

The veterinary surgeon must care for the pig cradle to grave. Our responsibility does not end at the farm gate.

Keywords: Pig, Loading, Transport, Movement, Slaughter, Postmortem.

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"Digital Transformation in Swine Farms: Bridging Innovation and Practical Implementation"

June 17, 2026, from 8:30 to 9:00

Asst. Prof. Dr. David Rosero
Iowa State University, Ames, Iowa, USA

Biography

Dr. David Rosero is an Assistant Professor of Animal Science at Iowa State University. His dynamic research program focuses on advancing swine nutrition and smart farming practices. His current research initiatives include 1) implementing nutritional and management strategies to improve pig livability, 2) advancing precision swine nutrition, and 3) accelerating the adoption of smart technologies in swine barns. Leveraging his past experience as the Technical Officer at The Hanor Company, he combines invaluable industry experience with academic pursuits. His research contributions were recently recognized by the George Foxcroft Lectureship in Swine Production for his efforts in bringing "Research to Reality."

ABSTRACT

The swine industry is experiencing a significant transformation driven by advances in Digital Technologies, including computer vision, wearable sensors, and automated data platforms, that are redefining how production systems monitor animal health, growth, and behavior. These digital tools offer opportunities to improve labor efficiency, enhance animal welfare, and enable real-time decision-making. However, despite rapid technological development, adoption in commercial swine systems remains limited due to concerns about the accuracy, reliability, implementation, and financial return of these technologies.

Recent research highlights the improved capability of computer vision systems to automate key production measurements, including pig counting, behavior monitoring, and body weight estimation. Studies conducted under commercial conditions demonstrated that camera-based systems can achieve high predictive accuracy relative to traditional scale measurements. Additionally, these systems provide continuous monitoring, enabling early detection of health issues.

Emerging wearable technologies further expand monitoring capabilities by capturing physiological and behavioral data such as temperature, movement, and vocalization patterns, with demonstrated potential for early disease detection. However, challenges such as device cost, battery life, and scalability remain barriers to widespread adoption.

A critical limitation across digital technologies is the lack of standardized validation frameworks, with only a small proportion of commercially available systems having undergone rigorous scientific evaluation.

Bridging the gap between innovation and implementation requires developing standardized evaluation protocols, improving system integration, and clearly demonstrating the economic value. The successful adoption of digital technologies will depend on their ability to deliver consistent, reliable performance across diverse production environments while addressing practical constraints.

Introduction and Objectives

Swine production systems are increasingly shifting from labor-intensive management practices toward automated, data-driven approaches. Digital technologies, including computer vision, wearable sensors, and environmental monitoring systems, are central to this transformation, enabling continuous monitoring of animal health, behavior, and performance.

Labor shortages and the need for improved efficiency are key drivers accelerating the adoption of digital technologies. Traditional monitoring methods, such as manual weighing and visual assessment, are time-consuming, subjective, and often insufficient for early detection of health or performance issues. These limitations limit the producer's ability to implement timely, targeted interventions.

Recent advancements in artificial intelligence and edge computing have enhanced the functionality of digital systems, allowing for automated data collection and real-time analysis directly within barn environments. Applications include pig counting, growth monitoring, behavior analysis, and environmental control. Despite these advancements, adoption remains constrained by uncertainty regarding system performance, integration challenges, and unclear return on investment.

A major concern is the lack of scientific validation, with only ~14% of commercially available technologies evaluated in peer-reviewed studies. This gap limits the producer's confidence and slows the adoption of these technologies in swine barns. Thus, the objectives of this paper include:

- To summarize current and emerging digital technologies used in swine production.
- To illustrate the evaluation of computer vision systems for body weight estimation under commercial conditions.
- To propose strategies that bridge the gap between technological innovation and practical implementation.

Computer Vision System: Evaluation

Data from commercial-scale studies evaluating the Swine SenseHub® camera system were analyzed. Cameras were installed above feeders to capture continuous image data for automated body weight estimation across multiple pens and production cycles.

The accuracy of the computer vision system was assessed using:

- Concordance Correlation Coefficient (CCC) to evaluate agreement with scale weights
- Mean Absolute Percent Error (MAPE) to quantify prediction accuracy
- Reliability, defined as the proportion of expected observations successfully captured

These metrics provided a comprehensive assessment of both accuracy and operational performance.

Results and Discussion

Computer vision technologies demonstrated strong performance for monitoring pig growth in commercial environments. Camera-based systems achieved high agreement with traditional scale measurements, with the CCC values ≥ 0.98 at the individual level and approaching 0.99 at the pen level. These results indicate that this computer vision system (Swine SenseHub®) can reliably estimate individual pig body weight continuously.

Reliability (% of data reported from expected measurements) ranged from 85% to over 90%, demonstrating these systems' ability to consistently collect meaningful data in commercial settings. However, variability in reliability across time points highlights the importance of optimizing system configuration and barn conditions.

Beyond body weight estimation, a wide range of emerging technologies are expanding the scope of digital swine management. Wearable sensors integrated into ear tags can capture temperature, movement, and behavioral data, enabling early detection of disease states before clinical signs are observed. Environmental sensors and thermal imaging systems provide continuous monitoring of barn conditions, supporting improved climate control and animal welfare. Automated feeding systems and electronic feeders enable precise measurement of feed intake and feeding behavior, thereby improving nutritional management.

Despite these advancements, significant challenges remain. The lack of standardized validation protocols limits comparability across technologies and reduces producer confidence. Integration of multiple data streams into cohesive decision-support systems remains complex, requiring advanced infrastructure and technical expertise. Additionally, concerns related to data ownership, privacy, and unclear economic returns continue to hinder adoption.

Conclusions and Recommendations

Digital transformation in swine production is advancing rapidly, with technologies such as computer vision, wearable sensors, and automated monitoring systems demonstrating strong potential to improve efficiency and animal management. Computer vision systems, in particular, have shown high accuracy, reliability, and scalability for applications such as body weight estimation.

However, rapid adoption in swine farms requires overcoming key barriers related to validation, implementation, and financial value. Technology development should focus on improving the accuracy and reliability of field systems. Additionally, quantifying the financial benefit of digital technologies will be critical to demonstrating their value in commercial operations.

The successful integration of validated digital tools will enable a transition toward more precise, proactive, and data-driven swine production systems, ultimately improving animal welfare, operational efficiency, and industry sustainability.

Keywords: Computer vision, Digital technologies, Swine farms, Technology adoption.

Acknowledgement: We would like to acknowledge collaborators at United Animal Health and Merck for their support and guidance throughout this analysis.

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"Application and Practice of Multistory Pig Farming: Planning and Configuration Process"

June 17, 2026; from 10:45 to 11:45

Dr. Zhichun Jason YAN
Beijing Precision Farm Technology, LLC, China

Biography

Zhichun Jason YAN completed a postgraduate degree in animal production in China in the late 1980s and was later admitted to a PhD program in swine epidemiology at the University of Minnesota before earning a degree in Agricultural Business from Kansas State University. He served as Director of Technical Programs at a U.S. organization, supporting Chinese pig producers during the industry's rapid industrialization in the late 1990s and 2000s. He then returned to China as Chief Scientist for a leading agribusiness, where he worked on farm planning, production, and herd health management for 10 years. After retiring from corporate roles, he continues to consult for major production companies and is actively involved in managing four farrow-to-finish farms, totaling approximately 16,000 sows.

ABSTRACT

Introduction and Objectives

The global swine industry, particularly in China, has undergone a radical structural transformation following the emergence of African Swine Fever (ASF) and high-pathogenic PRRS. The initial disregard, followed by panic, catalyzed a wave of innovation resulting in New Generation Test Removal (NGTR) protocols and upgraded biosecurity measures. This success in herd-level elimination restored production confidence, leading to an influx of over 300 billion RMB in new investment and the addition of more than 200 million head in production capacity since 2019. However, this rapid expansion collided with significant constraints: limited land availability in high-margin regions, stringent environmental regulations regarding odor and waste, and the logistical complexity of managing large populations. To maximize output per square meter of land, the industry pivoted toward multistory pig farming as a strategic necessity rather than a novelty. While initial doubts regarding disease transmission and vertical logistics were pervasive, the operational reality has proven these systems to be not only viable but often superior to conventional flat farms. The objectives of this paper are threefold: (1) to descriptively illustrate the science-based decision-making framework for configuring critical technologies within multistory structures; (2) to rationalize the capital budgeting methodology for comparing single-story versus multistory models; and (3) to present field observations on herd performance and operational efficiency within vertical swine production systems.

Materials and Methods

This study synthesizes empirical planning data and comparative operational analytics derived from

commercial swine operations implementing multistory systems. The methodology is divided into three core subsections:

2.1 Technology Configuration Decision Matrix

A systematic review was conducted to evaluate binary technology choices common to vertical farm design. This process prioritized scientific evidence from controlled applied research and practical empirical comparisons. The key evaluation nodes included: Building Integration (sow and post-weaning pigs in one building versus separate buildings); Pig Flow (wean-to-finish versus segregated nursery and finishing units); Waste Management (mechanical V-shape scrapers versus pull-plug pits); and Air Filtration (high-efficiency HEPA versus basic dust filtration). Selection criteria were weighted based on their impact on strict all-in/all-out compliance, maternal antibody cross-protection, and emission control.

2.2 Comparative Production and Financial Analysis

Operational and cost data were compiled and standardized across the same corporate entity to control for genetic and nutritional variance. The dataset compared 33 regular single-story sow farms against 14 multistory building farms. To ensure statistical relevance, data were aligned by identical year-week production groups. Cost analysis was normalized to a standard weaned pig weight (6 kg) to isolate the impact of facility design on fixed asset and sow depreciation per unit of output.

2.3 Capital Budgeting Framework

A Net Present Value (NPV) based model was employed to compare single-story versus multistory investment scenarios. Variables were normalized for farm type (breed-wean-finish), total land footprint, genetic stock, and a standardized cost of capital (10%). The analysis adjusted for structural depreciation periods unique to concrete civil construction versus standard equipment fencing.

Results and Discussion

The analysis revealed distinct patterns in both operational health and financial performance that differentiate multistory systems from their single-story counterparts.

Health and Production Flow Performance

Contrary to initial concerns that vertical housing might exacerbate disease spread, field observations from operations with both single and multistory farms reported above-average herd performance in the latter. This outcome is contingent upon a strict adherence to foundational health prerequisites: Freedom from Pseudorabies Virus (PRV) is deemed imperative, while elimination of wildtype PRRSv in the breeding herd is considered very necessary.

The architectural constraints of multistory buildings naturally enforce strict 28-day batch farrowing and internal gilt multiplication. These practices are not merely beneficial but are symbiotic with vertical design, drastically reducing internal logistics and animal contact events.

The adoption of HEPA filtration proved to be a cost-effective and worthwhile investment in this high-density context, offering protection against aerosol transmission that is more manageable within a single, controlled structure.

Infrastructure Configuration Insights

The decision-making process favored specific technological trade-offs:

- Pig Flow: Wean-to-finish systems were strongly preferred over separate nursery-finisher flows. While separate nurseries may save marginal floor space, the elimination of post-weaning group movement in wean-to-finish systems resulted in reduced fighting, less cross-contamination, and improved gain continuity within the vertical column.
- Waste Management: Mechanical V-shape manure scrapers were selected over traditional pull-plug pits. Despite higher initial mechanical cost, the significant reduction in in-barn odor and ammonia emissions, coupled with lower terminal waste treatment costs, was a critical determinant for operational permitting and neighbor relations in high-density areas.
- Building Integration: The choice between integrating sows and post-weaning pigs in the same building versus separate structures was nuanced. Integration saved hallway space and facilitated pig transfer; however, separation provided slightly better isolation for weaned pigs, a factor relevant for specific PRRS control programs. The discussion emphasized that strict all-in/all-out airflow management supersedes physical separation if hallway cross-contamination is not controlled.

Conclusions and Recommendations

The planning and operation of multistory pig farming projects require a shift from conventional intuition to a science-based, capital budgeting-driven approach. Key conclusions are:

1. Health is Non-Negotiable: Successful vertical farming is predicated on PRV-free, PRRS-stable herds, underpinned by strict 28-day batch farrowing and internal gilt replacement. These are not optional upgrades but operational imperatives for vertical systems.
2. Technology Selection Matters: Configuration choices - particularly the adoption of wean-to-finish flows and mechanical manure removal - directly impact biosecurity efficacy and odor control, which are the limiting factors for license-to-operate in high-density regions.
3. Economic Viability: Using Net Present Value (NPV) as the primary capital budgeting metric, multistory farms are comparable to or better than single-story farms on a constrained land footprint due to maximized output and extended structural depreciation benefits.

Future perspectives should focus on optimizing the capacity of ancillary systems, specifically water supply, backup power redundancy, and centralized waste treatment, as these elements, rather than the building footprint itself, represent the primary bottlenecks to sustainable intensification in vertical swine production.

Keywords: Multistory pig farming, Capital budgeting, All-in-all-out production, Biosecurity configuration.

PARALLEL SESSION 4: VIROLOGY AND VIRAL DISEASES I



"Porcine Reproductive and Respiratory Syndrome Virus How to Control this Master of Disguise?"

June 17, 2026, from 8:30 to 9:00

Prof. Dr. Hans Nauwynck
Laboratory of Virology, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium

Biography

Hans Nauwynck did his PhD in 1993 and became nominated as professor at Ghent University at the age of 30. In 2004, he took the lead of the Laboratory of Virology, Faculty of Veterinary Medicine, Ghent University and became Diplomate at the European College of Pig Health Management. In 2020, he became Chair of the Department of Translational Physiology, Infectiology and Public Health and Director of Research at the Faculty of Veterinary Medicine, Ghent University. At present, he lectures several courses on viral diseases in mammals, fish and shellfish at the Faculty of Veterinary Medicine and the Faculty of Bioscience Engineering. His research focuses on the cellular and molecular pathogenesis of viral diseases in humans and animals (including shrimp and honeybees), with special emphasis on (i) the entry of the virus in its host cell, (ii) the invasion of the virus in its host through barriers, via leukocytes and along neurons, (iii) the escape of the virus from immunity and (iv) the complex interactions of host-pathogen-environment (including microbiome). Better insights led to the development of new diagnostics, better viral disease control measures and tailor-made vaccines. He launched two spinoffs (Imaqua and PathoSense).

ABSTRACT

Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) continues to be one of the most challenging pathogens in swine health due to its extraordinary capacity to manipulate host immunity, establish persistent infection, and generate extensive genetic diversity. Although control strategies have improved, the virus's success is fundamentally rooted in its pathogenesis: a targeted assault on the porcine immune system by its replication in differentiated cells of the monocyte-macrophage lineage that delays antiviral responses, undermines adaptive immunity, and creates a permissive environment for long-term replication. This abstract synthesizes current understanding of PRRSV's macrophage tropism, immune-evasive mechanisms, within-host evolution, the immunological barriers that limit vaccine efficacy and the use of gene-edited pigs to control PRRS. A pathogenesis/immunity-centered perspective is essential for designing next-generation control tools capable of outmaneuvering this "master of disguise."

PRRSV Pathogenesis: A Targeted Attack on the Immune System

PRRSV pathogenesis is defined by its strict tropism for differentiated cells of the monocyte–macrophage lineage, such as porcine alveolar macrophages (PAMs). Viral entry is mediated by a coordinated interaction between sialic acid binding proteins (e.g. Sialoadhesin = Siglec-1, Siglec-10, DC-SIGN,..), CD163 and additional co-receptors, enabling efficient internalization and replication. The number of subsets of macrophages that are infected is dependent on the viral strain and explains the different clinical and pathological outcomes. In evolution, PRRSV evolved from a virus with a tropism for a restricted number of macrophage subsets to a virus with a tropism for many subsets. The increase of number of macrophages that become infected led to an increase in virulence and pathogenicity. Once inside differentiated macrophages, PRRSV profoundly alters their function: phagocytosis is impaired, antigen presentation is compromised, and cytokine secretion is skewed toward an anti-inflammatory profile. This early disruption of macrophage biology is the cornerstone of PRRSV's ability to delay innate immunity, establish high-titer viremia and hamper the adaptive immunity.

Viral nonstructural proteins are potent antagonists of type I interferon induction and signaling. By degrading key transcription factors, blocking IRF3 activation, and interfering with STAT pathways, PRRSV prevents the development of an antiviral state in infected and neighboring cells. The result is a prolonged window of uncontrolled replication during the first days of infection in macrophages at the respiratory mucosae and lymphoid tissues, followed by invasion via blood in which the virus replicates in intravascular monocytes that are differentiating upon adherence to endothelial cells. Via these infected migratory macrophages, the virus enters different regions in the body (e.g. lymphoid tissues, placenta), where it can persist for weeks to months.

Immune Evasion and Dysregulated Adaptive Responses

Adaptive immunity to PRRSV is slow, inconsistent and often insufficient. Neutralizing antibodies typically appear only after several weeks, and their breadth is limited by the virus's extensive antigenic variability. Within the host, escape mutants appear under the pressure of neutralizing antibodies. Even when present, neutralizing antibodies may not prevent reinfection with heterologous strains. PRRSV-specific T-cell responses are delayed and often weak, with limited cytotoxic activity. Regulatory T-cell induction and altered cytokine profiles contribute to an immunosuppressive environment that favors viral persistence. The virus's ability to modulate dendritic cell function further compromises the development of robust T-cell immunity. Collectively, these mechanisms explain why PRRSV can persist in lymphoid tissues long after clinical signs resolve and why sterilizing immunity is rarely achieved. Siglec-10, one of the binding receptors is present on B-lymphocytes and allow the virus to enter the cell. As CD163 is not expressed, PRRSV cannot become disassembled and stays in this cell for a very long time, leading to a reservoir.

Within-Host Evolution: Diversity Generated in Real Time

PRRSV's high mutation rate and propensity for recombination allow rapid diversification within individual animals. Selective pressures, including use of different binding receptors, innate immune responses, suboptimal adaptive immunity, and vaccine-induced immunity, drive the emergence of quasi-species populations.

These within-host variants may differ in receptor usage, replication efficiency, or antigenicity, complicating both immune clearance and vaccine protection. Persistent infection provides a longtime window for such evolution, making each infected pig a potential incubator for new variants. Understanding within-host viral dynamics is therefore essential for designing vaccines that target conserved epitopes and for predicting which viral features are most likely to escape immune recognition.

Immunological Barriers to Effective Vaccination

Modified-live vaccines (MLVs) remain the most effective tool for reducing clinical disease, but their protection is very strain-specific and incomplete. The fundamental challenge is immunological: PRRSV's early suppression of innate immunity limits the priming of strong adaptive responses, even when using live attenuated strains. The late induction of the adaptive immunity is restricting the success of attenuated vaccines. Inactivated vaccines are safe but work only in a homologous situation and when high antigenic masses are used. The protection obtained with new experimental vaccines are not very effective and therefore, there is little hope for finding a solution to the vaccination problem in the future. Maybe, better insights in the fusion process and how to immunologically block it may give a breakthrough.

May Gene-edited Pigs Help to Control PRRSV

Gene editing offers a promising way to control PRRS in pigs by altering specific genes that the virus uses to infect macrophages. Genetic engineering of the receptor CD163 inhibits PRRSV to replicate as it plays an important central role in the fusion process of PRRSV. However, one has to be careful as some strains may use alternative routes to infect macrophages. As the virus is extremely genetically unstable, this may lead to escape mutants that may dominate in the field. What the long-term clinical outcome will be is unpredictable. When it turns out to be safe, this approach will for sure reduce economic losses and improve animal welfare, though regulatory approval and public acceptance remain important challenges.

Conclusion

PRRSV's reputation as a "master of disguise" is earned through its sophisticated manipulation of the porcine immune system, its ability to persist in lymphoid tissues, and its rapid generation of genetic diversity. Effective long-term control will require tools that directly address these pathogenic mechanisms rather than relying solely on herd-level management. By integrating advances in immunology, molecular virology, and host genetics, the swine industry can move closer to sustainable control of this uniquely challenging virus.

Keywords: PRRS(V), Macrophage, Pathogenesis, Immunity, Vaccination, Gene editing.

PARALLEL SESSION 5: PIG PRODUCTION AND SUSTAINABILITY

"Managing the Peripartum Prolific Sow for Improved Piglet Production"

June 17, 2026, from 13:15 to 13:45



Assoc. Prof. Dr. Roy Kirkwood
Adelaide University, Roseworthy, SA, Australia

Biography

After completing his PhD on gilt management at Leeds, Roy researched the endocrinology of early weaned sows at Massey University, New Zealand and then moved to University of Alberta, and then the University of Saskatchewan, Canada and studied sow nutrition/reproduction interactions and control of reproductive function. During which period he went to vet school; graduating in 1995. After four years as a provincial government veterinarian, he returned to the UK for 3 yrs at the Royal Veterinary College, London, before moving to Michigan State University. After 10 yrs in the USA he moved to his current position as Associate Professor in Intensive Production (pigs) at the University of Adelaide, Australia. His research interests have mostly been to improve sow herd reproductive performance.

ABSTRACT

Introduction

A major objective of swine veterinarians is to enhance their clients' ability to cost-effectively market the maximum weight of pork. Underpinning this objective is the production of large, good quality litters with good pre-weaning growth and survival. Clearly, meeting these objectives will heavily depend on sow farrowing performance. When considering farrowing performance there is a tendency to focus on the farrowing event per se, although farrowing performance can be influenced by the preceding pregnancy management, especially during the 7 - 10 days pre-farrowing.

The underlying problem is an excessive fetal load relative to uterine capacity prepartum and too few teats for the number of piglets postpartum, which is a separate discussion. However, against this background, this review will discuss strategies for improving piglet pre- and post-natal growth and survival. Issues surrounding the large litters of prolific sows include the effects of intrauterine crowding causing lower average birthweights, increased birth weight variation, a physiological milieu providing for a suboptimal efficiency of piglet delivery, inadequate myometrial contractility, piglet hypoxia during prolonged deliveries, and litter mate competition post-partum. Potential management strategies for improving piglet survival in large litters will be examined, including farrowing kinetics, and neonatal piglet management.

Feeding the transition sow

Historically, nutritional management of sows during pregnancy has been contentious, with recommendations for feed restriction in early pregnancy to limit embryo mortality, and not 'over- feeding' in pregnancy to avoid reduced appetite in lactation. The former has largely been disproved and the latter being only relevant if the sow is over-fed to the point of being over-conditioned. Indeed, recent evidence has shown that sows ad libitum fed in the 7 to 10 days (Langendijk and Fleuren, 2018) or 2 to 3 days prepartum (Gourley et al., 2020) had improved lactation weight and backfat maintenance and higher litter weaning weights.

Another issue with higher sow feed intakes is the potential incidence of constipation, which will be uncomfortable or painful for the sow, depressing feed intake with consequences for colostrum and milk production. Further, the feces are a rich supply of lipopolysaccharide (LPS) and, with an effective fecal stasis, constipation can result in increased LPS absorption that interferes with prolactin and thyroid hormone release, and thus lactation, resulting in hypogalactia syndrome (Martineau et al., 1992). As documented by Oliviero et al. (2009), feeding a higher fiber diet can increase rate of passage and reduce the incidence of constipation. However, on entering the farrowing house sows are frequently switched from their lower energy higher fiber gestation diet to a higher energy, lower fiber, lactation diet, which can significantly reduce fiber intake (Kirkwood et al., 2021). Depending on the duration of low fiber feeding, this will predispose to some degree of constipation. Therefore, it would seem sensible to maintain sows on their gestation diet until (or at least near) farrowing.

In the immediate prepartum period, fetoplacental estrogen production increases. The estrogen promotes duodenal calcium absorption, increases myometrial gap junctions, up-regulates oxytocin receptors, and promotes cellular calcium entry needed for muscle contractions. Interestingly, stillbirth rates increase in older sows, notably from parity 5 through 7 and, although speculative, it is possible that older sows have lower prepartum estrogen levels. Indeed, a reduction in myometrial oxytocin receptor numbers has been noted in older sows (Adi et al., 2024). If reduced oxytocin receptors are associated with a reduced myometrial calcium influx, it would impair myometrial contractility, prolong fetal delivery, and so increase the risk for stillbirth. To counter this parity effect, an augmented blood calcium is required. This is further supported by a study showing a blood total calcium concentration at the start of farrowing of 2.385 mmol/L indicated a high likelihood of eutocic farrowing while lower concentrations were associated with increased incidence of dystocia (Blim et al., 2022).

One way to possibly increase circulating calcium levels is to provide an oral supplement but the results from this approach have been inconsistent. Recently, Craig et al. (2024) fed transition sows 40 g/d calcium chloride and while they documented a decreased urinary pH, no treatment effect on blood calcium concentrations or stillbirth rates were evident. However, when examined independent of treatment, sows with lower blood calcium concentrations or higher urinary pH had a higher incidence of stillbirths. This further demonstrated the importance of maintaining circulating calcium concentrations, but the limitations of feeding calcium to achieve this. An alternative approach would be to increase endogenous calcium mobilisation.

In dairy cows, peripartum calcium mobilisation is promoted by feeding negative dietary cation-anion difference (DCAD) diets (mEq K^+ plus mEq Na^+) - (mEq Cl^- plus mEq S^{2-}) to induce an acidemia, which promotes increased parathyroid sensitivity, increasing renal calcium resorption and activation of vitamin D to improve calcium mobilisation (Constable et al., 2017). A recent study of sows fed ammonium chloride (NH_4Cl) has provided evidence of a similar dietary DCAD effect in sows. The feeding of 20 g/d NH_4Cl during transition was associated with significantly increased blood ionised calcium, shorter farrowing durations, and fewer stillborns (Van et al., 2026).

Improving neonatal survival

In recent years, selection pressure for increasing litter size has impacted farrowing durations, which have increased from a maximum of < 5 h to an average of > 5 h (Bjorkman and Grahofer 2020). To deliver her piglets, the sow's uterus must undergo frequent contractions during which blood (and oxygen) supply to the litter is restricted. While not usually of major concern during early stages, the potential adverse effect of ongoing periodic fetal hypoxia increases with duration of parturition. Of immediate concern with prolonged farrowing is the higher numbers of stillborn piglets and the delivery of live pigs having lower birthweights, increased numbers of lower viability piglets, and increased birthweight variation which could result in an increased pre-weaning mortality.

When stillbirths and/or early neonatal mortality are deemed too high, an obvious response is to induce farrowing to allow improved supervision of deliveries. However, a frequent adjunct to a prostaglandin-induced farrowing is the administration of oxytocin, which has greater risks for piglet survival. For a full discussion of the risks of oxytocin for piglet survival, the reader is referred to the seminal works of Mota Rojas and co-workers, reviewed by Hill et al. (2022). When considering the administration of oxytocin, most protocols assume a problem exists, and so assistance is needed, when the interval between birth of two successive piglets is extended beyond (e.g.) 45 min. However, as described by Langendijk et al. (2018), stillbirths increased only when the piglet delivery interval exceeded 90 min, which was only 6% of the population. However, when stillbirth incidence was considered relative to the time since delivery of the first pig, the risk increased progressively from < 2 h to > 8 h; e.g., 2 - 4 h (6.9%), 6 - 8 h (13.4%) and > 8 h (27.3%). As stated above, myometrial contractions limited blood flow and oxygen supply to the fetuses and the cumulative result of limited, but repeated, fetal hypoxia is an adverse effect on fetal viability. This is why under 'normal' conditions, most stillbirths occur during the latter period of farrowing and, as such, argues against the use of oxytocin prior to about 240 min and/or delivery of piglets 7 or 8. Interestingly, a relationship between time taken to deliver the first 4 piglets and the total farrowing time was documented and indicated that if 4 pigs have not been born by about 90 min, it increased the likelihood of a prolonged farrowing (≥ 300 min) (Langendijk et al., 2018).

Pigs born later in the birth order and/or having lower birthweights are at heightened risk of neonatal mortality due to hypoxia during farrowing and being non-competitive for access to colostrum. Indeed, piglets suffering prolonged deliveries show progressively greater blood acetate concentrations and reduced viability.

This, in turn, would link to inadequate colostrum intake that, in association with the larger surface area to volume ratio and increased heat loss, increase the risk of mortality (Langendijk et al., 2018). It would seem intuitive that to counter these issues, newborn piglets should be oxygenated and assisted to consume colostrum. In a recent study, newborn piglets were placed for 15 min in a chamber with a fractional inspired oxygen level of 0.21 or an ambient control chamber (FiO2 0.16 - 0.18). In addition to measures of improved metabolic status, restoring normoxia resulted in reduced neonatal mortality (Thu et al., 2026).

There are various management procedures to enhance piglet colostrum intake, such as split suckling. However, a recent novel approach was the intraperitoneal injection of warm saline (Tucker et al., 2022), which proved very effective for increasing survival of low birthweight piglets. This does leave one question; do you want to save these small/disadvantaged pigs?.

Conclusions

With the ongoing selection for yet greater sow prolificacy, adverse impacts on farrowing performance and associated stillbirths, piglet birth weights, and post-natal performance are increasingly evident. Litter management protocols are needed to lessen this adverse impact, such as split suckling and more involved cross-fostering protocols. While the primary focus is the litter, we should not lose sight of the individual piglet, particularly the recognition of at-risk piglets, such as low birthweights and being born later in the birth order. Of particular importance is the achievement of an adequate colostrum intake which can, via improved immune status and piglet vitality, compensate for some other adverse impacts.

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"Porcine proliferative enteropathy: what is new about this important disease"

June 17, 2026; from 13:15 to 13:45

Prof. Dr. Roberto M.C. Guedes

Department of Veterinary Clinic and Surgery, Veterinary School, UFMG, Brazil.

Biography

Holds a degree in Veterinary Medicine from the Federal University of Minas Gerais - UFMG (1992), a master's degree in veterinary medicine from UFMG (1995), and a PhD in Veterinary Pathobiology from the University of Minnesota (2002). Postdoctoral studies in the proliferative enteropathy laboratory at the University of Minnesota (2003). Visiting professor at the Danish Technical University in Copenhagen (2008-2009). Currently, he is full professor at the Federal University of Minas Gerais. He was sub-coordinator and coordinator of the postgraduate program in Veterinary Sciences at the Veterinary School of UFMG from 2010 to 2016; head of the Department of Veterinary Clinic and Surgery from 2016 to 2018; and vice-dean of the Veterinary School of UFMG from 2018 to 2022. He is Treasurer of the Brazilian Association of Veterinarians Specialized in Swine, Minas Gerais region. Author of Lawsonia book-chapters at the Diseases of Swine, 12ed and the Pathogenesis of Bacterial Infections of Animals, 5th ed. Experience in Animal Pathology, mainly working with swine enteric diseases. Research focuses on the enteropathogens *Lawsonia intracellularis* and *Brachyspira hyodysenteriae*.

ABSTRACT

Porcine proliferative enteropathy (PPE), or ileitis, is one of the most prevalent diseases around the world and it is caused by an obligate intracellular bacterium, *Lawsonia intracellularis*. There are three presentations of this disease: the hemorrhagic form, also known as porcine hemorrhagic enteropathy (PHE), that affects replacement gilts and hogs close to market age causing bloody diarrhea and 15 to 30% mortality; the chronic form affects growing-finishing pigs from 6 to 20 weeks of age presenting transitory loose stools which impair growth performance; and the subclinical form, which is not associated with diarrhea but infected animals have reduced growth rate. Among these three forms, the last one is the most difficult to diagnose as no clinical manifestation is observed. Holtkamp (2019), based on published experimental challenge studies in pigs, has estimated losses on average daily gain, feed conversion rate and mortality due to ileitis on reduction of net profit (USD/per market pig) from 18.84 in unaffected animals to 12.86 in lower affected and to 1.90 in highly affected pigs.

As the prevalence of the disease in commercial swine herds is virtually 100%, it is imperative to understand the impact of the disease in your system. There are different ways to do that, such as following performance results very carefully, strict clinical evaluations of the pigs, seroprofiling the herd to understand the kinetics of *L. intracellularis* infection, detection of anti-*L. intracellularis* IgG in fluid samples or qPCR in fecal samples or oral fluids.

An evaluation of the efficacy of either modified-live or inactivated vaccines is also an interesting approach to evaluate the impact of the disease. Anyhow, as the infection is widely spread, the best way to control the disease is to have a controlled exposure of the animals to the bacteria using strategic medication or using vaccine.

Two important information that became available in the last few years regarding PPE was the association between the qPCR results and the impact of the disease in individual animal (Pedersen et al, 2012; Collins & Barchia, 2014) and the demonstration that reduction of environment infection pressure is obtained using lime in cleaned and disinfected facilities (Collins & Collins, 2024). Pedersen et al. (2012) have demonstrated that 10^6 *L. intracellularis* per gram of feces, detected by qPCR, demonstrate direct correlation with significant gross and microscopic lesions related to PPE, and Collins & Collins (2024) have demonstrated that the same number of bacteria or above is correlated to the reduction of average daily gain between 15 to 131 grams per day.

Moreover, qPCR in fecal sock-samples and oral fluids have been reported as alternative clinical samples to demonstrate the circulation of *L. intracellularis* in the environment; however, no correlation has been demonstrated with clinical disease or impact in performance (Eddicks et al, 2025).

Regarding pathogenesis of *L. intracellularis*, MacIntyre et al (2003), in a histological and immunohistochemical study of intestinal fragments from pigs at different stages of infection by *L. intracellularis*, demonstrated immunosuppression with a marked decrease in the number of B and T lymphocytes, but an increase in the number of macrophages in the lamina propria at the peak of infection by this bacterium. A Danish study (Boutrup et al. 2010) demonstrated, using fluorescent in situ hybridization, that *L. intracellularis* is still alive inside mononuclear cells in the lamina propria of infected pigs. Furthermore, our group demonstrated the pig macrophages, derived from blood monocytes, are susceptible to infection by *L. intracellularis*, *in vitro* (Pereira et al. 2020). Moreover, our group recently demonstrated, *in vitro*, using experimental infection of rat epithelial cells (IEC-18) in transwell plates, that *L. intracellularis* can infect these eukaryotic cells both through the apical surface and the basolateral surface (abstract in these proceedings, Correia et al 2026). Therefore, we hypothesize that macrophages may play a relevant role in the persistence of infection in the intestine and its dissemination also through the basolateral surface, in addition to the apical surface. Thus, the spread of infection would be potentiated, possibly justifying the persistence of infection for prolonged periods.

PPE is economic important disease, and all new information related to a better understanding of its pathogenesis, diagnostics and control will help to couple with the impact of it.

Keywords: *Lawsonia intracellularis*, Ileitis, Diagnostics, Prevention, Control.

Acknowledgement: RMCG has research fellowship from CNPq.

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"The Road Towards a Genetically Stable and Efficacious ASF Vaccine and Its Use in Pregnant Animals in A Field Situation"

June 17, 2026; from 13:15 to 13:45

Dr. Ruud Segers

MSD-Animal Health, Boxmeer, The Netherlands

Biography

Dr Segers obtained a PhD grade at the Veterinary faculty in Utrecht, The Netherlands, in 1991 on molecular studies on Leptospiraceae and since then been employed in R&D at MSD Animal Health. He is now globally responsible for the strategy and development of vaccines for swine and ruminants and leads a group of 90 researchers including 15 PostDocs. This research group has designed and developed more than 30 different veterinary vaccines currently marketed under the Porcilis®, Circumvent®, Bovilis® and Sequivity® brands. The vaccines prevent a variety of viral, bacterial and parasite diseases and contain a variety and combinations of inactivated, recombinant subunit, attenuated live as well as vectored type vaccines which can be administered by intramuscular, intradermal, subcutaneous and/or intranasal route.

ABSTRACT

Introduction and Objectives

Since the outbreak of African Swine Fever (ASF) in 2007 in Georgia, many attempts have been made to develop various types of vaccines to help reduce the spread of the virus. So far, only live attenuated vaccines have been proven to be reliably efficacious, and several of the vaccines have been proven to be safe in piglets. However, when tested under field situations, many of these vaccines proved to be unstable, revert to virulence and create serious issues in pregnant animals. Here we describe our results in the journey towards a vaccine that would be both effective as well as safe in commercial pigs and sows. In addition, it will be DIVA (Differentiating Infected from Vaccinated Animals) compatible with the right diagnostic tests and thus enabling culling while using vaccination as a tool in eradication. The results from small scale experiments with a promising live vaccine candidate are compared with the first testing of this vaccine in a field situation in the Philippines.

Materials and Methods

Selection of vaccine candidates

After various different inactivated or non-live approaches failed to protect pigs against experimental ASF challenge, a set of live attenuated Georgia-2007 lineage strains were licensed in (1,2). Strains with mutations in repetitive regions like the Multi Gene Family (MGF) were excluded from the screening because the MGF region of the genome is known to be prone to recombination and genetic instability.

The candidate vaccine strains were first tested for their ability to protect piglets after intramuscular vaccination against experimental challenge with the highly virulent strain Armenia/07. Subsequently the protective vaccine candidates were tested for genetic stability and safety in a reversion to virulence (RTV) animal study using 5 sequential passages in pigs. The resulting strains that were proven genetically stable were tested in a pregnant sow safety model. After none of the tested vaccines were considered to be both efficacious as well as safe enough, a third gene was deleted, and safety and efficacy testing was repeated.

Production of seed materials and vaccine

The selected strain ASFV-G-Δ9GL/ΔUK/ΔEP153R (Triple Mutant (TM)) was shown to grow on an immortalized porcine macrophage cell line and frozen cell and virus seeds stocks were produced and tested for purity and extraneous agents.

Preliminary safety testing of TM in naïve piglets and non-pregnant sows on a commercial farm in the Philippines

Strain TM was tested at a relatively high titer in 10 six-week-old naïve piglets cohoused with 7 sentinel pigs until 56 dpv. In parallel, the same dose was also tested in 10 gilts (6-10 months of age), cohoused for the same period with 7 sentinel gilts.

Safety testing of TM in naïve commercial piglets on 4 commercial farms in the Philippines

A total of 357 pigs were vaccinated twice at 5 and 8 weeks of age and subsequently housed comingled for 70 days with 180 non-vaccinated control animals. Local and systemic reactions were monitored, as well as vaccine strain excretion and transfer to control animals. The take of the vaccine was assessed through viremia measured by PCR and through serology by specific ASF ELISA.

Safety testing of TM in naïve pregnant sows on 4 commercial farms in the Philippines

A total of 37 sows in all stages of pregnancy were vaccinated twice and subsequently housed comingled for 70 days with 38 non-vaccinated control animals. Local and systemic reactions were monitored, as well as vaccine strain excretion and transfer to control animals and progeny. The take of the vaccine in the sows was assessed through viremia as measured by PCR and specific ASF ELISA.

Results and Discussion

Implementing rigorous safety testing in naïve pregnant sows, combined with RTV testing as a screening method has delivered the vaccine candidate TM and enabled us to discard other vaccine candidates that proved to be not safe enough for further development (3). Further the testing in limited numbers of piglets under contained conditions demonstrated that >90% of piglets vaccinated twice with strain TM were shown to be protected from experimental challenge with virulent ASF. As 95 - 100% of the animals in the field trial seroconverted, it is expected that most animals would be protected if exposed to virus.

After vaccination of piglets, excretion of TM was shown to be very limited and transfer to comingled sentinels could neither be measured in earlier contained trials nor in the field trial on the 4 farms (0/180 animals).

In the first field study in naïve gilts no excretion or transfer of TM was detected. However, in vaccinated pregnant naïve sows in the field we did measure limited spread from vaccinates to sentinel sows (2/34 animals). Transfer of TM from vaccinated sows to their progeny was very limited (1/62 animals tested), but nearly all piglets (60 of 62 tested) became seropositive after ingestion of immune colostrum.

Vaccination was confirmed to be safe for administration to naïve sows on all 4 farms in both semesters of pregnancy as only very limited and transient clinical reactions, no ASF related mortality, and no elevated rectal temperatures were noted. However, compared to the litters of the unvaccinated sows, an average reduction of 2.8 live-born piglets per litter was noted.

Conclusions and Recommendations

In conclusion, the rigorous safety testing protocols and the choice to rely on attenuation based on deletion of multiple non-repetitive genes has resulted in strain TM that has all the properties to be further developed and produced as a stable, safe and efficacious vaccine for the protection of naïve commercial piglets and gilts. Vaccination of naïve pregnant sows will protect the sows from ASF infection but is currently not advised and more research is required to develop suitable vaccination protocols for pregnant sows. In addition, the DIVA aspect of this strain (4) can be a powerful tool in future eradication programs.

Keywords: Vaccine, DIVA, ASF, Safety.

Acknowledgement: The work has been funded by MSD Animal Health.

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"Influenza Virus Spillover: Focusing on Viral Changes over The Past 20 years"

June 17, 2026, from 13:15 to 13:45

Prof. Daesub Song

College of Veterinary Me dicine, Seoul National University, Republic of Korea

Biography

Daesub Song, D.V.M. professor of College of Veterinary Medicine, Seoul National University, is an international expert on the virology including research of viral pathogenesis and development of viral vaccines and diagnostics. He received D.V.M in 2000 and his PhD of veterinary medicine in 2004 at Seoul National University. His research interests include animal virology, interspecies transmission of viruses, viral-host interaction, and several viral vaccine developments. He has worked as professor at College of Pharmacy, Korea University from 2015 to 2022. He also worked as a member in special task force team of MERS-CoV in the Korean Society of Virology and in the MERS-CoV Korea/WHO joint mission team in 2015. And he served as a member of board of directors in Korea Society for Zoonoses and The Korean Vaccine Society from 2016. He commercialized the oral porcine epidemic diarrhea virus vaccine that could induce the mucosal immunity and good protection in piglets for the first time in the world. He led the vaccine research team of several swine/canine vaccines and influenza vaccine in various animal species for the preclinical, clinical trials and registration in government. Recently, he focused his work to the preclinical evaluation of several viral vaccines and to develop the zoonotic viral vaccines with adjuvants. His work on interspecies transmission of avian origin flu to dogs and its' mutations led to the need of investigation of dogs as a potential mixing vessel of flu. He has published over 150 peer-reviewed articles.

ABSTRACT

Influenza virus reassortment represents a key evolutionary mechanism for human adaptation through spillover events across diverse species. Over the past two decades, the ecology of influenza viruses has undergone a profound shift, characterized by increased spillover frequency and expanding host range. The current highly pathogenic H5N1 virus is driving an unprecedented panzootic, facilitated by rapid genomic reassortment and frequent transmission into diverse mammalian hosts. Notably, interspecies transmission has been documented across multiple species, including transmission from birds to cattle, cattle to cats, and birds to pigs, with recent detection in sheep.

Beyond sporadic spillover events, avian-origin influenza viruses are increasingly capable of establishing sustained transmission in mammalian hosts and undergoing adaptive evolution. For example, avian-origin H3N2 influenza virus has successfully adapted to dogs, acquiring mammalian fitness-associated phenotypes through sustained dog-to-dog transmission. Our studies further demonstrate that co-circulation of canine H3N2 and pandemic 2009 (pdm09) H1N1 viruses enables reassortment in dogs, generating variants with enhanced virulence and transmissibility in animal models. In addition, we show that dogs are susceptible to multiple clades of highly pathogenic avian influenza (HPAI) viruses, including H5N1 (clades 1.1.2 and 2.3.2.1c) and H5N6 (clade 2.3.4.4). Notably, HPAI H5N1 viruses isolated from cats in 2023 harbored the PB2 D701N mutation, a well-recognized marker of mammalian adaptation, highlighting the potential role of companion animals as intermediate hosts for avian-human reassortment.

This diversification of intermediate hosts parallels a major shift in the role of pigs in swine influenza virus (SIV) ecology. Prior to 2000, SIV populations were largely dominated by the classical H1N1 lineage with limited genetic diversity. However, since the 2009 pandemic, pigs have become dynamic mixing vessels shaped by frequent reverse zoonosis. Human-origin influenza viruses introduced into swine populations continuously reassort with endemic lineages, accelerating viral diversification and the emergence of novel genotypes. Among these, the G4 Eurasian avian-like H1N1 virus carrying pdm09 internal genes exhibits key features associated with pandemic potential.

Consistent with these global trends, SIVs in Korea have evolved into diverse reassortant lineages incorporating pdm09-derived gene segments. These viruses have accumulated antigenic mutations and additional N-glycosylation sites, resulting in reduced cross-reactivity with human pdm09 vaccines. Notably, we report the first isolation of a G4-like H1N1 virus in Korea, possessing Eurasian avian-like surface genes and pdm09-derived internal genes, with the ability to infect multiple mammalian cell types. In addition, we identified established Eurasian avian-like H1N2 SIV lineages in Korean swine populations. Importantly, both G4-like H1N1 and H1N2 variants have shown limited cross-reactivity with current commercial swine vaccines.

Collectively, these findings highlight a paradigm shift in influenza virus evolution toward enhanced mammalian adaptation and increased spillover risk. The continued diversification of SIVs, driven by reassortment and reverse zoonosis, poses a significant challenge to existing vaccine strategies. These results underscore the urgent need for updated vaccine strains, strengthened surveillance, and proactive intervention strategies to mitigate the risk of future influenza pandemics before they emerge.



"Benefits of Functional Feed Additive on Pig Production Beyond the Gut"

June 18, 2026; from 8:30 to 9:00

Dr. Metta Makhanon

President of Thai Swine Veterinary Association; Swine Health Consultant, Bangkok, Thailand

Biography

Education

- 1988: Doctor of Veterinary Medicine (DVM), Chulalongkorn University, Bangkok, Thailand.
- 1997: Master of Business Administration (M.B.A.), Ramkhamhang University, Bangkok, Thailand.
- 2012: Ph.D. on Veterinary Pathobiology at Faculty of Veterinary Science, Chulalongkorn University, Thailand.

Work Experience

- President of Thai Swine Veterinary Association (2024 - 2028).
- 38 years experience in Asian Animal Health industry.
- Present: + Animal Health Consultant - Freelance, service in Asia.
  + Visiting Lecturer at Faculty of Veterinary Science, Chulalongkorn University, Thailand.

ABSTRACT

Introduction and Objectives

Antimicrobial used (AMU) in swine production is the highest proportion comparing to other animals from the year 2000 to 2040 as forecasted by UN-FAO (Acosta et al., 2025). This may cause the spread of antimicrobial resistant (AMR) in the industry. In order to reduce AMU and AMR, the alternative to antimicrobials (ATA) are developed for their benefits to microbiomes and gut health (Rahman et al., 2022). However, ATA may have more advantages than the benefit to animal gut health. The investigation by reviewed articles and conducted the field studies may increase our knowledge of ATA using.

Main Contents

This abstract concluded the potency of some ATAs used in swine production. Moreover, some studies have been conducted and illustrated. The key topics are as follows:

1. The key characterization of ATA,
2. ATA used in swine industry,
3. Some studies (*in vitro* and *in vivo*).

Results and Discussion

The key characterization of ATA (Rahmann et al., 2022)

The most important parameters needed to be investigated before choosing any ATA.

1. Physiochemical characterization including dosage and formulation, how to administration and how long or duration of administration.
2. Functional characterization including the bioavailability and pathway in target species.
3. Safety evaluation in animals, consumers, and environment such as AMR, toxicity, side effect to carcass quality, etc.

ATA used in swine production

1. Prebiotics: compound serve as food and energy of beneficial microorganisms in gut
2. Probiotics: live microorganisms to provide health benefit to host when supplemented in the appropriated amount
3. Postbiotics: the metabolic products derived from probiotics or beneficial microorganisms such as SCFA (butyric acid) and GABA
4. Phytobiotics/Phytochemicals/Herbs: non-nutritive chemical compound derived from plants
5. Antimicrobial Peptides (AMP): host defense peptides or bacteriocins produced by bacteria
6. Bacteriophages: the bacterial virus to disrupt bacterial metabolism and caused bacterial cell lysis
7. Quorum Quenching (QQ): the process to block bacterial communication
8. Minerals and organic substances including high dose of Zinc Oxide (2,000 - 4,000 ppm), Humic acid and Sodium Humate

(Song et al., 2025; Makhanon et al., 2019, 2020, 2023 & 2025; Liu et al., 2022; Kurata et al., 2022)

Some studies of ATA

1. Postbiotic: Butyrate for weaning pig diarrhoea and growth, GABA for improving breeder performance.
2. Organic substance: Humic acid and Sodium Humate to reduce ammonia in pig feces and its growth promoting effect in fattening pigs.
3. In vitro study, MICs of butyric acid and humic acid to pathogenic bacteria caused diarrhoea in animals.

Conclusions and Recommendations

ATAs illustrate their benefit beyond the gut.

Keywords: ATA.

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"An Update on PEDV Current Status in the USA: Molecular Detection, Genetic Evolution, Prevention and Control"

June 18, 2026; from 8:30 to 9:00

Prof. Dr. Jianqiang Zhang

Iowa State University, Ames, Iowa, USA

Biography

Dr. Jianqiang (JQ) Zhang is a professor and virologist at the Iowa State University Veterinary Diagnostic Laboratory. He currently holds the Lora and Russ Talbot Endowed Professorship in Veterinary Medicine. His work focuses on diagnostics, molecular epidemiology, pathogenesis, and vaccine development for viruses of veterinary importance. He has served as the Virology Editor of the book Diseases of Swine (11th and 12th editions). He has been the Virology Session Editor for the *Journal of Veterinary Diagnostic Investigation* since 2019. He is currently the Vice President of American Association of Veterinary Laboratory Diagnosticians (AAVLD).

ABSTRACT

Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) emerged in the United States in 2013 and has been circulating in U.S. swine populations for over a decade. The virus's ongoing evolution, the lack of effective modified live virus (MLV) vaccines, and gaps in biosecurity implementation present significant challenges to controlling PED in the USA. This presentation provides an update on the current status of PEDV in the USA, with a focus on advances in molecular detection, understanding of PEDV PCR positivity and genetic evolution, and prevention and control.

Molecular Tools for Detecting and Characterizing PEDV in the United States

Various PEDV strains have been identified worldwide, but genetic classification of global PEDV strains remains to be standardized. In the USA, "non-S INDEL" (clinically virulent) and "S INDEL" (clinically milder) are commonly used to describe and distinguish the circulating PEDV strains.

Screening real-time RT-PCR targeting conserved genomic regions are recommended for use to detect the presence of PEDV in a sample. Spike (S) gene-based differential real-time RT-PCR provides a faster alternative approach for distinguishing between non-S INDEL and S INDEL strains. However, the ongoing genetic evolution of PEDV, particularly in the S gene, poses significant challenges to the diagnostic performance of S gene-based differential PCR assays. Recently, we evaluated four S gene differential real-time RT-PCR assays for their ability to differentiate non-S INDEL and S INDEL PEDV strains.

Unfortunately, none of the four evaluated S gene differential PCR assays demonstrated satisfactory performance when tested on randomly selected clinical samples. Therefore, PEDV S gene differential PCR assays should not be used as stand-alone diagnostic tests without prior screening, as this may result in false-negative results.

Spike gene sequencing and/or whole genome sequencing can be conducted to further characterize the detected PEDV, including recombination analysis and comparison with other strains.

PEDV PCR Positivity and Genetic Evolution in the United States

Based on the U.S. Swine Disease Reporting System (SDRS) and the Morrison Swine Health Monitoring Project (MSHMP), PEDV screening PCR-positive rates were ~12 - 20% in winter and ~4 - 6% in summer in the past five years. PEDV has been detected in both sow and wean-finish farms, with slightly higher rates in the latter. Therefore, effective control of PEDV must consider wean-finish farms in addition to sow farms. In addition, the presence of PEDV in farm facilities and the surrounding environment is a significant concern.

Notably, most PEDV sequences were reported during the 2013 - 2014 epidemic phase, with fewer from the 2015-2025 endemic phase. Analysis of PEDV S gene sequences from 2013 to 2025 shows viral evolution as demonstrated by nucleotide and amino acid substitutions, insertions, and deletions. For example, among 898 U.S. non-S INDEL PEDV S1 sequences from 2013 - 2025, thirty sequences exhibited insertions or deletions compared to the non-S INDEL PEDV initially identified in the USA in 2013. One remarkable observation was a non-S INDEL PEDV variant recovered from a swine clinical sample in 2017 that harbors a 600-nucleotide deletion in the S1 region. Another interesting observation was that, since June 2024, a non-S INDEL PEDV variant harboring a 6-nucleotide deletion in the S1 region was detected from farms in Illinois and Iowa. Among 98 U.S. S INDEL PEDV S1 sequences from 2013-2025, six sequences exhibited deletions compared to the S INDEL PEDV initially identified in the USA in 2014. Interestingly, two S INDEL PEDV variants harboring large deletions in the S1 region (591-nucleotide deletion and 597-nucleotide deletion) were detected in 2024-2025. The phenotypes of these PEDV variants remain to be characterized.

Prevention and Control of PEDV in the USA

In the USA, a commercial killed vaccine and an RNA particle vaccine expressing the S protein are available but offer limited protection in naïve pigs. Modified live virus vaccines are under development. Control measures mainly include biosecurity (e.g., truck washing) and intentional exposure.

The substantive economic impact of PEDV, combined with low detection rates, short virus shedding, clear clinical signs, available diagnostics, and industry interest, supports efforts to eradicate the virus in the USA. In February 2024, the American Association of Swine Veterinarians (AASV) established a PEDV elimination task force, comprising practitioners, subject matter experts, and industry representatives, to lay the groundwork for a potential national eradication program. Strategic plans and roadmaps have been developed. This initiative will also strengthen federal-state-industry collaboration and provide valuable experience for future pathogen eradication efforts.

Keywords: Non-S INDEL PEDV, S INDEL PEDV, Diagnosis, Genetic evolution, Eradication.



"Factors Associated with Colostrum Consumption in Newborn Piglets"

June 18, 2026, from 8:30 to 9:00

Prof. Dr. Padet Tummaruk

Chulalongkorn University, Bangkok, Thailand

Biography

Professor Padet Tummaruk obtained his D.V.M. from Chulalongkorn University in 1997 and his M.V.Sc. and Ph.D. from the Swedish University of Agricultural Sciences in 2001. He is Head of the Centre of Excellence in Swine Reproduction, Faculty of Veterinary Science, Chulalongkorn University, Bangkok. He teaches swine reproduction, including reproductive biology, semen analysis, assisted reproductive technologies, ovarian function, and animal physiology. His research focuses on improving sow reproductive performance, particularly in gilt management, boar semen cryopreservation, artificial insemination, and neonatal piglet care. His work bridges fundamental reproductive physiology with practical applications to enhance productivity and sustainability in modern swine production systems under tropical conditions.

ABSTRACT

Introduction and Objectives

Colostrum is the first milk secreted by the mammary gland and plays a crucial role in the survival and early development of newborn piglets. During the first 24 h postpartum, piglets can absorb immunoglobulins, particularly IgG, through the gut, providing essential passive immunity. In addition to immune protection, colostrum supplies highly digestible energy, helping piglets maintain body temperature and cope with environmental stress immediately after birth. It also contains growth factors that support gastrointestinal development, enhance nutrient absorption, and promote intestinal health (Juthamanee et al., 2024).

Adequate colostrum intake is strongly associated with improved growth performance and survival rates. Piglets that consume sufficient colostrum tend to have higher body weight gains and better health outcomes during the pre-weaning and post-weaning periods. Conversely, insufficient intake increases the risk of mortality, particularly in the first few days of life. Studies suggest that piglets should consume at least 250 - 300 g of colostrum to ensure optimal immunity and growth (Adi et al., 2025).

Several factors influence colostrum consumption, including piglet vitality, birth order, litter size, and sow-related factors such as parity, nutrition, and hormonal status (Juthamanee and Tummaruk, 2021; Chaiyapatmaetee et al., 2025; Dumniem et al., 2025). Piglets with low birth weight or reduced vitality often face greater competition for teats, leading to inadequate intake (Dumniem et al., 2026). In large litters, competition further intensifies, increasing the likelihood of starvation or crushing.

Despite its importance, measuring colostrum intake under field conditions is challenging. Therefore, identifying risk factors associated with insufficient intake is essential for developing effective management strategies. Improving colostrum intake through better neonatal care and sow management can significantly enhance piglet survival and overall productivity in modern swine production systems.

Materials and Methods

Field-based studies in commercial swine production systems have provided valuable insights into factors influencing neonatal performance and colostrum intake in piglets (Juthamanee and Tummaruk, 2021; Laothong et al., 2024; Adi et al., 2025; Chaiyapatmaetee et al., 2025). Under tropical conditions, these investigations typically involve large populations of crossbred sows and their litters, reflecting modern hyperprolific genotypes. Sows of varying parities are commonly included and managed under uniform housing and feeding conditions, with insemination performed using standardized artificial insemination protocols.

A wide range of sow- and piglet-level parameters is routinely recorded to evaluate associations with early-life outcomes. At the sow level, key variables include parity, farrowing duration, and litter characteristics such as total born, born alive, stillbirths, and mummified fetuses, providing an overall assessment of reproductive performance and parturition dynamics. At the piglet level, detailed individual data are collected at birth, including birth order, time of birth, and birth weight prior to colostrum ingestion. Early postnatal performance is typically assessed by body weight at 24 h postpartum, reflecting both vitality and early nutrient intake. Birth interval and cumulative birth interval are also widely used as indicators of farrowing progression, as prolonged intervals may compromise piglet vitality and access to colostrum (Laothong et al., 2024).

To facilitate analysis, piglets and litters are categorized into biologically relevant classes, such as birth weight, litter size, and cumulative birth interval. These classifications help identify thresholds associated with inadequate colostrum intake and reduced survival. Although direct measurement of colostrum intake under field conditions is challenging, it is often estimated using indirect methods (Theil et al., 2014). Collectively, these approaches provide a comprehensive framework for identifying key determinants of neonatal success and for developing effective management strategies to improve piglet survival and performance.

Results and Discussion

Studies conducted under commercial conditions consistently demonstrate substantial variation in colostrum intake among neonatal piglets and highlight its critical role in early-life performance. On average, piglets consume approximately 400 - 420 g of colostrum; however, a considerable proportion, often exceeding 25%, fails to reach the recommended threshold of 300 g, required for optimal immunity and growth (Juthamanee and Tummaruk, 2021; Adi et al., 2025; Chaiyapatmaetee et al., 2025). Colostrum intake is influenced by multiple interrelated factors at both sow and piglet levels (Juthamanee and Tummaruk, 2021; Chaiyapatmaetee et al., 2025). Litter size is a major determinant, as larger litters reduce individual intake due to increased competition for teats. In addition, piglets born later during the farrowing process, reflected by longer cumulative

birth intervals, tend to consume less colostrum, likely due to reduced vitality and delayed access to functional teats (Juthamanee and Tummaruk, 2021; Laothong et al., 2024).

Consequently, the proportion of piglets with inadequate intake increases when birth occurs several hours after the onset of parturition, emphasizing the importance of efficient farrowing management. Birth weight is another key factor affecting colostrum intake (Juthamanee and Tummaruk, 2021; Chaiyapatmaetee et al., 2025). Heavier piglets generally consume more colostrum and exhibit improved early growth and thermoregulation, whereas low-birth-weight piglets, particularly those below 1000 g, are at greater risk of insufficient intake, especially in large litters. The interaction between birth weight and litter size is therefore critical, with lighter piglets in hyperprolific litters being the most vulnerable group (Chaiyapatmaetee et al., 2025).

Colostrum intake is also positively associated with early growth indicators, such as body weight at 24 h and weight gain, as well as physiological parameters like rectal temperature (Juthamanee and Tummaruk, 2021). Piglets with inadequate intake tend to exhibit impaired thermoregulation and increased mortality risk. Overall, these findings underscore the multifactorial nature of colostrum intake. Improving intake, through optimized farrowing management, targeted supplementation, and strategies to enhance birth weight, remains essential for reducing pre-weaning mortality and improving productivity in modern swine production systems.

Conclusions and Recommendations

Colostrum intake is a key determinant of neonatal piglet survival and early growth, and several important risk factors have been identified under field conditions. Among these, piglet birth weight, cumulative birth interval, and litter size are major factors influencing colostrum consumption. Low-birth-weight piglets are particularly at risk, as they generally consume less colostrum, especially in large litters where competition for teats is high. The negative effect of low birth weight is more evident in hyperprolific litters (14 - 17 and ≥ 18 piglets). Cumulative birth interval also plays a significant role. Piglets born later during farrowing exhibit reduced colostrum intake, with a noticeable decline when birth occurs 4.0 - 4.9 h after the onset of parturition and an even greater reduction beyond 5 h. This delay likely impairs piglet vitality and limits timely access to colostrum. Litter size further influences colostrum intake, as the proportion of piglets with inadequate intake increases from 13.2% in smaller litters (7 - 13 piglets) to 33.1% in large litters (≥ 18 piglets) (Juthamanee and Tummaruk, 2021). This effect is particularly pronounced in piglets with birth weights below 1000 g, whereas heavier piglets (≥ 1300 g) are less affected. These findings highlight the importance of targeted management strategies, including prioritizing low-birth-weight and late-born piglets, especially in large litters. Reducing farrowing duration and providing early colostrum supplementation can significantly improve piglet survival and growth in hyperprolific sow systems.

Keywords: Birth weight, Colostrum intake, Cumulative birth interval, Litter size, Piglet survival.

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"Old Enemies to New Challenges: The Changing Landscape of Swine"

June 18, 2026; from 13:15 to 13:45

Prof. Dr. Joaquim Segalés
Departament de Sanitat i Anatomia Animals, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB); Unitat mixta d'investigació IRTA-UAB en Sanitat Animal, CReSA

Biography

Veterinarian and PhD. Diplomate for the European College of Veterinary Pathologists and the European College of Porcine Health Management. Full professor at the Veterinary School of Universitat Autònoma de Barcelona and researcher at IRTA-CReSA. Director of the WOAH Collaborating Center for research and control of emerging and re-emerging swine diseases in Europe. He has been working for 33 years in swine diseases and 12 years in zoonotic coronavirus. He has co-authored more than 480 peer-reviewed publications in international journals.

ABSTRACT

Introduction

Swine production has historically faced the constant threat of infectious diseases that affect animal health, productivity, and the sustainability of the sector. While significant progress has been made in controlling several long-recognized pathogens through vaccination, diagnostics, and biosecurity, many of these "old enemies" remain endemic or have re-emerged in different epidemiological contexts. At the same time, the discovery of novel viruses and the evolution of existing pathogens are reshaping the infectious disease landscape in pigs. Globalization of production systems, increased animal movement, and ecological changes further contribute to this dynamic scenario. Understanding these evolving patterns is essential for improving disease prevention and control strategies in modern swine production.

Old enemies to new challenges

Swine production worldwide has long been challenged by infectious diseases that compromise animal health, productivity, and economic sustainability. Historically, a group of well-known pathogens, often referred to as the "old enemies", have shaped disease control strategies in the pig industry. These include agents causing diseases such as African swine fever, classical swine fever, porcine reproductive and respiratory syndrome (PRRS), porcine circovirus 2 PCV2) associated diseases, enzootic pneumonia or contagious pleuropneumonia.

Over decades, substantial scientific advances, including improved diagnostics, vaccination programs, biosecurity measures, and coordinated surveillance, have allowed the swine sector to mitigate the impact of many of these pathogens. However, despite these achievements, all these diseases remain endemic in many regions or have re-emerged, demonstrating the persistent threat posed by well-established pathogens.

In parallel, the landscape of swine infectious diseases has become increasingly complex due to the emergence of new pathogens or novel variants of known agents. For instance, the identification of PCV3 and PCV4, the continuous evolution of PRRS virus, and the emergence of Senecavirus A, highlight the dynamic nature of viral pathogens affecting swine. These agents often present diagnostic and epidemiological challenges, as their pathogenic potential, transmission dynamics, and interactions with other pathogens are not yet fully understood. Moreover, many swine diseases occur within multifactorial syndromes, where co-infections and environmental stressors play a critical role in disease expression.

Globalization of pig production, increased animal movement, intensification of farming systems, and ecological changes have further facilitated the spread and evolution of pathogens. The ongoing expansion of African swine fever across multiple continents illustrates how rapidly devastating diseases can spread in modern production systems, with profound economic and societal consequences. At the same time, improvements in molecular diagnostics and genomic technologies have revealed an unprecedented diversity of viruses circulating in pig populations, raising new questions about their clinical relevance and epidemiological significance.

Addressing these evolving challenges requires a multidisciplinary approach that integrates epidemiology, virology, pathology, as well as all issues related with production, management and biosecurity. Strengthening surveillance systems, improving early detection, and fostering international collaboration are essential components for effective disease control. Ultimately, understanding both the long-standing pathogens and the newly emerging agents will be crucial to safeguard swine health, ensure sustainable production, and protect global food security in the coming decades.

Conclusions

The epidemiology of swine infectious diseases is continuously evolving due to the coexistence of long-standing pathogens and newly emerging viral agents. Effective control will depend on strengthening surveillance, early detection, and multidisciplinary research. In addition, international collaboration and data sharing will be critical to address transboundary disease threats. A comprehensive understanding of both “old enemies” and new challenges will be key to safeguarding global swine health and production in the future.

Keywords: Swine pathogens, Evolution, emerging, Re-emerging, Surveillance, Disease control.



Prof. Dr. Roongroje Thanawongnuwech

Chulalongkorn University, Bangkok, Thailand

Biography

Prof. Dr. Roongroje Thanawongnuwech is a highly respect scientist and academic leader in the field of **Veterinary Pathology**. His research interest in animal virus pathogenesis has made significant contributions to the understanding of **major swine diseases** and has helped to develop new knowledge and control strategies. He is also a strong advocate for the advancement of veterinary education and research in Thailand and regional countries.

ABSTRACT

Introduction

African swine fever (ASF) is one of the most devastating transboundary animal diseases affecting the global swine industry. Since its introduction into Asia in 2018, the virus has spread rapidly across the region, resulting in massive economic losses, disruption of pork supply chains, and severe impacts on food security and rural livelihoods. The Asian experience represents the largest and most complex ASF epidemic recorded to date, affecting countries with highly diverse production systems ranging from smallholder backyard farms to intensive commercial operations. This presentation summarizes key lessons learned from ASF outbreaks across Asia, with particular focus on regional coordination, control strategies, and sustainable solutions for rebuilding a resilient swine sector.

The introduction of ASF into Asia was first reported in China in 2018, followed by rapid spread to several countries including Thailand. Thailand officially confirmed ASF in January 2022, although epidemiological evidence suggests earlier virus circulation. Across the region, ASF outbreaks had a disproportionate impact on smallholder and backyard pig farms where biosecurity practices were often limited, and disease detection was delayed. Consequently, many countries experienced dramatic reductions in pig populations and significant structural changes in their swine industries.

What have we learned from the Asian ASF epidemic?

One of the most critical lessons from the Asian ASF epidemic is the importance of regional coordination and transparency in disease reporting. ASF is a highly contagious transboundary disease that spreads through multiple pathways, including live pig movement, contaminated pork products, swill feeding, and informal trade networks that frequently cross-national borders. Strengthened collaboration among veterinary authorities, research institutions, and international organizations such as World Organisation for Animal Health and Food and Agriculture Organization has improved information sharing, surveillance capacity, and coordinated control responses. Regional initiatives have also supported joint research programs aimed at understanding virus epidemiology and identifying effective risk mitigation strategies.

Another key lesson relates to the importance of strengthening biosecurity throughout the entire pork value chain. Investigations during ASF outbreaks identified numerous transmission pathways including contaminated feed, transport vehicles, slaughterhouse practices, and improper disposal of infected carcasses. These findings highlight that ASF prevention requires integrated measures extending beyond the farm level to include traders, transporters, slaughter facilities, and consumers. Education campaigns and training programs have therefore become essential tools for improving practical biosecurity awareness, particularly among small-scale producers for local food security purpose.

The development and field use of ASF vaccines has recently emerged as a potential complementary tool for disease management. Vietnam has been among the first countries to approve and deploy commercial live attenuated ASF vaccines. Early field experiences suggest several potential advantages, including reduction in clinical disease severity, decreased mortality in vaccinated herds, and improved farmer confidence during herd repopulation. Vaccination may therefore contribute to stabilizing production in endemic regions and supporting recovery of the swine sector. However, important limitations and risks remain. Live attenuated ASF vaccines require stringent quality control, appropriate vaccination protocols, and continuous monitoring to ensure safety and efficacy. Concerns include variability in protective immunity, potential reversion to virulence, and the possibility of masking field infections, which could complicate disease surveillance and control efforts. Experiences from Vietnam and other countries indicate that vaccination should not replace conventional control measures but rather be integrated within comprehensive ASF management strategies that prioritize biosecurity, early detection, and rapid response.

The long-term recovery of the swine industry following ASF outbreaks also requires structural transformation toward more resilient production systems. Many countries have implemented programs focusing on farm biosecurity certification, compartmentalization, improved veterinary services, and enhanced diagnostic capacity. Supporting smallholder farmers while encouraging gradual modernization of production systems is essential to ensure equitable recovery and maintain stable pork supply chains.

In conclusion, the ASF epidemic in Asia has demonstrated that sustainable disease control requires a coordinated, multi-layered approach. Regional collaboration, transparent information sharing, and science-based policies are fundamental to managing transboundary animal diseases. Emerging tools such as vaccination may provide additional support but must be carefully integrated within broader control frameworks.

Take-home messages:

1. Biosecurity across the entire value chain remains the most effective preventive measure.
2. ASF vaccines may support control, but they must be implemented cautiously within integrated disease management strategies.
3. Sustainable recovery of the swine sector depends on resilient production systems and continued research collaboration.
4. ASF control requires regional cooperation and rapid information sharing.

Keywords: ASF, Biosecurity, Compartmentalization, Repopulation, Vaccine.

Acknowledgement: The author gratefully acknowledges the contributions of Nguyen Che Thanh (Andy), a dedicated PhD candidate at Chulalongkorn University, Faculty of Veterinary Science, Bangkok, Thailand, for his work on ASF research in Vietnam.

"Interaction and Vaccination of PCV2, PRRSV, and *Mycoplasmas*"

June 18, 2026; from 13:15 to 13:45



Prof. Dr. Chanhee Chae

Seoul National University, Seoul, Republic of Korea

Biography

He is a leading expert on the porcine circovirus type 2 (PCV2), porcine reproductive and respiratory syndrome virus (PRRSV), and *Mycoplasma hyopneumoniae*. His research focused on pathogenesis of viral and mycoplasmal diseases in pigs, with special emphasis on (i) interaction of PCV2, PRRSV, and *M. hyopneumoniae*, and (ii) evaluation of commercial viral and mycoplasmal vaccines. He is author of over 270 peer-reviewed publications and is a frequent speaker during international veterinary conferences and swine diseases.

ABSTRACT

Interaction and Vaccination of PCV2 and PRRSV

PRRSV vaccine enhanced PCV2 replication and that this is attributable to the failure of PRRSV vaccine in vaccinated dually infected pigs compared to non-vaccinated dually infected pigs. PRRSV vaccine induces enhancement of PCV2 replication as this vaccine is live attenuated strains and identical with a PRRSV/PCV2 co-infection. In contrast, the PCV2 vaccination alone is able to reduce the levels of PCV2 viremia and its associated lymphoid lesions in pigs regardless of the PRRSV infection status. Concurrent vaccination of pigs with PRRSV and PCV2 significantly reduces levels of PRRSV viremia, even in the dually infected pigs, compared to single challenge of PRRSV alone. In summary, the vaccination-dual challenge model suggests that the control of PCV2 infections by PCV2 vaccination may positively affect the efficacy of the PRRSV vaccine in dually infected pigs

Interaction and Vaccination of PCV2 and *M. hyopneumoniae*

Mycoplasmal vaccine was not able to reduce PCV2 replication in vaccinated dually infected pigs compared to non-vaccinated dually infected pigs. *M. hyopneumoniae* vaccination alone is not able to reduce PCV2 viremia or PCV2-associated lung and lymphoid lesions in dually infected pigs. Regardless of PCV2 infection, mycoplasmal vaccine alone is able to reduce the nasal shedding of *M. hyopneumoniae* and mycoplasmal-induced lung lesions in dually infected pigs.

Similarly, PCV2 vaccination alone is able to reduce PCV2 viraemia and its associated lung and lymphoid lesions but not able to reduce *M. hyopneumoniae*-induced lung lesions in dually infected pigs. Based on this independent interaction, it is necessary to vaccinate pigs with both *M. hyopneumoniae* and PCV2 for the control of co-infection with *M. hyopneumoniae* and PCV2.

Interaction and Vaccination of PRRSV and *M. hyopneumoniae*

Mycoplasmal vaccination alone can reduce *M. hyopneumoniae*-associated enhancement of PRRSV-induced respiratory diseases. Vaccination against PRRSV alone reduced PRRSV viremia and PRRSV-induced lung lesions in singular PRRSV-infected pigs but barely reduced the level of PRRSV viraemia and PRRSV-induced lung lesions in dual infected pigs. When *M. hyopneumoniae* and PRRSV vaccines are used in combination, there are significantly lower the levels of PRRSV viraemia than when the PRRSV vaccine is used alone in dually infected pigs.

Infection sequence between PRRSV and PCV2

PRRSV enhanced PCV2d replication and potentiated PCV2-associated lymphoid lesions in pigs infected either sequentially with PRRSV followed by PCV2d or simultaneously with PCV2d and PRRSV, but not in pigs infected with PCV2d prior to PRRSV.

Infection sequence between *M. hyopneumoniae* and PCV2

A sequential infection with *M. hyopneumoniae* followed by PCV2d, as well as a simultaneous infection with these pathogens, resulted in an increase of PCV2 genomic copy numbers in serum and enhanced PCV2-associated lymphoid tissues. These effects were not observed when PCV2d infection preceded *M. hyopneumoniae* infection.

Infection sequence between *M. hyorhinis* and PCV2

The potentiating effect of *M. hyorhinis* on PCV2-associated lymphoid lesions was shown to be dependent on infection sequence. Specifically, pigs sequentially inoculated with *M. hyorhinis* followed by PCV2b, or with PCV2b followed by *M. hyorhinis*, developed more severe PCV2-associated lymphoid lesions and clinical signs than pigs simultaneously inoculated with both pathogens.

Infection sequence between *M. hyopneumoniae* and PRRSV

The exacerbation of PRRSV-associated pneumonia was observed only when *M. hyopneumoniae* infection preceded PRRSV infection, whereas no potentiation occurred following PRRSV infection prior to *M. hyopneumoniae* infection or during simultaneous infection with both pathogens.

Infection sequence between *M. hyorhinis* and PRRSV

M. hyorhinis exacerbated PRRSV-induced pneumonia regardless of the infection sequence.

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PARALLEL SESSION 16: PIG FARMING PRACTICE

"Health and Production Management in Pig Farm"

June 18,, 2026 from 13:15 to 13:45

Asst. Prof. Dr. Pariwat Poolperm

Professional Training and Consultant, Co. Ltd., Thailand

Biography

Dr. Pariwat Poolperm is a senior veterinarian and swine health specialist with over 30 years of experience in academia, swine health and production management, and national veterinary leadership. He bridges the gap between high-level government policy and field-level execution. As the founder of Professional Training and Consultant Co., Ltd., he is providing high-level consulting to commercial swine farms and major animal health companies. His advisory work spans herd health improvement, reproductive management, and disease prevention across farms. He earned his Doctor of Veterinary Medicine from Kasetsart University, THAILAND, and later completed a Ph.D. in Physiology at North Carolina State University, USA, where his research focused on factors influencing boar semen quality and fertility. He is also a Diplomate of the Thai Board of Theriogenology. Pariwat's academic career includes over 25 years as a faculty member at Kasetsart University, he is a leading authority on swine health, contributing to expert panels for the FDA and the Ministry of Agriculture on critical issues like African Swine Fever (ASF) and Foot and Mouth Disease. He has co-authored peer-reviewed publications on swine disease epidemiology, reproduction, and herd management. His integrated expertise in research, policy, and field consultation positions him as a leading authority in swine production and veterinary services in Thailand.

ABSTRACT

Introduction

The Asian swine industry represents one of the most global pork production and consumption. Countries such as China, Vietnam, the Philippines, Thailand, and South Korea depend heavily on efficient swine farming to ensure food security and economic stability. However, this region faces a complex landscape characterized by a shift from traditional smallholder systems to intensive, large-scale commercial operations. Health and production management have become increasingly complex, requiring integrated approaches to improve productivity, animal welfare, and disease resilience, including the mitigation of transboundary, emerging and re-emerging diseases, with emphasis on strategies to enhance resilience and efficiency in modern production systems.

Biosecurity and Disease Surveillance Frameworks

Biosecurity, the foundation of herd health, remains the cornerstone of disease control in Asian pig farms, especially in regions affected by African Swine Fever (ASF), Foot and Mouth Disease (FMD), and Porcine Reproductive and Respiratory Syndrome (PRRS).

Asian farms increasingly adopt structured protocols involving controlled farm access, visitor hygiene procedures, vehicle disinfection, and clear separation between clean and contaminated zones. Quarantine programs for replacement gilts, systematic cleaning and disinfection of facilities, and robust pest control are essential to mitigate endemic and emerging diseases. Successful programs emphasize:

- Controlled farm access and visitor protocols
- Quarantine procedures for incoming animals
- Rodent, insect, and wildlife control
- All-in/all-out production systems
- Surveillance systems

Advancements in Reproductive Efficiency

Production management is fundamentally tied to reproductive success. Majority of regional experts emphasize that "the sow is the factory," and her health directly dictates herd throughput. Reproductive efficiency largely determines farm profitability. Key performance factors in breeding unit include:

- Gilt selection based on genetic merit,
- Gilt acclimation before introduces to the herd,
- Balanced nutrition for gestating and lactating sows,
- Effective heat detection and insemination techniques.

Piglet survival in the first 72 hours is critical. Essential practices include ensuring adequate colostrum intake, cross-fostering, implementing early-life interventions and proper vaccination protocol. Piglet survival and early growth depend mainly on:

- Colostrum intake within the first few hours,
- Temperature, humidity and heat stress index management and creep feeding,
- Hygiene in farrowing pens and cross-fostering strategies.

The Future Directions in Swine Business

The next decade will see intensified adoption of:

- Precision livestock farming technologies,
- Data-driven health monitoring systems,
- Regional disease surveillance networks and vaccine innovations,
- Sustainable production models integrating welfare and environment.

Farmers and policymakers must collaborate to standardize practices, strengthen research, and support training programs to elevate regional competitiveness.

Practices, and sustainable methods will be essential to meeting the growing demand and ensuring a sustainable food supply for safe and efficient pork production across Asia.

Conclusion

Health and production management in Asia is no longer just about treating sick animals. Rapid industry growth, coupled with significant disease and environmental pressures, requires farms to adopt integrated strategies encompassing biosecurity, preventive medicine, reproductive management, nutrition, and disease prevention.

As the industry continues to evolve, the adoption of scientific innovation, good management.

ORAL PRESENTATION



TOPIC 1: VIROLOGY AND VIRAL DISEASES (VVD)

INTESTINAL ORGANOIDS FROM EPTESICUS FUSCUS SUPPORT REPLICATION OF SELECT SWINE ENTERIC CORONAVIRUSES: INSIGHTS INTO BAT-SWINE VIRAL INTERFACE

Ning-Chieh Twu[1], Juan Carlos Mora-Díaz[1], Rahul Kumar Nelli[1], Lu Yen[1], Apoorva Saxena[1], Rachel Ruden[1], Panchan Sitthicharoenchai[2], Luis Giménez-Lirola[1*]

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Introduction and Objectives

Bats are recognized reservoirs for several zoonotic coronaviruses (CoVs), including SARS-CoV and MERS-CoV[GLG [1]. Understanding their susceptibility to other CoVs is crucial for assessing cross-species transmission risks. Swine CoVs such as PEDV and SADS-CoV are believed to have bat origins, and recent surveys have even detected PEDV in bat specimens. However, research using bats is constrained by ethical, ecological, and technical challenges. This study aimed to establish an in vitro model using intestinal organoids (enteroids) derived from the big brown bat (*Eptesicus fuscus*) to evaluate susceptibility to PEDV, TGEV, and PDCoV.

Materials and Methods

Small-intestinal crypts from three bats were isolated and cultured in Matrigel to generate differentiated bat enteroids (BEMCs). BEMCs were dissociated and seeded into transwell inserts (BETCs) to produce polarized epithelial monolayers. Native bat tissue, BEMCs, and BETCs were characterized by immunohistochemistry and gene expression analysis, including CoV receptor profiling. BETCs were inoculated with PEDV (USA/Colorado/2013), TGEV (Purdue P115 attenuated, BEI NR-43285; Miller [GLG[2] [NT3], BEI NR-447), and PDCoV (Michigan/8977/2014) in the presence or absence of trypsin and monitored for 48 h post-inoculation (hpi). Susceptibility was assessed by cytopathic effects (CPE), viral nucleocapsid (NP) detection via immunofluorescence (IFA), and viral RNA quantification via RT-qPCR.

Results and Discussion

Bat crypts consistently differentiated into enteroids that were sub-cultured for over 10 passages. BEMCs displayed crypt-villus organization and central lumens, whereas BETCs formed confluent, polarized monolayers within 5 - 7 days. Both structures recapitulated native intestinal morphology and expressed CoV receptors. Trypsin-treated infections produced moderate to severe CPE at 24 - 48 hpi, while non-trypsin groups showed mild or no CPE. Viral NP was detected in infected BETCs by IFA, with stronger fluorescence in trypsin-supplemented cultures. RT-qPCR confirmed viral RNA in all inoculated cultures.

Conclusion

This study established bat enteroid cultures and demonstrated susceptibility of *E. fuscus* enteroids to multiple swine enteric CoVs, independently of trypsin. The system provides a physiologically relevant platform to study viral pathogenesis, receptor usage, and interspecies transmission potential between bats and livestock.

Keywords: Bat, Intestinal organoids, Porcine epidemic diarrhea virus, Porcine delta coronavirus, Transmissible gastroenteritis virus.

EPIDEMIOLOGY OF AFRICAN SWINE FEVER IN NEPAL: OUTBREAK PATTERNS, CONTROL CHALLENGES, AND FUTURE DIRECTIONS

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Introduction and Objectives

African Swine Fever (ASF) has emerged as a major threat to Nepal's pig farming sector since its first outbreak in March 2022. The disease has significantly impacted both the pig population and pork production, severely affecting rural communities (MOALD, 2024). This study provides the first national-level analysis of ASF epidemiological patterns in Nepal, identifying key risk factors and control challenges, and offering evidence-based recommendations for future prevention and containment strategies.

Materials and Methods

ASF outbreak data for this study were sourced from the World Animal Health Information System (WAHIS) from March 2022 to June 2025 (WOAH, 2025). The data were analyzed and synthesized to generate epidemiological insights. These insights, along with a review of existing literature and local context, were used to identify major control gaps and challenges, ultimately leading to the development of evidence-based recommendations for Nepal.

Results and Discussion

A total of 48 ASF outbreaks were reported across all seven provinces of Nepal, resulting in 17,005 deaths and a case fatality rate of 92.91%. These outbreaks resulted in a 14.5% decline in the pig population and a 9.8% reduction in pork production. Spatial analysis revealed a weak positive correlation (Spearman's $r = 0.30$, $P = 0.006$) between pig density and outbreak frequency. Outbreaks peaked during the monsoon season ($\chi^2 = 9.17$, $P = 0.027$), indicating environmental influence. A confirmed case involving a wild boar further highlighted the risk of transmission between wild and domestic pig populations. Key risk factors included swill feeding, informal cross-border trade, poor biosecurity, and social-cultural practices such as communal pig slaughter under unhygienic conditions. Control efforts were hindered by limited veterinary infrastructure, weak surveillance, legislative gaps, and low farmer awareness.

Conclusion

ASF has had a major impact on Nepal's pig farming sector, causing economic losses and affecting food security. To reduce the spread of ASF, it is crucial to strengthen veterinary services, improve disease surveillance, enforce biosecurity measures, and raise public awareness. Regional cooperation and stronger policy enforcement are essential to prevent future outbreaks and ensure the long-term sustainability of Nepal's pig farming industry.

Keywords: African swine fever, Control challenges, Epidemiology, Nepal, Risk factors.

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2. WOAH (World Organization for Animal Health), 2025. WAHIS Events Management: Nepal - African Swine Fever Virus.

DISTRIBUTION AND GENETIC DIVERSITY OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUSES IN THE RUSSIAN FEDERATION

Anton Gennadievich Yuzhakov[1,2*], Oleg Anatolievich Verkhovsky[1], Alexei Dmitrievich Zaberezhny[1], Taras Ivanovich Aliper[1,2]

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Introduction and Objectives

Russia ranks among the top five global pork producers. The industry is dominated by large-scale farrow-to-finish pig farms that house tens and hundreds of thousands of sows, from farrowing to finishing. Porcine reproductive and respiratory syndrome (PRRS) is one of the most economically significant viral diseases affecting swine. The aim of our study was to investigate the distribution and genetic diversity of PRRS viruses.

Materials and Methods

The study was conducted between 2010 and 2021. During this period, a total of 2,796 samples (serum or tissue samples) from 51 farrow-to-finish pig farms located in 29 regions of Russia were analyzed. Material was collected from PRRS-positive farms that practiced vaccination and from non-vaccinating farms with an unknown PRRS status. The samples were screened for PRRSV RNA using commercial real-time PCR (Vetbiochem, Russia). To investigate viral diversity, the ORF7 and/or ORF5 regions of the genome were sequenced and/or analyzed.

Results and Discussion

Of the 51 swine farms tested, 30 (58.8%) were positive for PRRSV, located in 19 (65.5%) of the 29 study regions. Viral RNA was detected in 307 samples, accounting for 11% of the total. The PRRSV-1 was identified in the vast majority of samples (95%, 292 out of 307). The PRRSV-2 was detected in 5% of cases (15 out of 307) from four farms located in two Russian regions. Co-circulation of both European and American types of PRRSV was identified in all four cases. Genome segments of 45 field PRRSV strains were sequenced: 42 PRRSV-1 and 3 PRRSV-2. Based on ORF5 analysis, PRRSV-1 strains formed four clades (inter-clade nucleotide identity < 79%). Strains belonged to genotypes 1, 2, or were unclassified (Stadejek et al., 2008).

Conclusion

Our study confirms widespread circulation of the PRRSV in Russia. The pathogens belong to both the European and, to a lesser extent, the American species. PRRSV-1 strains are grouped into genotypes that differ significantly from those of viruses circulating in Western European countries. This fact is of interest for the perspective of understanding PRRSV evolution and its correlation with the geographic distribution of different PRRSV genotypes.

Keywords: Porcine reproductive and respiratory syndrome virus, Phylogenetic analysis, Russia.

Acknowledgement: We acknowledge Andrei Skrylev and other veterinary specialists from the farms provide samples for this research.

References

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CROSS-PROTECTIVE EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST THE NADC30 STRAIN

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11-21. The objective of this study was to evaluate the efficacy of that vaccine (Prevacent® PRRS) against PRRSV-2 lineage 1C strain NADC30 when administered to two-week-old pigs. First detected in Iowa in 2008, NADC30 and its variants have since spread worldwide, causing significant economic losses.

Materials and Methods

Forty-two two-week-old pigs were allocated to two groups of 21 pigs each and were injected by intramuscular route with either Prevacent® PRRS (Elanco) or a placebo. At 28 days post-vaccination, all pigs were challenged by intranasal and intramuscular routes with the PRRSV-2 lineage 1C strain NADC30. Efficacy was assessed by determining clinical scores (sum of scores for depression, respiratory distress, and loss of body condition), average daily weight gain (ADWG), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion

Despite relatively mild clinical signs, there were clear clinical and pathological differences between the vaccinated pigs and the controls. Indeed, the mean clinical score of the vaccinated pigs (0.238) was lower than the one of the controls (0.762) and the ADWG of the vaccinated pigs (0.533 kg) was higher than the one of the controls (0.424 kg). Also, the mean lung lesion score at 14 DPC of the vaccinated pigs (0.502) was lower than the one of the controls (15.964), resulting in a mitigated fraction of 0.977. Finally, the mean cumulative viral load in the sera (sum of viral loads at 3, 7, 10, and 14 DPC) was lower in the vaccinated pigs (26.742 $\log_{10}$) than in the controls (30.607 $\log_{10}$). Similarly, the mean viral load in the BAL fluids was lower in the vaccinated pigs (5.561 $\log_{10}$) than in the controls (7.780 $\log_{10}$).

Conclusion

The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, weight loss, lung lesions, and virus replication in blood and lungs following a challenge with PRRSV-2 lineage 1C strain NADC30.

Keywords: Cross-protection, Efficacy, Heterologous challenge, PRRSV, Vaccine.

CIRCULATION OF JAPANESE ENCEPHALITIS VIRUS IN SWINE HERDS OF VIET NAM

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Introduction and Objectives

Japanese encephalitis virus (JEV) is a mosquito-borne zoonotic pathogen in which pigs act as key amplifying hosts, usually showing no symptoms except reproductive losses in pregnant sows. JEV seropositivity in pigs was around 100% in Can Tho province (Lindahl et al., 2013) and 73.45% in some provinces of Vietnam (Lee et al., 2019). Recently, in Vietnam, many sow herds have reproductive disorder with unidentified causes. This study aimed to determine if JEV could contribute to this problem by detecting JEV in suspected samples and seroprevalence of sow herds in Vietnam.

Materials and Methods

A total of 508 sera from sows of 34 reproductive herds and 76 specimens, including 22 sow s' blood, 4 semen, 25 aborted fetuses, 19 tissues of nursing piglets with nervous signs, and 6 processing fluid samples, were collected across four regions of Vietnam in 2025 to detect JEV antibodies by ELISA kit (Median)-and JEV by Real-time RT-PCR (Median). The E gene of 6 JEV Real-time positive samples were amplified, sequenced, and analyzed to determine the genotype of these 6 JEV by using MEGA 7.0.26.

Results and Discussion

Overall, 100% of sow herds (34/34), but only 59.4% (302/508) of samples were seropositive for JEV, and the seropositive prevalence varied from 15.8% to 100% by herds. Seropositivity was highest in the Southeast (65.8%) and lowest in the Mekong Delta (15.8%). JEV RNA was found in 21.1% (16/76) of samples by Realtime RT-PCR, mainly in aborted fetuses (44.0%, 11/25 samples) and tissues (26.3%, 5/19 samples), while blood and semen were negative. The results showed a statistically significant difference ($P < 0.01$) between sample types in detection of JEV infection. All six E gene sequences analyzed showed the JEV detected in sow herds in Vietnam belonged to genotype Ia.

Conclusion

JEV is widely circulating and could be a cause of reproductive disorders in Vietnamese swine population. Findings highlight the need for ongoing surveillance, vector control, and vaccination strategies to ensure swine productivity and one health purpose.

Keywords: Genotype, JEV, Pig, Realtime RT-PCR, Serology.

Acknowledgements: The authors thank the Sistar Company Vietnam for the financial support and P&Y Livestock Services Company Limited, Vietnam with providing testing facilities.

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IMPACT OF SAMPLE MATERIAL AND DIAGNOSTIC LABORATORY ON NEONATAL PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS PCR MONITORING RESULTS

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Introduction and Objectives

Effective control of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in swine production also requires early detection in neonatal piglets. Various sample matrices - processing fluids (PF), tongue fluids (TF), and umbilical cord fluids (UC) - are used for PRRSV-1 PCR monitoring, but the comparability of results across sample types and diagnostic laboratories is unclear. This study aimed to evaluate whether qualitative (positive/negative) and quantitative (Ct value) PRRSV-1 PCR results from neonatal piglet samples are comparable across different sample materials and commercial diagnostic laboratories.

Materials and Methods

From 2024 to 2025, neonatal piglets from 152 PRRSV-1 infected sow herds in the Netherlands were sampled at the farrowing batch level. Farm staff, following practitioner instructions, collected PF, TF, or UC, which were pooled (up to 60 liters per pool) and submitted to two commercial laboratories (commercial tests Kylt and Indical). PCR testing was performed, and results were analyzed for both qualitative and quantitative comparability.

Results and Discussion

A total of 2680 samples were analyzed. The proportion of PCR-positive samples was not statistically different between laboratories: Merefelt (21.3%) and VLG (24.2%) ($P > 0.05$ with X2 test). However, significant differences in mean Ct values for positive samples were observed: Merefelt mean 27.2 (± 3.9), VLG mean 29.9 (± 4.5) ($P < 0.05$ with the Wilcoxon test after normality was rejected). Across sample materials, the percentage of PCR-positive pools and corresponding Ct values varied, but qualitative results remained consistent between laboratories. For example, Merefelt analyzed 1,076 PF (21.7% positive), 300 TF (16.7% positive), and 232 UC (25.0% positive). VLG analyzed 825 PF (25.2% positive) and 247 TF (20.6% positive); UC were not processed at VLG. Quantitative Ct values were not directly comparable between laboratories due to inter-laboratory variability.

Conclusion

The findings support the use of diverse sample matrices and laboratories for qualitative PRRSV-1 monitoring, while highlighting the need for caution when interpreting quantitative PCR data across different diagnostic settings.

Keywords: Diagnostic laboratory, Neonatal piglets, PRRSV, PCR, Sample material.

Acknowledgements: Lola Pailler Garcia and Carles Vilalta from the epidemiology department of IRTA-CreSA.

PRRSV-2 VARIANT-SPECIFIC EXPOSURE HISTORY AND ABORTION OUTCOMES IN U.S. SOW FARMS

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Introduction and Objectives

Homologous PRRSV exposure is generally thought to confer better immunological protection than heterologous exposure, though the relationship between genetic homology and clinical protection has rarely been quantified in field settings. We investigated how parity-specific abortion rates in U.S. farrow-to-wean farms were influenced by prior exposure to wild-type PRRSV-2 with varying genetic homology.

Materials and Methods

Production and surveillance data from three sow farms using live virus inoculation (LVI) for PRRSV-2 control were analyzed from 2018 - 2024. ORF5 sequences from LVI inocula and circulating viruses were classified to sub-lineage and genetic variant using PRRS-Loom1; sequences assigned to the same variant have high genetic homology (mean nucleotide identity: ~ 97.5%)1. Parity-specific abortion outbreaks were identified using exponentially weighted moving averages (EWMA); variant-specific exposure histories were reconstructed for each parity. Mixed-effects GLMs were used to quantify associations between abortions and parity, and exposure history to homologous and heterologous viruses.

Results and Discussion

25 abortion outbreaks were identified (~3.3 outbreaks/year/farm). Outbreaks were categorized as follows: 24% were caused by the introduction of a new sub-lineage, 32% by a new variant within a previously encountered sub-lineage, and 44% by a variant previously detected on that farm. Abortion odds were lower for parities 2-to-4 than parity 0 or ≥ 5. Controlling for parity, outbreaks caused by a repeat variant were associated with a large reduction in abortions ($P < 0.001$), translating to a decrease from a rate of 7% (IQR: 4 - 12%) for new variants to 2% (IQR: 1–4%) for repeat variants. In contrast, no significant difference was observed between outbreaks caused by a new sub-lineage versus a new variant within a previously encountered sub-lineage, suggesting that both are antigenically heterologous. This suggests that variant-level classification can cautiously be interpreted as an indicator of antigenic homology, though ongoing within-herd viral evolution may erode this relationship over time.

Conclusion

This study is among the first to evaluate PRRSV-2-associated abortion risk while integrating parity, immunological exposure history to viruses with variable levels of homology, and viral genetic distance. These findings help identify key drivers of abortion rates and inform parity-specific immunological intervention strategies in sow herds.

Keywords: Abortion risk, Genetic classification, Homologous immunity, Molecular epidemiology, PRRSV-2 epidemiology.

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ENHANCING PRRSV-2 MONITORING AND OUTBREAK TRACING BY ADOPTION OF FINE-SCALE CLASSIFICATION OF GENETIC VARIANTS IN NORTH AMERICA

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Introduction and Objectives

Existing genetic classification systems for porcine reproductive and respiratory syndrome virus 2 (PRRSV-2), such as restriction fragment length polymorphisms (RFLPs) and sub-lineages, are unreliable indicators of genetic relatedness or lack sufficient resolution for epidemiological monitoring routinely conducted by veterinarians. Here, we outline a fine-scale classification system for PRRSV-2 genetic variants that has been adopted in the U.S. and is being extended to Canada. We also present applied examples demonstrating how fine-scale classification can improve epidemiological insights in typical scenarios where veterinarians utilize sequencing

Materials and Methods

Based on > 38,000 U.S. open-reading-frame 5 (ORF5) sequences from 2015-present, sub-lineages were divided into genetic variants using a clustering algorithm; briefly, variant IDs are assigned to monophyletic clades that have bootstrap values of > 85 and meet thresholds for mean pairwise genetic distances. New sequences are incorporated every three months and new variants are systematically identified and labeled. A routinely updated webtool (https://stemma.shinyapps.io/PRRSLoom-variants/) was developed and is publicly available for end-users to assign newly generated sequences to a variant ID.

Results and Discussion

We demonstrate that the variant classification produced clinically useful results that are robust and reproducible across time and can dynamically accommodate new genetic diversity arising from virus evolution. Since 2020, 72 variants were identified, of which 17 were common (detected > 50 times). Median within-variant genetic distance was 2.3% (1.6 - 3.3% IQR). The mean distance to the closest related variant was 4.2%. Finally, we demonstrate how variant classification can better discriminate between previous and new strains on a farm, determine possible sources of new introductions into a farm/system, and track emerging variants regionally.

Conclusion

By enabling accurate and improved discrimination of PRRSV-2 genetic variants, adoption of this classification system has enhanced PRRSV-2 epidemiological monitoring, research, and communication, and improved industry responses to emerging genetic variants. This classification system relies on the U.S. and Canada sequences from 2015 onwards; further efforts are required to extend this system to older or international sequences.

Keywords: Diversity, Genetic classification, Evolution, Molecular epidemiology, PRRSV-2.

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NEW DIAGNOSTIC STRATEGIES IN PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS SURVEILLANCE IN DANISH PIG HERDS

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Introduction and Objectives

A national reduction plan for porcine reproductive and respiratory syndrome virus (PRRSV) was initiated in Denmark in 2022. Since then, producers, veterinarians and scientists have intensively collaborated to reduce the number of PRRSV infected herds. In 2025, the first region was declared PRRSV negative and nationally 73.1% of the Danish herds were PRRSV negative. This promising progress calls for new diagnostic strategies for fast detection of PRRSV by an intensified surveillance system that is economically affordable and feasible. The objective of this study is to test and evaluate alternative test materials that can strengthen the future surveillance of PRRSV in negative herds.

Materials and Methods

Diagnostic test materials have been collected from 18 PRRSV infected herds, and the goal is in 2025 and 2026 to include 50 herds in total. Ten of the sampled herds were farrowing units and eight were nursery units. PRRSV RT-qPCR analysis was performed on well-known (serum, processing fluid, oral fluid) and alternative (slurry) materials. Detection of PRRSV in serum, processing fluid and oral fluid samples was compared to findings in slurry. The diagnostic value of the alternative test material was calculated.

Results and Discussion

In 15 out of 18 tested herds (83%), the serum and slurry samples showed concordant results, being either PRRSV-negative (44%) or PRRSV-positive (39%). In the farrowing units, six out of ten herds tested PRRSV positive by one or more sample types, and the agreement between serum and processing fluid was 70%, the agreement between serum and slurry was 70% and the agreement between processing fluid and slurry was 80%. In the nursery units there was a 100% agreement between serum, oral fluid, and slurry, with five herds being PRRSV-positive and three herds being PRRSV-negative.

Conclusion

A new diagnostic approach is needed in PRRSV surveillance when areas are becoming PRRSV negative. The new system should include testing more often but be practical and economically affordable. Collection of alternative herd test material like slurry is promising when comparing the results of PRRSV detection to well-known diagnostic materials.

Keywords: Diagnostics, Porcine Reproductive and Respiratory Syndrome virus, Surveillance, Slurry.

EVALUATING NON-S INDEL AND S INDEL PORCINE EPIDEMIC DIARRHEA VIRUS DIFFERENTIAL REAL-TIME RT-PCR ASSAYS TARGETING SPIKE GENE AND ASSESSING DETECTION FREQUENCY OF THE TWO VIRUS STRAINS IN THE UNITED STATES

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) circulating in U.S. swine primarily includes non-S INDEL (clinically virulent) and S INDEL (clinically mild) strains that differ mainly in the spike (S) gene. PEDV screening PCR detects both strains but cannot distinguish them. Although S gene sequencing can distinguish strains, it is time-consuming, costly, and variably successful. S gene-based differential real-time RT-PCR provides a faster alternative, but the performance could be affected by PEDV genetic diversity. Additionally, the prevalence of non-S INDEL and S INDEL PEDV in U.S. herds remains unclear. This study aimed to (1) evaluate four S gene-based differential PCR assays and (2) determine detection frequencies of both strains in PEDV screening PCR-positive samples.

Materials and Methods

A commercial PEDV/TGEV/PDCoV real-time RT-PCR was used for PEDV screening. Three in-house-developed and one published S gene-based differential real-time RT-PCR assays were evaluated. Detection frequencies were assessed using 1749 PEDV screening PCR-positive samples collected from September 2024 to April 2025 and tested with differential PCR assays 1 and 2. A sample was considered strain-positive if either assay detected it.

Results and Discussion

All four differential assays showed no cross-reaction with 27 non-PEDV swine pathogens. Using gBlocks and PEDV isolates, all assays correctly differentiated the PEDV strains, except Assay 3, whose S INDEL primers/probes cross-reacted with the CV777 strain. Analytical sensitivity was comparable across all assays. All four assays detected both strains in mixed samples, although detection of the lower-concentration strain was compromised. During diagnostic performance testing using 91 randomly selected screening PCR-positive samples (Ct = 10.7 - 35.9), all four assays failed to detect a substantial proportion of positives. Among 1749 samples archived, 54.3% were positive for non-S INDEL, 21.9% positive for S INDEL, 0.8% positive for both strains, and 22.9% negative for both strains. Differences in strain distribution were observed across production stages and farm locations.

Conclusion

None of the four S gene-based differential PCR assays are fully reliable for detecting and differentiating two PEDV strains in clinical samples, underscoring the need for further assay refinement. Based on the tested and typeable samples, non-S INDEL PEDV was detected more frequently than S INDEL PEDV.

Keywords: Detection frequency, Non-S INDEL, PEDV, S-INDEL, S gene differential PCR.

Acknowledgements: This project was partially funded by Swine Health Information Center.

SCREENING AND THERAPEUTIC EVALUATION OF NATURAL COMPOUNDS AGAINST PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) severely impacts the global swine industry. Current vaccines offer limited cross-protection and carry virulence reversion risks, underscoring the need for alternative control strategies. Natural compounds, with diverse structures and mechanisms, represent a promising resource for antiviral discovery. The objective of this study was to screen a natural compound library to identify agents capable of inhibiting PRRSV infection and replication.

Materials and Methods

A high-throughput antiviral screening platform utilizing a NanoBiT-tagged recombinant PRRSV strain was employed (Wang et al., 2022). A library of 1,561 natural compounds was screened on MARC-145 cells. Compounds reducing viral load to < 25% of controls were selected for secondary screening. Candidates suppressing viral load to < 10% were further evaluated for 50% cytotoxic concentration (CC50) and 50% inhibitory concentration (IC50) in both MARC-145 cells and Porcine Alveolar Macrophages (PAMs).

Results and Discussion

From the initial screen, 36 compounds exhibited anti-PRRSV activity. Seven effective candidates were ranked by Selectivity Index (SI = CC50/IC50). Tetrandrine demonstrated the most potent activity, with SI values of 6.12 (CC50 = 43.06 μM, IC50 = 7.04 μM) in MARC-145 cells and 3.94 (CC50 = 15.57 μM, IC50 = 3.95 μM) in PAMs. Its safe concentration range in MARC-145 cells was 2.5 - 25 μM, indicating a favorable safety profile compared to other active compounds.

Conclusion

This study screened 1,561 natural compounds and identified several with anti-PRRSV activity. Notably, this is the first report of the anti-PRRSV efficacy of Tetrandrine, representing a significant advance in natural product-based antiviral strategies and offering a novel candidate for PRRSV control.

Keywords: Antiviral therapy, High-throughput screening, Natural compounds, PRRSV, Tetrandrine.

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FOOT-AND-MOUTH DISEASE VIRUS 3A ANTAGONIZES INNATE IMMUNE SIGNALING BY TARGETING MAVS AND TBK1

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Introduction and Objectives

Foot-and-mouth disease virus (FMDV) is a highly contagious pathogen that affects cloven-hoofed animals. The innate immune system is the host's first line of defense against viral infection, and several FMDV-encoded proteins have been shown to interfere with host immune responses. In this study, we aimed to elucidate the bipartite mechanisms by which the 3A protein subverts the type I interferon signaling pathway.

Materials and Methods

3A was cloned into Flag, Strep, and GST-tagged vectors. 3A-mediated luciferase reporter assays followed the initial luciferase screening. Interacting proteins were identified using luciferase assay and mass spectrometric results. Immunoprecipitation and immunofluorescence assays were then used to validate protein interactions. In vitro phenotype studies assessed surrogate virus replication in the presence of 3A. ELISA and qRT-PCR were used to evaluate cytokine secretion and interferon-stimulated gene (ISG) transcription.

Results and Discussion

3A inhibited RLR signaling and enhanced surrogate virus replication. Mechanistically, 3A blocked serine 172 of TANK-binding kinase-1 (TBK1), thereby inhibiting TBK1 phosphorylation and subsequent interferon regulatory factor 3 (IRF3) activation. Additionally, 3A was found to interact with caspase 3 to form a complex with Mitochondrial antiviral-signaling protein (MAVS), leading to caspase 3-mediated MAVS degradation. Collectively, this dual-targeting strategy profoundly impaired IFN signaling and pro-inflammatory cytokine production.

Conclusion

These findings establish FMDV 3A as a key virulence factor that simultaneously targets the central innate immune regulators TBK1 and MAVS, thereby promoting a cellular environment conducive to viral replication. By elucidating these previously unrecognized interactions, this study provides a molecular basis for the rational modification of 3A in the design of safe and effective live-attenuated vaccines against FMDV

Keywords: 3A, Foot-and-mouth disease, MAVS, TBK1, Type-1 interferon.

Acknowledgements: This work was supported by the National Research Foundation (RS-2021-NR060136).

COMPARISON OF SEROLOGICAL ASSAYS FOR PORCINE CIRCOVIRUS 2 (PCV2) ANTIBODY DETECTION FOLLOWING EXPERIMENTAL AND NATURAL EXPOSURE

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Introduction and Objectives

Serological monitoring of porcine circovirus 2 (PCV2) is useful for assessing herd immunity, dynamic infection, and subclinical infection. However, commercial ELISAs differ in antigen composition and may vary in sensitivity, which can affect antibody detection, particularly across PCV2 genotypes. In contrast, genotype-specific indirect immunofluorescence assays (IFA) represent an alternative approach to evaluate serological responses. This study compared two commercial ELISAs with genotype-specific IFAs (PCV2a, PCV2b, and PCV2d) for detecting PCV2 antibodies in non-vaccinated pigs under laboratory and field conditions.

Materials and Methods

In the first experimental-controlled study (Experimental 1), 24 cesarean-derived, colostrum-deprived piglets were inoculated with PCV2d, and serum samples were collected on days 0, 7, 14, and 21 post-inoculations. In the second controlled study (Experimental 2), 24 PCV2-seropositive pigs were inoculated with PCV2d at 7 weeks of age, with serum collected at 3, 7, 15, and 22 weeks. In the field study, serum samples were collected at 3, 5, and 9 weeks from 30 pigs originating from a $PCV2^{+}$/$PCVAD^{+}$ farm (Farm 1) and a $PCV2^{+}$/$PCVAD^{-}$ farm (Farm 2). Antibodies were evaluated using the BioChek ELISA, Ingezim ELISA, and genotype-specific IFAs.

Results and Discussion

In Experimental 1, by day 14 post-inoculation, IFA detected seroconversions for all genotypes, whereas BioChek showed limited detection and Ingezim detected no positive animals. By day 21, IFA positivity reached 80% for PCV2a and 100% for PCV2b and PCV2d, BioChek detected 80%, and Ingezim remained at 20%. In Experimental 2, IFAs and BioChek showed detection rates between 60 and 100%, while Ingezim ranged from 4.5 to 50% across time points. Under field conditions, all assays detected 100% seropositivity at 3 weeks of age. By 5 weeks, IFAs and BioChek showed high detection rates (93 - 100%), whereas Ingezim ranged from 57 - 70%. By 7 weeks, detection rates declined markedly for all assays, with IFAs and BioChek ranging from 28 - 41% and Ingezim detecting only 7% of samples, with more pronounced differences in the $PCV2^{+}$/$PCVAD^{-}$ farm. Agreement with IFA was moderate for BioChek and low for Ingezim.

Conclusion

These findings indicate that reliance on ELISA alone may underestimate serological responses, with implications for diagnostic accuracy and herd-level decision-making.

Keywords: Porcine circovirus 2, Antibodies, ELISAS, IFA.

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MARKET HOG TRANSPORTATION: A TRAILER STUDY MODEL FOR PATHOGEN DISSEMINATION IN THE U.S

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Introduction and Objectives

Pathogen dissemination across the United States represents a major economic and animal welfare risk. Preparedness strategies, including contingency plans and movement restrictions to limit pathogen spread, are central components of early intervention plans. When pathogens reach points of animal concentration, such as harvest facilities, dissemination may occur through contaminated trailers. However, limited data exist regarding the probability of trailer contamination at these high-risk locations. To address this knowledge gap, this study used four U.S. endemic swine viruses as surrogate models to evaluate the risk of trailer contamination during unloading at harvest facilities.

Materials and Methods

A total of 389 market hog trailers and unloading docks were sampled and tested by RT-PCR for PRRSV, PEDV, PDCoV, TGEV, and Senecavirus A over a year. Samples were collected both before and after unloading. We quantified clean trailers on arrival leaving the facility contaminated for each virus.

Results and Discussion

Among the 389 trailers, when evaluating each virus individually, 30.1%, 39.1%, 36.3%, and 30.3% of trailers arrived clean for PRRSV, PEDV, PDCoV, and Senecavirus A, respectively. Of those trailers arriving clean and unloaded at contaminated docks, 36.1, 57.2, 54.6, and 56.8%, respectively, became contaminated during unloading. Overall, 33% (102/389) of trailers arrived at the harvest facility negative for all four pathogens. However, after unloading contaminated docks, 74.6% of these trailers became contaminated with at least one virus. These findings demonstrate that a substantial proportion of clean trailers acquire viral contamination during unloading, whether considering individual pathogens (36.1 - 57.2%) or the combined status (74.6%). This highlights environmental contamination at harvest facilities as a critical risk factor for trailer contamination, posing an important threat for farm-level disease spread if trailers are not adequately cleaned and disinfected before usage.

Conclusion

Market hog trailers can become contaminated with swine viruses during unloading at harvest facilities, and these concentration points represent a substantial risk for pathogen dissemination via contaminated trailers. These results underscore the importance of implementing enhanced biosecurity measures at harvest facilities to mitigate trailer contamination and suggest that such facilities may also serve as valuable surveillance points for monitoring swine virus circulation.

Keywords: Market hogs, Foreign animal disease, Trailer contamination.

Acknowledgements: The authors thank to the Swine Health Information Center (SHIC), the American Association of Swine Veterinarians (AASV), the Swine Disease Eradication Center (SDEC) for founding the project and the harvest facility for allowing us to visit and collect samples.

AFRICAN SWINE FEVER IN WILD BOAR IN CATALONIA, SPAIN: EXPERIENCE OF AN ONGOING OUTBREAK

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Introduction and Objectives

On 28th November 2025, African swine fever (ASF) was officially declared in Spain after 30 years of a free status. Two wild boars were confirmed to be ASF virus (ASFV) PCR positive together with typical systemic hemorrhages that characterize acute cases of this disease. Following the detection of primary cases, intensified surveillance was implemented by the Official Veterinary Services, which is still ongoing at present (February 2026). This report summarizes the most recent epidemiological update of the outbreak.

Materials and Methods

An infected zone (IZ) of 20 km radius (subdivided into a core, high-risk zone of 6 km radius, and a lower-risk zone of 6 - 20 km radius) was defined, containing 95 municipalities. Enhanced passive and active surveillance were conducted within the designated IZ. Carcasses and hunted or trapped wild boars were sampled and analyzed following national diagnostic protocols. The date of the death was estimated for all the positive carcasses when feasible. Domestic pig farms of the IZ (n = 57) were tested for ASFV and subjected to reinforced surveillance.

Results and Discussion

By February 6th, 2026, 26 outbreaks (3 primary, 23 secondary) and 142 ASFV PCR-positive wild boar cases have been detected. An additional 938 cases tested PCR negative. All positive cases were found within the high-risk zone. Most PCR-positive necropsied carcasses displayed hemorrhagic lesions consistent with the acute form of ASF. Based on the estimated date of death, the most likely time when the virus entered Spain was between August and October 2025. No clinical signs or lesions compatible with ASF have been detected in any of the domestic pig farms located inside the IZ, which were all negative by PCR.

Conclusions

The current outbreak of ASF in wild boar in Spain demonstrated again the feasibility of this virus being found in distant regions from the nearest infected ones, pointing out human activity as the main driving force for transmission. So far, only PCR-positive wild boars have been detected in the 6-km radius IZ, which emphasize that reinforced biosecurity, enhanced passive surveillance, and strengthened physical barriers remain critical to prevent spread beyond the affected zone.

Keywords: African swine fever, Spain, surveillance, wild boar.

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ISOLATION AND CHARACTERIZATION OF SWINE INFLUENZA VIRUSES HARBORING PDM/09-DERIVED INTERNAL GENES IN SOUTH KOREA IN 2023

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Introduction and Objectives

Swine influenza viruses (SIVs) undergo antigenic drift and shift, enabling them to evade pre-existing immunity and potentially contribute to future pandemics. In 2023, we isolated one Eurasian avian-like (EA) H1N1 and two H1N2 strains in South Korea, which were identified as reassortants containing gene segments derived from pdm/09 H1N1 lineage, triple-reassortant swine lineages. In this study, we compared the novel reassortant viruses with classical swine H1N1, H1N2 and A/California/04/2009 to characterize their virological properties and assess their potential pandemic risk.

Materials and Methods

A total of 45 nasal swab samples were collected from domestic swine in South Korea in 2023, and viruses were isolated using embryonated chicken eggs via the allantoic cavity. The eight viral gene segments were amplified using segment-specific primers followed by sequencing on the Illumina platform. Phylogenetic trees were constructed using MEGA X (v10.2.6). Growth kinetics were evaluated in immortalized ferret and porcine epithelial cell lines. Cells were infected at a multiplicity of infection (MOI) of 0.005, and supernatants were collected at designated time points post-infection. Three-week-old female SPF swine were intranasally inoculated and monitored for 10 days. The contact group was co-housed with the challenged group from 1-day post-infection.

Results and Discussion

Phylogenetic analysis revealed that the PB1 and PA segments of A/swine/Korea/SNU01/2023(H1N1) and the PA segment of A/swine/Korea/SNU02/2023(H1N2) showed the highest genetic similarity to pandemic-like H1N1 viruses, indicating the retention of human-origin internal gene constellations following reverse zoonosis and reassortment in swine. All isolates replicated in immortalized ferret and porcine epithelial cell lines, with the novel reassortants exhibiting higher peak titers in ferret tracheal epithelial cells than classical strains. In vivo experiments using A/swine/South Korea/14/2023(H1N2) demonstrated efficient infectivity and transmissibility in swine. Elevated body temperatures exceeding 39°C were observed, and gross pathological examination revealed lung lesions in both inoculated and contact groups.

Conclusion

These findings highlight the importance of continuous surveillance of SIV and enhanced monitoring of reassortment events involving pdm/09 H1N1 internal genes, given their potential to facilitate swine-to-human transmission and increase pandemic risk.

Keywords: Influenza, Pandemic, Swine.

ORAL PRESENTATION



TOPIC 2: BACTERIAL AND PARASITIC DISEASES (BPD)

ENTERIC SNAP-SHOT (OCT–DEC 2025): CROSS-SECTIONAL CHARACTERIZATION OF ENTERIC PATHOGENS IN NURSERY AND FATTENING PIGS ACROSS GERMANY, FRANCE, AND SPAIN

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Introduction and Objectives

Enteric health in nursery and finishing pigs is shaped by an interplay of bacterial pathogens whose age-related distribution in commercial herds is insufficiently documented. This study aimed to characterize age-specific detection patterns of *Brachyspira (B) hyodysenteriae*, *B. pilosicoli*, *Lawsonia intracellularis* (LI), *Salmonella spp.*, ETEC F4/F18, and Shigatoxin (Stx2e), while comparing between diarrheic and non-diarrheic groups and across countries using sock sampling (Musse et al., 2022; Pedersen et al., 2015).

Materials and Methods

Between October and December 2025, 401 sock samples were collected across ages between weaning and end of fattening on 74 farms in Germany, France, and Spain. Herds included either reported *B. hyodysenteriae* circulation or recurrent diarrhea. Each sample, linked to age group and diarrhea status, was analyzed via qPCR.

Results and Discussion

Postweaning was dominated by ETEC (51% positive ETEC F4, 53% ETEC F18) and *Salmonella* spp. (42% positive). LI demonstrated an upward trend from late nursery into grower–finisher period. *B. hyodenteriae* was most prevalent in finishers (> 30% positivity in > 20 weeks of age). Samples of diarrheic pigs showed higher average numbers of pathogens, driven by ETEC and *Salmonella spp.*; LI and Stx2e frequently occurred in groups without diarrhea. This age layered patterns align with known etiologies of postweaning diarrhea (ETEC F4/F18 dominant) (Musse et al., 2022; Weber et al., 2015) and finisher dysentery (*B. hyo*), and with literature on LI ecology and co-infections (Reiner et al., 2011).

Conclusion

These findings confirm sock sampling as an effective tool for early detection of subclinical circulation in diarrheic herds. The resulting profiles support targeted, phase-specific interventions and improve herd-level decision-making through enhanced early warning in commercial pig production.

Keywords: *Brachyspira hyodysenteriae,* ETEC, Lawsonia, Sock sampling, Salmonella.

Acknowledgements: We sincerely thank the veterinarians, farmers, and colleagues whose dedicated support for farm sampling and metadata collection was essential to this work

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BASOLATERAL INFECTION OF INTESTINAL EPITHELIAL CELLS (IEC-18) BY *LAWSONIA INTRACELLULARIS* USING AN INVERTED TRANSWELL CULTURE MODEL

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Introduction and Objectives

Lawsonia intracellularis is an obligate intracellular pathogen responsible for porcine proliferative enteropathy, a disease associated with significant economic losses in global swine production (Kroll et al., 2005). Despite extensive research, important aspects of its pathogenesis, particularly those related to epithelial invasion routes, remain poorly understood. The aim of this study was to investigate the ability of *L. intracellularis* to infect intestinal epithelial cells via the basolateral surface using a polarized in vitro model.

Materials and Methods

An inverted transwell culture system was standardized using IEC-18 intestinal epithelial cells, allowing selective exposure of either the apical or basolateral surface to the pathogen. Monolayer integrity and polarization were assessed by confocal immunofluorescence (IFC) targeting tight junction proteins, paracellular permeability assays using FITC-dextran, and morphological analysis. Experimental infections with *L. intracellularis* were evaluated by confocal IFC, immunohistochemistry, Warthin-Starry staining, and quantitative PCR (qPCR) in both apical and basolateral compartments. Salmonella Typhimurium was used as a comparative model of epithelial invasion.

Results and Discussion

The results demonstrated that *L. intracellularis* was capable of crossing the porous transwell membrane and infecting IEC-18 cells via the basolateral surface, with an intensity comparable to that observed following apical infection. Infection did not cause significant disruption of monolayer integrity, as evidenced by preserved tight junction organization and maintained paracellular permeability. Quantitative analyses revealed similar bacterial detection levels between apical and basolateral infection conditions, confirming the reproducibility and robustness of the inverted transwell model.

Conclusion

This study demonstrates that *L. intracellularis* can invade intestinal epithelial cells through the basolateral surface at levels comparable to apical infection, supporting the hypothesis that infection may disseminate from the lamina propria toward the epithelium in vivo. The proposed model represents a relevant experimental tool for advancing the understanding of the pathogenesis and invasion mechanisms of this bacterium.

Keywords: Confocal immunofluorescence, Immunohistochemistry, Infectious diseases, Porcine proliferative enteropathy, Physiopathogenesis.

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A DEEP DIVE INTO *STREPTOCOCCUS SUIS* DIFFERENTIATION: FROM CULTURE TO PCR AND SEQUENCING

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Introduction and Objectives

Streptococcus (S.) suis is a major swine pathogen and an emerging zoonotic agent, causing significant economic losses in pig production. The species is genetically diverse, with virulence and epidemiology varying between serotypes and sequence types (ST) (Gottschalk et al., 2010; Goyette-Desjardins et al., 2014). While serotyping and multilocus sequence typing (MLST) are commonly used for epidemiological classification, they may not fully capture genomic differences relevant for outbreak investigations or the development of autogenous vaccines. This investigation presents a diagnostic and genomic analysis of 11 S. suis isolates from a single pig farm in Austria. The objective was to assess genetic relatedness and virulence factor profiles using whole genome sequencing (WGS), providing deeper insights beyond conventional diagnostic methods.

Materials and Methods

Brain swabs were obtained from clinically affected pigs between 2021 and 2023. Bacterial culture, species confirmation, capsular gene-based serotyping PCR, and MLST were performed at SAN Group. WGS, phylogenetic analysis, and virulence factor screening were conducted at PathoSense. Capsular serotyping targeted the cps gene cluster, and MLST followed the established S. suis scheme (Jolley et al., 2018). WGS data were used for phylogenetic analysis and screening of virulence-associated genes, including mrp, sly, epf, ofs, srtF, hylA and sao besides confirming the serotype and ST.

Results and Discussion

All isolates were identified as *S. suis* serotype 9. MLST assigned 10 isolates to ST 16, while one isolate could not be assigned to a known ST. Although serotyping and MLST suggested a high degree of homogeneity, WGS enabled a more detailed assessment of genetic relatedness and detection of heterogeneity not captured by classical methods. Genome-based screening of virulence-associated genes enabled comparison of closely related isolates and supported assessment of their pathogenic potential, particularly relevant for outbreak investigations and selection of suitable strains for autogenous vaccine development.

Conclusion

This investigation demonstrates that WGS may provide resolution beyond classical diagnostic methods for *S. suis*. Even within a single farm and a seemingly uniform serotype/ST background, relevant genomic and virulence-related differences may be identified. WGS-based analyses should therefore be considered an important tool in outbreak investigations and in autogenous vaccine design.

Keywords: MLST, Serotyping, *Streptococcus suis,* Virulence factors, Whole genome sequencing.

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BACILLUS B35 FERMENTATION BROTH ALLEVIATES *STREPTOCOCCUS SUIS* PNEUMONIA THROUGH BACTERIOSTASIS, PULMONARY MICROBES, AND IL-6/JAK/STAT/APOPTOSIS PATHWAYS

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Introduction and Objectives

Streptococcus suis (S. suis) is a major zoonotic pathogen responsible for severe diseases in pigs, including meningitis, arthritis, and pneumonia (Goldblatt et al., 2020). Currently, antibiotics remain the primary strategy for prevention and treatment. However, the increasing prevalence of antimicrobial resistance due to their long-term use compounds this issue, creating an urgent need for effective alternative therapies. To address this gap, this study investigated the therapeutic potential of B35 (a probiotic) fermentation broth against *S. suis*-induced lung injury in pigs and explored its underlying mechanisms.

Materials and Methods

The inhibitory effect of B35 fermentation broth against the CVCC607 strain was assessed using a combination of techniques: the MIC assay, time-kill curve analysis, TEM, and flow cytometry. A piglet model of S. suis infection was established to evaluate the therapeutic efficacy of orally administered B35 fermentation broth at doses of 100, 300, and 500 mg/kg. Putative interactions between active ingredients in the broth and core targets of S. suis infection were predicted through LC-MS and bioinformatics analyses, with predictions subsequently validated via in vitro cell experiment.

Results and Discussion

B35 fermentation broth showed a MIC of 15.6 μg/mL against CVCC607. It damaged bacterial cell membrane integrity, causing leakage of β-galactosidase and lactate dehydrogenase, increased PI uptake and membrane permeability, and inhibited biofilm formation. In a piglet infection model, oral administration of B35 fermentation broth dose-dependently alleviated clinical symptoms and lung pathological damage. It enhanced serum antioxidant activities (SOD, GSH, T-AOC), reduced MDA levels, downregulated pro-inflammatory genes (IL-6, TLR4, NF-κB), and upregulated anti-inflammatory genes (IL-4, IL-10). 16S rRNA sequencing indicated B35 broth reshaped the disordered lung microbiota post-infection. In vitro, 1.25 mg/mL B35 broth significantly inhibited S. suis-induced apoptosis of 3D4/2/1 Cells, reduced intracellular ROS levels, and stabilized mitochondrial membrane potential. Western Blot analysis showed B35 broth downregulated IL-6, JAK2, and STAT3 protein expression and inhibited the TNF/Caspase-3 apoptosis pathway.

Conclusion

B35 fermentation broth effectively combats S. suis infection through antibacterial action, modulation of oxidative stress and inflammation, and inhibition of the JAK2/STAT3 signaling pathway and apoptosis.

Keywords: Apoptosis, Lung microbiome, Fermentation broth of probiotics, *Streptococcus suis*.

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3D PORCINE TRACHEAL MODEL REVEALS *MYCOPLASMA HYOPNEUMONIAE*-INDUCED EPITHELIAL DAMAGE BEYOND BACTERIAL CULTURE STATUS

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Introduction and Objectives

The time-consuming and low-sensitivity nature of conventional bacterial culture (BC) limit studies on the actual role of *Mycoplasma hyopneumoniae* (*Mhp*) in complex respiratory diseases. Based on our previous demonstration that porcine airway epithelial cells cultured at the air-liquid interface (ALI-PRECs) support *Mhp* infection, we conducted a two-phase study to evaluate their suitability to assess *Mhp* viability from clinical tracheal swabs (TS).

Materials and Methods

In the initial study, tracheal-derived ALI-PRECs from three pigs were inoculated with *Mhp*-positive (BC-positive) or *Mhp*-negative TS, alongside positive (10^7 CCU/mL, *Mhp* 232) and negative controls. All inocula were removed after 2-h and cells were monitored every 24 h until 72 h post-inoculation (hpi). The second study addressed a clinically relevant scenario in which TS were qPCR-positive but remained BC-negative. Epithelial integrity was assessed by Transepithelial Electrical Resistance prior to inoculation. ALI-PRECs from a single animal were inoculated with three paired TS of known *Mhp*-infectious status collected from the same animal and monitored every 6 h for up to 24 hpi. All inocula were tested by *Mhp* qPCR and BC at inoculation. Infection was assessed by cytopathic effect (CPE), ciliary activity, immunofluorescence (IFA) for *Mhp* P46 and tight junction protein ZO-1, *Mhp* qPCR, BC, and cytotoxicity (LDH-Glo Cytotoxicity Assay, Promega).

Results and Discussion

Regardless of BC-status, *Mhp*-positive TS induced epithelial alterations, including CPE, reduced ciliary motility, ZO-1 disruption, detection of *Mhp* P46, and translocation of *Mhp* DNA to the basolateral compartment (indicative of epithelium damage). Significant differences in ALI-PRECs cytotoxicity between *Mhp*-positive and *Mhp*-negative TS treatments in both apical and basolateral fractions supported *Mhp*-associated cytopathic effects. qPCR confirmed Mhp DNA in inocula and *Mhp*-inoculated ALI-PRECs. In the first study, viable *Mhp* was recovered by BC at 18 days post-inoculation for TS, with evidence of biological activity detectable in ALI-PRECs earlier than by BC.

Conclusion

These findings indicate that ALI-PRECs can detect functionally active *Mhp* in clinical samples that may be missed by BC. This host-relevant model may serve as a complementary approach for assessing *Mhp* viability and offers insight into early pathogen-epithelial interactions.

Keywords: ALI-PRECs, Bacterial culture, *Mycoplasma hyopneumoniae*, Viability.

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DEVELOPMENT OF NOVEL ANTIMICROBIAL PEPTIDES AND THEIR ENGINEERING INTO NANOPARTICLES TO IMPROVE PERFORMANCE

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Introduction and Objectives

Antimicrobial resistance has become a major global health challenge. Antimicrobial peptides (AMPs) have emerged as promising antibiotic alternatives due to their unique bactericidal mechanisms and low propensity to induce resistance (Oliveira et al., 2025). Moreover, nano-delivery platforms can enhance the targeting capability, stability, and efficacy of AMPs (Si et al., 2023). This synergistic approach offers an innovative treatment strategy to combat difficult-to-treat bacterial infections.

Materials and Methods

Novel antimicrobial peptides were screened from random synthetic peptide using bacterial surface display system. One identified candidate peptide was subjected to sequence design, and the generated peptides were synthesized and characterized by evaluating their antimicrobial activity, stability, and biocompatibility. The mechanism of action of the AMPs was elucidated. The *in vivo* therapeutic potency was assessed using a mouse model of *E. coli* systemic infection. To further enhance the performance, two AMPs were engineered into zeolitic imidazolate framework-8 (ZIF-8), generating two nanoparticles. A *streptococcus suis*-induced infectious arthritis model was then used to evaluate the *in vivo* performance of the nanoparticles.

Results and Discussion

Novel AMPs were initially identified by screening from the synthetic random peptide library. Following rational design with one of the candidate peptides, a series of derivative peptides was obtained. In vitro characterization revealed that peptides WP-4 and WP-6 exhibited high antimicrobial activity and good biocompatibility. They demonstrated rapid bactericidal effects, a low propensity for resistance development, and in vivo therapeutic efficacy in a murine model of *E. coli* systemic infection. Studies on the antibacterial mechanism indicated that WP-4 and WP-6 act by targeting bacterial cell membranes, disrupting the proton motive force (PMF), and inducing excessive accumulation of reactive oxygen species (ROS). Two AMP-loaded nanoparticles using the ZIF-8 nanocarrier were successfully constructed, which showed improved in vitro activity and increased resistance to proteolysis. Moreover, these nanoparticles exhibited superior therapeutic efficacy in a *S. suis*-induced arthritis model.

Conclusion

This study identified AMPs with potent in vitro and in vivo activity. Engineering the AMPs into nanoparticles further enhances their performance and delivery. Our study paves the way for novel AMP development and engineering, providing a solution for combatting bacterial infection.

Keywords: Antimicrobial activity, Antimicrobial peptides, Peptide library, *Streptococcus suis*-induced arthritis, Zeolitic imidazolate framework-8.

Acknowledgements: This work was supported by grants from the National Key Research and Development Program of China (Grant Number: 2024YEE0104800).

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DEVELOPMENT OF A MURINE MODEL OF *STREPTOCOCCUS SUIS*-INDUCED ARTHRITIS TO SCREEN THERAPEUTIC DRUGS

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Introduction and Objectives

Arthritis is a frequent clinical manifestation of *Streptococcus suis* infection in both humans and swine (Bornemann et al., 2024; Huong et al., 2014). Antibiotics are commonly used to treat *S. suis* arthritis, although evidence-based regimens remain scarce. To address this gap, we established a murine infectious arthritis model using clinical joint-derived *S. suis* isolates. We constructed bioluminescent strains and applied an *in vivo* imaging system (IVIS) to enable real-time monitoring of infection and to screen candidate therapeutic agents, addressing the need for appropriate models and optimized treatment strategies.

Materials and Methods

A murine model of infectious arthritis was developed using clinical *S. suis* strains isolated from porcine joints. Two luminescent strains were constructed based on *S. suis* strain LXJ. A total of 82 joint-derived *S. suis* isolates collected from pig farms were tested by MIC assays to determine antimicrobial susceptibility profiles. Bioluminescent imaging was used to evaluate antibiotic efficacy *in vivo* and to support the development of therapeutic regimens.

Results and Discussion

Model development showed that intra-articular inoculation, but not intravenous or intraperitoneal inoculation, of the *S. suis* LXJ induced significant arthritis in C57BL/6 mice. Acute arthritis developed within 4 hours post-infection, with complete functional recovery by 9 days post-infection. Two luminescent strains based on *S. suis* LXJ were successfully constructed, and both *in vitro* and *in vivo* analyses demonstrated a positive correlation between bioluminescence signal intensity and bacterial load. Antimicrobial susceptibility testing indicated that over 90% of the isolates were resistant to macrolides and tetracyclines, and approximately 65% were resistant to sulfonamides and aminoglycosides. In contrast, over 76% of the isolates were susceptible to fluoroquinolones, chloramphenicol, and β-lactams. *In vivo* bioluminescence imaging further showed significant reductions in joint bacterial burden after treatment with compound amoxicillin, ceftiofur sodium, enrofloxacin, and florfenicol at multiple time points, supporting their therapeutic efficacy and administration routes.

Conclusion

This murine arthritis model, together with IVIS-based real-time infection tracking, provides a robust platform for evaluating therapeutic interventions for *S. suis*-induced arthritis. The effective drugs and regimens identified in this study also offer an evidence base to inform clinical treatment strategies.

Keywords: Antibiotic screening, Infectious arthritis, In vivo imaging system (IVIS), Mouse model, *Streptococcus suis*.

Acknowledgements: This work was supported by grants from the National Key Research and Development Program of China (Grant Number: 2024YEE0104800).

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HALF-LIFE OF MATERNAL DERIVED ANTIBODIES AGAINST *ACTINOBACILLUS PLEUROPNEUMONIAE* APX-TOXINS AND OMPA PROTEIN IN A COMMERCIAL FARM

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Introduction and Objectives
Swine pleuropneumonia caused by *Actinobacillus pleuropneumoniae* (App) is an infectious disease of worldwide distribution that affects pig herds, causing disease outbreaks mainly in the growing and fattening units. Maternal antibodies (MDA) play an important role in the prevention of clinical disease in early ages. The objective of this work was to determine in a positive herd the half-life of MDA against different toxins and proteins of App.

Materials and Methods
In an App-endemic commercial swine farm, 42 piglets from 7 sows were randomly selected and ear tagged at birth. Serum was sampled at 24 hours, and weekly, until the 10th week of life. These samples were analysed through five enzyme-linked immunosorbent assay (ELISA) tests against Apx toxins I, II, III (in-house tests), and IV and the OmpA protein (commercial kits), expressing the results in S/P value. So that the half-life of these antibodies could be determined as the time required to decrease 50% the s/p value detected at 24 hours of life.

Results and Discussion
24 hours after birth, the following values were detected: for ApxI: 0.733 (IC95% = 0.505 - 0.960), ApxII: 2.907 (CI 95% = 2.654 - 3.160), ApxIII: 1.098 (CI 95% = 0.956 - 1.241), ApxIV: 1.677 (CI 95% = 1.555 - 1.800) and OmpA:1.173 (CI 95% = 1.011 - 1.336). The half-life determined for each type of antibody was 9.56 days for ApxI, 35.49 days for ApxII, 11.79 days for ApxIII, 57.98 days for ApxIV and 17.8 days for OmpA.

Conclusion
The half-life of these MDAs can vary depending on the antigen used in the test, the serotype present in the herd and the sensitivity of the test used, with half-lives of less than 2 - 3 weeks for antibodies against the toxins ApxI, ApxIII, and the OmpA protein, and higher half-lives for the rest. This difference in half-life and in levels could explain, at least in part, outbreaks that appear sooner than expected and should be considered when implementing vaccination protocols.

Keywords: Colostral antibodies, MDA, half-life, App, *Actinobacillus pleuropneumoniae*.

ORAL PRESENTATION



TOPIC 3: COMBATING AFRICAN SWINE FEVER (ASF)

EVALUATION OF IMMUNOGENICITY AND REPRODUCTIVE SAFETY OF AN ASF LIVE-ATTENUATED VACCINE IN GROWING PIGS AND PREGNANT SOWS DURING COMMERCIAL USE

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Introduction and Objectives

Live-attenuated African swine fever (ASF) vaccines may support ASF control in endemic areas. We evaluated immunogenicity, virus detection in blood and secretions, and reproductive safety of the ASF-G-ΔI177L/ΔLVR live-attenuated vaccine under commercial conditions in the Philippines.

Materials and Methods

Two commercial farms participated. Growing pigs (total n = 200; per farm: 50 vaccinated, 50 controls) received a single intramuscular dose of 10^3 $TCID_{50}$ ASF-G-ΔI177L/ΔLVR. Serial sampling was performed in weeks 1, 2, 3, 4, 6, 8, 10, 14, and 17 post-vaccinations (200 pigs × 9 timepoints: 1,800 blood samples; 3,600 oral/rectal swabs). The ASFV genome was tested by p72 (B646L) real-time PCR using a commercial kit (AgPath-IDTM One-step RT-PCR reagents, Thermo Fisher Scientific). ASF antibody responses were assessed by commercial ELISA (Ingezim ASF 480, Gold Standard Diagnostics). Sows (total n=60; per farm: 15 vaccinated, 15 controls) were vaccinated 4 weeks before farrowing; blood was collected at 2 weeks post-vaccination and at farrowing. Piglets were sampled pre- and post-colostrum; a subset underwent necropsy at weaning.

Results and Discussion

No vaccine-related fever or systemic adverse reactions were observed in growing pigs or sows. Antibodies were detected at week 2 in 46 - 47/50 vaccinated pigs per farm (93% overall) and in 100/100 vaccinated pigs from week 3 onward. The vaccine genome was detected in the whole blood of approximately 48/50 vaccinated pigs per farm across weeks 1 - 17 (App. 95%); oral/rectal swabs were infrequently positive through week 4 (App. 5% of swab samples) and all swabs were negative from week 8 onward. Farrowing performance of vaccinated sows was comparable to controls; 154 total piglets were born to vaccinated sows with 3 stillbirths (1.9%). ASF antibodies were detected in all piglets after colostrum intake, and the vaccine genome was detected in major organs at necropsy, supporting transplacental transfer in utero. Sequencing of vaccine-specific deletion junctions from late timepoint qPCR-positive field samples to assess in-vivo genetic stability is in progress.

Conclusion

Single-dose vaccination showed a favorable safety profile, rapid seroconversion, limited detection in secretions, and reproductive safety under commercial farm conditions, supporting further evaluation for ASF control in Asia.

Keywords: African swine fever, Commercial farm trial, Live-attenuated vaccine, Philippines, Reproductive safety.

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PATHOLOGICAL CHARACTERISTICS OF THE EMERGING RECOMBINANT AFRICAN SWINE FEVER VIRUS GENOTYPES I AND II IN VIETNAM

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Introduction and Objectives

African swine fever (ASF) continues to cause serious losses in Vietnam, where highly virulent genotype II, low-virulent gene-deleted, and emerging recombinant genotype I/II (rASFV I/II) strains are co-circulating. The recombinant strains exhibit reduced susceptibility to licensed ASF vaccines, thereby complicating disease control. This study examines the virulence and pathological characteristics of VNUA/rASFV/HD1/23, a newly identified rASFV I/II strain in northern Vietnam, using an experimental pig infection model.

Materials and Methods

Sixteen seven-week-old pigs free of major swine pathogens were assigned to four groups and inoculated intramuscularly with 10^2, 10^3, or 10^4 HAD_{50}/mL of rASFV I/II strain of VNUA/rASFV/HD1/23; controls received PBS. Animals were monitored daily for clinical signs, rectal temperature, and survival. Blood and oral fluid samples were collected for ASFV genomic detection using real-time PCR. Complete necropsies and histopathological evaluations were performed on all pigs reaching humane endpoints.

Results and Discussion

All infected pigs developed acute disease with high fever, anorexia, depression, diarrhea, and recumbency, beginning 3 - 6 days post-infection (dpi). Mortality occurred between 4 and 10 dpi in a clear dose-dependent manner, with the highest dose (10^4 HAD_{50}/mL) producing the earliest clinical signs and shortest survival. Viremia was detected as early as 3 dpi, and viral shedding in oral fluids appeared at 2 dpi in the highest-dose group. Gross lesions consistently included splenomegaly with infarcts, hemorrhagic lymphadenopathy, pulmonary congestion, renal hemorrhage, and gastric hyperemia. Histopathology showed severe vascular injury, lymphoid depletion, necrosis, and inflammatory infiltration in multiple organs. The clinical progression, mortality pattern, and pathological findings closely resembled those caused by highly virulent ASFV genotype II strains, indicating that the recombinant VNUA/rASFV/HD1/23 strain retains high virulence.

Conclusion

This study characterized the pathogenicity of the emerging recombinant ASFV strain VNUA/rASFV/HD1/23 circulating in northern Vietnam. Experimental infections showed high virulence, with rapid disease progression, acute clinical signs, and high mortality within 4 - 10 days. Typical acute ASF lesions were observed, and disease severity was dose-dependent. The strain's virulence, comparable to genotype II ASFV, highlights urgent needs for improved diagnostics, strict biosecurity, and continuous surveillance

Keywords: African swine fever virus, Experimental infection, Pathology, Recombinant ASFV I/II, Virulence.

SAFETY CONCERNS AND RECOMBINATION RISKS ASSOCIATED WITH GENOTYPE − UNMATCHED LIVE ATTENUATED AFRICAN SWINE FEVER VACCINES

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Introduction and Objectives

African swine fever (ASF) is a highly lethal infectious disease of pigs and wild boars caused by ASF virus (ASFV), causing severe economic losses worldwide. ASFV comprises at least 23 genotypes, and protective immunity is largely genotype-specific with limited cross-protection. While the global epidemic is dominated by genotype II viruses, genotype I and recombinant genotype I/II strains have been reported in Asia. This study aimed to evaluate the risks of genotype-unmatched vaccination by assessing cross-immunity induced by a D250R gene-deleted attenuated strain (ASFVΔD250R, genotype II) against the virulent genotype I strain España 75 (Esp75).

Materials and Methods

Twelve eight-week-old castrated crossbred pigs (Landrace × Large White × Duroc) of both sexes were obtained from a commercial high-health-status herd. Prior to the study, all pigs were confirmed negative for ASFV and anti-ASFV antibodies by quantitative PCR and indirect ELISA. Pigs were vaccinated with ASFVΔD250R and subsequently challenged with 10^2 $TCID_{50}$ of either the homologous highly virulent genotype II strain or the Esp75, respectively, at 28 days post-vaccination. The challenged pigs were observed for 21 days. Survival rates and clinical signs were compared between vaccinated pigs and non-vaccinated control animals. Blood samples were collected from pigs longitudinally after challenge, and ten virus strains were isolated at each time point, and their genomes were analyzed.

Results and Discussion

Pigs immunized with ASFVΔD250R and subsequently challenged with Esp75 exhibited a higher survival rate compared with challenged non-immunized pigs inoculated with Esp75. However, immunized pigs challenged with genotype I Esp75 showed more severe clinical signs and reduced survival compared with pigs challenged with homologous highly virulent genotype II viruses. Importantly, genomic analysis of samples collected at 21 days post-challenge demonstrated recombination events between the genotype II ASFVΔD250R and the genotype I Esp75, resulting in the emergence of recombinant chimeric ASFV genomes.

Conclusion

This study shows that genotype-unmatched live attenuated ASF vaccines provide limited cross-protection but pose a significant risk of generating recombinant ASFV strains. These findings highlight careful risk assessment, along with surveillance and genetic characterization of circulating ASFV, is essential prior to vaccine deployment.

Keywords: African swine fever virus, Chimerization, Recombinant, Vaccine.

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AFRICAN SWINE FEVER (ASF) CONTROL AND REPOPULATION STRATEGIES IN MALAYSIA: EFFECTIVENESS OF CLEANING AND DISINFECTION PROTOCOLS

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Introduction and Objectives

Following the confirmation of African Swine Fever (ASF) in Malaysia in 2021, disease control has relied on stamping-out supported by rigorous cleaning and disinfection (C&D), and strict biosecurity. While disinfectant efficacy against African Swine Fever Virus (ASFV) has been widely reported in temperate regions, field-based evidence under tropical conditions remains limited. This study evaluated the effectiveness of current on-farm C&D practices in Malaysia to identify practical strategies for strengthening biosecurity and supporting repopulation.

Materials and Methods

A structured questionnaire assessing five biosecurity domains was administered to farm managers or owners from 37 pig farms across Malaysia. Environmental swab sampling was conducted in six ASF-affected farms in Peninsular Malaysia following routine C&D procedures. Swabs were tested for ASFV using real-time PCR (Ct cut-off: 38). Questionnaire and environmental data were analyzed using Chi-square tests, while differences in Ct values among farms were assessed using one-way ANOVA ($P < 0.05$).

Results and Discussion

Environmental ASFV detection and mean Ct values differed significantly among farms ($P < 0.05$). Lower levels of environmental contamination were associated with comprehensive C&D protocols incorporating foaming agents during wet cleaning, mandatory drying steps, appropriate disinfectant selection, and use of treated or underground water sources. In contrast, farms relying on water-only cleaning, lacking drying steps, or using untreated surface water showed higher frequencies of ASFV-positive environmental samples. Questionnaire analysis revealed significant differences ($P < 0.05$) in key biosecurity practices, including farm structural hygiene, personnel entry controls (mandatory showers), use of caustic soda, soaking of removable equipment, and water source management. Although ASFV DNA detection does not confirm viral infectivity, these findings demonstrate that multi-step, chemically assisted C&D protocols are critical for reducing residual ASFV contamination under tropical conditions.

Conclusion

Effective C&D remains the cornerstone of ASF prevention and repopulation in Malaysia. An optimal C&D sequence involving dry cleaning, wet cleaning with foaming agents, thorough rinsing, adequate drying, and appropriate disinfection was associated with reduced environmental ASFV contamination. Ensuring the use of underground or properly treated water further enhances biosecurity. Integrating environmental surveillance with targeted biosecurity assessment provides a practical, field-validated approach for ASF prevention and safe repopulation in tropical pig production systems.

Keywords: African swine fever, Biosecurity, Cleaning and disinfection, Repopulation.

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SUBTLE GENETIC SHIFTS OF AFRICAN SWINE FEVER VIRUS AMONG VIETNAMESE DOMESTIC SWINE FOLLOWING LIVE-ATTENUATED VACCINES COMMERCIALIZATION

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Introduction and Objectives

Since 2018, African swine fever (ASF) has been widely noted in outbreaks, devastating the Asian pig industry, particularly in Vietnam. The sole etiological pathogen of ASF, African swine fever virus (ASFV), is a linear, large double-stranded DNA virus with an estimated substitution rate of roughly 10^{-4} substitutions/site/year. The Vietnamese nationwide commercialization and implementation of live-attenuated vaccines (LAVs, approval in July 2022), alongside depopulation-repopulation efforts, necessitate a critical assessment of whether these strategies have inadvertently altered circulating ASFV strains.

Materials and Methods

Molecular surveillance of core genes was conducted on 298 pig-derived samples from numerous non-vaccinated farms across 11 randomly selected provinces, using available samples from service laboratories. These provinces are located across Central and Southern Vietnam, and comparisons were made between strains before (2019 - 2020) and after (late 2022 - 2023) LAVs' introduction. Additionally, the major genetic profiles of the two commercial LAVs were investigated.

Results and Discussion

The results confirmed spillover and ongoing field circulation of LAV-related strains and revealed a marked increase in genetic diversity, encompassing both vaccine-like and novel wild-type microvariants in the post-vaccine commercialization phase. Notably, these microvariants harbored non-synonymous single-nucleotide polymorphisms (SNPs) and large segmental deletions within the EP153R-EP402R genes, suggesting potential alterations in viral function. Most compellingly, a unique 15-AGACCAGCAACAAAC-nucleotide repeat in the E183L gene resulted in a five-amino-acid insertion (Arg-Pro-Ala-Thr-Asn) in the p54 protein, serving as a key marker for Vietnamese strains. Initial in silico analysis indicated that this novel p54 protein contained a longer alpha helix structure, which could influence viral movement and interactions with host cells.

Conclusion

Overall, these subtle yet significant genetic shifts suggest that ASFV may be evolving rapidly within the host under selective pressure from widespread immunization and/or diverse introduction routes during repopulation, potentially enabling it to evade the host immune system. This underscores the essential need for robust biosecurity protocols, stringent regulatory oversight of LAV deployment, and genetic surveillance. For diagnosis and management, the urgent development of reliable DIVA (Differentiating Infected and Vaccinated Animals) tools and real-time, adaptable molecular identification methods, coupled with a vaccination-tracking system, is necessary for accurate and sustained control of ASF.

Keywords: ASF virus, Genetic diversity, Live-attenuated vaccine, Spillover, Vaccine commercialization.

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EVOLUTION AND ADAPTATION OF BIOSECURITY MEASURES FOR LARGE-SCALE SWINE FARMS UNDER AFRICAN SWINE FEVER IN CHINA

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Introduction and Objectives
Since African swine fever (ASF) was first detected in China in 2018, biosecurity strategies in the swine industry have been fundamentally reshaped. Large-scale pig production enterprises rapidly implemented extensive biosecurity measures to mitigate ASF risks, yet the evolutionary patterns and convergence of these measures remain insufficiently examined. This study retrospectively analyzed the evolution of biosecurity strategies in large-scale Chinese swine farms in response to ASF and developed an evidence-based biosecurity knowledge map to support risk identification, training, and management decisions.
Materials and Methods
Three large-scale pig production enterprises in northern, central, and southern China were selected. From 2022 to 2023, seven pig farms were investigated through on-site biosecurity inspections focusing on facilities, operational procedures, and daily management. In-depth observations were conducted via six-month veterinary internships at four farms, supplemented by structured interviews with biosecurity veterinarians and reviews of historical records. Instead of applying a standardized quantitative biosecurity scoring tool, biosecurity was categorized into predefined external and internal components. The presence, modification, and introduction of specific biosecurity measures before 2018, during the ASF epidemic (2018 - 2021), and in the post-epidemic adjustment phase (2022 - 2023) were systematically documented. The evolution of biosecurity practices was compared using descriptive statistics and consistency analysis. This study described biosecurity evolution without quantitatively assessing disease prevention or farm productivity outcomes.
Results and Discussion
All three enterprises strengthened veterinary teams, expanded sow inventories, and established dedicated biosecurity management units. A total of 153 biosecurity measures were newly implemented or modified. During 2018 - 2021, the number and diversity of measures increased markedly, particularly for internal biosecurity and controls related to personnel, vehicles, and feed. From 2022 to 2023, enterprises maintained high biosecurity levels while optimizing resource allocation, including reduced personnel-related inputs. Increasing consistency of biosecurity measures among enterprises indicated convergence toward standardized biosecurity systems.
Conclusion
Large-scale swine farms in China have undergone a convergent evolution of biosecurity strategies in response to ASF. This study identifies priority, transferable biosecurity practices, including strict control of pig, vehicles, and personnel entry, enhanced feed and material biosecurity, routine multi-point monitoring, improved internal unit management, and targeted control of airborne and environmental risks.
Keywords: African swine fever, Biosecurity, Evidence-based medicine, Knowledge map, Swine production.

EVALUATION OF THE PERSISTENCE OF AVAC ASF LIVE VACCINE VIRUS IN PIGS POST-VACCINATION

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Introduction and Objectives

African swine fever (ASF) has caused devastating economic losses to the global swine industry for more than a century. Live attenuated ASF vaccines have recently been licensed in Vietnam, including AVAC ASF LIVE. This study aimed to: (i) determine the persistence and tissue distribution of the AVAC ASF LIVE virus in vaccinated pigs; (ii) assess viral infectivity from DNA-positive samples in cell cultures and in susceptible pigs.

Materials and Methods

The study was conducted in two commercial farms. In Farm I, 100 pigs were vaccinated; three pigs were necropsied on 14 and 28 days post-vaccination, and 10 pigs were examined at market age (5.5 months). In Farm II, 500 pigs were vaccinated; at market age (5 months), 15 pigs (10 healthy and 5 previously treated for unrelated diseases) were sampled. Blood and tissues were tested for ASFV DNA by real-time PCR. Positive samples at slaughter were further evaluated by virus isolation on DMAC cells and experimental inoculation of six 4-week-old pigs (3 intramuscular (IM) and 3 oral (PO) inoculation) to assess infectivity. Inoculated pigs were monitored clinically and tested by PCR and ASFV antibody ELISA for 60 days post-inoculation.

Results and Discussion

Low-level ASFV DNA was transiently detected within the first 28 days post-vaccination. At market age, the vast majority of pigs were PCR-negative, with only 10 - 20% showing weak DNA signals in selected tissues, primarily lymphoid organs, and occasionally liver or lung. Blood and carcass samples were negative in all healthy pigs; weak DNA detection in blood and muscle was observed in only one stunted pig that had received medical treatment. All DNA-positive samples failed to replicate in DMAC cells and showed no hemadsorption. Inoculation of six 4-week-old pigs (IM and oral) with pooled DNA-positive tissues caused no clinical signs, viremia, seroconversion, or detectable viral DNA during 60 days of follow-up.

Conclusion

Low-level ASFV DNA may persist in vaccinated pigs at market age; however, no replication-competent virus was detected. These findings confirm the long-term biosafety of AVAC ASF LIVE under field conditions and support its safe application in African swine fever control programs.

Keywords: African swine fever, AVAC ASF LIVE, Live attenuated vaccine, Viral persistence.

Acknowledgements: The authors would like to thank the AVAC staff for their support in caring for the animals during the experiment

GLOBAL DISTRIBUTION AND GENETIC CLASSIFICATION OF AFRICAN SWINE FEVER VIRUS

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Introduction and Objectives

African swine fever virus (ASFV) remains a devastating pathogen affecting global swine production. Despite the substantial increase in genomic data, global description of its molecular epidemiological distribution remains limited. Growing evidence of genetic variability and recombinant strains further emphasizes the need for more comprehensive molecular analyses. This study systematically analyzes ASFV sequence data to characterize the global molecular epidemiological distribution and to compare traditional genotyping based on partial p72 gene sequences with approaches based on whole-genome sequencing (WGS).

Materials and Methods

The study was conducted in three steps: input data processing, epidemiological distribution analysis, and genetic classification. ASFV nucleotide sequences and metadata were retrieved from GenBank and curated in R. Global temporal, spatial, and host-associated distribution patterns were analyzed and visualized. Genotype distribution was assessed using partial p72 gene and WGS data. Sequence alignment was performed using MAFFT and phylogenetic trees were reconstructed using the maximum-likelihood method in RaxML.

Results and Discussion

Temporal analysis of 15,614 ASFV sequences demonstrated a marked increase in data availability from 2017 to 2025 (12,421 sequences), following limited submissions between 1992 - 2002 and a moderate growth from 2003 - 2016. Spatially, Europe contributed the largest proportion of sequences (37.15%), followed by Asia (21.40%), notably Africa showed evidence of sustained ancestral circulation. In terms of host distribution, wild pigs represented the predominant host source (94.53%).

Phylogenetic analysis based on the p72 gene identified 24 genotypes, with the highest diversity observed in Africa and genotype II predominating in Asia and Europe. In contrast, WGS resolved six clades (clades 1 - 6). Clade 2 (corresponding to genotype II) was globally distributed (468 sequences), clade 3 and clade 4 corresponded to genotypes IX and X, respectively, and were restricted to Africa. Notably, clade 6 comprised recombinant strains (17 sequences, primarily from Asia) that were not detected by p72-based phylogeny, highlighting the higher resolution of genome-wide approaches.

Conclusion

This study highlights the spatiotemporal dynamics and global distribution of ASFV sequences, as well as the limitations of p72-based genotyping in resolving genetic diversity and detecting recombinant variants. These findings underscore the resolution of WGS in resolving ASFV evolution and genotype classification.

Keywords: African swine fever virus, Genetic classification, Global distribution, Molecular epidemiology.

ORAL PRESENTATION



TOPIC 4: EMERGING DISEASES IN SWINE (EDS)

EFFECT OF REPEATED SAMPLING ON TIME-TO-DETECTION IN ACTIVE PARTICIPATORY SURVEILLANCE FOR TRANSBOUNDARY PATHOGENS

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Introduction and Objectives

As ASFV has shown, notifiable pathogens may appear in any country at any time: ongoing surveillance is crucial to rapid detection and elimination. We previously showed that collecting and testing a small number of poor-doing pigs across many farms can detect low-prevalence notifiable pathogens cost-effectively (Trevisan et al., 2024). Herein, we evaluate the impact of repeated sampling on the probability of detection.

Materials and Methods

Using the 2017 USDA Census of Agriculture, we created a dataset of 66,637 farms in the contiguous 48 US (8,080,470 km^2). Each farm was identified by geolocation, production type, and inventory. The spread of a 'generic' pathogen within this region was simulated for 180 days over a range of spread parameter values (6,075 scenarios) using the USDA's Animal Disease Spread Model software (ADSM v3.5.10.0). The output for each scenario simulation (1,000 iterations per scenario) provided the infection status of each farm by day post-outbreak (DPO). Using the ADSM dataset, surveillance performance was expressed as the probability (P) of detecting ≥ 1 positive farm by DPO as a function of the percentage of participating farms, farm-level sensitivity, and disease prevalence (R v.4.3). The effect of sampling interval on P was evaluated by comparing P for a specific DPO (point-in-time sampling) vs an aggregate P (Pa) based on sampling every 14 days using Equation 1 (complementary probability formula), assuming independence across time points. (Equation 1) $Pa = [1 - (1 - P_{14}) \times (1 - P_{28}) \times \ldots (1 - P_{DPO})]$

Results and Discussion

The analysis revealed that, at low prevalence, a two-week sampling interval provided a higher probability of detection than a single sampling event. For example, given 29 infected farms among 66,637, a 40% producer participation (26,654 farms), and 10% farm-level sensitivity, achieved a 70% probability of detecting at least one positive farm. In contrast, repeated sampling (two-week interval) provided a 91% probability of detection.

Conclusion

Simplicity should guide surveillance programs. This surveillance design is highly adaptable to a variety of circumstances and provides low-cost, highly sensitive detection of ecdemic and endemic pathogens.

Keywords: Disease detection, Participatory surveillance, Repeated sampling, Transboundary pathogens.

Acknowledgements: The authors thank the National Pork Board for funding this study.

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EMERGENCE OF GETAH VIRUS IN HUBEI PROVINCE (CHINA), IN 2024

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Introduction and Objectives

Getah virus (GETV) is an emerging mosquito-borne alphavirus posing an increasing threat to the global swine industry. Due to the geographic expansion of mosquito vectors and the lack of commercial vaccine, GETV has become a significant concern for the swine industry. This study investigates a severe GETV outbreak in Central China.

Materials and Methods

In August 2024, an investigation was conducted at a farrow-to-finish farm located in a hilly area in Hubei Province. In June 2024, the farm introduced 149 pregnant sows. Following farrowing, the total population of suckling piglets reached approximately 1,800 heads. Samples of lung, spleen, kidney, tonsil, lymph nodes, brain, and intestinal tissues (~ 2g) were collected from three necropsied piglets. Pathogen detection was performed using qRT-PCR targeting the GETV NS1 gene.

Results and Discussion

The disease primarily affected suckling piglets aged 8 - 24 days, with younger piglets exhibiting the most severe clinical signs. Clinical progression began with depression, high fever (40.6 - 41°C), and constipation, while late-stage symptoms included yellow diarrhea and occasional vomiting, with death typically occurring within 10 hours of diarrhea onset. Physical examination revealed cyanosis on the abdomen, submandibular region, and snout, though no neurological symptoms were recorded. Within the population of 1,800 piglets, the morbidity rate exceeded 40% with the mortality rate around 25%. Necropsy revealed hemorrhagic and swollen inguinal and mesenteric lymph nodes, yellow intestinal contents, and hemorrhage in the cerebral dura mater. Laboratory analysis confirmed that GETV was systemically distributed in multiple tissues, with high viral loads detected via fluorescence RT-PCR: Ct values ranged from 18.37 to 21.17 in the lungs, spleen, and lymph nodes, and 20.10 to 25.68 in intestinal tissues. Furthermore, RT-PCR successfully amplified the target 596 bp band in all tested tissue samples, confirming GETV infection as the causative agent.

Conclusion

The outbreak in Hubei Province confirms that GETV can cause devastating losses in suckling piglets, characterized by rapid transmission and high case fatality rates. Given the seasonal nature of the outbreak (June - September) and the hilly location of the farm, effective mosquito control and rigorous biosecurity in farrowing houses are essential strategies for preventing the spread of this alphavirus.

Keywords: Getah virus, Epidemiological investigation, Outbreak, Swine Industry.

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A COMMERCIAL JAPANESE ENCEPHALITIS PIG VACCINE PROTECTS AGAINST THE AUSTRALIAN GENOTYPE IV VIRUS

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Introduction and Objectives

Japanese encephalitis virus (JEV) Genotype IV (GIV) first emerged in Australia in 2021–2022, resulting in a widespread outbreak across southeastern states and significant economic impacts on the Australian pig industry. Differences in levels of cross-genotype protection have been reported in experimental animal models and field studies in pigs, the amplifying host and target of vaccine programs in some endemic countries. However, there are limited studies on the antigenicity of the more divergent GIV virus in pigs and whether existing commercial GIII-based vaccines are fit for purpose (Fan et.al., 2022). The aim of this work was to establish an experimental pig infection model using a 2022 isolate of JEV (NSW/22) and assess the protective immunity of a JEV (GIII) commercial swine vaccine.

Materials and Methods

Groups of 7 - 8 eight-week-old pigs received two doses of vaccine or saline (sham) four weeks apart. At 14 weeks-old, cohorts were infected with JEV NSW/22 by intradermal injection. Baseline infection was determined by assessing viraemia, routes of virus shedding, antibody response, tissue tropism and clinical symptoms in sham-vaccinated pigs. Vaccine challenge studies were performed with two vaccination protocols using the Nisseiken JEV GIII swine vaccines: live attenuated/killed (JEL/JEK) and killed/killed (JEK/JEK).

Results and Discussion

No clinical signs were observed in sham-vaccinated pigs infected with JEV GIV. Viraemia was detected from day two post-infection (dpi) and typically lasted 2 - 5 days, with oral shedding detected from 4dpi. The virus was detected in post-mortem tissues of 8/8 pigs at 21dpi. Following the challenge of JEL/JEK vaccinated pigs, viraemia and shedding were not detected in 8/8 animals. Viral RNA was detected in post-mortem tissue of 1/8 of pigs. Two doses of the inactivated vaccine (JEK/JEK) provided 100% (7/7) protection against both viraemia/shedding and infection.

Conclusion

Our pig infection model contributes insight into the replication and transmission potential of JEV GIV in the amplifying host. Critically, we have demonstrated that two commercial GIII-based vaccine protocols protect against JEV GIV, providing the basis for potential vaccine options for the Australian pig industry and in other regions of the world where JEV GIV circulates.

Keywords: Arbovirus, Japanese encephalitis virus, Vaccine efficacy.

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PATHOGEN DYNAMICS IN THE U.S. SWINE INDUSTRY: A MACROEPIDEMIOLOGICAL PERSPECTIVE

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Introduction and Objectives

Emerging infectious diseases continue to challenge the U.S. swine industry. This study demonstrates how macroepidemiology, utilizing large-scale diagnostic data, monitors pathogen detection, strain diversification, and production phases to support population-level prevention and control.

Materials and Methods

The Swine Disease Reporting System compiles diagnostic data from six U.S. laboratories, covering over 98% of swine samples in the National Animal Health Laboratory Network. This study highlights trends in Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), Transmissible Gastroenteritis Virus (TGEV), Porcine Epidemic Diarrhea Virus (PEDV), Influenza A Virus (IAV), *Mycoplasma hyopneumoniae* (MHP), and Porcine Circovirus type 2/3.

Results and Discussion

PRRSV remained the most significant pathogen in 2025, reaching its highest PCR-positive rate in December in the wean-to-market category (52.9%). ORF5 lineage dynamics showed major shifts: L1C.5 increased from 161 detections in 2020 to 4,852 in 2025, driven by variant 1C.5.32, which spread across 14 states and predominated in IA (2,922), MN (626), MO (148), and IL (88). Lineage 1C.2 rose to 807 detections, while L1A and L1H declined to 1,078 and 597, respectively. Confirmed tissue diagnoses further highlighted PRRSV's impact, totaling 3,058 cases in 2025. MHP tissue diagnoses fell to 226, a 47% decrease from 2020, aligning with ongoing elimination efforts. TGEV was last detected in March 2021, with no positives among more than 210,000 submissions through 2025. PEDV reached record lows in adult/sow farms in 2025 (7% in winter, 5% in fall), while wean-to-market detections rose to 11% in fall, the highest since 2023. Transport and facility samples continued to show higher PEDV positivity than production sites in 2024 - 2025. IAV positivity in fall 2025 dropped to record lows since 2015 - 15% in adult/sow farms and 35% in wean-to-market herds. However, March 2024 monitoring showed an elevated overall positivity of 38.04%, with 51% of wean-to-market detections from lung samples. In 2025, PCV3 positivity remained higher in adult/sow farms, while PCV2 in wean-to-market herds fell to 40%, its lowest level since spring 2022.

Conclusion

Monitoring macroepidemiological patterns of pathogen detection provides a clear view of disease dynamics in U.S. swine herds. Continued surveillance is crucial for guiding herd health programs and enhancing industry preparedness.

Keywords: Lineage shifting, Macroepidemiology, Pathogen dynamics, PRRSV, Swine health.

PRRSV VARIANTS UNDER MONITORING (VUM): AN INITIATIVE FOR PROACTIVE NEAR REAL-TIME SURVEILLANCE

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Introduction and Objectives

PRRS-Loom, a Porcine Reproductive and Respiratory Syndrome Virus (PRRSV-2) variant classification tool, was developed for fine-scale viral classification to support epidemiological investigations (Kimberly et al., 2025). New PRRSV2 variants continue to emerge and spread with varied production impact. To support proactive identification of PRRSV2 variants that are, or could become, more impactful to the swine industry, a project to systematically identify and monitor variants with potential for widespread transmission was developed.

Materials and Methods

The tool requires two primary data streams: (1) spatiotemporally representative ORF5 sequences to continuously update PRRS-Loom variant classification reflecting the evolving viral landscape, and (2) near-real time routine field diagnostic/surveillance ORF5 sequences linked to unique Premises IDs to calculate new sites affected. In PRRS-Loom, a previously developed machine learning model was used to forecast variant growth and flag fast-growing variants (year-over-year growth rate > 20%) based on 27 sequence-level features (Pamornchainavakul et al., 2024). Variants with high predicted growth are designated as Variants Under Monitoring (VUMs). Then, using near real-time data from the Morrison Swine Health Monitoring Project (MSHMP), which captures sequences > 60% of U.S. breeding herds, VUMs are categorized by the number of new sites affected over the previous six months: Category 1 (< 30 sites), Category 2 (31 - 60), Category 3 (61 - 100), and Category 4 (> 100).

Results and Discussion

Reports showing updates on currently circulating VUMs are generated monthly, with further epidemiological description of VUMs category 2 or higher and known scientific information on each variant. If implemented at the time, this improved monitoring system would have likely classified variant 1C.5 as VUM Category 2 as early as December 2020, moving to Category 3 in January 2021, and Category 4 in May 2021. Similarly, a current variant rapidly spreading in the U.S. (1C.5.32) would have been flagged as Category 2 in November 2023, Category 3 in February 2024, and Category 4 in March 2024, illustrating the exponential growth of this variant over the first quarter of the year.

Conclusion

Altogether, this system allows for near real-time monitoring of PRRSV variant emergence and improved situational awareness, enhancing disease surveillance, preparedness, and communication.

Keywords: Disease Surveillance, Epidemiological Monitoring, Porcine Reproductive and Respiratory Syndrome Virus, Viral Variant Classification.

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A SURVEY OF CRITICAL CONTROL POINTS OF TRUCK WASHES OPERATED IN THE UNITED STATES AND CANADA

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Introduction and Objectives

Contaminated livestock trailers present a risk for pathogen transmission amongst swine farms and to national biosecurity. To mitigate this risk, trailers typically undergo a 3-step decontamination process: washing, disinfection, and drying. All 3 steps are critical to achieve trailer decontamination, since washing alone is insufficient for pathogen inactivation1-3. Using the concepts of HACCP, a survey of critical control points (CCPs) of the truck wash facility design and process is reported.

Materials and Methods

An instrument was created to focus on 4 CCPs: (1) Prevent Cross-Contamination; (2) Washing Phase; (3) Disinfection Phase; and (4) Drying Phase. Data was collected through visual, observational, and instrumental measurement from a convenience sample of 29 truck washes used by swine trailers in the United States and Canada.

Results

Notable findings are summarized by CCPs. The design of the entry and exit of the truck wash facility permitted the crossover of washed with unwashed trailers at 6 of the 29 facilities. The water temperature used for washing trailers ranged from 48 to 170 °F. Staff followed sanitation steps to prevent re-contamination of clean surfaces in 14% of wash events. Chemical disinfectant was found applied at/above label concentration to 33 (100%), where concentration was measured. Finally, in the drying phase, the maximum surface temperature of the trailer floor ranged from 93°F to 159.6°F. The maximum temperature maintained during the drying phase ranged from 5 to 40 minutes. While 76% of trailers began the drying phase with puddled water present, most (86%) trailers had a visibly dry surface upon cycle completion.

Discussion

All but one truck wash's water temperature measured lower than what was communicated as their critical limit. The observed lower-than-expected water temperatures may indicate potential concerns regarding the ability to remove organic material from trailer surfaces. While all trailers had chemical disinfectants applied at/above label concentration, 95% allowed enough wet contact time to deactivate pathogenic microbes. Only 36% of trailers reached a temperature consistent with science-based thresholds for deactivating PRRSV and PEDV. The survey revealed variability in facility design causing cross-contamination and processes that inconsistently address critical control points.

Keywords: Biosecurity, Disinfection, Decontamination, Livestock trailers.

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ORAL PRESENTATION



TOPIC 5: ADVANCEMENTS IN IMMUNOLOGY AND VACCINATION (AIV)

AN EMERGING TOOL TO ESTIMATE IMMUNOGENICITY: T CELL EPITOPE CONTENT COMPARISON OF A PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS MODIFIED LIVE VACCINE TO FOUR FIELD STRAINS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) continue to evolve creating highly diverse strains that are a significant challenge to control. The ability to quickly determine effectiveness of vaccines to emerging field strains has not been available to the swine veterinarian or pork producer. Effective PRRSv control necessitates a strong T cell mediated memory response. Using EpiVax's proprietary algorithms, PigMatrix and epitope content comparison (EpiCC), T cell content relatedness between a MLV vaccine Prevacent PRRS® and four PRRSV type 2 strains was predicted and compared to results from a previous challenge study. The study objective was to determine if EpiCC coverage scores are predictive of the efficacy ranking based on CD4 IFNg responses in published vaccine challenge study.

Material and Methods

Seven structural proteins (GP2, GP3, GP4, E, GP5, M, N) from Prevalent PRRS and four heterologous type 2 (PRRSV-2) challenged strains (NC174 lineage (L1C.unclassified), NADC30 (L1C.4), VR2332 (L5A.5), NADC20 (L9E.3)) were screened with a bank of putative class I and II Swine Leukocyte Antigen (SLA) in PigMatrix using a sequential analysis of 9mers of each structural protein. The 9mers over 1.64 standard deviations of all 9 mers were predicted to produce a T cell response creating an EpiCC score. Strain EpiCC scores divided by vaccine EpiCC scores were used to calculate an efficacy score.

Results and Discussion

The population analysis ranks the combined EpiCC coverage scores predicted efficacy as NADC20 (62.72%), VR2332 (61.34%), NADC30 (55.55%), and NC174 (52.76%). For the individual pig analysis, CD4 IFNg responses and EpiCC coverage scores have positive correlations, exception of GP5 which is negatively correlated. Positive correlations for E and M were statistically significant. Only EpiCC coverage scores for E and M proteins are statistically significantly correlated with CD4 IFNg response.

Conclusions

Higher EpiCC coverage scores were associated with higher vaccine efficacy in the population analysis. The individual animal analysis is preliminary as only four pigs were included due to lack of SLA identity. EpiCC coverage score may help veterinarians and pork producers determine a closely matched vaccine to field strains for better immunological fit and identify variants with a good immunological match.

Keywords: Efficacy, Epitopes, Heterologous challenge, Porcine Reproductive and Respiratory Syndrome Virus, T cells.

REDUCTION OF PNEUMONIA AND CLINICAL PROTECTION AGAINST PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* AFTER VACCINATION WITH A BIVALENT COMBO VACCINE IN A CHINESE COMMERCIAL FARM IN LIAONING PROVINCE: A CASE REPORT

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* cause economic losses to the pig industry. This case report aims to investigate the performance of different PCV2 and *M. hyopneumoniae* combo vaccines under field conditions in China.

Materials and Methods

The case report took place on a farrow-to-finish farm with a history of PCV2 and *M. hyopneumoniae* infections in Liaoning Province. Two consecutive batches of piglets were included in this case. Weaned piglets from one batch served as the historical control group (C; n = 1648), while piglets from the subsequent batch were selected as the Experimental group (E; n = 2210), leading to a batch-to-batch comparison. Group C was vaccinated at 14 days of age (combo PCV2-*M. hyopneumoniae* vaccine; historical vaccine used in the farm), while Group E was vaccinated at 21 days of age (Porcilis® PCV M Hyo). PCV2 viral load was quantified (qPCR) in sera randomly collected (10 pigs/group) at 3, 7, 11, 15, and 19 wk. Average daily gain (ADG) from weaning to slaughter was calculated at group level. At the abattoir, 100 lungs/group were randomly selected for pneumonia evaluation (Madec score). The prevalence of pneumonia and mortality % were analyzed by Fisher's exact test.

Results and Discussion

PCV2 was undetectable during most of the study, except at 19 wk when viral load was lower in E group (2.86 Log_{10}, [2.0, 3.7]) compared to C group (4.2 Log10 [3.8, 4.7]). Mortality was significantly lower in group E (2.90%) compared to group C (7.65%) ($P < 0.05$). Prevalence of pneumonia was significantly reduced in group E (53.0%) compared to group C (73.1%) ($P < 0.05$). The severity of pneumonia was also numerically lower in group E (1.92) vs group C (2.18). ADG was higher in group E (710.9 g/p/d) compared to Group C (695.6 g/p/d).

Conclusion

Under the conditions of this field observation, the tested vaccine significantly reduced the prevalence of pneumonia and mortality. The minimal pneumonia score and the insignificant PCV2 loads in viremic pigs confirmed excellent clinical protection against both PCV2 and *M. hyopneumoniae*. This was corroborated by the increased growth recorded (+15 grams/pig/day) compared to the control group.

Keywords: *Mycoplasma hyopneumoniae,* PCV2, Performance, Pneumonia, Vaccination.
Acknowledgements: The authors thank the producer for the field support during the trial.

ORAL IMMUNIZATION WITH MAIZE-EXPRESSED PEDV SPIKE PROTEIN-DERIVED ANTIGEN MODULATES MUCOSAL CELL-MEDIATED IMMUNITY AND CLINICAL OUTCOMES IN WEANED PIGS

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) is a major enteric pathogen in swine, causing high neonatal mortality and age-dependent growth retardation. Oral vaccines can target gut-associated lymphoid tissue, yet the coordination of mucosal and systemic immune responses during oral immunization remains poorly characterized. This study assessed a maize-expressed PEDV-S1 oral vaccine by characterizing clinical outcomes, fecal viral shedding, and lymphocyte cytokine expression and kinetics following PEDV challenge.

Materials and Methods

A feeding-based vaccination trial was conducted in sixty 3-week-old PEDV-negative pigs randomized into four groups (n = 15): Control, Vaccine-1, Vaccine-2 (with adjuvant), and Challenge (2x). Vaccinated groups received a prime-boost regime of maize-expressed S1 incorporated into feed prior to oral challenge with a non-S INDEL PEDV strain on day 35. The Challenge (2x) group received two live PEDV inoculations to mimic repeated natural exposure. Clinical signs, body weight, antibody response, and fecal viral RNA were monitored. Necropsies on days 7, 14, 21, 28, 37, and 45 provided feces, blood, spleen, and mesenteric lymph nodes (MLN) from the jejunum and ileum. Flow cytometry quantified T, B, γδ-T, NK, and regulatory cell subsets, including IFN-γ^+ and TNF-α^+ populations.

Results and Discussion

Oral vaccination altered disease progression and coordinated immune responses after challenge. Vaccine-1 pigs exhibited shorter diarrhea duration, while Vaccine-2 pigs showed mild but prolonged diarrhea, yet achieved greater body weight by day 45 compared with Controls ($P < 0.01$) and Challenge (2x) ($P < 0.05$). Viral shedding was highest in Controls ($P < 0.01$), intermediate in both vaccinated groups, and lowest in Challenge (2x) pigs, but only after the second exposure. MLN profiling showed increased $CD4^+$ T cell activation on day 21 in Challenge (2x) pigs and elevated B cells ($CD21^+$SLA-II-DR^+) on day 37 across all antigen-experienced groups. IFN-γ^+ $CD4^+/CD8^+$ cells were reduced at days 7–21 in antigen-experienced groups, consistent with trafficking from MLN. TNF-α^+ subsets remained low, whereas γδ-T cells increased from days 21-45 with group-specific patterns. $FOXP3^+CD25^+$ T cells remained stable.

Conclusion

Maize-expressed oral PEDV-S1 immunization generated regulated mucosal and systemic immunity, mitigated clinical disease, and improved growth performance, supporting its potential for enhancing gastrointestinal health in swine production.

Keywords: Cell-mediated immunity, Mucosal immunity, Maize-expressed antigen, Oral vaccination, Porcine epidemic diarrhea virus PEDV.

EXPLORATORY STUDY OF A NOVEL LIVE RECOMBINANT VACCINE AGAINST PORCINE EPIDEMIC DIARRHEA VIRUS IN SPF PIGLETS

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Introduction and objectives

Porcine epidemic diarrhea virus (PEDV) causes severe enteric disease in neonatal piglets, leading to high mortality and substantial economic losses. Maternal vaccination that elicits strong lactogenic immunity is a primary strategy to protect neonates during the critical early life period. This study evaluates the safety, immunogenicity, and preliminary efficacy of a live recombinant Paramyxovirus 1-vectored vaccine expressing PEDV Spike (AVX/PED S1S2) given to sows to provide passive immunity to SPF piglets.

Materials and Methods

Four pregnant SPF sows produced 39 piglets allocated to three groups: Group A (U/U) unvaccinated/unchallenged, Group B (U/C) unvaccinated/challenged, and Group C (V/C) vaccinated/challenged. Sows in Group C received 2.0 mL IM at 5 and 3 weeks prepartum. Weekly rectal swabs and blood were tested by PEDV qPCR and indirect ELISAs for nucleocapsid and Spike. Colostrum and piglet sera were sampled pre-colostrum and at day 3. Piglets in Groups B and C were orally challenged at 3 days old with a virulent Mexican PEDV isolate (Ct 19.3; 1.02×10^9 genome copies/mL). Clinical signs, mortality, and body weight were recorded. Sample size power was 0.918.

Results and Discussion

Vaccinated sows showed no adverse reactions. Group A (n = 12) remained healthy. Group B (n = 13) developed enteric disease within 24 hours, and all died or were euthanized by 96 hours. Group C (n = 14) had one death at 24 hours; the remaining 13 survived to scheduled euthanasia. Pre-challenge qPCRs were negative; qPCR was positive at sacrifice in challenged groups. Nucleocapsid ELISA remained negative pre-challenge across groups. Anti-Spike antibodies appeared only in vaccinated sows after the second dose and were detected in serum, colostrum, milk, and piglet sera in Group C. Growth differed significantly: Group C maintained normal growth (+26.8% vs Group A) while Group B lost weight (-14.3%; $P = 0.0049$ 2way ANOVA).

Conclusion

AVX/PED S1S2 was safe in sows, elicited maternal anti-Spike humoral responses, and provided lactogenic protection that reduced clinical disease and preserved piglet growth after PEDV challenge. Study limitations include small sample size, a single vaccination schedule and challenge dose, and absence of neutralizing titers, cell-mediated immunity, and longer follow-up.

Keywords: AVX/PED-S1S2 vaccine, Live recombinant vaccine, Nucleocapsid, PEDV, Spike.

IMMUNOGENICITY AND EFFICACY OF A *MYCOPLASMA HYO*PNEUMONIAE/ PORCINE CIRCOVIRUS TYPE 2 COMBINATION VACCINE AGAINST EXPERIMENTAL *MYCOPLASMA HYOPNEUMONIAE* INFECTION IN PIGS

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Introduction and Objectives

Vaccination is an important control measure against infections with *Mycoplasma hyopneumoniae* (*M. hyopneumoniae*), the primary pathogen of enzootic pneumonia in pigs. The combined vaccine against porcine circovirus type 2 and *M. hyopneumoniae* is safe, efficacious, and immunogenic. They induce humoral and cellular immune responses against *M. hyopneumoniae*. This study investigated local and systemic humoral and cell-mediated immune responses and the efficacy upon vaccination of piglets with a combined vaccine containing inactivated *M. hyopneumoniae* and porcine circovirus 2d (Cirbloc® M. Hyo, Ceva), followed by experimental *M. hyopneumoniae* infection.

Materials and Methods

45 piglets were assigned to a control (n = 20), vaccine (n = 20), and sentinel group (n = 5). Vaccination was performed in the vaccine group on D0, and a challenge infection was conducted in both the control and vaccine groups on D21. The sentinel group received Friis medium. 8 pigs of the vaccine and control groups were euthanized at two weeks after challenge (D35), the remaining pigs were at four weeks after challenge (D49). Blood, lung tissue, BALF, and bronchial lymph nodes were collected at different time points to evaluate antibody and cytokine responses with ELISA, vaccine-specific T cell responses with flow cytometry, clinical signs, and *M. hyopneumoniae* DNA load by qPCR.

Results and Discussion

The sentinel animals remained negative throughout the study. The vaccine group exhibited seroconversion on D21 and D35, with elevated levels of *M. hyopneumoniae*-specific IgA and IgG in BALF on D35. The vaccine group showed activation of IFN-γ^+/TNF-α^+CD4$^+$CD8α^+ T cells and T cell proliferation in blood on D7, which remained elevated through D21. Conversely, the concentrations of IL-10, IL-1β, TNF-α, CXCL-8, and IL-17A in BALF of the control group were higher on D49, correlating with higher *M. hyopneumoniae* DNA loads.

Conclusion

The combination vaccine elicited *M. hyopneumoniae*–specific humoral and cellular responses in blood, underscoring its protective efficacy.

Keywords: Cell-mediated immunity, Combination vaccine, *Mycoplasma hyopneumoniae*.

Acknowledgements: The authors thank colleagues from the Faculty of Veterinary Medicine, Ghent University.

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PROTECTIVE EFFICACY OF AN OIL-ADJUVANTED MONOVALENT FMD VACCINE AGAINST HETEROLOGOUS CHALLENGE IN PIGS

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Introduction and Objectives

Foot-and-mouth disease (FMD) is a highly contagious transboundary viral disease with major economic impact. The objective of this study was to evaluate the protective efficacy of a commercial oil-adjuvanted O1 Campos monovalent FMD vaccine by heterologous challenge in pigs. Virus-neutralizing (VN) antibody responses against homologous and heterologous strains were measured before and after challenge at SENASA.

Materials and Methods

FMD-naïve piglets were vaccinated intramuscularly with a monovalent oil-adjuvanted FMD vaccine containing the O1 Campos strain, Aftogen Oleo, Batch # 1128 (Biogénesis Bagó, Argentina), at a dose of 2 mL. Two vaccinated groups were included: G1 (n = 10), vaccinated once at 0 days post-vaccination (dpv), and G2 (n = 10), vaccinated at 0 and 28 dpv. A non-vaccinated control group (G3, n = 2) was included. The challenge test was conducted at SENASA, WOAH FMD Reference Laboratory in Argentina. Animals were challenged intramuscularly with 100,000 ID_{50}/mL/pig of a heterologous FMD virus strain (O/SEA/mya-98/VTN/24FS02/24) at 28 dpv for G1 and 28 days post-revaccination (dprv) for G2. Clinical protection was assessed post-challenge. Virus-neutralizing antibody titers against homologous and heterologous strains were measured at 26 dpv (G1) or 26 dprv (G2) and at 8 days post-infection (dpi) for both.

Results and Discussion

Complete clinical protection was observed in all vaccinated pigs (10/10) in both vaccination regimens, with the absence of generalized vesicular disease, whereas all control pigs developed clinical signs, confirming the validity of the challenge model. Vaccinated pigs developed robust VN titers against both the homologous strain O1 Campos (26 dpv: 2.06 $\log_{10}$; 26 dprv: 2.44 $\log_{10}$) and the heterologous strain O/SEA/mya-98/VTN/24FS02/24 (26 dpv: 2.10 $\log_{10}$; 26 dprv: 2.10 $\log_{10}$), with titers consistently exceeding the established 1.5 log10 cut-off values.

Conclusion

The oil-adjuvanted monovalent FMD vaccine Aftogen Oleo (O1 Campos) conferred complete clinical protection against heterologous viral challenge in pigs and induced neutralizing antibodies against homologous and heterologous strains. This study confirms the protective efficacy of the vaccine under heterologous challenge conditions.

Keywords: Foot-and-mouth disease, Heterologous Challenge, Oil-adjuvanted vaccine, Pigs, Protective efficacy.

EPIDEMIOLOGICAL INVESTIGATION OF *ACTINOBACILLUS PLEUROPNEUMONIAE* IN CHINA FROM 2021-2024 AND DEVELOPMENT OF A NOVEL BROAD-SPECTRUM DIVA LIVE ATTENUATED VACCINE

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Introduction and Objectives

Actinobacillus pleuropneumoniae, the pathogen of porcine contagious pleuropneumonia, has imposed substantial economic burdens on the swine industry (Perezchica et al., 2023). This study analyzed the serovar distribution and antimicrobial resistance of recent Chinese *A. pleuropneumoniae* isolates and developed a novel live attenuated vaccine with broad cross-protective potential.

Materials and Methods

The serovars and antimicrobial resistance of 90 *A. pleuropneumoniae* isolates collected from 20 provinces in China between 2021 and 2024 were analyzed. Based on a virulent serovar 1 isolate WH01, a live attenuated vaccine candidate WH01-3A, was constructed to meet DIVA requirements and simultaneously express three non-toxic Apx toxins (ApxIA, ApxIIA, ApxIIIA). The safety and protective efficacy of WH01-3A were evaluated in pigs.

Results and Discussion

Serovar 15 became predominant (36.7% overall, 52.6% in 2024), while serovars 1 and 7 declined. High resistance rates were observed against doxycycline (77.8%) and florfenicol (47.8%). Multidrug resistance increased sharply from 0% in 2021 to 42.1% in 2024, particularly in serovars 15 and 7. The WH01-3A vaccine candidate was safe in pigs and provided 66.7 and 100% protection against serovars 1 and 15, respectively, with significant reductions in lung lesion scores (42.6 and 67.8%). It induced antibodies against ApxI, ApxII, ApxIII, and whole-cell proteins of both serovars.

Conclusion

Serovar 15 has become the dominant serovar of *A. pleuropneumoniae* in China, and antimicrobial resistance is increasing. The constructed WH01-3A vaccine is safe and has the potential for cross-protection against serovars 1 and 15. Ongoing surveillance and rational vaccine application are essential for controlling *A. pleuropneumoniae* infections in China.

Keywords: *Actinobacillus pleuropneumoniae*, Epidemiological investigation, Live attenuated vaccine.

Acknowledgements: This research was supported by the National Natural Science Foundation of China (NO.32473032).

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HOLISTIC DISEASE CONTROL WITH 3FLEX: SIGNIFICANT IMPROVEMENTS IN PRODUCTIVITY METRICS IN A COMMERCIAL PIG FARM IN VIETNAM

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Introduction and Objectives
Porcine Reproductive and Respiratory Syndrome Virus, *Mycoplasma hyopneumoniae*, and Porcine Circovirus type 2 are primary contributors to Porcine Respiratory Disease Complex (PRDC), causing severe global economic losses. Control of these pathogens is key to pig health and productivity, but control strategies face many difficulties, especially in large-scale pig farms. This study evaluates a comprehensive stabilization program implemented on a 4800-sow farm to combat high mortality and instability.

Materials and Methods
Following a period of instability, high mortality in weaners caused by PRRS leading to PRDC, the farm transitioned from the previous vaccination regime to a new approach starting in August 2022. This approach included the application of Ingelvac PRRS MLV and FLEXcombo (*Mycoplasma hyopneumoniae* and Porcine Circovirus type 2) in a single injection. The implementation was paired with a comprehensive approach derived from farm audits, which incorporates enhanced biosecurity, pig flow, and management procedures to minimize vertical and horizontal pathogen spread. Key productivity indicators were recorded; statistical process control charts (SPC) were created to analyze variability and highlight deviation from normal behavior for both the sow herd and the nursery and grower stages.

Results and Discussion
The comprehensive disease control program resulted in the gradual stabilization of the health herd status, and improvement in productivity as demonstrated in the SPC charts. In the sow herd, the farrowing rate increased overtime from 88.13 to 91.21%. Total pigs born per litter also increased from 12.43 to 14.54 while the percentage of stillborn decreased from 4.6 to 3.2%. Consequently, the average pig born alive per litter improved from 8.20 to 12.30, and pigs weaned per litter increased from 10.57 to 11.90. The annual output, represented by Pigs Weaned per Sow per Year, rose from 23.30 to 28.90. Concurrently, weaner performance also improved significantly. The mortality rate decreased from 3.0% to a range of 1.8% to 2.2%, and the Feed Conversion Ratio decreased from 1.45 to 1.20.

Conclusion
Integrating targeted vaccination with rigorous biosecurity and management audits is highly effective for stabilizing herd health. Results from this study demonstrated in real time consistent and reliable performance maximizing output and controlling endemic diseases in large-scale in high-density porcine operations.

Keywords: 3FLEX, Boehringer, Holistic approach, PRRS, Productivity.

CROSS-PROTECTION CONFERRED BY INTRADERMAL UNISTRAIN® PRRS VACCINATION AGAINST A HIGHLY PATHOGENIC VIETNAMESE PRRSV2 STRAIN IN PIGS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a major swine pathogen, with PRRSV-2 highly prevalent in Vietnam. Information on the protection conferred by genetically divergent genotype 1–based vaccines against PRRSV-2 remains limited. This study evaluated the efficacy of the intradermal (ID) UNISTRAIN® PRRS vaccine (PRRSV-1 MLV) against a heterologous challenge with a highly pathogenic PRRSV-2 isolate from lineage L8E.

Materials and Methods

Twenty-eight 21-day-old piglets, confirmed negative for ASFV, CSFV, PRRSV, and PCV2, were allocated to two groups: vaccinated and challenged (VC, n = 12) and unvaccinated and challenged (UVC, n = 12). VC pigs received a single 0.2 ml intradermal dose of UNISTRAIN® PRRS (HIPRA, Spain) using the Hipradermic® needle-free device. Five weeks post-vaccination, VC and UVC pigs were intramuscularly challenged with 3 ml of 10^5 $TCID_{50}$ of highly pathogenic PRRSV-2 (lineage L8E). Clinical signs, rectal temperature, growth performance, viremia, serology, and pathological lesions were monitored for 28 days post-infection. Viremia was quantified as Area Under the Curve (AUC) based on Ct values and compared using Student's t-test.

Results and Discussion

All pigs were clinically healthy before challenge. After infection, UVC pigs developed marked pyrexia (> 40°C) from 2 dpi, peaking at 8 dpi, while VC pigs maintained normal temperatures ($P < 0.05$ at 4, 5, 9, and 10 dpi). Lung lesion scores were lower in VC pigs (12.66) than in UVC pigs (15.5; $P > 0.05$). Histopathology showed mild to moderate interstitial pneumonia in VC pigs versus severe, diffuse lesions in UVC pigs (scores 1.00 vs. 2.00; $P < 0.05$). Vaccinated pigs seroconverted between 14 and 21 days post-vaccination and showed higher antibody levels post-challenge (S/P 1.56 ± 0.63 pre-challenge vs. 2.10 ± 0.31 at 14 dpi; $P < 0.05$). Vaccination reduced viremia by 38.58% (AUC). Growth performance was slightly improved in VC pigs, and no mortality occurred. These findings suggest that intradermal vaccination enhances antigen presentation and cell-mediated immunity, supporting faster humoral responses and partial heterologous protection (Ferrari et al., 2011; Giudice et al., 2006).

Conclusion

Intradermal vaccination with UNISTRAIN® PRRS provides partial cross-protection against highly pathogenic PRRSV-2, reducing clinical signs, viremia, and pathological lesions while enhancing humoral immunity, supporting its use in PRRSV-endemic regions.

Keywords: Intradermal, Pig, Porcine reproductive and respiratory syndrome virus, Vaccine, Vietnam.

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IN VITRO ANTIGENICITY PROFILING PREDICTS BROAD IN VIVO PROTECTION INDUCED BY SAFESUI GLASSER ONE, THE FIRST SINGLE-DOSE INACTIVATED *GLAESSERELLA PARASUIS* VACCINE

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Introduction and Objectives

The antigenic diversity observed within and amongst *Glaesserella parasuis* serovars represents a major challenge for the effective control of Glässer's disease using conventional inactivated vaccines. Cross-protective immunity between serovars is generally limited, resulting in suboptimal field effectiveness. In 2024, we demonstrated, through a controlled immunization and experimental challenge study in specific-pathogen-free (SPF) piglets, that Safesui Glasser ONE - SGO (the first single-dose, inactivated, broad-spectrum vaccine against *G. parasuis*) induced robust clinical protection against homologous (SV1, SV4, SV5, and non-typable [NT]) and heterologous (SV7) serovars (Frandoloso et al., 2024). In the present study, we performed an in vitro analysis to characterize the antibody recognition profile induced by SGO against the most prevalent *G. parasuis* serovars circulating in Brazil.

Materials and Methods

A panel of eight sera obtained from SPF piglets immunized with the SGO vaccine was used for antigenicity assessment. Antigenicity was evaluated using the Smart Antigenicity Test (SAT) (Tamanini et al., 2024). The prediction of in vivo protection was based on an antigenicity index (AI) threshold of 1.52. This cutoff value was previously validated in an in vivo challenge study using *G. parasuis* serovar 7, a heterologous serovar relative to the antigenic composition of the SGO vaccine. A total of 39 clinical *G. parasuis* strains were evaluated, comprising serovars 1, 2, 4, 5, 7, 12, 13, 14, and non-typable (NT) isolates.

Results and Discussion

The SAT assay assesses the ability of vaccine-induced IgG to recognize antigens expressed on the bacterial surface. All clinical *G. parasuis* strains presenting an AI $\geq$ 1.52 were therefore predicted to be controlled by SGO-induced IgG. AI values for serovar 1 strains were $\geq$ 1.65, while serovar 4 strains showed AI values $\geq$ 2.07. Strains belonging to serovars 5, 7, and 12 presented AI values $\geq$ 1.59, $\geq$ 1.52, and $\geq$ 1.82, respectively. For serovars 13, 14, and NT, all isolates exhibited AI values $\geq$ 1.61.

Conclusion

Safesui Glasser ONE induces broadly cross-reactive IgG capable of recognizing surface antigens from the most prevalent *G. parasuis* serovars circulating in Brazil.

Keywords: Antigenicity, Cross-protection, *Glaesserella parasuis*, Safesui Glasser ONE, Vaccine.

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DEVELOPMENT AND EVALUATION OF TWO NANOPARTICLE VACCINES AGAINST *STREPTOCOCCUS SUIS*

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Introduction and Objectives

Streptococcus suis poses a significant threat to pig farming and public health, necessitating effective vaccines. Nanoparticle carriers can enhance antigen delivery, potently boosting immune responses. This study develops and evaluates two novel nanoparticle-based vaccines against *S. suis*.

Materials and Methods

Two nanoparticle vaccines loaded with *S. suis* protective antigens were constructed using the self-assembling protein nanoparticle I53-50 (Boyoglu-Barnum et al., 2021) and the metal-organic framework ZIF-8 (Zheng et al., 2025), designated Antigen-I53-50 and Antigen@ZIF-8, respectively. Humoral and cellular immune responses were assessed by ELISA for antigen-specific IgG titers and by ELISpot for γ-interferon production. Safety was evaluated by monitoring body temperature and clinical symptoms post immunization. For protection studies, mice were immunized intramuscularly twice, then challenged with lethal doses of *S. suis* serotypes 2, 7, and 9, with survival monitored (n = 6). In swine, a similar regimen (n = 6) with serotype 2 challenge was used, and protection was determined.

Results and Discussion

Two nanoparticle vaccines were successfully constructed. In mice, both vaccines elicited robust humoral responses, with significantly higher antibody titers than the antigen alone (mean endpoint titers: 1:81,920 for Antigen@ZIF-8, 1:163,840 for Antigen-I53-50 vs. 1:40,960 for antigen alone; $P < 0.05$). ELISPot revealed significantly enhanced γ-interferon production, indicating potent cellular immune responses. Immunization of up to 200 μg per mouse caused no significant body temperature increase or clinical symptoms, confirming favorable safety. In mice challenge studies, Antigen@ZIF-8 conferred survival rates of 100, 100, and 66.7% against *S. suis* serotypes 2, 7, and 9, respectively, and comparable rates of 100, 83.3, and 66.7% were observed for Antigen-I53-50, which both outperformed antigen alone (83.3%, 33.3%, and 33.3%, respectively) (n = 6). In swine, Antigen@ZIF-8 and Antigen-I53-50 at half the antigen dose of the commercial vaccine achieved protection rates of 66.7% and 50% (n = 6), respectively, demonstrating superior or equivalent efficacy compared to the commercial subunit vaccine (50%).

Conclusion

Two *S. suis* nanoparticle vaccines based on I53-50 and ZIF-8 were successfully developed. They elicit robust humoral and cellular immune responses and demonstrate cross-protection. Notably, both vaccines provide superior or equivalent efficacy compared to the commercial subunit vaccine in swine.

Keywords: *Streptococcus suis*, Self-assembling nanoparticle, Swine, Vaccine, Zeolitic imidazolate framework-8.

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TEN YEARS AFTER INTRODUCTION OF NADC30-LIKE STRAIN IN CHINA: A NOVEL CHIMERIC PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VACCINE CANDIDATE

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Introduction and Objectives

Since the introduction of lineage 1C NADC30-like (L1C) porcine reproductive and respiratory syndrome virus (PRRSV) in China, it has become the predominant variant. Current modified live vaccines provide limited heterologous protection and pose safety risks due to potential reversion and recombination (Sun et al., 2024). This study aimed to develop a safer vaccine candidate by exploiting the biological profile of a classical lineage 5A (L5A) BJ-4 backbone, characterized by lower in vivo fitness and higher safety, substituted with the protective immunogenic structural proteins of an L1C strain CHsx1401.

Materials and Methods

Three chimeric viruses RvBJ-4-(ORF2-4)SX, RvBJ-4-(ORF5-6)SX, and RvBJ-4-(ORF2-6)SX were constructed by substituting BJ-4 structural regions with CHsx1401 sequences. After in vitro characterization, pathogenicity and efficacy were evaluated in 29-day-old SPF pigs. Pigs were vaccinated with chimeras or the parental backbone and subsequently challenged with CHsx1401. Clinical signs, viremia, antibodies, and pathology were evaluated.

Results and Discussion

In vitro, RvBJ-4-(ORF2-6)SX demonstrated robust replication in MARC-145 cells. In the animal trial, all chimeric strains exhibited high safety profiles with no significant clinical signs during immunization, confirming the intrinsic attenuation of the L5A backbone. Upon challenge with CHsx1401, the RvBJ-4-(ORF2-6)SX group exhibited superior protection. This candidate substantially reduced viremia duration, achieving clearance within 14 days post-challenge. Rapid clearance of both the vaccine backbone and the challenge virus ensure safety and efficacy, minimizing the biological window for viral recombination.

Conclusion

The chimeric virus RvBJ-4-(ORF2-6)SX validates a novel vaccine design balancing safety and efficacy. Utilizing a L5A backbone with restricted in vivo persistence and incorporating L1C structural proteins confers effective protection while minimizing vaccine-derived recombination risks. This strategy offers a promising approach for controlling L1C PRRSV by limiting viral transmission and recombination.

Keywords: Chimeric vaccine, Cross-protection, Modified live vaccine, NADC30-like, PRRSV.

Acknowledgements: National Key Research and Development Program of China (2024YFD1800503).

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DEVELOPMENT, IMMUNOLOGICAL CHARACTERIZATION, AND EVALUATION OF THE CLINICAL EFFICACY OF VACCINES BASED ON *ACTINOBACILLUS SUIS*

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Introduction and Objectives

Actinobacillus suis is a clinically relevant swine pathogen associated with respiratory and septicemic disease, causing significant economic losses due to mortality and carcass condemnation (Ojha et al., 2010). Since 2023, clinical outbreaks attributed to *A. suis* have increased in Brazil (Machado et al., 2025). The pathogen produces toxins associated with severe necro-hemorrhagic lung lesions, like some *A. pleuropneumoniae* (App) serovars. Despite its importance, no licensed vaccines are currently available in Brazil. This study aimed to develop and evaluate experimental vaccines against *A. suis* as a platform for autogenous and licensed vaccine development.

Materials and Methods

Thirty-six piglets (23 days old) were randomly allocated into four groups (G1, n = 10; G2, n = 8; G3, n = 8; G4, n = 10). G1 received two intramuscular doses (D0, D14) of an inactivated A. suis vaccine formulated with Vaxxinova 01 adjuvant. G2 and G3 received inactivated A. suis vaccines combined with inactivated ApxI and ApxII toxins (100 IU and 200 IU, respectively) from App. G4 received sterile saline. Immunogenicity was assessed by indirect ELISA (D0, D14, D28). Animals were challenged on D28 with 10^7 viable *A. suis* cells via the endotracheal route and clinically monitored for 14 days. Lung lesion scores (LLS) were determined at necropsy (D42). The study was approved by the Animal Ethics Committee of AFK Imunotech (protocol no. 015/25).

Results and Discussion

All vaccine formulations were clinically safe, inducing only transient hyperthermia. Vaccinated groups (G1 - G3) showed a significant increase ($P < 0.05$) in antibody levels against *A. suis* antigens and ApxI/ApxII toxins, whereas no anamnestic response was observed in controls (G4). After challenge, vaccinated pigs showed mild clinical signs, faster recovery, and 100% survival, while control animals developed severe respiratory disease with 50% mortality. Lung lesion scores were significantly lower in vaccinated groups compared with controls (7.21 - G1; 4.61 - G2; 1.43 - G3; 47.39 - G4; $P < 0.001$), demonstrating strong vaccine-induced protection.

Conclusion

The experimental vaccines were safe and protective against *A. suis*, with ApxI and ApxII toxins playing a key role in enhancing clinical protection and reducing lung lesions.

Keywords: *Actinobacillus suis*, Apx toxins, Experimental vaccines, Immunogenicity, Lung lesions.

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LOCAL AND SYSTEMIC T CELL RESPONSES INDUCED BY *MYCOPLASMA HYOPNEUMONIAE* VACCINATION ASSOCIATE WITH PROTECTION IN PIGS

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Introduction and Objectives

Vaccination against *Mycoplasma hyopneumoniae* (*M. hyopneumoniae*) is widely used to control infection (Maes, 2008); however, vaccine-induced immunity remains poorly characterized, particularly regarding the expression of cell-mediated and humoral immune responses in different tissues, and blood. This study aimed to investigate short- and long-term tissue-specific immune responses following vaccination and subsequent challenge infection.

Materials and Methods

Forty-five piglets were randomly assigned to three groups (n = 15): vaccination without infection (V-NI), vaccination with infection (V-I), and no vaccination with infection (NV-I). The V-NI and V-I groups were vaccinated (MycoFLEX®, Boehringer Ingelheim) intramuscularly on D0. On D28, the V-I and NV-I groups were challenged with *M. hyopneumoniae*, while the V-NI group received Friis medium. Seven pigs from each group were euthanized on D42, and the remaining pigs on D86. Blood, lung tissue, bronchoalveolar lavage fluid (BALF), and bronchial lymph nodes were collected at multiple time points to assess humoral responses by ELISA, *M. hyopneumoniae*-specific T cell responses by flow cytometry, clinical parameters, and *M. hyopneumoniae* DNA load by digital PCR. Statistical analyses were performed using IBM SPSS Statistics (version 31). A linear mixed model was used to compare groups, with significance set at $P \leq 0.05$.

Results and Discussion

Vaccination induced early systemic cellular immune activation in blood at D28, characterized by increased IFN-γ^+ and TNF-α^+ $CD4^+CD8a^+$ T cells. After challenge, *M. hyopneumoniae*-specific cellular immune responses were observed in the bronchial lymph nodes. At D42, the V-I group exhibited increased frequencies of TNF-α+ and IL-17A+ T cells, indicating tissue-specific immune activation. By D86, functional IFN-γ+ T cells persisted in the bronchial lymph nodes of V-I pigs, reflecting sustained local memory responses. Serum IgG levels were increased in V-I group at D42, whereas IgA levels in serum and BALF showed no significant differences. Compared to NV-I pigs, V-I pigs showed significantly improved growth parameters, reduced disease severity, and lower pathogen burden at key time points post-challenge.

Conclusion

Early systemic T cell activation and sustained local cell-mediated immune responses induced by vaccination against *M. hyopneumoniae* were associated with protection against experimental *M. hyopneumoniae* infection.

Keywords: Immune responses, *Mycoplasma hyopneumoniae*, Vaccine.

Acknowledgements: The authors acknowledge the colleagues from the faculty of Veterinary Medicine of Ghent University.

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EVALUATION OF STREPTOCOCCUS SUIS IGM PROTEASE AS A CROSS-PROTECTIVE VACCINE ANTIGEN: DISTRIBUTION, GENOTYPING AND EFFICACY IN SWINE CHALLENGE MODELS

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Introduction and Objectives

Streptococcus suis infections are ubiquitous and a major driver of antibiotic usage. Unfortunately, available vaccines only provide serotype specific protection. Here we describe the development of a subunit vaccine based on IgM-protease (Seele et al., 2015) that provides serotype independent protection against > 90% of circulating strains. Further, a typing system has been set up that is predictive for cross-protectivity of the vaccine and proposed as a novel immunity-based typing system (Jacobs et al., 2024). Here we describe the extent of cross-protection provided by the vaccine, as demonstrated in a series of animal vaccination challenge experiments.

Materials and Methods

Bioinformatics, purification of rIde-14009-1, vaccine formulation, vaccination-challenge studies, IgM-protease typing, and PCR were done as described previously (Jacobs et al., 2024).

Results and Discussion

Based on sequence alignments of the IdeSsuis gene (Seele et al., 2015) encoding the IgM protease, a total of > 2000 *S. suis* clinical isolates were divided into 3 genetic groups (Jacobs et al., 2024). Of the clinical isolates, 90% belong to group A, 5% to group B, and 5% to group C. Group C contained mostly isolates from healthy animals. A vaccine based on the recombinantly produced group A IgM protease from strain 14009-1 (rIde-14009-1) was able to induce protection of piglets against all group A strains tested, i.e. strains of different serotypes (1, 2, 7, 9, and 14). However, it did not induce protection against infection with group B strains (mainly serotype 9 sequence type 16). There appear to be regional differences regarding the IgM protease group distribution. Therefore, clinical isolates from The Netherlands (two studies), Germany, Denmark, Italy, Spain (two studies), Brazil, USA, Canada (two studies), and China were classified by using the genome sequence or by a specific IgM protease typing PCR, and cross-protection was validated by vaccination challenge experiments.

Conclusion

From the observed cross-protection experiments, the vaccine is predicted to passively protect piglets that are born from vaccinated sows, from S. suis infection in more than 90% of the cases and for a period of at least 8 weeks. As opposed to bacterin-based vaccines, the observed cross-protection is serotype independent.

Keywords: Cross protection, passive protection, *Streptococcus suis*, vaccine.

Acknowledgements: The authors thank the Animal Research Department at MSD Animal Health in Boxmeer.

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A NOVEL ORAL *BACILLUS SUBTILIS* SPORE-BASED VACCINE INDUCES HUMORAL IMMUNE RESPONSES AGAINST PORCINE EPIDEMIC DIARRHEA VIRUS IN SOWS AND CONFERS LACTOGENIC IMMUNITY TO THEIR OFFSPRING

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Introduction and Objectives

PEDV burdens the swine industry and food security. Neonatal piglets are highly susceptible to infection with a mortality rate of up to 100%. The cross-protective and lactogenic immunity are major concerns of available vaccines. Humoral immunity responses play a key role in PEDV inhibition. Especially, *Bacillus subtilis* spores exhibit a promising platform to deliver a mucosal vaccine and potentially induce mucosal immunity.

Materials and Methods

The PEDV immunogens (PEDVSME and PEDVCOE) were engineered and expressed on the spore surface of recombinant *B. subtilis* 186. The immunogenic spores were harvested and used as top dressing in pig feed. The study was conducted in a PEDV-free herd status, verified by qPCR, of gestating sows (n = 60). The immunization protocols were categorized into 6 groups: G1-PEDVSME 1 x 10^9 CFUs, G2-PEDVCOE 1 x 10^9 CFUs, G3-Control (PBS), G4-PEDVSME 1 x 10^9 CFUs-probiotics, G5-PEDVSME 5 x 10^7 CFUs-probiotics, and G6-PEDVSME 5 x 10^7 CFUs. They were administered once daily for 7-consecutive-day as a prime-boost regimen, at 10-week gestation (prime) and 13-week-gestation (boost). Serum, colostrum, and milk samples were collected for immunological analysis.

Results and Discussion

The results from ELISA exhibited an increasing tendency of IgA and IgG in sow sera at 3-different-point. Especially, the sera of 16-week-gestation sows G1 showed the highest level of IgG when compared to others and the control. The lactogenic immunity was verified by the existence of IgA and IgG in colostrum/milk. The colostrum/milk samples from the sow G4 declared the highest levels of IgA and IgG in colostrum. Furthermore, the decreasing tendency of IgA and IgG levels in the milk of all groups was sharply declined ($P < 0.05$). Interestingly, the sera of 7-day-old piglets showed the presence of PEDV-specific-IgG from all immunized groups.

Conclusion

The *B. subtilis* spore-based oral vaccine triggers the humoral immunity in sows, resulting in the increasing level of IgG and IgA in serum. The multispecies-probiotics supplement with oral vaccine prototype synergistically affects and exhibits the presence of IgA and IgG in colostrum. Ultimately, the successful transfer of PEDV-specific lactogenic immunity from immunized sows to piglets is noted. These findings support further novel oral vaccine platforms against PEDV.

Keywords: Bacillus subtilis spore, Lactogenic immunity, Mucosal vaccine, Oral immunization, PEDV.

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ORAL PRESENTATION



TOPIC 6: HERD HEALTH MANAGEMENT (HHM)

STUDY TO SEARCH FOR ASSOCIATIONS BETWEEN BIOSECURITY MEASURES AND PRRS STATUS OF SOW HERDS IN THE NETHERLANDS

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) remain a major challenge for swine production in the Netherlands, with herd status influenced by various biosecurity measures. This observational study investigates the association between biosecurity practices and PRRS status in Dutch sow herds.

Materials and Methods

A cross-sectional biosecurity survey was conducted among 19 sow farms using the online biosecurity tool Combat® (100 questions on internal and external biosecurity, transport, management). PRRS status was determined by PCR on pooled samples in a period of 8 weeks around the time of the biosecurity audit. Samples of neonatal piglets were either processing fluids or tongue tip fluids. Samples end of nursery (9W) consisted of oral fluids from 3 pens of piglets and were taken at the beginning and the end of the 8-week period. Farms were categorized into low (Ct < 30.9), medium (31 < Ct < 35), Ct groups. Possible associations were demonstrated using the Pearson correlation coefficient (r) calculated in Microsoft Excel.

Results and Discussion

A strong negative correlation was found between the number of farms within 3 km and the Ct value end of nursery on a farm (r = -0,6488, *P* = 0,0089). For the number of farms within 1 km this correlation was weak and non-significant (r = -0,3920, *P* = 0,1484) Farms with medium to high Ct values tended to be located further from the nearest pig farm (3 - 8 km). A weak negative correlation was found between the length of the quarantine period on the farms and the Ct value end of nursery (r= -0,3934, *P* = 0,1469). Contact between different age groups of piglets occurred in all Ct groups.

Conclusion

The only significant findings suggest that greater physical distance from other pig farms and longer quarantine periods for incoming gilts are associated with higher Ct values end of nursery. However, many biosecurity practices were inconsistently applied across farms. It is unclear whether farms adopt more biosecurity due to recent PRRS outbreaks, or if those without outbreaks reduce measures. In all farms the planned discussion on the results attributed to more awareness and action points were formulated.

Keywords: Biosecurity, Combat, PRRSv.

QUANTIFYING TOTAL BIRTH-TO-MARKET LOSSES PER LITTER UNDER DIFFERENT SOW FARM PRRS STATUS SCENARIOS IN A MIDWEST US COMMERCIAL SWINE PRODUCTION SYSTEM (2022 - 2025)

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Introduction and Objective

Porcine reproductive and respiratory syndrome virus (PRRSV) remain one of the most economically significant pathogens affecting swine production1. However, understanding the total losses attributed to PRRS from birth-to-market, under different herd prevalences, remains a challenge due to the multi-site multi-phase characteristics of modern swine production. This study aimed to address this challenge by measuring total birth-to-market losses per litter by sow farm PRRSV status.

Materials and Methods

Whole-herd production and diagnostic data from an integrated Midwest US system (273,349 sows; 1,682 weaned weekly cohorts; 2022-2025) were analyzed with records linked across production phases and outcomes weighted by the proportion of pigs transferred to each group of pigs. Sow farm PRRS status at weaning was categorized as Unstable 0 - 16 weeks post-outbreak, Unstable ≥ 17 weeks post-outbreak, Stable, or Provisionally negative/Negative. Birth-to-market losses included mummies, stillborn, pre-weaning mortality, nursery and finisher mortalities, and transportation losses. A linear mixed model (Negative Binomial, log-link, farm as random effect, sows farrowed as offset) was used to measure birth-to-market losses per litter, adjusting for PEDV status, season, year, and post-weaning PRRS lateral outbreaks. Additionally, partial budget analysis (PBA) for all pairwise comparisons quantified economic differences in marginal benefits and costs using historical data.

Results and Discussion

PRRSV status was significantly associated with birth-to-market losses ($P < 0.0001$), where Unstable 0 - 16 weeks post-outbreak showed the highest birth-to-market losses at 7.80 pigs/litter farrowed (95% CI: 6.46 - 9.48), followed by Unstable ≥ 17 weeks post-outbreak at 6.36 (95% CI: 5.28 - 7.65), Stable at 4.64 (95% CI: 3.81 - 5.64), and Provisionally Negative/Negative at 3.80 (95% CI: 3.17 - 4.54). PBA valued each pig difference per litter at US$ 112 across all production phases combined. The 4.00 additional pigs lost in Unstable 0 - 16 weeks versus Negative status represented $448 per litter in economic losses, justifying interventions for PRRSV infection prevention and management.

Conclusion

This framework demonstrates the value of sustainable data integration, linking whole-herd production data with disease monitoring classifications to better understand the whole-herd economic impact of diseases under field conditions. This system-specific approach provides system managers with evidence-based data to benchmark against historical performance for quantitatively justifying investments in PRRSV stabilization and elimination efforts.

Keywords: Birth-to-market losses, Evidence-based management, Herd health management, PRRSV monitoring.

LAURIC ACID GLYCERIDE SUPPLEMENTATION IN SOW DIETS IMPROVES PIGLET PERFORMANCE, LITTER UNIFORMITY, AND PASSIVE IMMUNITY

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Introduction and Objectives

Glycerides of lauric acid (GLA) have demonstrated immunomodulatory properties in monogastric species, improving immune responses and resilience against bacterial and viral pathogens. This study aimed to evaluate the impact of GLA supplementation in sow diets on maternal immune transfer, piglet performance, and robustness during lactation and early post-weaning.

Materials and Methods

Forty-five gestating sows were randomly allocated to two groups: a control group (n = 24) and a GLA-supplemented group (at 2 kg/T; n = 21). Groups were strictly balanced for body weight (BW, P = 0.18), parity (P = 0.87), body condition score (P = 0.97), and serum IgG levels (P = 0.51). The trial lasted five weeks, including two weeks pre-farrowing and three weeks of lactation. Sow performance (BW, feed intake, backfat thickness) and piglets' performance (BW and survival at birth and weaning, 21 days of age) were recorded. Colostrum and milk composition were analyzed, and antibody concentrations were quantified in sow and piglet serum. Data were compared using Student's T-test, X^2 test and uniformity was tested using O'Brien's test.

Results and Discussion

Sow zootechnical parameters and litter sizes were unaffected by treatment (18.7 *vs.* 18 live-piglets/sow, P = 0.578). However, GLA supplementation significantly increased the proportion of live-born piglets (89.2% *vs.* 83.1%; P = 0.026) and reduced stillbirths (9.4% *vs.* 15.1%; P = 0.026, n = 21/group). Weaned piglets from supplemented sows exhibited higher BW (+6.2%; P = 0.021), total weight gain (+8.6%; P = 0.016), and average daily gain (+10.1%; P = 0.007, n > 233/group). Litter uniformity significantly improved (CV = 0.35 *vs.* 0.44; P = 0.049). Immunological analysis revealed a numerical increase in colostrum IgG (+ 12%, n = 21/group) and a significant 86% increase in piglet serum IgG at five weeks of age (P < 0.05, n = 12/group), indicating improved passive immunity. No effect of parity or litter size was observed on these parameters.

Conclusion

GLA supplementation during late gestation and lactation improved piglet viability, growth performance, and litter homogeneity, likely through enhanced colostrum quality and maternal immune transfer. These findings support GLA as a nutritional strategy to optimize sow productivity and piglet health during lactation and early post-weaning.

Keywords: Glycerides of lauric acid, Litter homogeneity, Maternity phases, Passive immunity.

MATERNAL HYDROXY-SELENOMETHIONINE SUPPLEMENTATION IMPROVES PERFORMANCE AND IMMUNE COMPETENCE OF SOWS AND PIGLETS UNDER HEAT STRESS

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Introduction and Objectives

Selenium (Se) plays a critical role in antioxidant defense and immune regulation, particularly during gestation and under thermal stress. Inadequate Se status in sows can impair reproductive outcomes and compromise piglet health. Organic Se sources, such as hydroxy-selenomethionine (OH-SeMet), exhibit superior bioavailability compared to seleno-enriched yeast (SeY) and inorganic sodium selenite (NaSe). This study evaluated the effects of maternal OH-SeMet supplementation on performance and immune resilience in sows and their offspring exposed to heat stress.

Materials and Methods

Sixty Landrace × Yorkshire sows of similar parity and body weight were randomly assigned to three dietary treatments (n = 20): basal diet supplemented with 0.3 mg/kg Se as NaSe, SeY, or OH-SeMet. The trial spanned gestation to weaning (day 21) during summer conditions (THI > 75). Sows were vaccinated against PED and TGEV on gestation day 85. Blood samples from sows (gestation day 107, lactation day 14) and piglets (days 14 and 21) were analyzed by ELISA for inflammatory and stress biomarkers (Moya *et al.*, 2007, Martínez-Miró et al., 2016) and PED- and TGEV-antibody titers (Wang et al., 2025). Data were analyzed using one-way ANOVA and Tukey's honestly significant difference (HSD).

Results and Discussion

OH-SeMet significantly improved piglet survival and reduced diarrhea incidence ($P < 0.05$). Litter weight and weight gain were higher compared to NaSe and SeY groups ($P < 0.05$). In sows, OH-SeMet and SeY reduced IL-1β and IL-6 ($P < 0.05$), while OH-SeMet further decreased CRP, haptoglobin, and TNF-α, and increased IL-10 and PED- and TGEV-specific antibody titers ($P < 0.05$). Piglets mirrored these benefits, showing lower IL-6, CRP, cortisol, MAP, and LPS levels with OH-SeMet supplementation. SeY supplementation exhibited intermediate effects.

Conclusion

OH-SeMet supplementation improved immune function and growth performance in sows and piglets under heat stress, highlighting its potential as a superior Se source for swine production systems.

Keywords: Heat stress, hydroxy-selenomethionine, Maternity phases, Passive immunity.

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SURVEILLANCE OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME (PRRS) USING PCR IN VIETNAM, 2014 - 2025

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) cause major economic losses in swine production. This retrospective study aims to analyze porcine reproductive and respiratory syndrome (PRRS) surveillance in Vietnam from 2014 to 2025, utilizing PCR and Realtime-PCR diagnostic submissions. The specific objectives were to assess differences in positivity rates across farm types, pig production groups, and sample categories, as well as to characterize genotype distribution among sequenced isolates.

Materials and Methods

Between 2014 and 2025, samples were collected from sow herds and finishing farms across Vietnam. Specimens included lungs, lymph nodes, pooled tissues, blood, oral fluid (OF), and family oral fluid (FOF), all of which were tested using conventional PCR and Realtime-PCR assays. Analyses were performed at the individual sample level; farm-level classification was not possible due to incomplete identifiers. Sequencing was conducted on a limited subset of samples, and North American (NA) lineage subtyping was not undertaken.

Results and Discussion

Of 2,836 samples analyzed, 594 were PRRS-positive (20.9%). Positivity was significantly lower in sow farms compared with finishing farms (11.0% vs. 40.9%; $P < 0.001$), reflecting increased viral circulation following piglet transfer and highlighting the need for health controls at the sow level. Infection rates differed by pig group ($P < 0.001$): 20.0% in pre-weaning piglets versus 73.3% in post-weaning pigs (4 - 10 weeks), underscoring heightened susceptibility during the nursery phase. Diagnostic tissues (lungs, lymph nodes, pooled tissues) yielded higher detection rates (42.9–58.1%) than screening samples (blood, OF, FOF) (24.6 - 32.6%), supporting lesion-guided sampling while confirming oral fluids as a non-invasive alternative. Genotyping revealed predominance of North American strains (67.0%), followed by highly pathogenic North American (17.0%), European (9.2%), and mixed infections (7.0%). Sequencing was limited, precluding detailed NA lineage subtyping.

Conclusion

PRRSV continues to circulate in both sow and finishing farms in Vietnam, with high detection rates in post-weaning pigs underscoring the need for strengthened nursery health management. Non-invasive samples provide effective tools for surveillance, while tissue specimens remain valuable for diagnostic confirmation. Sustained molecular monitoring and expanded sequencing capacity are essential to support effective PRRSV control strategies.

Keywords: Detection, Non-invasive samples, PRRS, Surveillance, Screening.

Acknowledgements: We would like to express our sincere gratitude to the diagnostic laboratories, Nong Lam University and farm staffs whose efforts made this study possible. We greatly appreciate the technical support provided by the Boehringer Ingelheim Animal Health (BIAH) Vietnam team.

SEASONAL EFFECT ON THE WEANING-TO-ESTRUS INTERVAL IN WINTER: A CASE REPORT FROM A FINNISH FARM

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Introduction and Objectives

Seasonal infertility in sows is often characterized by a decrease in the proportion of animals exhibiting estrus within the expected weaning-to-estrus interval of seven days, typically observed in late summer and early autumn.

Materials and Methods

This case report describes a Finnish farm where this decline started at the end of autumn, with the lowest proportion of sows showing heat during the winter months of January and February in 2024 and 2025 (approximately 18%). However, the proportion improved in March and April (11%), returning to normal levels (around 5%) between May and November. The lighting schedule on the farm is as follows: 13 hours in the gestation unit, 15.5 hours in the farrowing and lactation unit, and 17 hours in the insemination unit. The prevalence of sows not returning into heat after weaning was only observed in sows of second parity or higher.

Results and Discussion

Ultrasound investigation of 20 sows not returning to estrus one week after weaning revealed that approximately 80% had corpora lutea measuring about 10 mm, indicating ovulation one to two weeks prior. The remaining sows had abnormal follicular development leading to anestrus, silent estrus, and a few sows developing follicular cysts. These sows having large corpora lutea returned to heat, on average, 18 days after weaning. This study concludes that 80% of the sows not returning to estrus within seven days, had ovulated during the week before weaning, suggesting a lactational estrus.

Conclusion

This is the first report of a seasonal pattern in lactational estrus with an atypical winter decline in the proportion of sows returning to estrus after weaning. Some publications state that milk production could be reduced if there is less than 16 hours of light in the lactation unit. Although not measured during the investigations, a possible explanation for this could be a reduction in prolactin levels during the darker months, i.e., due to increased levels of melatonin. This increase in melatonin and decrease in prolactin could lead to reduced milk production and therefore a more positive energy balance, facilitating onset of follicular development during the last week of lactation.

Keywords: Lactational estrus, Prolonged weaning-to-estrus interval, Seasonal infertility, Ultrasound, Corpora lutea.

SAMPLE AND POOLING STRATEGIES FOR EARLY DETECTION OF PRRS VIRUS IN BOAR STUDS

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Introduction and Objectives

Epidemiological surveillance in boar studs is essential to prevent porcine reproductive and respiratory syndrome virus (PRRSV) transmission through semen. Serum and blood swab samples are commonly tested by RT-PCR using pools of five samples; however, the effect of larger pool sizes on PRRSV detection sensitivity is not well defined. The objective of this study was to compare PRRSV RT-PCR detection in known positive serum and blood swab samples at different pooling ratios (1:5, 1:10, and 1:15) using different commercial PCR kits.

Materials and Methods

Nine PRRSV-positive serum samples were classified by viral load as high (HVL; Ct < 30), low (LVL; Ct 30 - 34), or suspect viral load (SVL; Ct > 34) and pooled with negative samples at 1:5, 1:10, and 1:15 ratios. Samples were tested using two commercial PCR kits (A and B). Additionally, eleven PRRSV-positive blood swab samples (3 HVL, 3 LVL, and 5 SVL) were diluted according to viral load and tested in triplicate using two commercial PCR kits (A and C). In total, 120 PCR reactions were performed. Results were analyzed using Kruskal-Wallis and Dunn's post hoc tests ($P < 0.05$).

Results and Discussion

All HVL and LVL samples were detected by RT-PCR across all pooling ratios, sample types, and PCR kits. Eight PCR-negative results (Ct > 42) were observed, all originating from SVL samples and occurring at all dilution ratios, with greater frequency at 1:15. No significant differences in mean Ct values were observed between PCR kits for serum samples ($P > 0.05$). In contrast, significant differences were detected between PCR kits and pooling ratios for blood swab samples ($P < 0.05$).

Conclusion

These results indicate that pooling up to 15 samples does not compromise PRRSV detection when viral loads are moderate to high but increases the risk of false-negative results in samples with very low viral loads.

Keywords: Detection, PRRSv, PCR, Pooling, Size.

Acknowledgements: The authors thank the Pig improvement company Mexico for the support with providing testing facilities.

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EFFICIENCY AND COMPLIANCE OF VACCINATION PRACTICES IN BRAZILIAN PIG FARMS BASED ON THE PIGCARE AUDVAC DATABASE (2024-2025)

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Introduction and Objectives

Vaccination in swine production is an essential practice to ensure animal health against various pathogens. Implementation of Good Vaccination Practices is necessary to guarantee maximum process efficiency (Gazmararian et al., 2002; Rose & Andraud, 2017; Yadav et al., 2025). Through an audit program, it is possible to evaluate and monitor the efficiency of the vaccination procedure. Thus, the aim of this study was to analyze the internal database of the PigCare AUDVAC® audit vaccination system to identify critical control points related to the vaccination process.

Materials and Methods

Between January 2024 and December 2025, a database was created from the PigCare AUDVAC® system to evaluate results obtained during this period. Each audit included responses of 19 topics such as: vaccine storage and monitoring, age of vaccination, doses interval, vaccine administration, needle replacement frequency, presence of backflow or bleeding, and use of Personal Protective Equipment (PPE). The compiled data were analyzed as percentages, and graphs were generated using Python code.

Results and Discussion

A total of 591 audits were conducted covering 84 companies (including independent farms, cooperatives, and industries) across nine Brazilian states. The audits yielded an average score of 88.31 (scale 0–100), with a minimum of 31.82 points and a maximum of 100 points. Were evaluated 686,797 animals and non-compliance was observed across the 19 evaluated topics, with notable findings including backflow and bleeding in 30%, reuse of vaccines outside the temperature range (9%), lack of temperature monitoring (27%), animals vaccinated outside the recommended age range in 13,1%, inadequate needle size (21%), needle replacement frequency above recommendations (piglets 1:50 and breeders 1:10) in 23%, absence of PPE use in 26%, and lack of verification of application volume in 24% of audits. A high percentage of farms fail to ensure Good Vaccination Practices, which significantly affects vaccine response. Continuous training and regular audits are essential to mitigate these challenges, which have a significant impact on the sustainability of national swine production.

Conclusion

According to the present study, many critical aspects of vaccination are not regularly followed. The adoption of these measures contributes to improving herd health and productivity in swine production.

Keywords: Animal health, Good Vaccination Practices, PigCare AUDVAC® system, Swine production, Vaccination practices.

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THE 3D CONCEPT: DATA, DIAGNOSTICS AND DECISION A DEEP AND BROAD-SPECTRUM VIEW OF THE PRODUCTION

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Introduction and Objectives

Respiratory diseases are leading causes of economic loss in swine production, reducing growth, efficiency, and carcass value. To address the need for a structured, data-driven approach to quantify and prioritize such losses, we developed the '3D' methodology, which integrates field information, performance, diagnostics, and slaughterhouse outcomes. Although respiratory data were the initial application due to the high impact, the methodology is broadly applicable across health and production challenges, supporting evidence-based decisions that enhance productivity.

Materials and Methods

Between January and July 2024, data from a cooperative in Paraná, Brazil, including 856 flocks (1,036,983 pigs), were analyzed using histology, microbiology, molecular diagnostics, performance, and slaughterhouse losses. Statistical methods included representative sampling, comparisons, correlations, and multivariate analyses. This approach provided a holistic view of herd health, linking it to respiratory disease status, quantifying economic impacts, and guiding strategies for disease control and productivity improvement. The dataset was stratified to isolate the bottom 25% of flocks, enabling clearer assessment of risks and inefficiencies and directing corrective actions toward the most impactful areas, maximizing financial return through targeted decision making.

Results and Discussion

Slaughterhouse respiratory condemnations were used as primary indicator of herd health impact. A wide diversity of pathogens was detected in field and slaughter tissues, with *Mycoplasma hyopneumoniae* predominating and often associated with secondary bacterial agents, reinforcing the multifactorial nature of Porcine Respiratory Disease Complex. The quartile distribution for condemnations due to respiratory problems was 0.62; 1.48; 2.68 and 9.66% of slaughtered animals. Comparing this bottom quartile with the overall population, mortality was 18.5% higher (4.27 vs. 3.6%; $P < 0.001$), resulting in 1,732 more deaths and a loss of R$ 995,946.00. These findings demonstrate the strong link between respiratory disease, productivity, and economic losses, highlighting the value of integrating slaughter data with field diagnostics to identify high-risk groups and their impact.

Conclusion

Accurate identification of factors driving losses is essential for effective and strategic herd management. By integrating data information, the "3D" methodology enables prioritization of areas with greatest impact. Focusing on high-risk groups supports targeted, evidence-based actions that maximize economic return and deliver measurable improvements.

Keywords: Condemnations, Data-driven, Productivity, Respiratory health, Sustainability.

NEONATAL DIARRHOEA PROBLEMS IN ASIA: DIGGING INTO ITS EPIDEMIOLOGY, AGENTS, LOAD, AGE, AND COINFECTIONS

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Introduction and Objectives

Neonatal diarrhoea (ND) is a common polymicrobial process, initiated after birth by primary pathogens such as viruses and/or bacteria that increases in severity once other pathogens frequently present in healthy animals also get involved, causing production losses (Lee et al., 2023). This passive study includes samples from farms around Asia with ND problems, and its objective was to describe the epidemiology of ND.

Materials and Methods

A total of 126 breeding farms and 439 litters distributed from China, South Korea, The Philippines, and Thailand with ND problems between 2024 and 2025, were included in this analysis. Scours from three litters per farm were fixed on FTA-Elute cards using Enterocheck PLUS and analysed by a multiplex qPCR against Rotavirus type A and C (RVA and RVC), Porcine Epidemic Diarrhoea (PED), *Clostridium perfringens* type A and C (CpA, CpC), Enterotoxigenic *Escherichia coli* - F4, F5 and F6 fimbriae, and LT toxin, and *Clostridioides difficile*. Results were classified into 'High' (HL) and 'Mid" loads (ML), except for PED.

Results and Discussion

C. difficile was found in 51% of litters (28% HL), CpA in 97% (65% HL), *E. coli*-fimbriae in 29% (11% HL), *E. coli*-LT Toxoid in 34% (11% HL), RVA in 46% (22% HL), RVC in 18% (10% HL) and PED in 8%. 51% of samples were from litters of 0-8 days of age, and 49% were from 9 to 28 days, with differences observed in both pathogen positivity and load across age groups. Regarding co-infections, 90% of the samples were positive for ≥ 2 agents, and 62% for ≥ 3 agents. Samples from litter >14 days, the number of agents was significantly higher than in younger litters. Overall, sample age, pathogen positivity, and coinfections differed significantly from previously reported results in Europe (Boix et al., 2025). These differences could be explained by differences in the preventive and control tools used between the two continents. In Asia, antibiotic use is higher than in Europe, which may influence the disease dynamics and age distribution.

Conclusion

This data provides useful insights into ND epidemiology in Asia and may support the development of proper preventive and control strategies in the future.

Keywords: Coinfections, bacteria, Neonatal diarrhoea, virus.

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CONTAINMENT OF A PRRSV OUTBREAK IN A BOAR STUD THROUGH RAPID BIOSECURITY AND MANAGEMENT INTERVENTIONS

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Introduction and Objectives

A PRRSv-negative boar stud housing 528 boars in two barns (N1 and N2), detected PRRSv by PCR on April 7, 2024, in the regular monitoring. An emergency protocol was immediately implemented, including sanitary closure, withdrawal and testing of all produced semen doses, and activation of a contingency plan to maintain supply. Subsequent testing confirmed that 11 of 261 boars in barn N2 were PCR positive, while all 267 boars in N1 were negative. The two barns are identical and separated by 10 meters, with negative-pressure ventilation and no filtration. A race against time began to contain the outbreak, preserve genetics, and restart production quickly.

Materials and Methods

The primary goal was to maintain PRRSv-free N1 population to quickly resume production:
Immediate isolation and internal zoning: Communication between barns was blocked; independent flows for staff, tasks, materials, and waste were implemented.
N2 staff entrance was redirected externally with showers.
N2 was completely depopulated April 9 - 12.
Biosecurity after N2 depopulation:
Ventilation in N2 was shut down; N1 ventilation was reduced to minimum.
High-pressure washing was initially avoided to prevent the spread of aerosols. Manual removal of organic matter was carried out, followed by the application of disinfectants in weeks 3 and 5 after depop.
Heat treatment was applied to surfaces in weeks 4 and 5; deep cleaning with water pressure soap and disinfection were in week 6; sanitary downtime began in week 7.

Results and Discussion

Operational Recovery: Semen sales from N1 resumed May 12 after two full-herd blood tests and weekly monitoring (PCR and ELISA) returning all negative. N2 remained inactive until cleaning, disinfection, downtime, sentinel introduction, and repopulation were completed. Failure to properly remove mortality was identified as the most likely cause of virus introduction. Corrective measures included switching carcass disposal to hydrolysis system, installing motion-sensor security cameras, maintaining independent personnel access for both barns, and assigning an on-site veterinarian.

Conclusion

Rapid response and adaptive biosecurity enabled successful biocontainment. Preserving N1 minimizes downtime and genetic supply disruption. In high-density pig regions, contingency protocols are essential for survival.

Keywords: Biocontainment, Boar Study, PRRSv.

QUALITY COLOSTRUM PROFILE AND IMMUNOGLOBULINS TRANSFERENCE IN BRAZILIAN SWINE PRODUCTION

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Introduction and Objectives

Genetic selection in recent decades has increased litter size in hyperprolific sows. This progress, however, brings challenges such as greater litter heterogeneity and limitations in the sow's capacity to provide sufficient, high-quality colostrum. These factors contribute to higher variability at weaning and the development of piglet subpopulations with uneven passive immunity. While the importance of colostrum intake has been well documented, the quality of colostrum receives less attention. To address this gap, the present study provides an overview of colostrum quality in sows from commercial farms in Brazil.

Materials and Methods

A total of 2,533 colostrum samples from 93 commercial Brazilian sow farms were collected up to 3 hours after first piglet delivery in parity order (PO) PO1 (559), PO2 (565), PO3 (507) and PO4+ (902). Immunoglobulin concentration was measured using the %BRIX method with a digital refractometer (MA871, Milwaukee), following Hasan et al. (2016). Each sample was analyzed in triplicate and classified as adequate (%BRIX ≥ 25) or inadequate (%BRIX < 25). A Linear Mixed Model evaluated the effects of Genetics (A-131; B-648; C-566; D-84; E-465; F-639) and PO on BRIX values, with Farm added as a random effect (R Core Team, 2021).

Results and Discussion

The average %BRIX was 25.3 ± 3.8 (range: 2.2 - 40.8). Overall, 54.8% (n = 1,387) of colostrum samples were quality adequate, while 45.2% (n = 1,146) were inadequate, showing low quality. Genetics ($P = 0.006$) and Farm ($P < 0.005$) significantly influenced BRIX values, suggesting the factors affect meaningfully the colostrum quality. Parity showed no overall effect ($P = 0.159$), but PO2 and PO3 had slightly lower BRIX values than PO1 (-0.43, $P = 0.05$ and -0.41, $P = 0.062$, respectively). These results indicate that gilt development programs are effective, yet multiparous sows may be experiencing a decline in colostrum quality, increasing the vulnerability of their offspring in field conditions. This pattern suggests that management practices may be overly focused on primiparous sows, highlighting the need for a more balanced approach in hyperprolific systems.

Conclusion

Assessing colostrum quality is a valuable tool for diagnosing passive immunity transfer in piglets and helps reduce the proportion of animals that remain vulnerable to field conditions.

Keywords: BRIX refractometry, Colostrum quality, Early management, Hyperprolific sows, Passive immunity.

ENHANCING BIOSECURITY IN SWINE OPERATIONS: INVESTIGATING WILDLIFE INTERACTIONS ON MORTALITY MANAGEMENT STRUCTURES OF SWINE FARMS

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Introduction and Objectives

Wildlife activity around swine mortality management structures is often reported, however, the species, frequency and extent to which they interact with these structures are unknown, hindering precise evaluation of how these animals compromise farm biosecurity. There is concern wildlife interacting with mortality management structures (dead boxes or composting bins) may facilitate pathogen spread to surrounding farms and potentially lead to disease spillovers into swine herds (e.g., Influenza A). The objectives are to monitor wildlife visiting dead animal handling structures and characterize the species, frequency and behaviors observed around these structures.

Materials and Methods

Motion-activated cameras were installed near mortality management structures on 30 commercial US swine farms in four different states and set to record videos of 15 seconds when triggered over a 12-month period beginning in December 2025. Here, we summarize preliminary results to Jan 22nd, 2026, containing information from ~900 farm-days, and present findings on the species of wildlife interacting with these structures. The number of videos recorded per camera per day were used to atypical days, defined as those exceeding the $\bar{x}$ + 2 SD. All recordings from typical days were manually reviewed, while 50 random recordings from atypical days were reviewed. Recorded videos were reviewed to identify wildlife species and characterize observed behaviors.

Results and Discussion

Approximately 67,100 videos have been recorded so far, representing roughly 93 hours of footage. Wildlife activity was detected in 0.93% of the recordings. Species identified, listed in order of frequency of detection, include black and turkey vultures, coyotes, domestic animals (dogs and cats), rodents, skunks, cattle, opossums, owls, eagles, and others. Wildlife was more frequently recorded at night and around farms that perform rendering, although visits to composting bins were also documented. Direct interaction and consumption of carcasses by wildlife were observed.

Conclusion

Our findings indicate a diverse set of wildlife species intermittently interact with swine mortality management structures, engaging in behaviors that could facilitate mechanical movement of contaminated material and presenting potential spillover risk. Strengthening biosecurity and designing mortality management systems that restrict wildlife access (enclosed structures, for example) are likely to help limit these risks.

Keywords: Disease spread, Mortality management structures, Wildlife activity, Wildlife behavior.

Acknowledgements: The authors thank the Swine Health Information Center (SHIC) for providing funds for this project.

SHEDDING PATTERNS OF FECAL BACTERIAL AND VIRAL TAXA IN NEWLY INTRODUCED BREEDING GILTS

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Introduction and Objectives

Introducing purchased breeding gilts into pig farms without compromising herd health remains challenging (Garza-Moreno, 2018). Such introductions may affect the composition of fecal microbiota due to environmental changes, stress, and dietary transitions (Patil, 2020). Despite the importance of intestinal health, little is known about shedding patterns of specific bacteria and viruses in the feces during quarantine and early gestation. This study employed a diagnostic metagenomic assay to longitudinally characterize the detection patterns of viral and bacterial taxa in the feces of newly introduced breeding gilts.

Materials and Methods

Two batches of 7-month-old breeding gilts (n = 12 per batch) were purchased and introduced into the quarantine of a commercial farm in Belgium. Fecal samples were collected at four time points: T1 (arrival of gilts in the quarantine unit), T2 (10 days in quarantine), T3 (end of quarantine), and T4 (1 month of gestation). At each time point, samples from three animals were pooled prior to sequencing, yielding four pooled samples per batch per time point. Nanopore sequencing was performed using a diagnostic metagenomic assay, and the presence of specific viral and bacterial taxa was evaluated.

Results and Discussion

Picobirnavirus was detected in all pooled samples across all time points, representing the most consistently identified viral agent. *Treponema* spp. became consistently detectable from T3 onward and remained consistently detected through early gestation. Other viral taxa - including rotavirus, astrovirus, and enteric adenovirus - were detected only sporadically, at low detection frequencies. The range of detectable taxa varied more between pools at T1 than at later time points. Detection profiles became increasingly homogeneous over quarantine, with some agents consistently present and others appearing intermittently or disappearing. No consistent shifts were observed between T3 and T4, indicating stabilization occurred by quarantine end and was maintained after mixing with farm sows. Some batch-to-batch variation was observed, reflecting individual differences in shedding or colonization dynamics.

Conclusion

The consistent and transient detection patterns of bacterial and viral taxa highlight key dynamics during gilt adaptation and provide practical reference data for interpreting routine health monitoring results.

Keywords: Breeding gilts, Fecal shedding, Nanopore sequencing, Quarantine.

Acknowledgements: The authors acknowledge the colleagues from the Faculty of Veterinary Medicine of Ghent University.

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LATE GESTATION PHASE-FEEDING REDUCES GROWTH PLATE DYSPLASIA IN NEONATAL AND WEANED PIGS

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Introduction and Objectives

Osteochondrosis and growth plate dysplasia contribute to lameness, premature culling, and economic loss in commercial swine production systems worldwide. Maternal nutrition during late gestation may influence skeletal programming; however, nutritional strategies to reduce early structural lesions have not been established. This study replicated previous findings1 and evaluated whether late-gestation phase-feeding reduces growth plate dysplasia at birth and weaning under commercial conditions.

Materials and Methods

Sows were assigned during the final 70 days of gestation to either a control diet (CON; 11% CP, 0.52% SID lysine, 1.48 × NRC trace minerals, vitamins ≥ NRC) or a late-gestation phase-fed diet (LG-Phase; 16% CP, 0.87% SID lysine, 2.48 × NRC trace minerals, > 2× NRC vitamins). Growth plates from the 5th - 7th ribs were evaluated histologically by a board-certified pathologist blinded to treatment and scored for lesion severity. Twelve 2-day litters (7 CON, 5 LG-Phase) and fifteen 17-day litters (9 CON, 6 LG-Phase) were assessed. Data analysis was performed in OpenEpi to calculate odds ratios and 95% confidence intervals using the Taylor series method, with litter as the experimental unit.

Results and Discussion

Body weights did not differ between treatments within age groups. Moderate or worse lesions occurred in 57 vs 27% of neonatal pigs and 85 vs 50% of weaned pigs (CON vs LG-Phase). The odds of moderate-or-greater lesions were 3.6 times higher in neonatal CON pigs (OR = 3.6, 95% CI: 0.84 - 15.38) and 5.8 times higher in weaned CON pigs (OR = 5.8, 95% CI: 1.41 - 23.49). Lesions progressed from birth to weaning in control pigs, whereas late-gestation phase-feeding reduced both prevalence and severity. These replicated findings confirm consistency across cohort groups and support maternal nutritional programming as a modulator of early endochondral ossification and skeletal maturation.

Conclusion

Late-gestation phase-feeding significantly reduced growth plate dysplasia at birth and weaning. Maternal nutritional management represents a practical herd-level preventative strategy to enhance structural soundness and potentially reduce early-life skeletal risk in high-prolificacy commercial swine systems globally.

Keywords: Bone, Gestation feeding, Growth plate dysplasia, Herd health, Structural soundness.

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FEASIBILITY AND APPLICATION OF TONGUE TIP SAMPLING FOR INFLUENZA A VIRUS SURVEILLANCE IN PIGS FROM WEANING THROUGH NURSERY PHASE

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Introduction and Objectives

Oral fluid sampling has become a widely adopted method for surveillance of pathogens in commercial pigs, including for influenza A virus (IAV). More recently, tongue tips were evaluated for PRRSV and IAV surveillance as an alternative sample type, demonstrating comparable sensitivity to oral fluids (Osemeke et al., 2025). In this study, we evaluated tongue tip sampling as a tool to aid in the surveillance of IAV in nursery pigs and interpretation of source farm IAV status in pigs at weaning.

Materials and Methods

Three commercial wean-to-finish sites were enrolled at weaning. Tongue tips were excised from pig mortalities and placed into a sterile plastic bag and labeled by date. Samples were stored in an on-site freezer until processing. Oral fluid (n = 6 per 30 pens) and oropharyngeal swab samples (n = 15) from pigs identified as having received individual antibiotic treatment were collected weekly. All samples were processed as previously described (Paploski et al., 2025; Henao-Díaz et al., 2020) and tested for IAV by RT-qPCR. Samples with Ct ≤ 38 were considered positive.

Results and Discussion

IAV was detected in all sample types. Detection in tongue tip samples occurred as early as 1 and 7 days post-placement into the nursery at two sites supplied by a common source sow herd. At a third site sourced from a different sow herd, IAV detection occurred 27 days post-placement. Individual tongue tips frequently yielded lower Ct values than the date-level mean Ct despite co-storage. Mean tongue tip Ct values by date ranged from 22.6 - 36.7, 23.7 - 35.6, and 27.5 - 37.1 at sites A, B, and C, respectively, with lower minimum Ct values observed compared to both oral fluid (28.6 - 35.0) and oropharyngeal swab samples (31.0 - 35.4).

Conclusion

Tongue tip sampling provides a convenient means of determining IAV herd status in nursery pigs. This sample type offers the possibility to characterize the IAV status of pigs at weaning and assess the status of sow herds which would facilitate interventions to control IAV. The ease and inherent frequency of tongue tip sampling compared to other sample types should facilitate improved determination of onset of infection and transmission dynamics.

Keywords: Influenza A virus, Surveillance, Tongue tip sampling.

Acknowledgements: The authors thank the University of Minnesota, Minnesota Agricultural Experiment Station for funding

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ORAL PRESENTATION



TOPIC 7: PIG PRODUCTION AND SUSTAINABILITY (PPS)

INFRARED THERMOGRAPHY: AN ALLY TO EVALUATE PIG GROWTH EFFICIENCY

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Introduction and Objectives

Optimizing feed efficiency is a critical goal in swine production to improve sustainability and to reduce cost. While traditional methods using feed stations provide accurate performance data, they are time- and labor-intensive. Infrared thermography (IRT) offers a non-invasive, real-time method to assess physiological indicators related to growth efficiency. This study evaluated the use of the Thermal Efficiency Index (TEI), calculated as mean surface temperature divided by body weight, as a potential selection criterion for sustainable pig production.

Materials and Methods

A total of 22,579 Duroc pigs from a high-health nucleus herd in Canada were monitored using IRT and traditional feed intake recording equipment. Performance metrics were monitored from approximately 50 to 130 kg body weight. Genetic parameters were estimated using mixed models, and genetic correlations between TEI and performance traits were assessed.

Results and Discussion

TEI showed moderate heritability (0.23 ± 0.04) and strong negative genetic correlations with body weight (-0.82), average daily gain (-0.80), and feed intake (−0.66), suggesting high-performance animals emit less radiant heat. Feed-efficient animals also showed higher TEI values. These findings highlight a trade-off: selecting for lower TEI could increase growth rates but may compromise feed efficiency. Efficiency of correlated response values indicated that TEI could be a practical indirect selection trait, improving key performance indicators by 53 - 74% of direct selection effects.

Conclusions

A near-perfect genetic correlation (0.95) between mid-test and end-test TEI supports its early use in selection programs. Integrating TEI with conventional methods enhances the ability to identify high-performance pigs while supporting welfare and sustainability.

Keywords: Body temperature, Genetic correlation, Residual feed intake, Swine production, Thermal efficiency index.

Acknowledgements: The authors are grateful at the Hendrix Genetics Swine nucleus selection center in Bon Accord (Canada) for their involvement in collecting animal measurements as well as for their expert technical assistance.

EVALUATION OF COLIPROTEC F4/F18 FOR CONTROL OF POST-WEANING DIARRHEA IN AN ANTIBIOTIC-FREE PIG PRODUCTION SYSTEM IN THAILAND

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Introduction and Objectives

Post-weaning diarrhea (PWD) remains a major challenge in antibiotic-free production systems, particularly where enterotoxigenic *Escherichia coli* (ETEC) harboring toxin genes (STaP, STb, LTb) are endemic. Coliprotec® F4/F18, an oral live vaccine targeting F4 and F18 ETEC strains, offers an alternative to antimicrobial interventions and promotes beneficial gut microflora in piglets. This study evaluated vaccine performance under commercial raised-without-antibiotics (RWA) conditions in Thailand, examining fecal consistency, mortality, growth performance, ETEC prevalence, and microbiome composition.

Materials and Methods

The trial was conducted at a 6,000-head RWA commercial farm in Lopburi, Thailand. 600 piglets were distributed across four groups in two barns, with 150 animals per group. Two groups served as non-vaccinated controls, while two groups received Coliprotec® F4/F18 according to label recommendations. Fecal consistency was evaluated using a 0 - 2 scale at days 0, 7, 14, and 28 post-weaning. Body weights were recorded at weaning (day 0, 21 days old) and day 28 from 15 representative pigs per group. Mortality was monitored throughout. Fecal samples collected on days 0 and 28 underwent PCR analysis for ETEC fimbriae (F4, F18) and toxin genes (STaP, STb, LTb). Microbiome characterization was performed via 16S rRNA gene sequencing.

Results and Discussion

Vaccinated groups exhibited consistently lower fecal scores and reduced PWD signs compared to controls. Body weights at weaning and day 28 were significantly higher in Coliprotec® F4/F18-treated pigs ($P < 0.001$ to $P < 0.05$). After removing outliers, average daily gain improved in vaccinated animals (500 vs. 470 g/day, $P = 0.064$). Post-weaning mortality was numerically reduced in treatment groups (3.3% vs. 6.7%). ETEC detection at day 28 showed reduced F4 prevalence in vaccinated pigs. Microbiome analysis revealed enhanced intestinal ecology following vaccination, with the Coliprotec® F4/F18 day-28 group displaying the highest microbial richness and alpha diversity (Shannon index 4.34 - 4.62). Beta diversity analysis confirmed distinct clustering between groups (PERMANOVA $P = 0.00999$). Beneficial taxa including Prevotella spp. were enriched in vaccinated animals.

Conclusion

Under commercial antibiotic-free conditions, Coliprotec® F4/F18 vaccination improved fecal consistency, enhanced growth performance, and supported healthier gut microbiota profiles, demonstrating effective reduction of PWD-associated losses while promoting intestinal resilience in RWA production systems facing endemic ETEC challenges.

Keywords: Antibiotic-free production, Coliprotec, Microbiome, Post-weaning Diarrhea, Swine.
Acknowledgements: This study is supported by Elanco (Thailand).

RELATIONSHIP BETWEEN KETOSIS AND THE BODY CONDITION OF GILTS AT FARROWING AND DURING LACTATION

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Introduction and Objectives

Metabolic challenges during late gestation and early lactation are an increasing concern in modern hyperprolific sows. Among these, subclinical ketosis (SK) has gained relevance due to its association with reduced feed intake, excessive mobilization of body reserves, and impaired metabolic robustness. Recent reports indicate that more than 25% of sows may experience SK (Ros et al., 2024), highlighting its importance as a widespread yet often overlooked disorder. This work investigated objective indicators associated with SK risk and improvement related to Mefreponic acid.

Materials and Methods

A total of 250 gilts were included in this study and allocated to four groups: untreated control (CON; n = 50), treatment with mefepronic acid 24 hours after farrowing (24HAF), one week before farrowing (1WBF), and two weeks before farrowing (2WBF). Body weight was recorded 24 hours before farrowing and at weaning. Backfat thickness (BFT) and loin depth (LD) were measured by ultrasound at treatment, 24 hours after farrowing, and at weaning. β-hydroxybutyrate (BHBA) concentrations were assessed at the same time points using a handheld glucometer. Feed intake was recorded during lactation. Sows with BHBA ≥ 0.01 mmol/L were classified as having SK (Ros et al., 2024).

Results and Discussion

The frequency of SK was 22% in CON, 4% in 24HAF, 3% in 1WBF, and 12% in 2WBF ($P = 0.001$). Sows with ketosis exhibited lower body weight before farrowing and at weaning ($P < 0.001$), reduced BFT at all measurement points ($P < 0.001$), and lower LD throughout the study period ($P < 0.05$). These sows also tended to consume less feed during lactation ($P = 0.057$) and to lose more body weight ($P = 0.051$). Despite their compromised metabolic status, SK sows were not removed from the herd more frequently than non-SK animals. These findings indicate that sows entering lactation with limited fat and muscle reserves are more prone to SK, suggesting impaired metabolic adaptation to lactation.

Conclusion

Objective body condition measurements, particularly BFT and LD, may represent practical and predictive tools for identifying sows at increased risk of SK and supporting targeted herd-level management strategies. In addition, the use of mefepronic acid contributed to a reduction in the frequency of subclinical ketosis.

Keywords: back fat thickness, Fibrate, ketosis, loin depth, mefepronic acid.

Acknowledgements: The authors thank the personnel in Olimaporc farm (JISAPS) for the support during the trial and to Francisco Murciano because of the acquiring of data.

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USE OF FIBRATES IN GILTS WITH ELECTRONIC-AUTOMATIC FEEDING: EFFECT ON METABOLISM

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Introduction and Objectives

Hyperprolific sows experience metabolic overload during gestation and lactation due to their large litters (Cantin et al., 2025). This is especially true in gilts and primiparous sows, as they are still growing. This is sometimes exacerbated by deficiencies in feed (quality and/or quantity). In this study, we investigated the influence of fibrates (Liverfine, Mefepronic acid) on multiparous sows with automatic feeding and increased voluntary intake.

Materials and Methods

A total of 250 gilts were used in this experiment, divided into four groups: untreated control (CON; n = 50), treated with Liverfine 24 hours post-farrowing (24HAF), treated one week before farrowing (1WBF), and treated two weeks before farrowing (2WBF). The sows were weighed at farrowing and weaning. Backfat thickness (BFT) and loin depth (LD) were measured using ultrasound at the time of treatment, at farrowing, and at weaning. Beta-hydroxybutyrate (BHBA) measurements were also taken using a glucometer at the time of treatment, 24 hours after farrowing and at weaning. Feed consumption records were taken during lactation.

Results and Discussion

A significant difference was found in weight loss, with a loss of between 2.5 and 1.9 kg less in the treated groups ($P < 0.001$). A difference was also observed in BFT, with a loss of 0.38 mm in CON and -0.15, 0.03 and -0.05 in the 24HAF, 1WBF and 2WBF groups ($P < 0.003$). A trend towards difference was observed in feed consumption, but it was significant in kg of feed consumed/kg of live weight lost when comparing the CON group with 24HAF ($P = 0.01$) and with 1WBF ($P < 0.001$) and a trend with 2WBF ($P = 0.059$). The frequency of ketosis was 22% in the CON group, 4% in 24HAF, 3% in 1WBF and 12% in 2WBF ($P = 0.001$). The fact that better results were found in the 1WBF group indicates that in the last week of gestation, when metabolic expenditure is highest, the use of fibrates produces greater metabolic improvement by improving hepatic lipid metabolism.

Conclusion

The use of fibrates, administered between 1 week before farrow and 24h after farrow, improves hepatic lipid metabolism. This advantage is maximized when animals can voluntarily increase their feed intake.

Keywords: Back fat thickness, Fibrate, gilt metabolism, loin depth, mefepronic acid.

Acknowledgements: The authors thank the personnel in Olimaporc farm (JISAPS)-for the support during the trial and to Francisco Murciano-for acquiring of data.

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EFFECTS OF IMMUNOLOGICAL CASTRATION ON GROWTH PERFORMANCE CARCASS QUALITY, AND ECONOMIC RETURNS IN FATTENING FEMALE PIGS

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Introduction and Objectives

Immunization against endogenous gonadotropin-releasing factor (GnRF) using Improvac® is an established alternative to physical castration in male pigs. Its application in fattening female pigs has gained interest due to potential improvements in growth performance and economic return without compromising carcass quality. This study evaluated the association between Improvac® administration and production efficiency, carcass traits, and economic return under commercial production conditions in Vietnam.

Materials and Methods

A total of 120 Large White × Landrace female pigs were randomly allocated to three treatment groups (n = 40/group). Each group was housed in a separate pen under standardized commercial management conditions (pen was considered the experiment unit). Treatment included: Control (no Improvac), Improvac 1 mL (two doses of 1 mL, extra-label), and Improvac 2 mL (two doses of 2 mL). Vaccinations were administered subcutaneously at 16 and 20 weeks of age. Individual body weight and pen feed intake were recorded daily until slaughter at 26 weeks. Average daily gain (ADG), average daily feed intake (ADFI), feed conversion ratio (FCR), mortality, carcass traits, and benefit-cost ratio were evaluated. Data are presented as mean ± SD and analyzed using one-way ANOVA ($P < 0.05$).

Results and Discussion

The approved 2mL regimen was associated with significantly higher ADG (0.947 ± 0.096 kg/day) and market weight (123.5 ± 6.5 kg) compared with controls (0.874 ± 0.104 kg/day; 118.3 ± 7.1 kg; $P < 0.05$), while FCR and mortality did not differ among groups. The 1mL-twice regimen showed modest improvement, but lower performance compared with the full dose 2mL regimen. Economic evaluation based on benefit-cost ratio indicated higher returns in the 2 mL group under the observed production and pricing conditions. No significant differences were detected in lean meat percentage, fat percentage, or other carcass traits. The findings are consistent with published meta-analyses reporting improved growth performance in immunized gilts without adverse effects on carcass quality.

Conclusion

Under the conditions of this study, Improvac immunological castration was associated with improved growth performance and economic return in fattening female pigs under commercial conditions without compromising carcass quality. Sub-dosing was associated with reduced economic benefit.

Keywords: Carcass quality, Economic return, Fattening female pigs, Growth performance, Improvac.

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METHIONINE HYDROXY ANALOG BIS-CHELATED COPPER COMPARED WITH TRIBASIC COPPER CHLORIDE IN A REDUCED-COPPER STRATEGY FOR WEAN-TO-FINISH PIGS

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Introduction and Objectives

Copper supplementation above basal requirements is used in swine diets as a growth promoter, typically from inorganic sources at ~150 mg/kg. However, inorganic Cu sources such as tribasic copper chloride (TBCC) increase environmental excretion due to the inclusion rate and level of bioavailability. Methionine hydroxy analogue bis-chelated Cu (MHAC; MINTREX® Cu trace mineral) might have greater relative bioavailability compared with TBCC that may allow for a lower inclusion strategy. This study compared TBCC at 150 mg/kg with reduced level of Cu as MHAC from wean-finish.

Materials and Methods

A total of 360 weaned barrows 7.27 kg of body weight (BW) were assigned to pens to a randomized complete block design with three dietary treatments (8 pens/treatment): A Control: 20 mg/kg inorganic Cu, TBCC: 150 mg/kg Cu, and MHAC: 80 mg/kg Cu during nursery and reduced to 50 mg/kg during grow-finish. Growth performance and mortality were evaluated. Pen as experimental unit and initial BW as blocking factor.

Results and Discussion

At nursery exit, BW was similar for Control, TBCC, and MHAC (28.5, 28.3, and 29.0 kg, respectively; SEM = 0.963; $P = 0.766$). Feed conversion rate (FCR) improved with TBCC vs. Control (1.57 vs. 1.61; $P < 0.050$), and MHAC further improved FCR vs. both Control and TBCC (1.52 vs. 1.61 and 1.57; SEM = 0.012; $P < 0.050$). During the grow-finish phase, FCR was improved with TBCC compared with Control (2.309 vs. 2.370; SEM = 0.013; $P < 0.050$). Pigs fed MHAC had the lowest FCR (2.240), which was improved compared with both Control (2.370; $P < 0.010$) and TBCC (2.309; $P < 0.010$). Final BW was similar for Control, TBCC, and MHAC (109.2, 109.3, and 111.8 kg, respectively; SEM = 2.01; $P = 0.428$). Feed intake tended to be reduced in pigs fed MHAC (1.606 kg/d) compared with Control (1.683 kg/d; $P < 0.100$). FCR improved with TBCC vs. Control (2.15 vs. 2.20; $P < 0.05$), with further improvement in MHAC vs. both TBCC and Control (2.07 vs. 2.15 and 2.20; SEM = 0.019; $P < 0.05$). Mortality did not differ among treatments ($P = 0.824$).

Conclusions

MHAC improved feed efficiency throughout wean-to-finish production while reducing total Cu supplementation compared with TBCC. These results may support reducing Cu strategies without sacrificing Cu supplementation benefits.

Keywords: Copper, Feed conversion, Organic trace minerals, Wean-to-finish pigs.

ASSOCIATIONS AMONG SOWS' BODY MEASUREMENTS IN DIFFERENT ANIMAL POPULATIONS: DATA FROM A CROSS-SECTIONAL STUDY

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Introduction and Objectives

Accurate assessment of sow body condition is essential for improving longevity, reproductive performance, and herd sustainability. On-farm measurements differ in their ability to reflect fat and muscle reserves, and these associations may vary across parities (Maes et al., 2004). This study assessed associations among different body condition measurement methods across parities.

Materials and Methods

50 farms, with body condition assessed in 50 sows per farm across different parities and stages of gestation. Visual body condition scoring (scale 1 - 5; NFACC, 2014) was conducted first to minimize bias, followed by flank circumference (measuring tape placed between the two groin folds), caliper measurement at the last rib, and ultrasound mode B, positioned at P2 position to measure backfat thickness (BF) and loin depth (LD). Associations among measurements were evaluated using Pearson correlation coefficients.

Results and Discussion

Total 544 gilts, 523 parity 2 sows, and 737 older sows (≥ parity 3) were included. In gilts, LD was not significantly associated with BF and, between the parameters analyzed showed its strongest association with visual body condition scoring ($r = 0.43$), with overall lower R^2 values compared with older parities. In parity 2 sows, all body condition measurements were significantly associated, although the correlation between LD and BF was moderate ($r = 0.27$). BF was more strongly associated with flank circumference and caliper, whereas LD was most closely associated with flank measurements. Similar patterns were observed in parity ≥ 3 sows, where all measurements were significantly associated, but the correlation between LD and BF remained moderate ($r = 0.24$). Associations were also similar between different genetics. The consistently low correlations between fat and muscle-related parameters indicate that these represent distinct components of sow body condition, highlighting the added value of including muscle measurements.

Conclusion

Different body condition methods capture different components of sow body condition, but after the first parity, they are moderately to well correlated. Fat and muscle-related measurements provide complementary information, suggesting that reliance on a single method may be insufficient, particularly in younger sows. Incorporating objective measurements and taking the parity into consideration may improve on-farm decision-making and support sustainable sow management.

Keywords: Backfat thickness, Caliper, Loin depth.

Acknowledgements: The authors thank all the technicians who visited the farms and VLAIO for the sponsorship of the project.

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ENVIRONMENTAL PERFORMANCE OF PIG MANURE BIOCONVERSION USING BLACK SOLDIER FLY LARVAE IN SUSTAINABLE PIG PRODUCTION SYSTEMS

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Introduction and Objectives

Pig manure management contributes to ammonia emissions, greenhouse gases, and nutrient losses that affect environmental sustainability. Black Soldier Fly (Hermetia illucens) larvae (BSFL) offer a promising alternative by enabling nutrient recovery while reducing environmental impacts (Mertenat et al., 2019). This study evaluated the environmental performance of pig manure bioconversion by BSFL, focusing on waste reduction, nitrogen stabilization, and potential mitigation of nutrient-related emissions.

Materials and Methods

Fresh pig manure was used as the main substrate under standardized conditions (70% moisture, fixed larval density and feeding rate) in a completely randomized design. Waste reduction index (WRI), biomass yield, and feed conversion ratio (FCR) were measured. Nitrogen in substrate, larvae, and frass was analyzed to assess stabilization, while apparent nitrogen losses were estimated to infer potential ammonia reduction and compare environmental performance with untreated manure.

Results and Discussion

BSFL reduced pig manure mass by 50 - 60%. Nitrogen recovery into larval biomass reached 20 - 25%, while apparent nitrogen losses were reduced by 25 - 35% compared with untreated storage. Waste reduction and nitrogen stabilization were highest at moderate manure inclusion, whereas excessive inclusion increased nitrogen losses due to ammonia buildup. These results highlight the environmental benefits of BSFL in improving nutrient retention and reducing manure-related impacts.

Conclusion

Black Soldier Fly larvae bioconversion improves environmental performance of pig manure management by reducing waste volume, stabilizing nitrogen, and generating valuable insect protein. BSFL technology represents a scalable and sustainable solution to mitigate environmental impacts in modern pig production systems.

Keywords: Black Soldier Fly larvae, environmental performance, pig manure, sustainability, waste reduction.

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ORAL PRESENTATION



TOPIC 8: AIOT IN PIG HEALTH AND PRODUCTION (AIOT)

INTEGRATION OF GENERATIVE ARTIFICIAL INTELLIGENCE IN VETERINARY EDUCATION: EVALUATION OF MICROSOFT COPILOT IN A CROSSOVER STUDY

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Introduction and Objectives

Digital decision-support tools are increasingly relevant for veterinarians managing complex health problems. This study evaluated the use of generative Artificial Intelligence (AI) as a didactic aid in veterinary education, including a focus on structured clinical reasoning for pig herd health cases. Within the AIoT framework, we assessed whether AI-assisted case analysis improves learning outcomes in undergraduate training for future veterinarians.

Materials and Methods

Following a comparative screening of generative AI tools, Microsoft Copilot was selected due to institutional accessibility and compliance with European data protection requirements. A user-oriented 'Cheat Sheet' was developed, providing prompt-engineering guidance (e.g. structuring clinical questions, requesting differential diagnoses, and critical appraisal steps), rather than veterinary medical content. A targeted prompt guided students through systematic case analysis. A randomized crossover study was conducted in the course Leitsymptome at the University of Bern including one session using an authentic pig herd health case with reproductive disorders. Approximately 60 fourth-year veterinary students were randomly assigned to AI-assisted or conventional case-solving, with instructors blinded to group allocation. Learning outcomes were assessed via student questionnaires and blinded lecturer evaluation of oral case presentations.

Results and Discussion

Thirty-eight student responses showed that 68% perceived AI support as helpful for structuring information and identifying diagnostic pathways. However, the overall learning benefit was rated as moderate. Lecturer assessments revealed no statistically significant performance difference between AI-assisted and control groups (P = 0.464). Qualitative feedback indicated improved organization and reflection, but also limitations such as superficial outputs and insufficient contextual depth for complex pig herd problems.

Conclusion

AI can support structured clinical reasoning in various parts, including swine veterinary education, particularly for herd health case analysis, but does not automatically enhance learning outcomes. Effective integration requires didactic framing, critical evaluation skills, and awareness of AI limitations. Future research should compare different AI models and assess long-term effects on competence development also in pig health management.

Keywords: Clinical reasoning, Large language model, Veterinary education.

ESTABLISHMENT OF TEN DETECTION METHODS FOR PIG PATHOGENS BASED ON NANOPORE SEQUENCING

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Introduction and Objectives

Intensive swine production increasingly faces co-circulation of multiple respiratory and enteric pathogens, making singleplex diagnostics time-consuming and incomplete for differential diagnosis. We established a nanopore targeted sequencing workflow combining mPCR enrichment and real-time long-read sequencing to simultaneously detect ten clinically important swine pathogens and evaluated analytical performance and clinical agreement with qPCR.

Materials and Methods

Ten targets were included: *Actinobacillus pleuropneumoniae*, *Mycoplasma hyopneumoniae*, PRRSV-1/2, PCV2/3, PRV, *Lawsonia intracellularis*, *Erysipelothrix rhusiopathiae*, and TGEV. Primers were designed from pathogen-specific genomic regions, screened by BLAST, and verified by singleplex PCR and; amplicons from clinical positives were confirmed by Sanger sequencing. Cross-reactivity was tested against a mixed panel of ten non-target swine pathogens. Multiplex primer concentration was optimized by NTS readout across gradient concentrations. Analytical sensitivity was assessed using serially diluted mixed templates. Clinical evaluation compared NTS and qPCR on field specimens (n = 201). Reads were analyzed in a cloud pipeline, generating structured outputs for AIoT monitoring and decision support. Positivity-rate differences were tested using χ^2 ($P < 0.05$), and agreement was assessed using Cohen's kappa.

Results and Discussion

All primer pairs produced single bands at expected sizes, with no amplification from the non-target pathogen panel. In multiplex optimization, only primer concentrations of 3 μM and 5 μM enabled detection of all ten targets; 5 μM was selected for subsequent experiments. Sensitivity varied by target: several pathogens were consistently detected at 9×10^1 copies/mL, whereas others required 9×10^2 copies/mL; at 5 μL of 9×10^2 copies/mL, all positives were detected across 4/4 replicates. In clinical specimens (n = 201), NTS yielded higher positivity than qPCR for five targets-PRRSV-2 (15.9 vs 11.4%), PCV2 (30.3 vs 24.9%), *L. intracellularis* (12.9 vs 6.5%), PCV3 (67.7 vs 59.7%), and TGEV (7.0 vs 2.5%). Agreement was good-to-excellent, and total coincidence rates ranged from 89.55% to 99.50% across pathogens. In an edge-cloud-client architecture, on-farm NTS devices can act as biosensors and fuse sequencing outputs with IoT streams for cloud analytics and real-time alerts.

Conclusion

Multiplex NTS enables same-day detection of ten swine pathogens with qPCR agreement and extra positives. As a core AIoT module, it delivers actionable insights for real-time monitoring and targeted intervention.

Keywords: Clinical concordance, mPCR, qPCR, Swine pathogens.

DIGITAL BIOSECURITY: ENHANCING INTERNAL BIOSECURITY THROUGH BEHAVIOR-BASED MODIFICATION OF WORKERS' MOVEMENT PATTERNS IN A COMMERCIAL SWINE FARM IMPACTED BY PRRSV

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Introduction and Objectives

Internal biosecurity failures in intensive swine systems are mainly driven by compliance issues. Worker habits, time pressure, and risk normalization often lead to poor protocol adherence and indirect pathogen spread. The hypervirulent PRRS virus serves as an effective model for examining behavior-mediated transmission pathways. This study sought to quantitatively evaluate internal biosecurity risks arising from worker compliance behaviors and to determine whether implementing feedback-driven, behavior-oriented adjustments to movement protocols could mitigate risk.

Materials and Methods

Between April and September 2025, worker movements were systematically monitored on a Spanish commercial farrow-to-finish farm utilizing the Biorisk Internal® digital biosecurity system. The system combines on-farm edge data capture (worker ID, production zones, timestamps via fixed checkpoints) with a cloud-based analytics layer that reconstructs movement networks and runs probabilistic simulations, feeding a web dashboard. A total of 11,447 movements were documented. Directed zone-to-zone networks were developed to detect non-compliant routes and biosecurity amplifiers. Individual worker compliance risk profiles were established, and Markov chain simulations were utilized to assess the effectiveness of targeted, behavior-based interventions.

Results and Discussion

In total, 28.3% of movements were designated as non-compliant (0.136 events per hour), reflecting structurally embedded behavioral risk. Most of the cumulative risk was attributed to fattening-to-fattening movements (50.6%), with additional contributions from fattening-to-gestation (9.7%) and nursery-to-farrowing routes (7.9%). The fattening unit demonstrated a significant amplification effect (PR out = 0.856). Risk distribution among workers exhibited significant heterogeneity, with one individual responsible for 55.1% of the aggregate risk. Instances of non-compliant movements were most frequent during early working hours (05:00 - 11:00 h). Simulation results, displayed as scenario-based dashboards, indicated that focused intervention targeting high-risk routines and individuals effectively diminished transmission rates.

Conclusion

Internal biosecurity risks are localized within specific routines, zones, and personnel. A layered digital architecture integrating on-farm data capture, cloud analytics, and dashboard visualization enables both real-time alerts on non-compliant movements and retrospective review of cumulative risk patterns, predictive and behaviour-oriented decision-making. Digital monitoring and tailored feedback convert compliance into quantifiable and actionable behavioral outcomes, offering a scalable solution for AIoT-based internal biosecurity management in pig production.

Keywords: Digital biosecurity, Movements, PRRS, Workers.

DIGITAL BIOSECURITY MOBILITY-BASED FACILITATES THE DETECTION OF SUPERSPREADER CENTERS AND AGENTS USING REAL-TIME NETWORK ANALYSIS

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Introduction and Objectives
Indirect transmission of pathogens such as Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), Porcine Epidemic Diarrhoea Virus (PEDV), and African Swine Fever Virus (ASFV) remains a major constraint in pig production systems. Conventional biosecurity audits often fail to capture real-world mobility patterns of people and vehicles that drive cross-farm sanitary risk. This study aimed to: (1) characterize movements of people and vehicles among farms and sites; (2) identify operational super-spreaders of disease; and (3) support prioritization of biosecurity measures and targeted training strategies.
Materials and Methods
Visitors and vehicle logs (including live animals, feed, and semen deliveries) were obtained from the Biorisk External® system. Movements were captured automatically via GPS/geolocation of authorized vehicles or through manual QR-code check-ins, generating a standardized digital logbook. Data was processed in R to reconstruct directed networks between centers using company downtime and C&D rules. Edges were weighted using network analysis incorporating frequency and directionality. Network metrics (degree, strength, betweenness, and out-strength) were integrated into two indicators: EPI score (centers) and EPI index (agents). Super-spreaders were defined as actors within the $\geq 90^{th}$ percentile of combined metrics. Sensitivity analyses assessed model stability with respect to parameters β (transmission rate), λ (case-resolution rate), and μ (node exit rate through removal or inactivation).
Results and Discussion
The dataset comprised 34,699 movements among 211 centers. Vehicles exhibited the highest epidemiological impact, particularly feed and maintenance vehicles. Several workers showed EPI_index values above 0.8, acting as connectors across farm types. Feed mills and washing stations emerged as dominant hubs driving sanitary-risk flow.
Conclusion
A limited subset of vehicles, workers, and centers accounted for most indirect transmission potential. The proposed solution combines edge data-capture (GPS and QR events) with a cloud-based processing layer and a web dashboard for farm-level visualization, enabling near-real-time operation in settings with continuous or frequent connectivity and intermittent synchronization in regions with less mature technical infrastructure. This enables the identification of operational super-spreaders not detected by traditional audits, reduces the indirect spread of diseases, and provides a scalable implementation-agnostic framework to strengthen biosecurity in pig production systems with heterogeneous digital readiness.

Keywords: Digital biosecurity, Network analysis, Real-time, Superspreaders.

DEPLOYMENT OF AUTOMATED SYSTEM FOR LUNG LESIONS AND PLEURITIS EVALUATION

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Introduction and Objective

The modernization of the pork industry requires objective, scalable technologies to replace subjective and labor-intensive inspection methods and enable a more integrated data ecosystem. This study describes the development and deployment of a fully automated image-analysis system in a high-throughput pig slaughterhouse in Spain. The primary objective was to apply machine learning for real-time, standardized pathological assessment at slaughter, with the long-term goal of linking slaughterhouse findings to farm-level production data.

Materials and Methods

The system was developed using a large data set comprising 485,687 images collected over seven months, representing 4,344 production batches. The machine learning model was trained on several thousand lungs per lesion severity grade to automate pathological assessment. Pulmonary lesions were quantified using an ordinal severity scale ranging from 0 (no lesions) to 5 (maximum severity), and pleuritis was recorded as a binary variable (presence/absence), regardless of the extent of the affected pleural surface. Model performance was evaluated on an independent validation set of approximately 700 lungs, annotated by expert assessors. Following validation, the model was deployed on a cloud-based platform that automated the workflow, including image acquisition, batch-level prediction, and integration with slaughterhouse telemetry data. Accuracy metrics were analyzed using mixed-effects models in JMP® 18.2.1, accounting for batch-level variability.

Results and Discussion

The automated system achieved an overall accuracy of 88.1% for classifying the presence or absence of pathological lesions on the validation set. Additionally, the system enabled continuous, real-time assessment without line stoppages, providing a standardized and observer-independent alternative to conventional visual inspection. The integration of slaughterhouse pathology data with farm-level production information, stratified by animal origin and production system, created a feedback loop allowing the exploration of associations between farm-side factors and slaughter outcomes.

Conclusions

This fully automated image-analysis system provides a rapid, standardized, and quantitatively robust approach to pathological assessment in swine slaughterhouses. By reducing subjectivity and transforming visual inspection into high-throughput structured data, the system supports improved process control, targeted interventions, and data-driven improvements in farm management and herd health. Overall, it contributes to a more transparent, integrated, and efficient pork production chain.

Keywords: Automated model, Lung scoring, Machine learning, Performance.

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HARNESSING MACHINE LEARNING TO IDENTIFY PREDICTORS OF PIGLET SURVIVAL IN COMMERCIAL BREEDING HERDS

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Introduction and Objectives

Early piglet mortality remains a major source of biological and economic loss in commercial swine production systems (Salgado-López et al.,2025; Björkman et al., 2022). Neonatal mortality arises from complex, non-linear interactions among piglets, sows, litter, and farrowing-related factors. Machine learning (ML) methods can accommodate these interactions to identify high-risk piglets and actionable predictors of early survival. Therefore, this study aimed to identify predictors of piglet survival within five days post-farrowing using comprehensive ML approaches in a commercial breeding herd.

Materials and Methods

Data were obtained from three commercial sow farms in Brazil between 2021 - 2023 and included 5,008 piglets born to 685 sows, with 27 predictors. Early piglet survival (5 days post-farrowing) was modeled as a binary outcome. The dataset was split into 80% for training and 20% for testing with three repeats of 10 - fold cross-validation. Class imbalance was addressed using data-level techniques (random up-/down-sampling, ROSE, and SMOTE) and algorithm-level strategies, including cost-sensitive elastic net regression, scaled XGBoost, and balanced random forest approaches. Model performance was evaluated using accuracy, recall, and F1-score. Model interpretability was achieved using variable importance, partial dependence plots, and Shapley Additive Explanations (SHAP).

Results and Discussion

Balanced random forest and scaled XGBoost models outperformed traditional classifiers, achieving 82% accuracy, 83.2% recall, and F1 Score of 89.7%. Across models, birth weight, average daily gain (ADG) at 24 hours, colostrum intake, postnatal temperature (24 h), and farrowing duration consistently emerged as key predictors. Survival plateaued after 380 minutes of farrowing; ADG was protective at 250 g/day. SHAP analysis revealed nonlinear associations between piglet colostrum intake and ADG at 24 hours on survival, underscoring the critical importance of adequate colostrum transfer and early growth dynamics. Early mortality was concentrated among low-birth-weight piglets, further amplified by thermal stress and poor colostrum intake.

Conclusion

ML models identified predictors of piglet survival, including birth weight, 24h average daily weight gain, and colostrum intake. These predictors enable identification of high-risk piglets and can be integrated into farm operational systems to support risk- stratification and prioritization of neonatal interventions, such as split suckling, supplemental colostrum, and strategic cross-fostering, thereby improving pre-weaning survival in commercial herds.

Keywords: Class imbalance, Early piglet mortality, Machine learning, Precision swine management.

Acknowledgements: The authors thank the Federal University of Rio Grande do Sul, Brazil, and the collaborating production systems for their support in providing access to the data.

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ORAL PRESENTATION



TOPIC 9: NUTRITION AND GUT MICROBIOTA (NGM)

A NOVEL DIETARY DAIRY BIOACTIVE (FXP™) ENHANCES POST-WEANING ENTERIC HEALTH IN NURSERY PIGS

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Introduction and Objectives

Post-weaning pigs experience multifactorial stressors that disrupt gastrointestinal health, predisposing them to enteric pathogens, which exacerbate diarrhea and lead to morbidity and mortality. A novel dairy-derived bioactive (FXP™) enriched with colostrum-associated compounds, particularly IgA, exhibits broad-spectrum gut health and antipathogenic activity at low dietary inclusions, offering partial mitigation of post-weaning enteric health challenges in nursery pigs. Our study objectives were to demonstrate growth and gut health efficacy in nursery pigs supplemented with FXP™ and to show antipathogenic effects against several common enteric viral and bacterial pathogens in vitro using porcine epithelial cell models.

Materials and Methods

An in vivo study evaluated dietary FXP™ (0.50%) in nursery pigs (10 replicate pens with 4 pigs/pen) for 21 days post-weaning. Enteric stress was induced by 24-hour feed/water deprivation on day 3. Growth performance, diarrhea scores, and ileal histology were measured. Four in vitro experiments tested FXP™ against Rotavirus (RV, serotype A), Enterotoxigenic Escherichia coli (ETEC F4/F18), Salmonella species, and Streptococcus suis using porcine epithelial cells. Treatments included control, pathogen only, and pathogen + 0.50% FXP™. Cytotoxicity (LDH), barrier integrity (TEER/FITC-dextran), and pathogen-specific infectivity mechanisms were measured to determine FXP™ antipathogenic effects.

Results and Discussion

Dietary supplementation of FXP™ improved cumulative ADG ($P \leq 0.05$), reduced diarrhea scores ($P = 0.04$), and increased the ileal villus height to crypt depth ratio ($P = 0.03$). In vitro, co-incubation with FXP™ reduced RV infectivity ($P < 0.01$), tended to decrease ETEC F4 and F18 adhesion ($P < 0.10$), lowered Salmonella species adhesion and invasion ($P < 0.05$), and reduced Streptococcus suis adhesion and translocation ($P \leq 0.02$). Furthermore, co-incubation of 0.50% FXP™ with porcine pathogens tended to partially improve intestinal barrier integrity ($P \leq 0.10$). These results show broad-spectrum antipathogenic benefits to FXP™ against key nursery pig enteric pathogens in-vitro along with improved performance and gastrointestinal health in nursery pigs.

Conclusion

FXP™ supplementation improved growth performance, reduced diarrhea, and enhanced intestinal morphology in nursery pigs under enteric stress. In vitro, FXP™ demonstrated broad-spectrum antipathogenic activity and partially preserved epithelial barrier integrity, highlighting its potential as a novel nutritional strategy to support gut health and resilience against post-weaning enteric challenges.

Keywords: Colostrum, Enteric pathogens, Gastrointestinal health, Nursery pig.

MILK FAT GLOBULE MEMBRANE (MFGM) IMPROVES PERFORMANCE OF PIGLETS DURING THE WEANING PHASE

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Introduction and Objectives

Scientific research in infant nutrition indicates that MFGM has the potential to benefit the brain gut axis through better cognitive development, reduced infection risks (respiratory tract infections and diarrhea), and shaping the gut microbiome activity and function. MFGM is a natural bioactive component of cow's milk. In neonatal piglets, orally administrating MFGM during the first postnatal week stimulated short-chain-fatty-acid producing bacteria colonization, enhanced intestinal barrier functions, and consequently improved the growth performance on 21 d (Wu et al., 2020). The hypothesis is that supplementation of these natural bioactive milk molecules in piglet feed at weaning improves post-weaning performance.

Materials and Methods

In total 1008, 24d old piglets (Danbred x Pietrain) were divided on sex and body weight (BW, 5.43 ± 0.6kg) over three treatments, in a 6-week post-weaning piglet trial. Each treatment contained 14 replicates with 24 piglets per pen. Piglets had free access to weaner diet (d0 - 14), starter 1 diet (d15 - 28) and starter 2 diet (d29 - 42). In the control treatment, diets were not supplemented with MFGM. In treatment 2, the weaner diet was supplemented with MFGM containing supplement (2kg/T). In treatment 3, MFGM supplement (2kg/T) was added to the weaner and starter 1 diet. BW was determined per pen on day 0, 14, 28 and 42. Feed intake (FI) was measured per diet phase to calculate FCR. Medication, morbidity, and mortality were recorded daily. SAS proc mixed was used to analyze performance data and PROC GENMOD was used to analyze medication, mortality, and morbidity data.

Results and Discussion

MFGM supplementation in treatments 2 and 3 resulted in a significant increase in final BW (d42) with 0.67 and 0.56 kg, respectively, resulting in an increased ($P < 0.05$) ADG. FI increased by 22 ($P < 0.05$) and 10 g/d, respectively. FCR was improved by 0.005 and 0.03 ($P < 0.10$) g/g, respectively. Individual medications tended to decrease linearly with increased duration of MFGM supplementation with 12.5 and 27.0% ($P < 0.10$), respectively. No differences in morbidity or mortality were found.

Conclusion

MFGM supplementation during the first 2 to 4 weeks after weaning improved piglet performance and decreased individual medications till the end of nursery.

Keywords: Milk Fat Globule Membranes, Nursery medication, Nursery performance, Piglet.

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EFFECTS OF NATURAL 1,25-DIHYDROXY VITAMIN D3 GLYCOSIDES ON INFLAMMATION AND REPRODUCTIVE EFFICIENCY IN SOWS

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Introduction and Objectives

Farrowing and lactation represent physiologically demanding periods for sows, marked by substantial metabolic adaptations and markedly increased requirements for energy and key nutrients such as calcium, phosphorus, and vitamin D_3 (Becker et al., 2024). Therefore, active forms of vitamin D_3 may play an important role. The present study evaluated the hypothesis that dietary supplementation with 1,25-dihydroxyvitamin D_3 glycosides (1,25-$(OH)_2$-D_3) enhances sow performance and litter outcomes during farrowing and early lactation.

Materials and Methods

At approximately 5 days before their due date, 24 mixed parities (one animal per group primiparous, 7 animals per group multiparous) were assigned equally by parity to three treatment groups. Control was fed a basal diet (the standard diet of lactating sow) containing vitamin D_3 at 1,800 IU/kg of feed. The basal diet was then supplemented with either 100 g/t (T1) and 150 g/t (T2) natural 1,25-$(OH)_2$-D3 (The natural 1,25-$(OH)_2$-D_3 product was applied in the study in a diluted premix form; however, the supplementation levels reported in this abstract refer to the equivalent active ingredient concentrations). Parameters evaluated included farrowing and litter performance, including individual piglet weights at birth, after cross-fostering and at weaning. Serum interleukin-1 beta, IL-1β, calcium metabolism (parathyroid hormone [PTH] and calcium level).

Results and Discussion

Supplementation with 1,25-$(OH)_2$-D_3 reduced farrowing duration and pre-weaning piglet mortality compared with the control group ($P < 0.05$). These improvements led to higher piglet average daily gain and body weight at weaning ($P < 0.05$). Sow supplementation 1,25-$(OH)_2$-D_3 showed lower IL-1β concentrations at farrowing and at the end of lactation ($P < 0.05$). Parathyroid hormone levels at the end of lactation were also significantly reduced ($P < 0.01$), indicating improved calcium homeostasis. Enhanced calcium availability may support myometrial contraction, contributing to improved farrowing performance.

Conclusion

A natural source of 1,25-$(OH)_2$-D3 could improve farrowing performance and calcium metabolism (represented by lower PTH excretion). In our study, 100 g/t natural 1,25-(OH)2-D3 in the feed was the most cost-effective dose.

Keywords: Natural 1,25-dihydroxyvitamin D_3, inflammation, farrowing time, sow's productivity.

Acknowledgements: The authors thank the Universitat degli Studi di Milano, Italy for the support in providing testing facilities.

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ETIOLOGICAL INVESTIGATION OF MELANOSIS COLI IN SLAUGHTER PIGS

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Introduction and Objectives

Melanosis coli, a well-documented human condition marked by brown/black colonic mucosal pigmentation, is linked to chronic anthraquinone laxative use. These anthraquinone purgatives cause colonic epithelial cells apoptosis and deposition of brown pigments on the colonic membrane. (Yang et al., 2020; Jian et al., 2011). Since November 2023, melanosis coli has occurred regularly in fattening pigs at a northern China slaughterhouse, despite sharing identical genetics, feed formulations, and pen facilities. Some batches even reached 35%, prompting this etiological study.

Materials and Methods

In January 2024, colon samples from fattening pigs with melanosis coli, including one normal (No. 1) and three blackened (No. 2 - 4) specimens from the same slaughter batch were collected. Pathological examination and atomic absorption spectrometry were performed to assess tissue pathology and copper/iron content.

Results and Discussion

Sample 1 (normal colon) showed intact mucosal epithelium, sparse lamina propria inflammation, clear submucosal adipose structure, and unaffected intestinal glands. Samples 2 - 4 displayed mucosal epithelial necrosis/shedding and increased lamina propria inflammation. Samples 3 and 4 exhibited enhanced glandular secretion. Sample 4 showed suspected brown granular deposits in lamina propria macrophage cytoplasm. Copper-specific staining revealed yellowish-green granules in the cytoplasm of lesioned mucosal epithelial cells and macrophages, with scattered granules also noted. Copper and iron ion analysis showed iron was undetectable in both samples. Copper measured 5.76 mg/kg in the normal colon (No. 1) and 12.5 mg/kg in the melanosis coli sample (No. 4).

Conclusion

Melanosis coli was rare in swine. Prior studies linked it to low vitamin E levels, oxidative damage, high-sulfate drinking water, or dietary inert pigment accumulation (Wilberts *et al*., 2015; Rodríguez *et al*., 2021). This study showed black colon exhibited mucosal epithelial necrosis and abnormal copper deposition. These findings suggest a potential association between copper accumulation and melanosis coli that warrants further investigation to elucidate causal relationships. Enhanced glandular secretion observed in samples 3 and 4 may be associated with abnormal copper deposition, which requires further examination. Potential factors that may lead to abnormal copper deposition, such as water quality, additives, stress, and pathogens, should be investigated to identify the true etiology.

Keywords: Colon, Copper, Melanosis Coli, Investigate.

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BLACK INTESTINE IN FINISHER PIGS: INSIGHTS FROM GUT MICROBIOME PROFILING AND HISTOPATHOLOGY

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Introduction and Objectives

In several Thai finishing farms, slaughterhouses have reported pigs showing black discoloration of the colon, resulting in carcass price deductions and reduced buyer confidence. Despite its economic relevance, scientific information on this condition is scarce. This study aimed to characterize the gut microbiome and intestinal histopathology of pigs exhibiting black intestine compared with pigs with normal colons, and to identify microbial or structural factors associated with this condition to support farm-level corrective strategies.

Materials and Methods

Samples were collected from a slaughterhouse receiving pigs from one farm with recurrent black-intestine cases. Colon contents were collected from normal pigs (Normal group, n = 8) and pigs with black intestine (Black group, n = 8). Contents were placed on ice, subjected to DNA extraction, and analyzed by 16S rRNA V3–V4 sequencing using the Illumina platform. Intestinal segments showing discoloration were fixed in 10% neutral buffered formalin, sectioned, and stained with hematoxylin and eosin for histopathology.

Results and Discussion

Histopathology revealed reduced goblet cell numbers and crypt narrowing in the crypts of Lieberkühn, accompanied by luminal accumulation of cellular debris, with similar lesions observed in both groups. Microbiome profiling identified 14 phyla. The phylum *Campylobacterota* was significantly enriched in the Black group ($P < 0.001$). At the genus level, *Campylobacter*, *Enterococcus*, and *Lawsonia* were significantly more abundant in the Black group than in the Normal group ($P < 0.001$).

Conclusion

Although black discoloration suggests a severe condition, histopathology revealed comparable structural changes in both groups. In contrast, gut microbiome analysis demonstrated clear dysbiosis in pigs with black intestine, characterized by increased abundance of pathogenic or inflammation-associated genera. These findings suggest that microbial imbalance, rather than distinct tissue pathology, may underlie this condition. Enhancing farm hygiene, pathogen control, and nutritional strategies to support gut health may help reduce the incidence of black intestine and the associated economic losses.

Keywords: Black intestine, Dysbiosis, Finisher pigs, Gut microbiome, Histopathology.

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EFFECT OF DIFFERENT INCLUSION LEVELS OF A COMMERCIAL PRODUCT IN POST-WEANING DIETS ON THE PRODUCTIVE PERFORMANCE AND THE INFLAMMATORY AND OXIDATIVE STATUS OF NURSERY PIGLETS

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Introduction and Objectives

Weaning is a critical moment for piglets, which face numerous stressful changes that can lead to a transient but long-lasting immune stimulation (De Groot et al., 2021), resulting in a loss of intestinal integrity (Ramis et al., 2023). The objective of this study was to evaluate the changes in different biomarkers related to inflammation, immune stimulation, and intestinal integrity related to the use of different concentrations of a nano-encapsulated fitogenic blend in feed as previously described.

Materials and Methods

Seven hundred and two healthy weaned piglets, were individually weighed and allocated to three experimental treatments (18 replicates; 234 animals each): control group (CON) receiving a basal diet, Group lower dose (DI-L) receiving basal+1.25 kg/tonne of the additive and Group Higher dose (DI-H) receiving basal diet+2.50 kg /tonne of the additive. From each pen, one average piglet was selected for faecal sampling on days 4th, 17th and 40th. The gene expression was performed on fecal samples for: Calprotectin (CALP), Occludin (OCDL), Zonulin (ZON), IFNγ and TGFβ (Ramis et al., 2023).

Results and Discussion

At 40 days after weaning, significant differences in CALP were observed between CON and the DI-L experimental group (5 folds lower; $P = 0.025$), this group showed a significant reduction in CALP compared to the control group. In terms of OCDL, 17 days post-weaning, significant differences were observed between the CON and DI-L (6 folds lower; $P = 0.012$), with the DI-L obtaining better results for OCDL quantity. Likewise, it was demonstrated that there are no significant differences but a trend to significance ($P = 0.067$) between DI-H and DI-L indicating that at a higher concentration of product, piglets will show a greater amount of OCDL. However, although numerically higher levels of IFNγ were obtained in the experimental group, no significant differences were found between CON and DI-L ($P = 0.101$).

Conclusion

The results suggested that a low concentration of fitogenic blend produced CALP reduction, OCDL gene expression increasing and non-significant increase of ARNm for IFNγ. All together suggests a lower inflammation and better intestinal integrity after weaning, and highlights the relation between the immune system, inflammation, and intestinal integrity.

Keywords: Calprotectin, IFN-gamma, Intestinal integrity, Occludin, Vegetal extract.

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EFFECT OF DIETARY ANTIOXIDANT SUPPLEMENTATION WITH A NATURAL SOURCE OF SUPEROXIDE DISMUTASE ON OXIDATIVE STRESS BIOMARKERS AND PERFORMANCE IN POST-WEANING PIGLETS UNDER HEAT STRESS CHALLENGE

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Introduction and Objectives

Oxidative stress during the post-weaning period compromises piglet health and growth, particularly under challenging conditions such as heat stress (Barbé et al, 2015). This study aimed to evaluate the effects of supplementing post-weaning piglet diets with a natural source of primary antioxidant enzymes (Lallès et al., 2011), on physiological and productive responses under heat-induced oxidative stress.

Materials and Methods

A 28-day trial was conducted at AB Neo's Centre of Excellence in Aragón, Spain, using 1,152 piglets (24 days old) allocated into 48 pens (24 piglets/pen) in a closed facility. After a 1-day adaptation, piglets were assigned to 2 treatments and randomly allocated to the different treatment diets, considering equal distribution of sex and weight category between treatments: Control: Standard feed, Average Initial Weight (AIW), 6.49 kg/piglet. Treatment: Standard feed supplemented with MELOFEED (20 g/tn during phase 1 (days 1 - 14) and 10 g/tn during phase 2 (days 14 - 28)). AIW: 6.53 kg/piglet. Oxidative stress was induced by cyclic heat challenge (temperature rose to 37ºC for 8 h. on two consecutive days during days 7 - 8 and 21 - 22). Blood samples collected on days 9 and 23 were analyzed for oxidative biomarkers (Total Antioxidant Capacity (TAC), Total Oxidative Status (TOS), Haptoglobin and Hemolysis score). Growth performance (Body weight, Average Daily Gain) was recorded at days 14 and 28 after weaning.

Results and Discussion

Dried melon juice supplementation improved antioxidant status, evidenced by reduced Total Oxidative Status ($P < 0.01$), higher TAC/TOS ratio ($P < 0.1$), lower Haptoglobin levels ($P < 0.05$) and better hemolysis score distribution compared to the control. Piglets receiving dried melon juice exhibited higher ADG ($P < 0.05$) and higher weight 28 days after weaning (13,44 vs. 13,92 kg, $P < 0.05$), suggesting enhanced resilience under heat-induced oxidative stress. These findings indicate that dietary primary antioxidants can mitigate oxidative damage and support physiological adaptation during critical production phases.

Conclusion

MELOFEED effectively reduced oxidative stress and improved growth performance in post-weaning piglets exposed to heat challenge as an example of oxidative stress. Incorporating primary antioxidants into diets represents a practical strategy to enhance animal welfare and productivity under stress conditions.

Keywords: Haptoglobin, Heat Stress, Melofeed, Superoxide Dismutase (SOD), Total Oxidative Status (TOS).

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EFFECT OF BACILLUS SUBTILIS DSM 29784 SUPPLEMENTATION ON POST-WEANING PIGLETS RAISED UNDER NATURAL *ESCHERICHIA COLI* PRESSURE

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Introduction and Objectives

Weaning is a critical phase in pig production, increasing susceptibility to enteric pathogens like *Escherichia coli*. Probiotics like Bacillus subtilis DSM29784 (Bs) may support gut resilience by modulating microbiota and reducing pathogen colonization. This study evaluates Bs impact on *E. coli* and gut microbial composition in weaned pigs.

Materials and Methods

The antimicrobial potential of Bs against *E. coli* strains was evaluated in vitro using a zone-inhibition test. The in vivo efficacy was assessed on a farm endemically infected with *E. coli* confirmed by qPCR. 192 piglets, randomly allocated to 3 x 8 pens of 8 piglets weaned at 21 days were assigned to three diets: Negative control (NC: no AB, ZnO 150ppm), Positive control (PC: AB: Halquinol D0 - 14, Bacitracin D15 - 39, ZnO 2,575 ppm), and Bs (NC + Bs: 10^8 cfu/kg). Growth and fecal scores were recorded. Fecal samples were taken on days 1, 7, 14, 28 and 39 for ETEC F4 and F18 loads by qPCR and for microbiota analysis using 16S rRNA gene sequencing. Data was analyzed using ANOVA.

Results and Discussion

The in vitro assay showed Bs exhibiting larger zone-inhibition against ETEC (15.74 mm) and EPEC (23.76mm) compared to an industrial benchmark, 13.58mm and 16.23mm, confirming its strong antimicrobial potential. In vivo, fecal scores remained similar across treatments (D14 NC 3.25; PC 3.25 and BS 3.38 (P = 0.96)). During the trial period, ADG of PC (465 g/d) was higher than NC (415 g/d) (P = 0.04) but not significantly different from BS (443 g/d), while from day 29 to 39 in the nursery period, the BS supplemented piglets showed higher ADG (772 g/d) than NC (697 g/d) (P = 0.04). ETEC F18 was absent in Bs pigs from day 1 to 28, whereas it persisted in NC and PC groups, while F4 load was not different across the groups. Butyrate producers like Ruminococcaceae and Lachnospiraceae evolved similarly across groups, but BS showed the highest presence at the study end. Bifidobacteriaceae remained consistently higher in BS versus NC and PC, with significant differences at D28 (P = 0.045).

Conclusion

The current study showed the potential of Bs to support in control of *E. coli*, by inducing healthier gut conditions and improved productivity in piglets.

Keywords: Gut Health, Post-weaning, Probiotic.

POSTBIOTICS AND PHYTOGENICS REDUCED DIARRHEA BY ENHANCING INTESTINAL BARRIER AND MODULATING IMMUNE PROFILE WHEN INCORPORATED FROM WEANED DIETS

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Introduction and Objectives

Early weaning and diet transition impair piglet gut integrity and immunity, increasing diarrhea risk and reducing growth (Smith et al., 2010; Yin et al., 2014). With antibiotics and ZnO restrictions, we assessed how postbiotics and phytogenics may improve performance, intestinal health, and immune function in weaned piglets.

Materials and Methods

A total of 192 piglets (25 days old; 6.0 kg) were assigned to four treatments (20 pens/treatment): a negative control (NC; basal diet without ZnO), a positive control (PC; basal diet with ZnO), a postbiotic additive (2 kg/T from day 0 - 14, then 1 kg/T), or a phytogenic additive (1 kg/T). Growth parameters (body weight, ADFI, ADG, FCR) and diarrhea incidence were monitored. Blood, jejunal tissue, and colonic digesta were collected on days 7, 15, 17, and 28 to assess antioxidant biomarkers, cytokine profiles, intestinal morphology, and expression of barrier-related and inflammatory genes. Data were analyzed using SPSS with parametric (t test, ANOVA with Duncan post hoc) or non-parametric methods (Mann–Whitney, Kruskal–Wallis with Dunn adjustment), and diarrhea rate was evaluated via χ^2. Results are expressed as means with significant value as $P \leq 0.05$ and a trend $P \leq 0.10$.

Results and Discussion

Both additives improved performance and health relative to NC. Diarrhea rate declined from 14.4% (NC) to 11.7% (-19%) and 9.0% (-38%), and FCR improved by 5% with phytogenics ($P < 0.05$) and showed an 8% trend with postbiotics. By day 17, antioxidant status improved to PC-like levels: GSH-Px increased by +12% and +8%, while MDA declined by –31% and -26% ($P < 0.01$). Cytokine modulation included increased TGF-β1 ($P = 0.05$) and decreased TNF-α (-5% and -9%), with a stronger effect for phytogenics. By day 28, both additives enhanced intestinal barrier function, increasing VH:CD (+9% and +12%), reducing serum D-lactate (-34% and -33%; $P < 0.01$), and showing a trend for lower DAO (-24%). These effects aligned with greater tight-junction gene expression and reduced pro-inflammatory signaling. Responses were broadly comparable to PC.

Conclusion

Postbiotics and phytogenics thus may offer promising ZnO-free strategies to sustain gut integrity, immune competence, and performance in pig production under increasing regulatory and consumer pressure.

Keywords: Diarrhea, Feed additive, Immune regulation, Intestinal barrier, Weaned piglets.

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DIETARY SUPPLEMENTATION WITH FREE MCFA IMPROVES SOW PERFORMANCE, COLOSTRUM QUALITY AND OFFSPRING GROWTH

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Introduction and Objectives

Increased litter size in sows limits colostrum and nutrient intake per piglet, leading to higher mortality and morbidity. Medium-chain fatty acids (MCFA) are known to provide antimicrobial activity, modulate lipid metabolism and support immune function. This study evaluated the effects of MCFA supplementation on sow performance, colostrum composition and immunity of sows and their offspring.

Materials and Methods

A total of 91 multiparous sows (Landrace × Yorkshire; parity 3.84 ± 1.15) were allocated to two treatments: a control diet or a MCFA-supplemented diet (1.0 g/kg; Agrifirm, Belgium) throughout gestation and lactation. Diets were corn-soybean based and formulated to meet NRC requirements, ensuring equal nutrient levels in both treatments (2935 kcal/kg ME and 3266 kcal/kg ME for gestation and lactation diets, respectively). The MCFA product consisted of free MCFA from C8 to C12. Sow performance and litter outcomes were analyzed using the sow as the experimental unit. Colostrum composition, immunoglobulin concentrations, and microbiota profiles were assessed. Immune transfer was evaluated in 10 litters per treatment (2 piglets/litter). Post-weaning growth was monitored for 5 weeks in piglets from 10 litters/group (4 littermates/pen) with the pen as the experimental unit.

Results and Discussion

MCFA supplementation tended to increase total piglets born, 24-hour survival and litter birth weight (P = 0.06 - 0.08), coinciding with a higher number of functional teats and improved colostrum quality, as indicated by elevated Brix scores and protein content ($P < 0.05$). Sows receiving MCFA showed higher plasma IgG and IgM levels, which translated into enhanced passive immune transfer, evidenced by increased plasma IgG and IL-10 levels post-colostrum intake ($P < 0.05$). LEfSe analysis revealed greater relative abundances of Lactobacillus amylotrophicus and Amylolactobacillus in colostrum from MCFA-supplemented sows, suggesting a role in establishing a resilient microbial community, as described elsewhere (Fan et al., 2025). These maternal effects likely influenced gut and immune development in offspring, as reflected by improved post-weaning growth performance ($P < 0.05$).

Conclusion

Maternal supplementation with a specific MCFA blend improved colostrum quality, immune transfer, and piglet performance post-weaning. These findings highlight the potential of MCFA-based strategies to enhance sow-mediated support and to give piglets a better start.

Keywords: Immunity, MCFA, Microbiota, Pig, Reproductive performance.

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EFFECTS OF NATURAL GROWTH PROMOTER IN DIETS ON THE PERFORMANCE OF GROWING PIGS

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Introduction and Objectives

Removing antibiotic growth promoters in swine has raised disease incidence and lowered productivity (Laxminarayan et al., 2015). Although many alternatives exist, their results are inconsistent and rarely match the effectiveness of antibiotics. A holistic approach is needed, emphasizing gut health and supporting the immune system. This study aimed to evaluate the effects of a natural growth promoter (Varium®) in diets on growth performance, feed efficiency, and gut health of growing pigs.

Materials and Methods

A total of 200 growing pigs (25.39 ± 4.0 kg) at 70 days old were assigned to one of the 2 treatments with 4 replicates (pens) per treatment and 25 pigs per replicate. Pigs in the control treatment (CON) received diets without Varium, while the VARIUM treatment was fed diets containing 1 kg/ton of Varium. Body weights of pigs were measured at 70, 98, and 120 days of age, and feed intake was recorded daily. On day 98, 16 fecal samples (2 pigs per pen) were collected by the SWAB method, immediately stored in a cool box, and sent to the lab for measuring *Escherichia coli* spp., *Lactobacillus* spp., and *Clostridium perfringens*. Parameters were compared between treatments using ANOVA, with statistical significance set at $P < 0.05$.

Results and Discussion

Feeding Varium diets to growing pigs did not affect the live weight, average daily gain (ADG), feed intake, and feed efficiency of growing pigs ($P > 0.05$) at any time points or phases; however, pigs fed the Varium diets were given better ADG and feed conversion ratios. Besides, pigs fed the Varium diets tended to be lower in *E. coli spp*. and higher in *Lactobacillus spp*. ($P = 01.47$) and had significantly fewer days of disease incidence (9.14 vs. 12.1%; $P < 0.001$). Consequently, compared to the CON treatment, the production cost of the pigs fed the Varium diets was 95.25%, and the veterinary medicine cost of the VARIUM treatment was 59.25%.

Conclusions

Feeding Varium diets to pigs tended to improve daily gain, efficiency, and bacterial profile. It also lowered the incidence of disease, lowered the cost of veterinary care, and increased the farm's profit.

Keywords: Growing Pigs, Gut Health, Natural Growth Promoter.

Acknowledgements: The authors express their appreciation to Amlan for providing VARIUM® and funds for conducting this experiment.

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EFFICACY OF A MICROENCAPSULATED ESSENTIAL OIL COMPLEX IN CONTROLLING SWINE DYSENTERY IN FATTENING PIGS

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Introduction and Objectives

Swine dysentery (SD), caused by *Brachyspira hyodysenteriae*, remains a major enteric disease in commercial pig production, leading to mucohemorrhagic colitis and severe economic losses (Burrough, 2017). This study evaluated the efficacy of a specific microencapsulated essential oil complex (MEO), containing cinnamaldehyde, carvacrol, thymol, and eugenol, in controlling natural SD outbreaks in a commercial fattening system.

Materials and Methods

The field trial was performed in a Spanish feedlot facing recurrent SD outbreaks. A total of 3,000 fattening pigs were allocated to the three treatments using a randomized block design: 1) Negative Control (standard diet); 2) MEO group 500 g/ton grower; 300 g/ton fattener phases); and 3) Competitor group (oregano, Zn, Cu, and inulin blend at 500 g/ton). Clinical signs (bloody diarrhea), mortality, and antibiotic interventions were recorded daily. Mass water medication with lincomycin was only triggered if > 4 pens in a warehouse exhibited clinical signs; otherwise, only individual injectable treatment (tiamulin) was applied.

Results and Discussion

The Control group required mass water medication in 100% of pens during both grower and fattening phases due to severe outbreaks. The Competitor group managed the grower phase but required mass medication in the fattening phase. Remarkably, the MEO group required zero mass water medication treatments throughout the entire trial, indicating effective suppression of disease transmission. Cumulative mortality was significantly reduced in the MEO group (3.85%) compared to the Control (7.69%) and Competitor (6.73%). Furthermore, the MEO group achieved the best Feed Conversion Ratio (3.05 vs. 3.15 in Control), reflecting improved gut integrity.

Conclusion

Dietary inclusion of the microencapsulated essential oil complex significantly reduced SD-associated mortality, improved feed efficiency, and eliminated the need for mass antibiotic water medication in a commercial setting. The findings support its potential use as a sustainable strategy for Swine Dysentery management in the post-antibiotic production era.

Keywords: Antimicrobial reduction, Essential oils, Gut health, Microencapsulation, Swine dysentery.

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MURAMIDASE SUPPLEMENTATION IMPROVES GROWTH AND GUT FUNCTIONALITY OF POST-WEANING PIGLETS

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Introduction and Objectives

Post-weaning piglets commonly experience intestinal inflammation, compromised barrier function, and reduced nutrient utilization. Peptidoglycan (PGN) released during bacterial turnover can stimulate TLR2-mediated inflammation, while its breakdown product, muramyl dipeptide (MDP), activates NOD2 and supports immune tolerance. Muramidase (MUR) is a glycosyl hydrolase that hydrolyzes PGN fragments without antimicrobial activity. This abstract presents an integrated summary of five controlled trials evaluating dietary MUR supplementation (50,000 LSU(F)/kg) on growth performance, gut health, and nutrient utilization in nursery pigs.

Materials and Methods

Three performance and two mechanisms of action trials were included. Four studies weaned pigs at 28 d (28 - 42 d duration; 2 studies with 2 piglets/pen, 2 studies with 10 piglets/pen) and one at 21 d (14 d duration; 16 piglets/trt) with 20 - 64 replicate pens per treatment depending on the study. Diets differed in crude protein level and environmental challenge intensity. Depending on the study, measurements included growth performance, diarrhea scores, plasma urea nitrogen (PUN), vitamins A and E, fecal lipocalin-2, cytokine gene expression, antioxidant enzyme activity, and jejunal morphology.

Results and Discussion

Across trials, MUR supplementation improved key performance and health indicators. Average daily gain increased from 495 to 511 g/d ($P < 0.05$), and diarrhea scores decreased from 0.25 to 0.19 ($P < 0.05$). In high protein challenged piglets, fecal lipocalin-2 was reduced substantially (1655 vs 298 ng/mL; $P = 0.04$). IL17B expression in lamina propria declined from a 3.45-fold increase in controls to -1.86-fold in MUR-supplemented pigs ($P < 0.05$). Likewise, MUR reduced PUN (20.8 vs. 16.1 mg/dL; $P = 0.02$) and increased plasma vitamin A levels (205.9 vs. 239.5 ng/mL; $P = 0.03$). Antioxidant enzyme activity increased from 15.0 to 17.6 U/g protein ($P = 0.005$) and jejunal epithelial thickness improved (30.1 vs 36.5 µm; $P = 0.013$). These outcomes align with the expected benefits of reducing PGN-driven inflammation and improving mucosal integrity.

Conclusion

This integrated analysis demonstrates that muramidase supplementation during the nursery period supports gut health by lowering inflammatory and oxidative stress markers, enhancing nutrient utilization, and improving growth and barrier function, offering a practical non-antimicrobial strategy to optimize post-weaning piglet performance.

Keywords: Gut functionality, Immune modulation, Muramidase, Nutrient absorption, Post-weaning diarrhea.

APPLICATION OF SHRIMP PEPTIDE IN PIG PRODUCTION: EFFECTS ON FEED INTAKE, GROWTH PERFORMANCE, AND HEALTH

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Introduction and Objectives

Vietnam's agricultural sector generates over 160 million tons of by-products annually, including approximately 400,000 - 500,000 tons of shrimp heads and shells. These materials are rich in proteins, minerals, and bioactive components, presenting significant potential as alternative feed ingredients. This study evaluated the nutritional efficacy of shrimp-derived peptides on the performance of sows, piglets, and growing-finishing pigs.

Materials and Methods

Low-molecular-weight peptides (230 - 300 Da) were extracted from shrimp by-products through fractionation and protease-mediated enzymatic hydrolysis. These peptides, enriched with free amino acids, were incorporated into basal diets at defined levels. The experimental design covered various production stages: a sow trial (20 lactating sows), a piglet trial (60 piglets aged 42 - 70 days, 11.04 ± 1.24 kg) a grower trial (396 pigs, 10.30 ± 0.39 kg), and a finisher trial (110 pigs, 95.5). Measured parameters included feed intake (FI), average daily gain (ADG), feed conversion ratio (FCR), sow lactation performance, piglet weaning weight, serum immunoglobulins (IgA, IgG, IgM), lysozyme activity (LZM), health status, and carcass traits. Data were analyzed using ANOVA with significance $P < 0.05$.

Results and Discussion

The supplementation significantly enhanced feed intake and animal performance. In sows, voluntary feed intake during lactation increased by 14% compared to the control group. Piglets from supplemented sows achieved weaning weights 9.4% higher than the control. For piglets aged 42–70 days, continuous peptide use led to an 11% reduction in Feed Conversion Ratio (FCR). Furthermore, immune parameters (IgA, IgG, IgM, and LZM) in growers aged 35 and 49 days showed substantial increases, ranging from 18 to 89%. Growing-finishing pigs from 80 days old, the treatment resulted in improved growth performance. Economic analysis, calculated based on feed cost, shrimp hydrolysate supplementation cost, market selling price, and labor expenses, revealed that 2% peptide supplementation increased profit per marketed pig by 120.9%.

Conclusion

The addition of shrimp-derived peptides via direct on-farm mixing with commercial pelleted feed improves feed intake, growth performance, immunity, and economic outcomes in swine production. These findings highlight their potential as high-value functional feed ingredients. Further research is recommended to optimize inclusion levels across diverse production systems.

Keywords: Alternative protein sources, Functional nutrition, Piglet performance, Shrimp peptides, Sow feed intake.

Acknowledgements: The authors thank Nong Lam University HCMC, Vietnam for the support with providing testing facilities.

ORGANIC ACID AND ANIONIC DIETS AS NUTRITIONAL STRATEGIES TO MODULATE URINARY PH AND ACID–BASE BALANCE IN GESTATING GILTS

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Introduction and Objectives

Gestation increases the risk of genitourinary infections, compromising sow welfare and longevity. Organic acids and anionic diets can reduce urinary pH and help inhibit bacterial growth through dietary acidification; therefore, this study evaluates their use as a nutritional strategy to acidify the genitourinary tract.

Materials and Methods

A total of 19 gilts (182.95 ± 6.67 kg BW; 30 days of gestation) were allocated in a randomized complete block design (body weight and backfat thickness) into three treatments: CON (control diet; 170 mEq/kg; n = 7), ACID (supplementation with 6.5 kg/ton of a blend of organic acids (citric, benzoic, formic, and lactic); n = 6), or ANION (anionic diet; 9.05 kg/ton of calcium chloride; 45 mEq/kg; n = 6) for 15 days. All diets were balanced to be isonutritive (3050 Kcal/kg ME; CP: 14.91%; Total Ca: 1.23%). Blood and urine samples were collected on days 0 and 15. Blood was obtained by jugular venipuncture into heparinized syringes and blood pH, pO2 and pCO2 were immediately analyzed. First-morning urine pH was determined by spontaneous urination using a benchtop pH meter. Data were analyzed using mixed models in RStudio, with treatment, time, and their interaction as fixed effects and sows as a random effect. Means were compared by Tukey's test.

Results and Discussion

On day 0, both urinary and blood pH were similar among treatments ($P > 0.10$). By day 15, the ANION diet reduced urinary pH (6.75 ± 0.22) compared with the CON group (8.04 ± 0.36; $P = 0.020$) and tended to be lower than the ACID group (7.46 ± 0.22; $P = 0.092$), indicating that the anionic strategy reduced urinary pH. For blood gas analysis on day 15, blood pH in the ANION group tended to be lower (7.348 ± 0.018) compared with the CON group (7.412 ± 0.029; $P = 0.082$), not differing from the ACID group ($P > 0.10$). No differences were observed for pO_2 or pCO_2 ($P > 0.10$).

Conclusion

Our results indicate that the anionic diet effectively promoted urinary acidification. In contrast, organic acid supplementation did not affect urinary or blood pH.

Keywords: Acidosis, Cystitis, Genitourinary tract, Metabolism, Urine.

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EFFECTS OF PHYTOGENIC SUPPLEMENT ON GROWTH PERFORMANCE, NUTRIENT DIGESTIBILITY, IMMUNE SYSTEM BIOMARKERS IN BLOOD, GUT MICROBIOME AND MUCOSAL HEALTH OF PIGLETS CHALLENGED WITH *E. COLI*

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Introduction and Objectives

The post-weaning period in piglets is characterized by intestinal immaturity, microbiota instability, and high diarrhea risk, often impairing growth (Gresse et al., 2017). Pharmacological zinc oxide has been widely used to control these effects but faces regulatory restrictions (EFSA, 2017, Tang et al.,2024). Plant-derived saponins, including Quillaja saponaria extracts, may support gut health and performance as promising alternatives (Upadhaya & Kim, 2021). The objective of this study was to evaluate the effects of Quillaja saponaria supplementation on growth performance, gut health, and immune response in weaned piglets challenged with E. coli, compared with zinc oxide.

Materials and Methods

Forty-eight weaned pigs ([Landrace × Yorkshire] × Duroc; 8 kg BW) were used in a 4-week randomized trial with four treatments: non-infected control, infected control, Quillaja Extract 250 (375 g/t, QS), and zinc oxide (1,000 g/t, ZnO). Each treatment had six replicates with two pigs per pen. On day 14, pigs (except the non-infected control) were orally challenged with E. coli (5.2×10^9 CFU/pig). Growth performance, blood biomarkers, fecal microbiology, and intestinal morphology were assessed. Data were analyzed by ANOVA and Tukey's test ($P < 0.05$).

Results and Discussion

All Quillaja saponin (QS) treatments improved performance under E. coli challenge. QS produced the greatest BW gain vs. infected control (+0.79 kg; $P < 0.05$), with higher ADG, feed intake (+2.7%), and improved G:F, matching or exceeding ZnO. QS alone increased BW (+1.4% FI) with no difference vs. ZnO. TNF-α decreased ($P < 0.05$) while IgG remained stable, indicating controlled immune modulation. Antioxidant enzymes (SOD, GPX, CAT) increased ($P < 0.05$). QS enhanced villus height by +35.1 µm (+9.0%) vs. +18.8 µm (+4.8%) for ZnO, improving absorptive capacity. Total VFA increased up to +14.5% ($P < 0.05$), increasing butyrate and modulating microbiota. Ileal pH rose to 6.74 - 6.88 (+4%), while cecal pH decreased, indicating improved fermentation and gut integrity.

Conclusion

Quillaja saponaria supplementation improved gut health, immunity, and growth in weaned piglets, especially under E. coli challenge. It enhanced microbiota balance, gut integrity, nutrient absorption, and feed efficiency, while reducing inflammation and oxidative stress.

Keywords: *E. coli* challenge, Immune response regulation, Gut health modulation, Growth performance enhancement, Quillaja Saponaria.

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ORAL PRESENTATION



TOPIC 10: ONEHEALTH, AMR AND PIG WELFARE (OAW)

REDUCING ANTIBIOTIC USE BY TARGETED TREATMENT OF DIARRHEA IN DANISH NURSERY PIGS

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Introduction and Objectives

Batch medication of diarrhea outbreaks is the main driver of antibiotic use in Danish pig production. According to national statistics (2024), an average pig received 6.5 days of oral antibiotic medication during the nursery period. The purpose of this study was to reduce antibiotic use by replacing oral batch medication of diarrhea with parenteral individual animal treatment and refined treatment criteria in nursery pigs.

Materials and Methods

The study was conducted on a farm suffering from diarrhea outbreaks caused by enterotoxigenic *Escherichia coli* F4 and subsequently *Brachyspira pilosicoli* and *Lawsonia intracellularis*. In each of 137 separate nursery pens an indicator pig was selected and followed from insertion at weaning to planned exit. All focal pigs were clinically evaluated daily and individual average daily gain (ADG) was recorded. Pigs received parental antibiotic treatment for three days if two criteria were met simultaneously: 1) diarrhea (back-part staining/diarrheic feces) and 2) clinical complications: Depression, dehydration, sunken flanks, ill-thrift. Pigs with diarrhea but no clinical complications were not treated with antibiotics or electrolytes.

Results and Discussion

A total of 41 pigs (30%) developed treatment-requiring diarrhea, while 80 pigs (58%) developed uncomplicated diarrhea. The remaining 16 pigs (12%) remained without diarrhea. The average daily diarrhea prevalence was 10% and the average daily diarrhea treatment prevalence was 0.8%. Pigs with treatment-requiring diarrhea had longer diarrhea periods (average 8.0 diarrhea days). Pigs with uncomplicated diarrhea had shorter diarrhea periods (average 2.9 diarrhea days) and recovered well without antibiotic treatment. The ADG in pigs with treatment-requiring diarrhea (485 g) was significantly ($P < 0.05$) reduced compared to pigs without diarrhea (549 g). ADG in pigs with uncomplicated diarrhea (514 g) did not differ significantly from pigs without diarrhea.

Conclusion

The study showed that most diarrhea cases were uncomplicated and did not require antibiotic treatment and had growth rates similar to pigs without diarrhea. In conclusion, individual animal treatment combined with refined treatment criteria reduced the number of diarrheas treated animals by 70% compared to batch medication.

Keywords: AMR, Antibiotic, Diarrhea, Pig, Treatment.

Acknowledgements: Financial support was received from the European Union, project "Alternatives to Veterinary Antimicrobials" (Grant Agreement No. 862829).

EFFECTS OF PLANT-DERIVED ISOQUINOLINE ALKALOIDS ON CORTISOL AND SALMONELLA SHEDDING IN TRANSPORTED PIGS

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Introduction and Objectives

Salmonella contamination remains a major concern for human salmonellosis, as pork products may become contaminated and act as a source of *Salmonella* transmission, especially during transportation. Plant-derived isoquinoline alkaloids (IQ) have demonstrated anti-inflammatory and antimicrobial properties, suggesting their potential use as a feed additive to mitigate transportation-induced stress and *Salmonella* shedding in pigs.

Materials and Methods

A total of 82 Landrace × Berkshire barrows and gilts (initial body weight: 47.9 ± 7.2 kg) were orally challenged with 15 mL of a *Salmonella* cocktail (10^8 CFU/mL) on days 0 and 9. On day 14, pigs were randomly assigned to three treatments: NC (negative control, no IQ), T1 (IQ at 150 g/t of feed), and T2 (IQ at 150 g/t of feed for two weeks, followed by water-soluble IQ at 100 g/1,000 L for the final three days). All pigs were transported to the slaughterhouse on day 28. Saliva, fecal, and carcass swab samples were collected at designated time points. Salivary cortisol and *Salmonella* concentrations in feces and carcass swabs were analyzed.

Results and Discussion

Salivary cortisol levels significantly increased after transportation (D28) in the NC group (1.87 to 5.48 ng/mL; $P < 0.0001$) and were higher than in T1 and T2 ($P \leq 0.0002$). *Salmonella* prevalence in fecal samples on D28 was significantly higher in the NC group (100%) compared to the T1 (73.7%) and T2 (71.4%) groups. Additionally, the amount of *Salmonella* contaminating the carcasses in the NC group was significantly greater than in T1 and T2 ($P = 0.01$). This study found a positive correlation between saliva cortisol levels and the quantity of *Salmonella* shed in feces, reinforcing the notion that stress contributes to increased *Salmonella* shedding.

Conclusion

Transportation induces stress in pigs, increasing cortisol levels and *Salmonella* shedding. Supplementation with isoquinoline alkaloids (IQ) may reduce stress responses and fecal *Salmonella* shedding, thereby improving animal welfare and food safety.

Keywords: Isoquinoline alkaloids, *Salmonella* shedding, Cortisol, Animal welfare.

Acknowledgements: The authors thank Ohio State University for the support with providing testing facilities.

THREE-YEAR LONGITUDINAL SURVEILLANCE OF INFLUENZA A VIRUS AT THE HUMAN-SWINE INTERFACE IN MIDWEST SWINE FARMS IN THE UNITED STATES

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Introduction and Objectives

Active surveillance helps track endemic IAV in swine and assess potential threats to public health. This study, conducted from 2022 - 2025, characterized the IAV detected in farm employees, and associated pre-wean and nursery pigs, at the human-swine interface across conventional production systems in the Midwest United States.

Materials and Methods

Active surveillance was performed in 30 farms targeting employees, pre-wean piglets at 15 breeding herds, and piglets in 15 downstream nurseries in 5 states for a minimum of 12 months. Farm employees were surveyed to assess demographic data, including human-seasonal vaccination status within the prior year. Farm employees self-collected a nasal swab monthly and swine samples included 10 udder wipes and 15 nasal wipes from breeding herds and 15 nasal wipes and 4 oral fluids from the nursery each month. Samples RT-rtPCR- positive for IAV were subtyped, and whole genome sequencing was attempted.

Results and Discussion

The project enrolled 189 farm employees and survey results indicated 66.32% were male and 33.68% female, 39.38% were included in the 26-35 age category, 79.27% worked with swine < 10 years, and only 43.01% received the human-seasonal influenza vaccine the previous year. During the 3-year period, 6 human nasal swabs (0.40%; n = 1484) tested IAV positive from 4 farms. Five hemagglutinin (HA) sequences were generated and revealed 2 H3N2 from the 2022–2023 human influenza season, 1 H1N1 pandemic from 2025, and 2 H1 1A.1.1.3 swine-lineage IAV that were detected in 2024 - 2025 and reflected zoonotic transmission. IAV RNA detection in swine was 29.8% (n = 7665) positive across all farms. Approximately 25.09% (n = 4400) and 36.20% (n = 3265) were IAV positive in pre-wean and nursery pig samples, respectively. Hemagglutinin sequencing also detected 7 distinct phylogenetic swine-lineage groups across 4 evolutionary lineages: H1 1A.1.1.3, 1A.3.3.3, 1B.2.2.2, 1B.2.1, and H3 1990.4, 1990.4.a, and 2010.1.

Conclusion

Human-seasonal IAV was not detected in swine thus far from these farms. However, swine-lineage H1 1A.1.1.3 was detected in 2 employees on different farms during the surveillance period. Active surveillance involving both humans and swine is critical to understanding IAV circulation at the human-swine interface, impact on bidirectional transmission, and developing methods of control.

Keywords: Active surveillance, Swine; Influenza A virus, Farm employee, Nursery pigs, Pre-weaning piglets.

PHAGE DRIVEN ANTIBIOTIC SUSCEPTIBILITY SHIFTS IN MULTIDRUG RESISTANT EXTRAINTESTINAL PATHOGENIC *ESCHERICHIA COLI*

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Introduction and Objectives

Antimicrobial resistance (AMR) in swine production is accelerating the emergence of multidrug-resistant (MDR) pathogenic *Escherichia coli*, which complicates disease therapy and antibiotic use (Li et al., 2025). Bacteriophage therapy is a targeted alternative; however, phage resistance poses a significant limitation, often resulting from remodeling of lipopolysaccharide (LPS) and outer membrane protein (OMP) that leads to pleiotropic changes in antibiotic sensitivity (Burmeister et al., 2021). This study aims to isolate phages against MDR *E. coli*, select phage-resistant mutants, assess antibiotic susceptibility shifts relative to parental strains, and conduct genomic analysis.

Materials and Methods

A total of 10 porcine-derived multidrug-resistant extraintestinal pathogenic *E. coli* (ExPEC) strains (Li *et al*., 2024) were used as hosts. Lytic phages were isolated from 113 pig-farm sewage samples across China using the agar overlay method. Phage-resistant mutants were selected at MOI 0.1, profiled by Kirby–Bauer antibiotic testing, and mutants exhibiting altered susceptibility were subjected to whole-genome sequencing, with SNPs identified and analyzed.

Results and Discussion

Pleiotropic shifts in antibiotic susceptibility were observed following the emergence of phage resistance. In total, 195 lytic phages were isolated against MDR *E. coli*, yielding 232 phage-resistant *E. coli* mutants, of which 8.6% of the mutants showed antibiotic phenotype changes. The phage-resistant *E. coli* mutant M-A208-181-2 regained moxifloxacin (MXF) susceptibility (inhibition zone, 16 mm) compared with 0 mm in parental *E. coli* A208, and mutant M-A216-88 became amikacin (AMK) susceptible (inhibition zone, 17 mm) compared with 0 mm in wild-type *E. coli* A216. Whole-genome sequencing of mutants with antibiotic shifts detected SNPs in LPS/OMP associated loci, supporting a link between phage-selected envelope remodeling and collateral antibiotic re-sensitization.

Conclusion

Phage resistance evolution in swine-derived MDR *E. coli* was accompanied by antibiotic susceptibility shifts, indicating pleiotropic trade-offs rather than resistance alone. Single nucleotide polymorphisms in LPS/OMP loci suggest that envelope remodeling is a catalyst for modified drug response. These results endorse the application of lytic phages for bacterial management and the investigation of antibiotic resensitization possibilities in MDR strains. In vivo validation and comprehensive strain testing are required to verify robustness and translational significance.

Keywords: Antibiotic susceptibility, Lytic bacteriophages, MDR Escherichia coli, Phage resistance, Surface receptors.

Acknowledgements: The authors thank the Huazhong Agricultural University, Wuhan, China, for the support with providing testing facilities.

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ESTABLISHMENT AND APPLICATION OF A METHOD FOR DETECTING ANTIBIOTIC RESISTANCE GENES IN SWINE RESPIRATORY PATHOGENS BASED ON NANOPORE SEQUENCING TECHNOLOGY

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Introduction and Objectives

Porcine respiratory disease complex (PRDC) often involves polymicrobial bacterial infections, driving empirical antimicrobial use and dissemination of antimicrobial resistance genes (ARGs). Routine diagnostics typically separate pathogen identification from resistance profiling and seldom resolve the bacterial host of ARGs, limiting timely targeted therapy and epidemiological tracing. We developed a targeted nanopore sequencing workflow for same-day, multiplex detection of major PRDC-associated bacteria and clinically relevant ARGs, with long-read–based ARG-to-host assignment to support antimicrobial decision-making and surveillance.

Materials and Methods

An ultramultiplex primer pool was designed to enrich informative loci from Actinobacillus pleuropneumoniae, Glaesserella parasuis, Pasteurella multocida, Streptococcus suis, and Bordetella bronchiseptica, together with representative ARG markers related to β-lactams, tetracyclines, macrolides, sulfonamides, and quinolones. After single-tube multiplex PCR enrichment, rapid barcoded libraries were sequenced on MinION for real-time analysis. A bioinformatics workflow performed basecalling, demultiplexing, and mapping to a curated pathogen/ARG database. ARG-to-host attribution combined read-level co-mapping with targeted local assembly and flagged uncertain calls for confirmatory testing. Feasibility was evaluated using mock/spiked materials and field respiratory specimens, benchmarked against routine culture and/or targeted PCR, and assessed for genotypic–phenotypic consistency when susceptibility data were available.

Results and Discussion

The workflow produced actionable outputs within a same-day timeframe, and real-time sequencing enabled early preliminary pathogen calls followed by iterative refinement as coverage increased. Across evaluation materials, targeted enrichment supported simultaneous detection of the intended pathogens and ARG markers, including scenarios consistent with mixed infections and low-abundance targets. Long-read information improved interpretability by enabling direct linkage of ARG signals to their most likely bacterial hosts, supporting pathogen-specific therapeutic guidance and source-oriented tracing. The pipeline also incorporated quality-control reporting and uncertainty handling to reduce false-positive reporting and to guide confirmatory testing when needed.

Conclusion

Targeted nanopore sequencing offers a practical approach for integrated PRDC bacterial diagnosis and resistance profiling, providing host-resolved ARG information to support precision antimicrobial use and on-farm AMR surveillance.

Keywords: Antimicrobial resistance; Multiplex PCR; Nanopore sequencing; PRDC; Targeted sequencing.

CORRELATION OF TOXIC ELEMENT CONCENTRATIONS WITH SEMEN QUALITY PARAMETERS IN BOARS: THE ROLE OF TIN AND OTHER HEAVY METALS

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Introduction and Objectives

Certain chemical elements can serve as essential nutrients in trace amounts but may become toxic with chronic exposure to elevated levels. Globally, industrial activities are increasing environmental concentrations of these elements, coinciding with a decline in fertility and sperm quality in humans.

Materials and Methods

This study aimed to assess the concentrations of 21 potentially toxic chemical elements in ejaculated semen of 30 boars aged 7 to 34 months and to correlate these concentrations with common sperm quality parameters measured using a CASA system (Androvision, Minitube). The semen was collected on a Finnish boar stud farm, and the boars were imported from Norway (n = 15), Denmark (n = 9), and the Netherlands (n = 6). Kruskal-Wallis test was used to compare concentrations of different elements between countries of origin, and Spearman's rho test to correlate these elements with sperm parameters.

Results and Discussion

The highest concentrations were found for tin (Sn, 143 µg/L), molybdenum (Mo, 237 µg/L), barium (Ba, 406 µg/L), manganese (Mn, 407 µg/L), and lead (Pb, 2259 µg/L). Boars from Norway exhibited the highest levels of strontium (Sr, $P = 0.002$), thallium (Tl, $P = 0.004$), Mo ($P = 0.005$), uranium (U), and Sn (both p = 0.05). A significant negative correlation was observed between mercury (Hg) and sperm concentration (Spearman's rho: -0.4; $P < 0.05$). Positive correlations were noted between vanadium (V), cobalt (Co), Sr, Hg, Tl, and U concentrations and the percentage of sperm with proximal droplets (Spearman's rho > 0.4; $P < 0.05$). Additionally, U concentration negatively correlated with the percentage of sperm with normal morphology (-0.456; $P < 0.05$). Sn concentrations showed significant negative correlations with normal morphology, motility, progressive motility, and vitality (Spearman's rho > 0.4; $P < 0.005$).

Conclusion

This study demonstrates that high concentrations of toxic chemical elements can be detected in boar semen, with tin having the most pronounced correlation with sperm quality. This study also shows differences in the concentration of chemical elements in boar semen depending on country of origin. It is the first study linking tin concentrations in boar sperm to alterations in major sperm parameters.

Keywords: Heavy metals, Tin, CASA, Sperm Quality Parameters.

TRAINING COMMUNITY ONE HEALTH TEAMS TO PREVENT *TAENIA SOLIUM* IN RURAL RWANDA

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Introduction and Objectives

Small-scale pig farming is an important form of livelihood and economic advancement for many families in LMIC. However, in areas with poor hygiene where pigs roam freely, neurocysticercosis due to Taenia solium is a leading cause of epilepsy. Epilepsy is a consequence of humans consuming tapeworm eggs, whereas the adult tapeworm is the result of people consuming undercooked, infected pork. In Rwanda, a pig with cysts on its tongues has significantly reduced value, leaving the farmer with little to no profit. The objective was to provide workshops about preventing *T. solium* to One Health Teams (OHTs), enabling them to share this knowledge with community members.

Materials and Methods

In this cohort study, monthly workshops were delivered to 255 people who formed OHTs in 85 villages in rural Rwanda. Each OHT included a community health worker, animal health worker and hygiene and sanitation officer. OHT members were surveyed before and after each training to measure knowledge acquisition.

Results and Discussion

The proportion of OHT members who correctly described the transmission of T. solium to people increased from 71 to 91% and to pigs from 32 and 91% from before to after the training. Few participants recommended washing hands to prevent neurocysticercosis before training (11%) whereas 40% did after training. Most responses also included consumption of pork. Participants did not separate the behaviors needed to prevent taeniasis versus neurocysticercosis. Due to these inaccuracies, we delivered additional training in February 2026 and provided a training booklet and poster. Results of this training will be available by June.

Conclusion

The *T. solium* lifecycle and the development of neurocysticercosis are complex. After training, most OHT members knew how people acquired the tapeworm through pork, and pigs became infected through consuming eggs. However, without understanding that inadvertent consumption of tapeworm eggs causes neurocysticercosis, behavior changes among community members will not occur. The OHTs role in disseminating information to their communities relies on an accurate understanding of zoonotic disease prevention.

Keywords: Community One Health Teams, LMIC, Taenia solium, Trainings, Zoonoses.

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STRENGTHENING SMALLHOLDER PIG FARM THROUGH THE FARMVETCARE APP USING ONE HEALTH APPROACH WITH LAB-SUPPORTED DIAGNOSTICS

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Introduction and Objectives

Smallholder pig farms are particularly at risk to infectious diseases due to low levels of biosecurity and vaccination coverage. This study aimed to support farmers' access to animal health information, enhance biosecurity awareness, and enhance early detection of zoonotic and infectious animal diseases, especially African swine fever (ASF), in smallholder pig farms in Phu Tho and Lao Cai provinces, Vietnam.

Materials and Methods

This study developed a disease surveillance app, called "FarmVetCare", and applied it in pig farms, coupled with laboratory diagnostics in a One Health manner. FarmVetCare included three modules for farmers, animal health workers in the field, and veterinary staff at the provincial level. Farmers were trained in biosecurity practices, vaccination schemes, responsible antibiotic use, and the practical application of the FarmVetCare App in their farming context. As part of a One Health - aligned surveillance process, whole blood, serum, or homogenized tissue samples were collected for suspected ASF cases and analyzed using real-time PCR assays. Sample collection and testing were offered free of charge to support farmers and strengthen disease surveillance.

Results and Discussion

Through the collected responses to before and after training evaluation, the preliminary assessment of the effectiveness of the training showed positive impact on the awareness of pig smallholders, recorded a clear improvement, especially about the use of antibiotics in livestock farming, the correct answer rate increased sharply from 32.9% to 83.1%. Participated farmers actively use FarmVetCare App to report clinical signs and seek information, enhancing a platform for animal health record-keeping, and quick access to veterinary consulting support. During follow-up surveillance, 45 out of 56 samples collected from ASF-suspected pig farms were positive with ASF virus. These findings indicate the effectiveness of app-based reporting in facilitating early case identification and targeted diagnostic follow-up.

Conclusion

The combination of the FarmVetCare App, interactive training and diagnostic support provides a practical One Health-oriented model for strengthening disease detection and biosecurity measures in smallholder pig systems. Equipping farmers and local veterinarians with digital tools, along with trainings and interventions shows strong potential for broader application in Vietnam to reduce zoonotic and infectious disease risks in pig production.

Keywords: African swine fever, Biosecurity, FarmVetCare, One Health, Pig farms, Surveillance.

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DIFRUCTOSE ANHYDRIDE III SUPPLEMENTATION IN LACTATING SOWS REDUCES SUCKLING PIGLET MORTALITY AND ENHANCES BODY WEIGHT UNIFORMITY OF WEANING PIGLETS

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Introduction and Objectives

Difructose anhydride (DFA) III is a plant-derived prebiotic shown to improve IgG absorption in calves (Escartín et al., 2024), but its effects on lactating sows are unknown. This study investigates whether DFA III supplementation can improve sow reproductive performance, with emphasis on piglet mortality and growth.

Materials and Methods

Thirty pregnant sows were randomly assigned to a control (n = 15) or DFA-treated group (n = 15). Treated sows received 12 g/day of DFA III from 7 days pre-farrowing to 21 days postpartum, while controls were fed the basal diet. IgG and IgA titers against PRRSV and PEDV were determined by immunoperoxidase monolayer assay (IPMA). Piglet outcomes (total born, born alive, and mortality during days 1 - 3), body weight at birth, day 1, and weaning (day 21), and estimated milk yield and litter weight were recorded. Cross-fostering, when necessary, was performed within groups. Data were analyzed using the GLM procedure in SAS 9.4, with group as the main effect.

Results and Discussion

Compared with the control group, the treatment group showed a 1.73-fold increase in PRRSV-specific IgA and a 1.89-fold increase in PEDV-specific IgG titers in sow colostrum ($P < 0.001$). Piglet mortality by day 3 was lower in the treatment group (4.2 vs. 10.4%, $P = 0.016$), along with reduced body-weight variation at day 21 (CV: 11.3 vs. 15.3%, $P = 0.029$). At weaning, the treatment group tended to have higher milk yield (+ 1.68 kg, $P = 0.092$) and total litter weight (+ 9.98 kg, $P = 0.080$). These findings suggest that DFA III supplementation improves milk immunoglobulin quality, enhancing preweaning survival and growth uniformity through passive immunity (Muns et al., 2016).

Conclusion

This is the first study to evaluate the impact of difructose anhydride III on the reproductive performance of lactating sows. DFA III supplementation appeared to improve milk quality and increased IgG and IgA concentrations against PEDV and PRRSV in sow colostrum, which contributed to lower suckling piglet mortality and more uniform weaning weights.

Keywords: Milk yield, Passive immunity, Pig, Prebiotics, Suckling piglets.

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ORAL PRESENTATION



TOPIC 11: REPRODUCTION TECHNOLOGIES AND LACTATION (RTL)

IMPACT OF MATERNAL AND FARROWING PARAMETERS ON COLOSTRUM QUALITY IN A FREE FARROWING SYSTEM

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Introduction and Objectives

Colostrum plays a critical role in the survival and performance of neonatal piglets, with both its quantity and quality being key determinants of health and welfare. The objective of this study was to evaluate the influence of sow-related and farrowing-associated parameters on colostrum immunoglobulin G (IgG) concentration.

Materials and Methods

A total of 151 crossbred sows were included and sow-related parameters such as parity, body weight, body condition score, backfat thickness, induction of farrowing, and gestation length were recorded alongside farrowing parameters, including total number of piglets born, farrowing duration, obstetrical intervention, placental expulsion, litter weight, and placental weight. Ambient temperature and relative humidity were measured within 24 hours prior to farrowing. Colostrum samples were collected after expulsion of the first piglet and analysed for IgG concentration using enzyme-linked immunosorbent assay (ELISA), with concurrent assessment by digital Brix refractometry. Linear regression analyses were performed using log-transformed IgG concentrations. Predictor variables were selected based on biological relevance and descriptive statistics. The final model included total piglets born, parity, induction of farrowing, relative humidity, and the interaction between parity and induction.

Results and Discussion

Brix refractometry values were strongly correlated with ELISA-measured IgG concentrations ($r = 0.66$, $P < 0.001$). The final regression model explained 43% of the variance in IgG concentration ($R^2 = 0.43$, $P < 0.001$) and identified significant effects of parity ($P < 0.001$), induction of farrowing ($P = 0.001$), relative humidity ($P = 0.004$), and the parity × induction interaction ($P = 0.032$). Higher parity was associated with increased colostral IgG levels, whereas induction of farrowing was linked to reduced IgG concentrations, particularly in gilts, with the effect diminishing in older sows. Although a positive association between ambient humidity and IgG concentration was observed, its biological significance remains unclear.

Conclusion

Colostrum IgG concentration was significantly influenced by parity, induction of farrowing, and environmental conditions. The negative effect of farrowing induction underscores the importance of careful periparturient management. Furthermore, digital Brix refractometry appears to be a practical and reliable on-farm tool for assessing colostrum quality and may be effectively integrated into sow and piglet management strategies.

Keywords: Brix refractometry, Birth induction, Immunglobulin G, Parity, Sow.

DIETARY AMMONIUM CHLORIDE IN LATE GESTATION AND FARROWING DURATION, COLOSTRUM PRODUCTION AND PIGLET PERFORMANCE

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Introduction and Objectives

Colostrum plays an important role in piglet health and growth. Colostrum yield and volume are influenced by sow health, which is related to farrowing duration. Prolonged farrowing duration occurs more often in older sows. Presumably, due to lower circulating calcium concentrations impairing myometrial contractility, piglet expulsion is prolonged so increasing farrowing duration. Previous studies found that administering ammonium chloride (NH4Cl) orally or by infusion improved serum calcium concentrations (Beck and Webster, 1976; Vagg and Payne, 1970). This project aims to investigate the effects of feeding NH4Cl in late gestation of older sows on farrowing duration, colostrum production, and piglet performance.

Materials and Methods

On day 101.1 ± 0.1 of gestation, 72 (Landrace × Large White) sows of parity 4 to 8 were selected and assigned equally to two groups. Control sows were fed the basal diet, and treatment sows were fed the basal diet supplemented with 20 g/day NH4Cl until farrowing. Piglets were weighed at birth and 24 h to measure colostrum yield, and litter weight was recorded on days 3, 10, and 18 post-farrowing to calculate average daily gains (ADG) to weaning. Colostrum intake was estimated by using the equation by Devillers et al. (2004). Treatment comparisons for farrowing duration, colostrum yield, and litter ADG were performed using generalized linear mixed models fitted with 'glmmTMB' package, in R version 4.4.3.

Results and Discussion

The average farrowing duration of treated sows was shorter than for control sows (288.8 ± 26.4 min vs 384.4 ± 24.1 min; $P < 0.05$). Colostrum yield from treated sows was higher than control sows (3.33 ± 0.45 kg vs 2.04 ± 0.42 kg, respectively; $P < 0.05$). The ADG of treated piglets of sows from birth to day 3, and from day 10 to day 18 were higher compared to piglets from control sows (173.98 ± 6.39 g vs 151.88 ± 7.03g, and 312.75 ± 5.23 g vs 291.22 ± 5.44 g, respectively; $P < 0.05$ for both).

Conclusion

These results demonstrate that sows fed 20g/day NH4Cl for 2-weeks before farrowing exhibited reduced farrowing durations, improved colostrum yield and ADG until weaning.

Keywords: ADG, Ammonium chloride, Colostrum, Farrowing duration, Late pregnancy.
Acknowledgements: This work was supported by Adelaide University and SunPork Piggery. The authors thank the staff and students from the School of Animal and Veterinary Science, Adelaide University and SunPork Roseworthy Piggery for their help and providing facilities.

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EFFECT OF DIETARY PHYTOGENIC ADDITIVES ON SERUM CYTOKINE CONCENTRATIONS OF LACTATING SOWS

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Introduction and Objectives

The peripartum period in sows is characterized by marked physiological and inflammatory changes that may impair immune function and reproductive performance. Phytogenic additives have been proposed as natural modulators of immune responses. This study evaluated the effects of dietary phytogenic additives on serum cytokine concentrations in lactating sows.

Materials and Methods

A total of 75 sows were allocated in a randomized complete block design, with genetic line, parity order, and experimental batch as blocking factors. Animals were assigned to one of three treatments: a control diet without additives (CONT); phytogenic additive 1 (PA1), composed of herbs, plant extracts, and essential oils from the Fabaceae, Liliaceae, and Theaceae families; and phytogenic additive 2 (PA2), derived from the Lauraceae, Schisandraceae, and Myrtaceae families. Each treatment included 25 sows selected based on average body weight. Blood samples were collected at 109 days of gestation and at 2 and 10 days postpartum. Serum concentrations of IL-1β, IL-4, IL-6, IL-8, IL-10, IL-12p40, IFN-α, IFN-γ, and TNF-α were determined. Data were analyzed using mixed models in RStudio, with treatment, sampling time, and their interaction as fixed effects, block as a random effect, and sow as the experimental unit. Statistical significance was declared at $P < 0.05$.

Results and Discussion

Cytokine concentrations were primarily affected by sampling time. IL-6 showed a significant time × treatment interaction ($P = 0.012$), with higher levels in PA1 during gestation, in PA2 at 2 days postpartum, and in CONT at 10 days postpartum. IFN-α was affected by time ($P = 0.002$) and tended to interact with treatment ($P = 0.089$), showing higher levels in PA1 during gestation and lower levels in both supplemented groups at 10 days postpartum. Other cytokines (IL-1β, IL-4, IL-8, TNF-α, IL-12p40) did not differ among treatments ($P > 0.05$) but varied over time ($P \leq 0.018$). IFN-γ and IL-10 did not differ over time or among treatments ($P > 0.05$).

Conclusion

Peripartum physiology primarily shapes cytokine profiles, while phytogenic additives selectively modulate IL-6 and possibly IFN-α without broadly affecting cytokine homeostasis.

Keywords: Immune modulation, Inflammation, Phytogenics, Peripartum.

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POSTPARTUM DISEASE IN SOWS: THE ROLE OF RED BLOOD COUNTS, FRUCTOSAMINE, UTERINE ECHOGENICITY AND INFLAMMATORY MARKERS IN PREDICTING PIGLET SURVIVAL AND UTERINE INVOLUTION

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Introduction and Objectives

Postpartum diseases in pigs result in infertility in sows and are often characterized by inadequate milk production, leading to reduced growth and increased mortality in nursing piglets. Recent research suggests that prolonged systemic stress and inflammation are key contributors to postpartum diseases, such as postpartum dysgalactia syndrome. Aim of this study was to better understand the link between systemic stress and inflammation during the early postpartum (pp) and clinical findings in the sows.

Materials and Methods

A study was conducted involving 45 sows with a parity of two to four and an average litter size of 17.3 piglets. Clinical examinations were performed on days 3 and 5 pp, assessing appetite, vulvar discharge, and mammary gland, along with ultrasound evaluation of the uterus. The uterine exams were analyzed for diameter, intra-luminal fluid accumulation, and echogenicity using the Weasis DICOM Viewer (v. 4.6.5.). One blood and saliva sample was collected each day to measure inflammatory (IL-6, TNF-α, Aldolase), stress (cortisol, Chromogranin A (CgA)), oxidative stress (ROS, Carbonyl, TBARS), and metabolic (IGF-1, Glucose, Fructosamine) markers, as well as blood counts. Litter characteristics, including size, mortality, and weight gain during lactation, were recorded.

Results and Discussion

The results revealed positive correlations on day 3 between high uterine echogenicity and levels of Aldolase ($P < 0.05$). On day 5, concentrations of Cortisol, Aldolase, and CgA were positively associated with piglet mortality before weaning ($P < 0.05$). Additionally, fructosamine levels on days 3 and 5 positively correlated with red blood cell counts and hemoglobin levels on those days, as well as red blood cell counts on day 3 negatively with uterine size at weaning. These findings indicate that inflammation and stress levels in sows during early lactation positively correlate with uterine hyperechogenicity, while negatively impacting piglet survival.

Conclusion

Ultrasound assessment of the uterus on day 3 could serve as a predictive tool for piglet survival; a hyperechoic uterine appearance suggests higher inflammation and stress levels in the sows. Additionally, the results highlight a possible connection between red blood cell counts and fructoseamine during early lactation, and uterine size at weaning.

Keywords: Metabolic biomarkers, Post-partum disease, Stress biomarkers, Ultrasound, Uterine health.

INVESTIGATION OF WHETHER REPEATED PGF2A TREATMENT INDUCES DEPENDENCE IN PORCINE OVARIAN GRANULOSA CELLS IN VITRO

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Introduction and Objectives

Exogenous synthetic Prostaglandin F2α (PGF2α) is used to regulate female livestock's estrus and parturition. In production practice, repeated PGF2α injections are administered to induce synchronous estrus. Whether multiple PGF2α injections exert adverse effects on animal physiological functions and induce dependence remains unclear. This study explored the effects of repeated PGF2α treatment on porcine granulosa cells (GCs) proliferation, apoptosis, hormone secretion and receptor expression, providing experimental data for assessing the potential occurrence of hormone dependence (a state in which GCs exhibit abnormal proliferation, apoptosis, hormone secretion or receptor expression due to repeated exposure to PGF2α) in vitro.

Materials and Methods

GCs were divided into the control group, and the single-treatment, double-treatment, and triple-treatment with 200 μg·mL-1 PGF2α-T groups. All samples were collected simultaneously. CCK-8, TUNEL, ELISA, qRT-PCR and Western Blotting were used to detect proliferation, apoptosis, hormone secretion, and receptor expression. All experiments were conducted with 3 independent biological replicates, each including 3 technical replicates.

Results and Discussion

Following single and double treatments with 200 μg·mL-1 PGF2α-T, no significant changes were detected in the cell proliferation compared with the control group, while triple treatments promoted the proliferation. The counts of apoptotic cells and the expression of Follicle-Stimulating Hormone Receptor (FSHR) and Luteinizing Hormone Receptor (LHR) remained similar across all groups. Compared with the control group, single and double treatments had no effect on hormone secretion, whereas triple treatments reduced estrogen and progesterone secretion. Additionally, single treatment had no effect on the expression of Prostaglandin F Receptor (PTGFR), whereas double and triple treatments significantly up-regulated the expression. Given the promoted proliferation and reduced hormone secretion following triple treatments, the upregulated expression of PTGFR indicates that repeated treatments increase the sensitivity of GCs to PGF2α-a adaptive response that suggests the possibility of dependence induction in vitro. Due to the passage limitation of primary GCs, we were unable to detect the long-term effects, so we will continue to monitor the long-term effects in vivo experiments in the future.

Conclusion

Under the tested in vitro conditions, repeated PGF2α exposure did not induce overt apoptotic or functional impairment of granulosa cells.

Keywords: Dependence, Granulosa cells, Porcine, Prostaglandin F2α Tromethamine.

Acknowledgements: We gratefully acknowledge the financial support for this study provided by Ningbo Sansheng Biotechnology Co., Ltd.

REPRODUCTIVE PERFORMANCE OF REPLACEMENT GILTS AFTER ESTRUS SYNCHRONIZATION WITH DIFFERENT ALTRENOGEST FORMULATIONS

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Introduction and Objectives

The reproductive performance of sows is key for increasing profitability of pig farms (Yang et al., 2009; Li et al., 2015). Altrenogest is used to regulate estrus cycle in gilts and impacts their reproductive performance. This study aimed to investigate reproductive performance after estrus synchronization of gilts using different altrenogest formulations, comparing their effect on estrus rate, farrowing rate, and average litter size.

Materials and Methods

The experiment was conducted at a new breeding herd in Nong'an County, Jilin Province (China). During the establishment of the farm, a total of 1160 Danish hybrid replacement gilts were used to restock the farm during 8 consecutive batches (three-week system). At arrival, gilts from each batch were randomly assigned to either Group A or Group R. Each gilt was allocated alternately to ensure random distribution (e.g., one to Group A, the next to Group R). The groups were housed in two separate but similar partitions within the same herd facility. For estrus induction, Group A (n = 569) received Altresyn® (Ceva), while Group R (n = 560) was treated with Regumate Porcine® (MSD Animal Health). The first batch of gilts was allowed to show natural estrus without synchronization, while Altrenogest was used for estrus induction starting from the second batch until the eighth batch. Reproductive performance was recorded and the estrus rate % (ER), farrowing rate % (FR) and litter size (LS) were calculated. Data from ER and FR were analyzed by Fisher's exact test and LS by ANOVA test.

Results and Discussion

In general, ER%, FR% and LS were improved in most of the batches from Group R compared to group A. The overall ER% was significantly higher in group R (94.95%) compared to group A (89.29%) ($P < 0.05$). The overall FR% was numerically higher in group R (91.91%) than in group A (88.22%) ($P = 0.07$). The average LS was significantly larger in group R (14.3 ± 2.7) compared to group A (13.8 ± 2.4) ($P < 0.05$).

Conclusion

Under the conditions of this experiment, the reproductive performance of gilts varies depending on the altrenogest formulation used. Gilts synchronized with altrenogest from Group R had a significantly higher estrus rate, and a significantly larger litter size.

Keywords: Altrenogest, Estrus rate, Farrowing rate, Litter size, Reproductive performance.
Acknowledgements: The authors thank the producer for the field support during the trial.

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THE PLANT *SOLANUM GLAUCOPHYLLUM* REDUCES FARROWING DURATION AND INCREASES EARLY PIGLET SURVIVAL

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Introduction and Objectives

Farrowing duration and colostrum intake are critical determinants of piglet survival until weaning. Increasing evidence suggests an important role of vitamin D in sow reproductive performance (Yang & Ma, 2021). The plant *Solanum glaucophyllum* (SG) contains 1,25$(OH)_2$D3-glycosides, which support vitamin D metabolism in pigs. This study aimed to evaluate the effects of long-term dietary SG supplementation on farrowing performance and early piglet survival.

Materials and Methods

In a commercial Brazilian breeding-to-finishing farm, farrowing performance of 139 DanBred gilts (F1; Landrace x Large White) was monitored. The animals received a standard diet (CON; 70 sows) or CON supplemented with dried and ground SG-leaves (Panbonis®, Herbonis Animal Health, CH; SG; 69 sows) from weaning onward. SG was included throughout the trial with 100 g/ton. At 1st parity farrowing duration (first to last piglet), litter characteristics at birth, 24 h and 10 days, and sow rectal body temperature (RT) postpartum (pp) were assessed. Cross-fostering within the treatment group was performed within 48h pp. Colostrum intake was calculated according to (Devillers et al., 2004) and composition was measured by wet chemistry.

Results and Discussion

The number of total born piglets was 18.3 in CON and 18.7 in SG ($P = 0.548$). However, the proportion of live-born piglets was higher in SG (92.9%) compared to CON (89.3%; $P = 0.042$). Farrowing duration was reduced by 92 min in SG ($P < 0.001$), resulting in shorter expulsion time per piglet (16 min vs. 23 min, $P < 0.001$). RT was numerically lower during the first two hours pp and significantly lower than 4h pp in SG ($P < 0.001$). Total fat and solids in colostrum were slightly reduced in SG, but colostrum intake per piglet was 38 g higher. Litter size ($P = 0.053$) and piglet weight at 10 days ($P = 0.094$) tended to be higher in SG.

Conclusion

Dietary supplementation of SG to sows improved the farrowing process and increased the number of live-born piglets. Enhanced colostrum intake suggests earlier and more effective suckling behavior, potentially stimulating colostrum production. The slightly lower fat and total solid content may reflect greater overall colostrum yield in sows fed SG.

Keywords: Colostrum intake, Dietary supplementation, Farrowing performance, Piglet survival, Vitamin D.

Acknowledgements: The authors thank the staff of InsideSui and the farm for their time and dedication to the trial.

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ORAL PRESENTATION



TOPIC 12: PIG FARMING PRACTICE (PFP)

IMPROVING PIGLET WEANING OUTCOMES THROUGH PRECISION CREEP-FEEDING MANAGEMENT

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Introduction and Objective

Creep feed intake during lactation is essential for preparing piglets for weaning and contributes to improved post-weaning growth performance (Sulabo et al., 2025). However, many Thai swine farms tend to over-provide creep feed, which often leads to post-feeding diarrhea and reduced weaning weight. This study aimed to train farm staff to provide creep feed at appropriate amounts prior to weaning.

Materials and Methods

A 5,000-sow commercial farm with four production units was used in this study. Approximately 55 sows farrowed weekly under an all-in all-out system. Piglets received creep feed from 5 to 25 days of age, with amounts precisely measured using a scale and calibrated scoops. The feeding program consisted of 7 g/piglet/day from days 5 - 14, 15 g/piglet/day from days 15 - 20, and 25 g/piglet/day from days 21 - 25. Feed was offered twice daily at 10:00 and 14:00. Piglet weaning weight and the number of piglets weaned per litter were recorded to assess the effectiveness of the controlled creep-feeding regimen.

Results and Discussion

Piglets consumed an average of 285 g/piglet of creep feed. No severe diarrhea cases were observed in the farrowing unit throughout the study. The average weaning weight reached 6.5 kg at 25 days of age, with 16.0 piglets weaned per sow. Providing creep feed at accurate, controlled amounts for at least 15 days prior to weaning demonstrated clear benefits for farm productivity (Muro et al., 2023). Controlled intake helped prevent digestive upset and supported consistent growth and uniformity within litters.

Conclusion

The findings indicate that suckling piglets should receive appropriately controlled creep feed throughout the lactation period. Proper feed quantity and consistent feeding management are essential for supporting pre-weaning development.

Keywords: Creep feed, Farm performances, Feeding program, Suckling pigs
Acknowledgements: The authors deeply thank SN Breeder farm, Nakhon Ratchasima province for providing and sharing farm data

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ASSESSING BEHAVIORAL READINESS FOR BIOSECURITY ADOPTION AMONG VIETNAMESE PIG FARMERS USING THE ADKAR METHODOLOGY

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Introduction and Objectives

Biosecurity is a cornerstone of disease prevention and sustainable pig production, yet its adoption varies across production systems. Understanding farmers' behavioral readiness is critical for designing effective interventions. This study applied the ADKAR behavioral-change framework to assess Vietnamese farmers' readiness to adopt biosecurity practices and to examine how behavioral readiness relates to on-farm biosecurity implementation.

Materials and Methods

A cross-sectional study was conducted among 72 pig farms in two Vietnamese provinces, Đồng Nai (n = 35) and Hà Nội (n = 37), representing company-led indoor farms (n = 8), privately owned indoor farms (n = 28), and backyard/household production systems (n = 36). Farmers participated in semi-structured interviews to generate individual ADKAR profiles, with each component scored on a five-point scale (1 - 5). Biosecurity implementation was quantified using Biocheck.Ugent methodology, generating standardized scores (0 - 100) for biosecurity. Statistical analyses evaluated differences by province, farm type, and farm size, and explored associations between ADKAR profiles and biosecurity scores.

Results and Discussion

Across both provinces, farmers demonstrated high motivation to improve biosecurity, with desire to show the highest average score. In contrast, Awareness, Knowledge, and Ability consistently scored below the threshold required for successful change, indicating widespread behavioral barriers. Only 8.3% of farms exhibited no ADKAR-related blockages. Farmers in Dong Nai scored significantly higher than those in Ha Noi for Awareness and Knowledge, while Desire and Ability did not differ significantly by province. Farm type and size were the strongest determinants of behavioral readiness: company-led and large-scale farms showed higher ADKAR scores and more comprehensive biosecurity implementation, whereas backyard and household farms exhibited persistent gaps despite high motivation. Farms with high ADKAR profiles generally achieved higher biosecurity scores, supporting a positive relationship between behavioral readiness and effective biosecurity implementation.

Conclusion

Vietnamese pig farmers show strong willingness to improve biosecurity, but behavioral gaps limit implementation, particularly among small-scale producers. Behaviorally informed, scale-specific interventions that strengthen foundational ADKAR components are essential to translate motivation into sustained biosecurity improvements across the sector.

Keywords: Biosecurity, Behavioral change, Disease prevention, Pig production.

ASSESSMENT OF PERSONAL PROTECTIVE EQUIPMENT (PPE) USAGE BY TRUCK DRIVERS DURING MARKET HOGS UNLOADING AT A US HARVEST FACILITY

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Introduction and Objectives

Market hog truck drivers play a crucial role in the swine industry as they are one of the few individuals who move between multiple pig sites daily. Their practices during loading/unloading can influence trailer contamination and animal welfare. This study aims to characterize market hog driver practices and perceptions of biosecurity.

Materials and Methods

As part of a larger study focused on assessing trailer contamination during market hog unloading, truck drivers were engaged through a survey administered at a Midwestern U.S. harvest facility. A convenient sample of 182 drivers participated in the study, in which each driver answered a questionnaire.

Results and Discussion

When arriving at the harvest facility, some drivers changed into unloading/loading dedicated shoes and/or clothes before entering the lairage area. The most common footwear used was rubber boots (92.5%), followed by leather boots (7.5%). In some cases, drivers also wore disposable plastic booties (7.7%) or shoe covers (8.5%) over their footwear. A total of 57.8% of the drivers used fabric coveralls, 13.1% used disposable coveralls, and 22.4% used regular pants/shirts, and 6.7% used shorts and shirts/t-shirts. Most drivers (85.9%) wore fabric gloves, while 7.2% used latex gloves and 6.9% wore no hand protection. The combination of PPE a driver varied between the above-mentioned options. The most common combination was the use of rubber boots, fabric coveralls, and fabric gloves (49.1%). When 112 drivers were asked why they chose to use the PPE they used, 40.2% admitted that it ~~is~~ was to remain clean, 25% of them did not know why they were using PPE, 4.5% used it for both comfort and to stay clean, 8% comfort only, 3.6% used it because they were required to, and only 8% responded that these were for biosecurity reasons.

Conclusion

These results show that PPE usage during unloading is variable among market hog truck drivers, which is an important risk factor for trailer contamination if the PPE is not properly disposed of or cleaned between loads. It also highlights that a small proportion of drivers understand why PPE is important, showcasing the importance of training and educational opportunities within this group.

Keywords: Biosecurity, PPE, Truck drivers, Unloading.

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EFFECT OF AN ACTIVATED ZINC OXIDE TO REPLACE PHARMACOLOGICAL ZINC OXIDE IN PIGLETS TO CONTROL POST-WEANING DIARRHEA

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Introduction and Objectives

Post-weaning diarrhea (PWD) is a major challenge in pig production prevented with high amounts of zinc oxide (ZnO) and treated with antibiotics contributing to the risk of antimicrobial resistance (Lallès et al., 2007). A novel activated ZnO source with modified physiochemical properties leads to improved reactivity and antimicrobial activity, especially against gram-negative bacteria, such as Escherichia coli (*E. coli*) (Ma et al., 2013). Thus, the aim of the present study was to assess the effect of an activated ZnO on growth performance, diarrhea incidence, and intestinal permeability of weaning piglets compared to pharmacological ZnO.

Materials and Methods

A feeding trial was conducted with 1480 piglets (BW: 6.7 kg) weaned at 26 d. Piglets were randomly selected and placed in one of ten pens with 37 piglets. Piglets were fed in four phases post-weaning. A basal diet was supplemented with three different concentrations of an activated ZnO (high, medium, low) for each phase compared to the pharmacological feed-grade ZnO control (2400, 2100, 1800, 1500 ppm Zn): Phase 1 (800, 600, 400 ppm Zn); Phase 2 (700, 525, 350 ppm Zn); Phase 3 (600, 450, 300 ppm Zn); and Phase 4 (500, 375, 250 ppm Zn). The trial was conducted as a complete randomized block design. Fecal consistency was visually evaluated. Intestinal permeability was assessed by using a non-absorbable fluorescent marker (Vicuña et al., 2015).

Results and Discussion

The average daily gain was greater ($P < 0.05$) for medium and low activated Zn than high ZnO and pharmacological ZnO groups in phases 2, 3, 4 and overall. The feed conversion was lower ($P < 0.05$) for medium and low activated ZnO compared to high and pharmacological ZnO groups in phase 2 and 3. The diarrhea incidence did not differ ($P > 0.05$). The intestinal permeability was lower ($P < 0.05$) for high, medium and low activated ZnO compared to pharmacological ZnO.

Conclusion

The results of the present study demonstrate the potential of a novel activated ZnO source to control PWD as a suitable alternative to pharmacological feed-grade ZnO for feeding concepts aiming to minimize E. coli induced PWD.

Keywords: Activated zinc oxide, diarrhea, *Escherichia coli*, growth performance, piglet.

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SURVEY OF THE CURRENT STATUS OF BIOSECURITY IN SELECTED PIG FARMS IN VIETNAM USING THE PIGHEALTH SECURITY-X SOFTWARE

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Introduction and Objectives

Biosecurity is a cornerstone of infectious disease prevention in pig production and a prerequisite for sustainable livestock systems. Therefore, the present study aimed to (i) evaluate biosecurity performance across different housing systems, farm scales, and production types in Vietnam, and (ii) identify critical weaknesses that require context-specific interventions to strengthen biosecurity and support sustainable pig production.

Materials and Methods

A spatial biosecurity assessment framework was implemented to evaluate pig farms, in which each farm was partitioned into external and internal zones. The internal zone was further delineated into three functional subzones: risk, buffer, and cleanliness. Biosecurity practices were surveyed using the PigHealth Security-X questionnaire, administered to 106 representative farms across Vietnam. External biosecurity was assessed through 30 targeted questions, while internal biosecurity was evaluated using 135 targeted questions, with scores averaged across the three subareas. The overall biosecurity index (BStot) was calculated as the means of the external and internal biosecurity scores.

Results and Discussion

Most closed-house farms achieved biosecurity scores exceeding 60 points, with large-scale sow farms attaining the highest mean score (81.35), indicative of substantial investment in infrastructure and compliance with standardized procedures. In contrast, open-house farms generally scored below 60; however, large-scale farrow-to-finish operations reached 75.98, suggesting that farm scale can partially offset structural limitations. Small-scale, open-house and grower-to-finish farms recorded the lowest mean score (37.66), underscoring limited awareness and implementation of biosecurity practices. Comparative analysis across farm type, scale, and production system demonstrated that closed-house facilities, large-scale operations, and sow farms consistently achieved higher scores across all zones. The weakest component across all farms was feed and water hygiene within the clean zone, representing a persistent critical gap. Buffer and risk zones were particularly vulnerable in open-house and small-scale farms, largely due to deficiencies in personnel management, equipment handling, and operational practices.

Conclusion

Biosecurity performance in Vietnamese pig farms exhibits substantial variation across housing systems, farm scales, and production types. Furthermore, feed and water management remain the most pervasive weakness across the sector, underscoring the urgent need for targeted, context-specific interventions to enhance biosecurity and mitigate the risk of disease outbreaks.

Keywords: Biosecurity, Pig farm type, Production operation, Scale.

Acknowledgements: The authors thank Nong Lam University HCMC, Vietnam for the support with providing testing facilities.

EVALUATION OF DEPLOYABLE FAN COVERINGS FOR BIOCONTAINMENT OF AIRBORNE PARTICLES ASSOCIATED WITH SWINE VIRAL TRANSMISSION

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Introduction and Objectives

Pathogens such as PRRSV and IAV are spread by respiratory secretions, dust, and other microscopic particles (Otake et al., 2010). Studies have shown that virus detectability and viability are influenced by particle size, with PRRSv and IAV isolated from particles larger than 2.1 µm (Zuo et al., 2013; Alonso et al., 2015). This study aimed to evaluate whether rapidly deployable exhaust fan coverings reduce expelled airborne particles that may facilitate transmission of swine pathogens, such as PRRSV.

Materials and Methods

One wean-to-finish site was selected featuring various fan sizes (24" - 50"). Three materials were compared to a fan with no covering: PolyKlean™ synthetic media (Blue Poly), Nylon, a tear-resistant fan sock (Fan Sock) staked to the ground to redirect airflow, and a Polyethylene privacy screen (Black Screen). Airborne particle counts were collected 1 meter from the fan interior and 1, 2, and 3 meters from the fan exterior using an optical particle counter. Three consecutive measurements were performed at each distance and location to calculate an average particle count, with three replicates per treatment and fan. A two-way repeated measure ANOVA was conducted to evaluate the effects of fan cover treatment and fan size on air particle quantity measurements.

Results and Discussion

At 1 meter from the fan, the fan sock treatment had a lower average particle count of 5.0 µm than no cover or the blue poly treatments ($P = 0.046$). At 1 meter in front of the fan on the inside of the barn, the 50" fan had significantly lower particle counts of particles measuring 1.0 µm ($P = 0.002$) and 5.0 µm ($P = 0.003$), and overall ($P < 0.001$). Differences in air particle counts based on fan size were not observed ($P > 0.10$). Fan sock treatment had the greatest impact on reducing particles 1 meter outside of a fan. However, as the distance from the fan increased, there was no difference in air particle quantity across treatments.

Conclusions

This pilot study suggests that rapidly deployable fan coverings may reduce exhausted air particle quantity at short distances from the barn, thus questioning their role in improving biocontainment of aerosolized particles that may carry pathogens.

Keywords: Aerosol, Biocontainment, Biosecurity, Fan covering, PRRS.
Acknowledgements: Funding for this project was provided by the Swine Health Information Center.

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KNOWLEDGE, ATTITUDES, AND PRACTICES TOWARD TRANSBOUNDARY ANIMALS AND EMERGING ZOONOTIC DISEASES AMONG PIG FARMERS IN NORTHERN VIETNAM

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Introduction and Objectives

Vietnam was one of the hotspot countries for transboundary animal and emerging zoonotic diseases (TAEZDs) in Southeast Asia. This cross-sectional study aimed to explore knowledge, attitudes, and practices (KAP) regarding TAEZDs and its associated factors among household-scale pig farmers in Lao Cai and Phu Tho provinces.

Materials and Methods

A structured questionnaire was used to collect socio-demographic and KAP information from 294 pig farmers across twelve communes. The study was done between December 2024 and June 2025 as part of the ICT4 health project. Descriptive and statistical analyses, such as Wilcoxon rank sum test, linear regression, were performed using RStudio to identify potential factors associated with knowledge, attitudes, and practices.

Results and Discussion

The overall mean knowledge, attitudes and practices scores toward TAEZDs and their prevention were 27.3 out of 35, 3.8 out of 4, and 7.3 out of 10, respectively. Key factors associated with better knowledge of TAEZDs included being male ($P = 0.04$), married and primarily responsible for caring for pigs ($P = 0.03$), and attending livestock production training ($P = 0.04$). Moreover, farmers from Phu Tho province ($P = 0.03$), and those with higher education ($P = 0.008$) showed more positive attitudes toward TAEZDs compared to farmers from Lao Cai province and with lower education. Factors associated with better TAEZDs prevention practices were being female ($P = 0.01$), younger age, married group ($P = 0.02$), and primarily responsible for caring for pigs ($P = 0.02$). In particular, larger farms had significantly higher knowledge and practice scores ($P < 0.01$) but not attitudes scores. Interestingly, farmers who reported that pigs had previously gotten Streptococcosis and leptospirosis had higher knowledge and attitude scores ($P < 0.05$), however no differences in scores were found among farmers who reported cases of African swine fever. Pearson correlation analysis revealed a significant positive relationship between knowledge and practice ($r = 0.2$, $P < 0.001$), attitude and practice ($r = 0.1$, $P < 0.05$), although the correlations were modest.

Conclusions

Smallholder pig farmers in northern Vietnam demonstrated positive attitudes but only moderate levels of knowledge and practices regarding TAEZDs. Targeted interventions should focus on localized, peer-led and hand-on training approaches that include gender and farming responsibility aspects. These efforts are essential to bridge the gap between positive attitudes, knowledge and effective biosecurity practices.

Keywords: Biosecurity, Disease prevention, KAP, Pig farms.

Acknowledgements: We sincerely thank the Lao Cai Provincial Sub-Department of Crop and Plant Protection, Animal Health and Fishery; Phu Tho Provincial Sub-Department of Animal Husbandry, Veterinary, and Fishery; and local veterinary and animal health officers for their valuable support. We also acknowledge Ministry of Agriculture, Food and Rural Affairs of the Republic of Korea (MAFRA) and Sustainable Animal and Aquatic Foods (SAAF) program for their financial support.

COLOSTRUM COMPOSITION IN RELATION TO FARROWING DYNAMICS AND REPRODUCTIVE PERFORMANCE OF SOWS

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Introduction and Objectives

Colostrum is essential for neonatal piglets, providing not only energy and immunoglobulins but also hormones and bioactive compounds critical for early survival. In addition to its nutritional function, colostrum may reflect the sow's physiological and endocrine status during the periparturient period. This study investigated the associations between colostrum composition, farrowing characteristics, and reproductive performance of sows housed in a free-farrowing system.

Materials and Methods

Sixty sows were monitored, and colostrum samples (5 - 10 mL) were collected following the birth of the first piglet. Concentrations of progesterone, albumin, and α-lactalbumin were quantified in colostrum serum. Farrowing traits and litter outcomes were recorded.

Results and Discussion

A total of 897 piglets were born, with a mean farrowing duration of 242 min. Mean colostrum concentrations were 21.6 ± 10.8 ng/mL for progesterone, 7.33 ± 1.47 mg/mL for albumin, and 1602.7 ± 506.9 ng/mL for α-lactalbumin. Progesterone concentrations were positively correlated with albumin ($r = 0.29$; $P = 0.02$) and α-lactalbumin ($r = 0.38$; $P = 0.002$). Additionally, colostrum progesterone showed positive associations with log-transformed farrowing duration ($r = 0.27$; $P = 0.03$), piglet-to-placenta expulsion interval ($r = 0.26$; $P = 0.04$), and the incidence of severe meconium staining ($r = 0.27$; $P = 0.04$). Sows requiring more than one obstetrical intervention had significantly higher colostrum progesterone concentrations (25.9 ng/mL) compared with sows requiring none or one intervention (19.3 ng/mL; $P = 0.02$).

Conclusion

This study is the first to demonstrate associations between specific colostrum traits and farrowing outcomes in a free-farrowing system. Although correlations were modest, colostrum progesterone may serve as a potential indicator of prolonged or more difficult farrowing.

Keywords: α-lactalbumin, Albumin, Progesterone, Obstetrical intervention.

POSTERS

TOPIC 1: VIROLOGY AND VIRAL DISEASES (VVD)

MICROBIAL COMMUNITY AND METABOLOME ANALYSIS OF THE PORCINE INTESTINAL DAMAGE MODEL INDUCED BY THE IPEC-J2 CELL CULTURE-ADAPTED PORCINE DELTACORONAVIRUS (PDCOV) INFECTION

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Introduction and Objectives

Porcine deltacoronavirus (PDCoV) is a newly emerged enteropathogenic coronavirus associated with swine diarrhea, the pathogenic mechanisms of PDCoV are still poorly documented and warrant further exploration. To date, no metabolomic analysis of PDCoV has been reported. Understanding the intricate interplay between PDCoV infection, piglet susceptibility, and the consequential alterations in intestinal microbiota and metabolism is imperative for devising effective preventive and therapeutic strategies.

Materials and Methods

Oral PDCoV-inoculated piglets were monitored daily for symptoms. Intestinal samples were fixed in 10% buffered formalin, processed for H&E staining (histopathology) and immunofluorescent staining to elaborate on the pathological changes. The mid-intestinal digesta were sterilely collected, frozen in liquid nitrogen for 16S rRNA sequencing. Stool samples underwent microbial community profiling and LC-MS-based metabolomics analysis.

Results and Discussion

PDCoV disrupted intestinal structure, increased permeability, and induced mucosal pathological abnormalities, with inoculated piglets exhibiting persistent watery diarrhea (PID 1 - 4), gross intestinal lesions, and severe ileal villous atrophy, while controls and other organs were unaffected. Additionally, PDCoV induced an imbalance in the intestinal flora and disturbed its stability. Microbial community profiling revealed bacterial enrichment (e.g., Proteobacteria) and reduction (e.g., Firmicutes and Bacteroidetes) in the PDCoV-inoculated piglet model. In addition, metabolomics analysis indicated that 82 named differential metabolites were successfully quantified, including 37 up-regulated and 45 down-regulated metabolites. Chenodeoxycholic acid, sphingosine, and oleanolic aldehyde levels were reduced in PDCoV-inoculated piglets, while phenylacetylglycine and geranylgeranyl-PP levels were elevated. Correlation analysis indicated a negative correlation between Escherichia-Shigella and choline, succinic acid, creatine, phenyllactate, and hippuric acid. Meanwhile, Escherichia-Shigella was positively correlated with acetylcholine, L-Glutamicacid, and N-Acetylmuramate. Roseburia, Lachnospiraceae_UCG-010, Blautia, and Limosilactobacillus were negatively and positively correlated with sphingosine, respectively.

Conclusion

These data suggested PDCoV-inoculated piglets exhibited significant taxonomic perturbations in the gut microbiome, which may result in a significantly altered metabolomic profile.

Keywords: Intestinal damage, Metabolome analysis,Microbial community profiling, Porcine deltacoronavirus, Piglets.

Acknowledgements: This work was supported by the Shanghai Agriculture Applied Technology Development Program, China (No. 2019-3-3).

ENHANCING SURVEILLANCE OF ENTERIC CORONAVIRUSES IN SWINE HERDS: EVALUATION OF A MULTIPLEX RT-QPCR ASSAY FOR SIMULTANEOUS DETECTION OF PEDV, PDCOV, AND TGEV RNA

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV), porcine deltacoronavirus (PDCoV), and transmissible gastroenteritis virus (TGEV) are highly contagious RNA viruses causing severe enteric disease in swine. Accurate diagnosis is essential for surveillance and control. Previous studies reported RT-qPCR assays for these viruses; however, most focus on single-virus or duplex detection and often lack internal controls, limiting efficiency and reliability (Niu et al., 2022; Lazov et al., 2023). This study evaluates a multiplex RT-qPCR assay designed to simultaneously detect and differentiate PEDV, PDCoV, and TGEV RNA in one reaction.

Materials and Methods

The RealPCR PEDV/PDCoV/TGEV Multiplex RNA Mix (IDEXX) was developed for simultaneous identification of PEDV, PDCoV, and TGEV RNA. The assay includes an internal sample control (ISC) targeting endogenous swine RNA to verify sample quality, addition, extraction, and amplification. Inclusivity, exclusivity (including PRCV and common swine pathogens), and limit of detection were assessed. Study 1 evaluated diverse sample types (fecal swabs, feces, intestinal content, oral fluids, and environmental samples), including pooled specimens (1:10). Study 2 compared diagnostic performance with a commercial RT-qPCR test using 51 field samples.

Results and Discussion

The assay showed high inclusivity, no cross-reactivity, and a detection limit of 10 copies/reaction. In Study 1, agreement with a reference PCR was 99.4% for PEDV, 99% for PDCoV, and 100% for TGEV. Pooled samples showed Ct delays of 3 - 5 cycles. In Study 2, IDEXX PCR detected five more PEDV positives than PCR-B (83.9% agreement); PDCoV agreement was 98%, with one additional positive identified by IDEXX PCR. The ISC ensured confidence in negative results, supporting surveillance programs. For environmental samples where endogenous RNA may be scarce or absent, adding an optional internal positive control is recommended.

Conclusion

The RealPCR PEDV/PDCoV/TGEV Multiplex RNA Mix demonstrated strong analytical performance, with high inclusivity, no cross-reactivity, and a detection limit of 10 copies per reaction. It consistently detected targets in pooled samples and reliably differentiated swine enteric coronaviruses in a single reaction.

Keywords: Coronavirus, PCR, PDCoV, PEDV, TGEV.

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ANALYTICAL COMPARISON OF RNA EXTRACTION METHODS FOR PRRSV-1 AND PRRSV-2 RNA DETECTION USING MULTIPLEX RT-QPCR

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a significant challenge to swine health worldwide, necessitating highly sensitive, reliable diagnostic approaches. This study aimed to evaluate and compare the analytical performance of two RNA extraction methods for detecting PRRSV-1 and PRRSV-2 using multiplex RT-qPCR.

Materials and Methods

Quantified PRRSV-1 and PRRSV-2 strains were spiked into PRRSV-negative serum and semen samples, both individual and pooled (1:5). Serial 10-fold dilutions were prepared and extracted using two commercial kits: IDEXX Extraction Kit (RealPCR DNA/RNA Magnetic Bead Kit, IDEXX Laboratories) and a second leading commercial kit (Kit B). For each sample type: individual serum, pooled serum, individual semen, and pooled semen, 80 RNA extracts per extraction method were tested (640 total). All extracts were analyzed using the RealPCR PRRSV-1/PRRSV-2 Multiplex RNA Test. The limit of detection (LOD) for each extraction method was defined as the lowest viral concentration consistently detected in 8 of 8 replicates.

Results and Discussion

The IDEXX Extraction Kit showed consistent detection of PRRSV-1 and PRRSV-2 across all tested sample types, indicating high analytical sensitivity. For individual serum and semen samples, the LOD was 6.3 $TCID_{50}$/mL for PRRSV-1 and 15.8 $TCID_{50}$/mL for PRRSV-2, comparable to the performance of the extraction Kit B. In pooled serum samples, both extraction methods achieved a low LOD for PRRSV-1 (1.26 $TCID_{50}$/mL), while detection thresholds for PRRSV-2 remained consistent at 31.6 $TCID_{50}$/mL. Ct values exhibited a progressive shift toward earlier cycles with increasing viral concentrations, consistent with the expected dynamics of quantitative PCR. These results reflect the performance of the complete analytical workflow and confirm its sensitivity and reproducibility across both extraction protocols.

Conclusion

The IDEXX Extraction Kit demonstrated robust analytical performance for the detection of PRRSV-1 and PRRSV-2 in serum and semen samples, including pooled specimens. Its sensitivity was comparable to that of the extraction Kit B, with both methods achieving low detection thresholds across sample types. When paired with the RealPCR PRRSV assay, the IDEXX Extraction Kit enables reliable and efficient molecular detection of PRRSV, supporting its application in routine diagnostic workflows and surveillance programs in swine health-.

Keywords: Extraction, PRRSV, RT-qPCR, Semen, Serum.

NLRX1 MEDIATES THE DISRUPTION OF INTESTINAL MUCOSAL FUNCTION CAUSED BY PORCINE ASTROVIRUS INFECTION VIA THE ERK/MLCK PATHWAY

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Introduction and Objectives

Porcine astrovirus (PAstV) is a widespread enteric virus with zoonotic potential (Rawal et al.,2022), yet its cellular pathogenesis remains poorly understood. Our previous proteomics study identified mitochondrial protein NLRX1 as significantly upregulated during PAstV-4 infection (Tao et al., 2022). This study aims to investigate the role of NLRX1 in PAstV-4 replication and its impact on intestinal mucosal barrier function.

Materials and Methods

Caco-2 cells were infected with PAstV-4 strain SH/2022/CM1. Viral propagation was confirmed by immunofluorescence and $TCID_{50}$ assays. Barrier integrity was assessed via qPCR and Western blot analysis of tight junction proteins (Occludin, ZO-1) and MUC-2. NLRX1 was silenced using siRNA to examine its role in viral replication ($TCID_{50}$), mitophagy (LC3-II), and barrier function upon infection. To investigate the signaling pathway, cells were pretreated with inhibitors (PD98059, 3-MA, or ML-7), followed by Western blot analysis of p-ERK, p-MLC, and barrier proteins to link NLRX1 to ERK/MLCK activation.

Results and Discussion

PastV-4 infection up-regulated NLRX1 and mitophagy in Caco-2 cells significantly, while silencing of NLRX1 or treatment with mitophage inhibitor 3-MA inhibited PastV-4 replication. Additionally, PastV-4 infection triggered the activation of the extracellular regulated protein kinases/ myosin light-chain kinase (ERK/MLCK) pathway, followed by down-regulation of the tight-junction proteins (Occludin and ZO-1) as well as MUC-2 expression. Silencing of NLRX1 or treatment of 3-MA inhibited myosin light-chain (MLC) phosphorylation and up-regulated the Occludin and ZO-1 protein. Treatment of the ERK inhibitor PD98059 also inhibited the MLC phosphorylation, while MLCK inhibitor ML-7 mitigated the down-regulation of mucosa-related protein expression induced by PastV-4 infection. Yet, adding PD98059 or ML-7 could not affect the NLRX1 expression. In summary, this study preliminarily explained that NLRX1 played an important role in the disruption of intestinal mucosal function triggered by PastV-4 infection via the ERK/MLC pathway.

Conclusion

Our findings first establish that NLRX1 is a key regulator mediating PAstV-4-induced mucosal barrier damage through the ERK/MLCK pathway. By elucidating this mechanism, this study provides a foundational basis for targeting NLRX1 in the development of therapeutics for porcine viral diarrhea.

Keywords: ERK/MLCK, Intestinal mucosal barrier, Mitophagy, NLRX1, Porcine astrovirus.

Acknowledgements: This work was funded by the Shanghai Agricultural Technology Development Program, China (Grant No. T20210106) and the SAAS Program for Excellent Research Team (Grant No. [2022]012).

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COMPARATIVE FIELD EFFICACY STUDY OF FLEXCOMBO® AND PORCILIS® PCV M HYO IN A KOREAN FARM

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Introduction and Objectives

Porcine circovirus type 2 causes porcine circovirus diseases (PCVD). After the introduction of PCV2 vaccines, PCVD symptoms disappeared in most farms in Korea. However, there's no guarantee that all PCV2 vaccines have the same level of efficacy under commercial conditions. This study compares two PCV2 vaccines in terms of efficacy in field conditions.

Materials and Methods

The study was conducted on 12 consecutive batches of piglets from a production site with 200 sows, with weekly weaning cycle. A total of 1283 piglets were divided into 3 groups of 4 consecutive batches in each group (i.e. group A batch 1 - 4, group B batch 5 - 8 and group C batch 9 - 12). Vaccine treatment was allocated by group at weaning. Pigs from Group A & C received 1 dose of Ingelvac CircoFLEX® with MycoFLEX® (FLEXcombo®, freshly mixed) and pigs from Group B received Porcilis® PCV M Hyo (ready to use product). Fisher's exact test was used for statistical comparison, and Bonferroni correction was applied to adjust for multiple comparisons.

Results and Discussion

Comparisons between the FLEXcombo® as 'A','C' groups and Porcilis® PCV M Hyo as 'B' group, demonstrated a significant difference in mortality rate between these 2 treatments (p-value 0.0167). Mortality of Group A was 11.13% lower than Group B, while Group C was 10.75% lower than Group B. Compared to Group B, Group A and C reduced the batch mortality by 71.2 and 68.8%, respectively, compared to Group B.

Conclusion

As many other cases demonstrated before in Korea, PCV2 vaccination is the best tool to reduce mortality caused by PCVD. But not all vaccines demonstrate the same level of efficacy. In this study, the two FLEXcombo® groups demonstrated better performance than the Porcilis® PCV M Hyo vaccine group. And no difference was observed between the 2 FLEXcombo® groups, which means a putative change of environmental factors during the trial can be excluded as cause of difference in vaccine efficacy. In the Porcilis® PCV M Hyo vaccine group, some dead pigs with clinical signs of wasting, coughing and anorexia were necropsied. And necropsy showed enlarged and swollen inguinal lymph nodes.

Keywords: FLEXcombo®, Porcilis® PCV M Hyo, Porcine circovirus type 2, Vaccine efficacy.
Acknowledgements: The authors thank the 200-sow farm in Gangwon-do, South Korea for the support with providing pigs for the study.

CEREBLON PROMOTES INFLUENZA VIRUS REPLICATION THROUGH AMPK UBIQUITINATION

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Introduction and Objectives

Infection with influenza A and B viruses activates cereblon (CRBN), which binds AMP-activated protein kinase alpha subunit (AMPKα) and promotes the ubiquitination and degradation of AMP-activated protein kinase gamma subunit (AMPKγ), shifting metabolism toward anabolism and inducing lipogenesis. This early lipogenic reprogramming supplies lipids for efficient viral replication. Genetic or IMiDs-mediated CRBN inhibition reduces lipid droplets and robustly suppresses diverse influenza strains, highlighting CRBN-AMPK as a promising broad-spectrum antiviral target.

Materials and Methods

Materials: MDCK, A549 cells were cultured in DMEM at 37°C in 5% CO2. Media were supplemented with 10% fetal bovine serum, 100 U/mL penicillin, and 100 µg/mL streptomycin. The strains of IAV, IBV used included Puerto Rico/8 (PR8) (H1N1), California/04/2009 (H1N1) (2009 Pandemic H1N1-like), Brisbane/10/07 (H3N2), and Chicken/Korea/01310/2001 (H9N2), Austria/1359417/2021 (B/Victoria) and Phuket/3073/2013 (B/Yamagata).

Methods: Cytotoxicity assessment, duolink proximity ligation assay (DPLA), transfection of siRNA, treatment of inhibitory chemicals to cells, immunoprecipitation assay, immunohistochemistry staining (IHC), western blot (WB), real-time quantitative PCR (RT-qPCR), immunofluorescence assay (IFA), hematoxylin and eosin staining (H&E)

Results and Discussion

In vivo, CRBN knockout (KO) mice are resistant to influenza A virus infection with all WT mice challenged with the mouse-adapted PR8 strain died within 10 days, whereas 80% of homozygous KO ($Crbn^{-/-}$) mice survived the IAV challenge. *In vitro*, Lipid droplet (LD) numbers in IAV-infected cells increased from the early stage of infection, peaked at the mid-stage, and then declined, mirroring CRBN expression in both mRNA and protein levels, but inversely correlating with phosphorylated AMPKα levels. In parallel, levels of ubiquitinated proteins rose up to 8 hours post-infection (hpi) then reduced. Significant suppression of viral replication was observed during CRBN inhibitor treatment. The safety and broad-spectrum antiviral of CRBN were confirmed across different IAV strains and other different viruses. CRBN inhibitor protected mice from IAV challenge in a dose dependent manner, and (*R*)-Thalidomide showed synergistic activity with oseltamivir in protecting mice against IAV infection.

Conclusion

This research underscores CRBN as a crucial regulator of host metabolism during viral infection, revealing the CRBN-AMPK axis as a promising host-targeted therapy for pan-influenza antiviral development.

Keywords: Anabolism, AMPK ubiquitination, Cereblon, Influenza virus, Lipogenic reprogramming.

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PARALLEL, RANDOMISED FIELD EFFICACY, AND RETURN-ON-INVESTMENT STUDY OF A NEXT GENERATION PRRSV2-MLV VACCINE COMPARED TO A CONVENTIONAL LINEAGE 7 BASED PRRSV2 MLV VACCINE

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a major challenge in global swine production. A next-generation PRRSV modified live virus (MLV) vaccine, developed by Synthetic Attenuated Virus Engineering (Coleman et al., 2008). Via targeted attenuation by codon pair deoptimization, a significantly reduced speed of NSP1 translation is achieved. The subsequent reduced viral replication and immune deviation are indicated to provide very high efficacy, cross-protective capacity, and safety (Park et al., 2021). This study aimed to compare the effectiveness of the CPD-PRRSV2-MLV with a conventional PRRSV2-MLV in reducing production losses and improving economic outcomes on a commercial wean-to-finish farm under natural PRRSV infection.

Materials and Methods

The trial was conducted on a wean-to-finish farm with a history of PRRSV2 circulation during the fattening phase, confirmed by longitudinal serum PCR; attempts at sequencing the field strain were unsuccessful. The farm routinely used a conventional PRRSV2-MLV as part of its disease control strategy. All piglets originated from a 2,000-sow PRRSV-negative breeding herd. A total of 1,258 piglets were assigned randomly into two groups housed in separate barns with similar management. The CPD-MLV group (n = 625) received a CPD-lineage 5 PRRSV2-MLV (PersoporcTM, Ceva, France) according to farm management traditions, at five weeks of age, while the Con-MLV group (n = 633) received a conventional lineage 7 PRRSV2-MLV. Growth performance, mortality, and economic data were collected throughout the cycle. Economic return was calculated using Gompertz standardization and current local prices.

Results and Discussion

The CPD-MLV group showed better performance, with lower cumulative mortality (1.44 vs. 1.74%), higher average daily gain (709 vs. 676 g/day), and improved feed conversion ratio (2.73 vs. 2.76). Economic analysis revealed higher net profit per pig (51.28 vs. 41.23 €), of 10.05 € in favor of the CPD-MLV group. Under the given endemic PRRSV2 management conditions, the CPD-MLV vaccine demonstrated to be a valid alternative to a traditional MLV vaccine, shown in health, production, and economic outcomes compared to the conventional vaccine.

Conclusion

These findings support the value of the next-generation CPD-MLV vaccine in PRRSV2 control programs, offering benefits for herd health, animal welfare, and profitability.

Keywords: Next-generation, Profitability, PRRSV2, Return-on-investment, Vaccine.

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UNRAVELLING BETWEEN-HERD PRRS TRANSMISSION AND EVALUATING CONTROL STRATEGIES IN DENMARK

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) remains endemic in most pig-producing countries, including Denmark. A national control program was launched in 2022, followed by 2023 legislation mandating routine testing, PRRS status reporting, loss of PRRS-free status after purchases from non-free herds, and region-specific coordination of control activities. The effectiveness of these measures remains uncertain. This study aimed to (i) describe PRRSV transmission dynamics before 2022, (ii) quantify contributions of local and movement-mediated transmission, (iii) map herd-level basic reproduction numbers (R_0), and (iv) assess the expected impact of targeted interventions.

Materials and Methods

We developed a stochastic between-herd compartmental model using Danish PRRS surveillance and pig movement data from 2020 - 2021. Herds transitioned through four states: susceptible (S), highly infectious (I_h), lowly infectious (I_l), and detected (D). Transmission occurred via local spread and pig movements. The model estimated herd-level R_0 values, identified hotspots of sustained transmission, and simulated interventions including depopulation-repopulation (DPRP), increased testing frequency, and stricter risk-based trading.

Results and Discussion

Over 50% of herds had R_0 >1, indicating substantial potential for sustained transmission. Both local and movement-mediated transmission contributed, but local spread primarily explained spatial clustering. Although only 17% of infectious herds were undetected under current surveillance, they accounted for ~60% of onward transmission, highlighting impact of hidden infections. DPRP rapidly reduced observed prevalence but had limited effect on true transmission due to undetected herds. Simulations showed that combining more frequent testing, within-herd PRRS elimination, and stricter risk-based trading greatly increases the likelihood of national eradication. Our model is novel integrating the national surveillance system-blood testing and clinical inspections into a between-herd PRRSV framework, allowing assessment of intervention effectiveness under realistic detection. Calibrated with Danish SPF surveillance data, it enables national-scale, data-driven predictions. However, only herd-level data were available, so within-herd transmission is not explicitly represented; persistence is captured via prolonged herd-level infectious periods.

Conclusion

PRRS persistence in Denmark is driven by local transmission and undetected infections. Effective eradication requires improved surveillance, targeted within-herd control, and stricter trading practices. The model identifies key transmission routes and regional hotspots, providing evidence-based guidance for national PRRS control.

Keywords: Basic reproduction number, Control, PRRS, Surveillance, Transmission model.

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VALIDATION OF THE ENZYMATIC HYDROLYSIS PROCESS OF PORCINE PLASMA AS SAFETY STEP FOR INACTIVATION OF PORCINE EPIDEMIC DIARRHOEA VIRUS (PEDV), PORCINE REPRODUCTIVE AND RESPIRATORY VIRUS (PRRSV) AND PORCINE CIRCOVIRUS-2 (PCV-2)

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Introduction and Objectives

The spray-dried plasma (SDP) manufacturing process has demonstrated efficacy against multiple swine viruses (Blázquez et al., 2020). A current commercial product is based on bioactive peptides obtained through enzymatic hydrolysis of porcine plasma. This study aimed to determine whether the plasma enzymatic hydrolysis process inactivates PEDV, PRRSV and PCV-2 when viruses are inoculated into liquid plasma prior to hydrolysis.

Materials and Methods

PEDV CV777 was propagated in VERO cells, PCV-2 genotype b isolated Sp-10-7-54-13 in PK-15 cells, and PRRSV VP21 strain in MARC-145 cells, each under standard growth conditions. A total of 1.5 kg of bovine plasma (used to avoid antibodies against the target viruses) was divided into three 0.5 L sub-batches. Plasma was heated to 50°C under continuous stirring, after which protease was added, and each sub-batch was inoculated with 50 mL of virus. Hydrolysis was conducted for 5 h under optimal temperature and pH conditions, and the full procedure was performed in triplicate. Samples collected before and after hydrolysis were stored at -75°C. Infectivity was assessed in Vero (PEDV), PK-15 (PCV-2) and MARC-145 (PRRSV) cells using a microtiter assay adapted to 24-well plates. PEDV was evaluated by cytopathic effect (CPE), whereas PCV-2 and PRRSV detection relied on quantitative PCR, comparing Ct values at 0 and 3 dpi to assess potential viral replication.

Results and Discussion

For PEDV, CPE at T0 was detectable up to dilution -3, while no CPE was observed after 1 - 5 h of hydrolysis (T1 - T5), suggesting inactivation through enzymatic activity and/or temperature. For PCV-2 and PRRSV, quantitative PCR analysis of triplicates at T0, T1 and T5 showed no Ct decrease over time, indicating the absence of viral replication and suggesting that the detected genomes were non-infectious. Cytotoxicity in all cell lines limits the suitability of culture-based titration, particularly for PCV-2 and PRRSV.

Conclusion

PEDV was inactivated during enzymatic hydrolysis, while PCV-2 and PRRSV showed no evidence of replication after treatment. Overall, enzymatic hydrolysis of liquid plasma appears to stop or substantially limit viral replication, although further studies are needed to confirm complete inactivation under diverse conditions.

Keywords: Enzymatic hydrolysis, Plasma, Porcine circovirus type 2, Porcine epidemic diarrhea virus, Porcine reproductive and respiratory virus.

References

1. Blázquez, et al., 2020. *Porcine Health Management* 6, 16.

INACTIVATION OF AVIAN INFLUENZA VIRUS INOCULATED IN SPRAY-DRIED BOVINE PLASMA

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Introduction and Objectives

Avian influenza virus (AIV) is a major concern for the livestock industry due to its ability to infect birds and potentially mutate to affect other species, including ruminants and humans. Spray-dried plasma (SDP) has previously demonstrated safety against several swine viruses (Blázquez et al., 2020). This study aimed to evaluate the survival of low-pathogenicity AIV H1N1 inoculated onto spray-dried bovine plasma (SDBP) and stored at room temperature (RT; 22°C) for 0, 7, 14 and 21 days.

Materials and Methods

A H1N1 strain was propagated in 10-d old embryonated chicken eggs (ECE) to obtain a high-titer stock. Commercial SDBP was gamma-irradiated at 10 KGy to ensure the absence of microorganisms, and a 10 g subsample was stored at -75°C as a negative control. Sixty grams of SDBP were inoculated with 9 mL of virus by spraying the inoculum gradually while shaking to ensure homogenization. One gram of inoculated material was placed into each of nine glass tubes (0.5 cm inner diameter) and stored at RT. Three tubes were collected at each time point (0, 7, 14 and 21 days) and kept at -75°C until titration. Viral titration was performed in ECE using undiluted samples and 10-fold dilutions (10^0 to 10^{-7}). Five eggs per dilution were inoculated with 100 µL of sample and monitored for 7 days. The assay limit of detection was $10^{1.5}$ EID_{50}/mL. Viral reduction was calculated as the difference between the initial inoculum titer and the titer detected in treated samples.

Results and Discussion

The initial virus titer in the 9 mL inoculum was $10^{7.7}$ EID_{50}/mL. SDBP samples analyzed immediately (day 0) showed a mean titer of $10^{3.95\pm0.25}$ EID_{50}/mL. All SDBP samples stored at RT for 7, 14 or 21 days had no detectable infectivity for H1N1 in ECE. The calculated viral reduction was $\geq 10^{2.42}$ EID_{50}/mL ($\geq$ 99.6% inactivation), indicating rapid loss of infectivity after inoculation onto SDBP, suggesting that the low water activity of SDBP reduces the viability of AIV.

Conclusion

AIV H1N1 inoculated onto SDBP lost infectivity within 7 days at room temperature supporting the safety of SDBP as an ingredient for animal feed.

Keywords: Avian influenza virus, Inactivation, Spray-dried plasma, Storage.

References

1. Blázquez, et al., 2020. *Porcine Health Management* 6, 16.

INACTIVATION OF AVIAN INFLUENZA VIRUS DURING MANUFACTURING PROCESS OF BOVINE SPRAY-DRIED PLASMA AND RED BLOOD CELLS

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Introduction and Objectives

Avian influenza virus (AIV) is a major concern for the livestock industry due to its capacity to infect birds and potentially mutate to affect other species, including ruminants and humans. This study evaluated the infectivity of a low-pathogenicity AIV H1N1 in plasma and red blood cells after spray-drying (SD) and subsequent storage at room temperature (RT).

Materials and Methods

H1N1 strain was propagated in 10-d old embryonated chicken eggs (ECE) to obtain a high-titer virus stock. Spray-dried bovine plasma (SDBP) and spray-dried bovine red cells (SDBRC) were γ-irradiated and reconstituted at 25% solids. Bovine sources were selected to avoid interference from porcine influenza virus antibodies. Three 900 g liquid sub-batches of plasma and red cells were inoculated with 100 g of virus immediately before spray-drying. Samples were processed in a Büchi 290 spray-dryer under standardized conditions (inlet 200 ± 5°C; outlet 80 ± 1°C; dwell time 0.41 s), with disinfection between batches. Dried samples were subdivided into 0.5 g aliquots, heated at 90 ± 3°C for 60 s (≈ 80.7°C in powder) to simulate commercial thermal exposure and stored for 14 days at 22 - 25°C before analysis. Viral titration was performed in ECE using undiluted samples and 10-fold serial dilutions (10^0 - 10^{-7}). Five eggs per dilution were inoculated with 100 µL of sample and monitored for 7 days. Viral reduction was calculated as the difference between virus titers before and after SD.

Results and Discussion

Initial virus titers before SD were $10^{6.46\pm0.07}$ and $10^{6.35\pm0.16}$ EID_{50}/mL for plasma and red cells, respectively. SD reduced H1N1 infectivity in plasma by 3.90 - 4.40 logs with further reduction to 4.76 - 5.20 logs after storage. In red cells, SD achieved reductions of 2.07 - 2.40 logs with further reduction to 3.41 - 4.45 logs after storage. Spray-drying and 14-day storage at RT inactivated > 5.0 ± 0.25 $\log_{10}$ EID_{50}/mL of H1N1 in plasma and 3.91 ± 0.52 $\log_{10}$ in red cells, supporting their safe use in animal feed.

Conclusion

The H1N1 reductions achieved during SD and subsequent storage at RT under low water activity conditions are consistent with other virus inactivation results for safe use of spray-dried blood products (Blázquez et al., 2020).

Keywords: Avian influenza virus, Blood products, Inactivation, Post-drying storage, Spray-drying.

References

1. Blázquez, et al., 2020. *Porcine Health Management* 6, 16.

EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE IN PREGNANT GILTS

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the efficacy of that vaccine (Prevacent® PRRS) when administered to gilts at six weeks prior to breeding by a challenge at 90 days of gestation.

Materials and Methods

Twenty nine gilts were distributed among three groups. Six weeks prior to breeding, fourteen gilts were injected intramuscularly with Prevacent® PRRS (Elanco), and another ten and five gilts were injected with a placebo, which were included as positive and negative control gilts, respectively. At approximately 90 days of gestation, the vaccinated gilts and the positive control gilts were challenged intranasally and intramuscularly with PRRSV-2 lineage 8 strain NADC20. The five negative control gilts remained unchallenged. Efficacy was assessed by determining viral loads in the gilts' sera, piglet viability, and birth weight.

Results and Discussion

Viremia was detected in all ten positive control gilts at 3 and 7 days post-challenge (DPC) and in nine gilts at 14 DPC, while viremia was only detected at 3 and 7 DPC in thirteen and two out of the fourteen vaccinated gilts, respectively. The mean cumulative viral load in the sera (sum of viral loads at 3, 7, and 14 DPC) was lower in the vaccinated gilts (5.475 log10) than in the positive control gilts (16.410 log10). The percentage of viable piglets from the vaccinated gilts (59.8%; 116/194) was lower than that of the negative control gilts (88.0%; 44/50), but higher than that of the positive control gilts (11.3%; 16/141). Further, the birth weight of the offspring of the vaccinated gilts (1.28 kg) was lower than that of the negative control gilts (1.39 kg), but higher than that of the positive control gilts (1.17 kg).

Conclusion

A vaccination of gilts six weeks prior to breeding with Prevacent® PRRS proved to be efficacious, as evidenced by a higher piglet viability and birth weight and a lower viremia in the vaccinated gilts than in the non-vaccinated challenge control gilts upon a challenge at 90 days of gestation.

Keywords: Challenge, Efficacy, PRRSV, Reproduction, Vaccine.

SAFETY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE IN PIGLETS UNDER FIELD CONDITIONS IN THE UNITED STATES

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Introduction and Objectives
Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the safety of that vaccine (Prevacent® PRRS) when administered to two- to four-week-old pigs on swine farms located in the main swine-producing states of the United States.
Materials and Methods
On nine swine farms located in six different states of the United States (i.e., Alabama, Illinois, Indiana, Iowa, Minnesota, and North Carolina), a total of 6,512 two to four-week-old pigs were selected, among which 5,055 pigs were vaccinated by intramuscular route with Prevacent® PRRS (Elanco) and 1,457 pigs were injected at the same time by the same route with the diluent of the vaccine. All vaccinated and control pigs were observed for local and systemic reactions.
Results and Discussion
There were no differences in the incidence of injection site and systemic reactions between the vaccinated pigs and the control pigs. Only eleven out of the 5,055 vaccinated pigs (0.2%) and three out of the 1,457 control pigs (0.2%) developed injection site reactions following their treatment. None of the 5,055 vaccinated pigs and 1,457 control pigs showed anaphylactic-like reactions following their treatment. A total of 841 out of the 5,055 vaccinated pigs (16.6%) and 242 out of the 1,457 control pigs (16.6%) exhibited health abnormalities within 21 days following their treatment. All were events that could be expected in commercial swine production sites (e.g., unthriftiness, loss of condition, anorexia, coughing, diarrhea). Further, none of the 34 (0.7%) and 13 (0.9%) deaths in the vaccinated and control pigs, respectively, were attributed to the vaccine or the diluent.
Conclusion
A vaccination of two- to four-week-old pigs with Prevacent® PRRS proved to be safe under field conditions in the United States, as evidenced by the absence of differences in immediate adverse events, injection site reactions, and abnormal health observations between vaccinated pigs and control pigs.
Keywords: Field, PRRSV, Respiratory, Safety, Vaccine.

DURATION OF IMMUNITY AFTER VACCINATION WITH A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE

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Introduction and Objectives
Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to assess the duration of immunity of that vaccine (Prevacent® PRRS) by a challenge with PRRSV-2 lineage 8 strain NADC20 at 182 days post-vaccination (DPV).

Materials and Methods
Seventy two two-week-old pigs were allocated to two groups of 36 pigs each and were injected intramuscularly with either Prevacent® PRRS (Elanco) or a placebo. At 182 DPV, all pigs were challenged intranasally (4 mL/nostril) and intramuscularly (2 mL) with 7.3 $\log_{10}$ TCID50 of PRRSV-2 lineage 8 strain NADC20. Efficacy was assessed by determining clinical scores (sum of scores for depression, respiratory distress, and loss of body condition), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion
There were clear clinical, pathological, and virological differences between the vaccinated pigs and the controls. Indeed, the mean clinical score of the vaccinated pigs (35.64) was lower than that of the controls (40.70), even though the very high individual clinical scores of two controls that were found dead at 10 and 13 DPC were not included in the calculation. Also, the mean lung lesion score at 14 DPC of the vaccinated pigs (1.547) was lower than that of the controls (22.264) resulting in a mitigated fraction of 0.7639. Finally, the mean cumulative viral load in the sera (sum of viral loads at 7 and 14 DPC) was lower in the vaccinated pigs (3.072 $\log_{10}$) than in the controls (10.688 $\log_{10}$). Similarly, the mean viral load in the BAL fluids at 14 DPC was lower in the vaccinated pigs (3.244 $\log_{10}$) than in the controls (6.818 $\log_{10}$).

Conclusion
The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, lung lesions, and virus replication in blood and lungs upon a challenge with PRRSV-2 lineage 8 strain NADC20 at 182 DPV, supporting a duration of immunity up to the end of the fattening period.

Keywords: Duration of immunity, Efficacy, Challenge, PRRSV, Vaccine.

IMMUNOLOGICAL EVALUATION OF NON-INTERFERENCE OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE ON THE CLASSICAL SWINE FEVER C-STRAIN VACCINE IN PIGS

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Introduction and Objectives

Classical swine fever virus (CSFV) and porcine reproductive and respiratory syndrome virus (PRRSV) are major pathogens causing significant economic losses in swine production worldwide. Live attenuated vaccines are commonly used to control these diseases. The objective of this study was to determine the non-interference between the PRRSV-2 vaccine Prevacent® PRRS and a CSFV vaccine.

Materials and Methods

Twenty three pigs were allocated to a treatment group (n = 12) and a control group (n = 11). At 17 days of age, pigs in the treatment group received Prevacent® PRRS (Elanco). Fourteen days later, all pigs were vaccinated with a live attenuated CSFV C-strain vaccine. Blood samples were collected at 0, 14, and 28 days post-CSFV vaccination (DPV) for detection of antibodies against CSFV by a virus-neutralization (VN) assay, monoclonal antibody-based competitive ELISA (mAb cELISA), and CSFV E2-specific ELISA (anti-E2 ELISA). Antibody levels were expressed as VN titers, percentages of inhibition, and OD450 values, respectively.

Results and Discussion

All pigs were negative for antibodies against CSFV at 0 DPV. At 14 DPV, some pigs of both groups had developed antibodies against CSFV. Indeed, five (41.7%), seven (58.3%), and ten (83.3%) out of the twelve Prevacent® PRRS-vaccinated pigs tested positive for antibodies against CSFV in the VN assay, mAb cELISA, and anti-E2 ELISA, respectively. Similarly, six (54.5%), seven (63.6%), and nine (81.8%) out of the eleven control pigs tested positive for antibodies against CSFV in the VN assay, mAb cELISA, and anti-E2 ELISA, respectively. At 28 DPV, all pigs of both groups had developed antibodies against CSFV. There were no statistically significant differences in the amounts of antibodies as measured with the three serological assays between both groups, except for a slightly higher VN antibody titer in the Prevacent® PRRS-vaccinated pigs (493.33) than in the control pigs (320.00) at 28 DPV ($P = 0.0314$).

Conclusion

The administration of Prevacent® PRRS had no negative impact on the pig's ability to mount an immunological response to a subsequent vaccination against CSFV, as evidenced by the absence of differences in the serological response against the live attenuated CSFV C-strain vaccine between the Prevacent® PRRS-vaccinated pigs and the control pigs.

Keywords: CSFV, Immunity, PRRSV, Serology, Vaccine.

CROSS-PROTECTIVE EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST A HIGHLY PATHOGENIC LINEAGE 8 STRAIN

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the cross-protective efficacy of that vaccine (Prevacent® PRRS) against a highly pathogenic (HP) PRRSV-2 strain belonging to lineage 8 when administered to two-week-old pigs.

Materials and Methods

A total of 36 two-week-old pigs were allocated to three groups of twelve pigs each and were injected by intramuscular route with either Prevacent® PRRS (Elanco) (at either 4.0 $\log_{10}$ $TCID_{50}$/dose or 5.2 $\log_{10}$ $TCID_{50}$/dose) or a placebo. At 28 days post-vaccination (DPV), all pigs were challenged by intranasal and intramuscular routes with the HP-PRRSV JX strain. Efficacy was assessed by determining the mortality rate up to 14 days post-challenge (DPC).

Results and Discussion

One out of the twelve control pigs died prior to the challenge due to an umbilical infection, leaving only eleven control pigs left for the challenge. Upon the challenge, all eleven non-vaccinated challenge control pigs died between 7 and 11 DPC, whereas only two out of the twenty-four vaccinated pigs died. The two vaccinated pigs that died had been vaccinated at a dose of 4.0 $\log_{10}$ $TCID_{50}$. Because of the 100% mortality rate in the non-vaccinated challenge control pigs, other efficacy parameters that were recorded, such as rectal temperatures, average daily weight gain, lung lesion scores, and viral loads in serum samples and broncho-alveolar lavage fluids, could not be analyzed, but the results were always in favor of the vaccinated pigs.

Conclusion

The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce the mortality rate following a very severe lethal challenge with a highly pathogenic PRRSV-2 lineage 8 strain, suggesting that Prevacent® PRRS can provide broad cross-protection against HP-PRRSV lineage 8 strains in pigs, which still circulate widely in Asia.

Keywords: Cross-protection, Efficacy, Heterologous challenge, PRRSV, Vaccine.

ONSET OF CROSS-PROTECTIVE IMMUNITY AFTER VACCINATION WITH A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to assess the cross-protective efficacy of that vaccine (Prevacent® PRRS) by a challenge with PRRSV-2 lineage 8 strain NADC20 at 28 days post-vaccination (DPV).

Materials and Methods

Eighty two-week-old PRRSV-seronegative pigs were allocated to four groups of 20 pigs each and were injected intramuscularly with either Prevacent® PRRS (Elanco) (three groups, each with a different dose) or a placebo. At 28 DPV, all pigs were challenged intranasally and intramuscularly with $10^{5.20}$ TCID50 of PRRSV-2 lineage 8 strain NADC20 (GenBank MK837936.1). Efficacy was assessed by determining clinical scores (sum of daily scores ranging from 0 to 3 for depression, respiratory distress, and loss of body condition), average daily weight gain (ADWG), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion

The mean clinical scores of the vaccinated groups (5.85, 6.95, and 6.95) were lower than that of the controls (16.10), and the ADWG of the vaccinated groups (0.361, 0.327, and 0.316 kg) were higher than that of the controls (0.054 kg). Also, the mean lung lesion scores at 14 DPC of the vaccinated groups (5.925, 5.288 and 5.050) were lower than that of the controls (54.610) resulting in mitigated fractions of 0.9200, 0.9450, and 0.9789. Finally, the mean viral loads in sera at 14 DPC were lower in the vaccinated groups (6.450 $\log_{10}$, 6.565 $\log_{10}$, 6.445 $\log_{10}$) than in the controls (9.049 $\log_{10}$). Similarly, the mean viral loads in BAL fluids at 14 DPC were lower in the vaccinated groups (6.127 log10, 6.260 $\log_{10}$, 6.334 $\log_{10}$) than in the controls (8.907 $\log_{10}$).

Conclusion

The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, weight loss, lung lesions, and virus replication in blood and lungs upon a challenge with PRRSV-2 lineage 8 strain NADC20 at 28 DPV, supporting an onset of immunity of four weeks against a heterologous strain.

Keywords: Cross-protection, Efficacy, Heterologous challenge, Lineage 8, Vaccine.

CROSS-PROTECTIVE EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST THE NC174 STRAIN

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Introduction and Objectives
Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the attenuated PRRSV-2 lineage 1 strain SD 11 - 21 (Prevacent® PRRS). The objective of this study was to evaluate the efficacy of that vaccine (Prevacent® PRRS) against PRRSV-2 lineage 1A strain NC174 when administered to two-week-old pigs.

Materials and Methods
A total of 40 two-week-old pigs were allocated to two groups of 20 pigs each and were injected by intramuscular route with either Prevacent® PRRS (Elanco) or a placebo. At 28 days post-vaccination (DPV), all pigs were challenged by intranasal and intramuscular routes with PRRSV-2 lineage 1A strain NC174. Efficacy was assessed by determining clinical scores (sum of scores for depression, respiratory distress, and loss of body condition), average daily weight gain (ADWG), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion
One out of the 20 vaccinated pigs died three days prior to the challenge in poor body condition, leaving 19 vaccinated pigs for the challenge. There were clear clinical and pathological differences between the vaccinated pigs and the control pigs upon the challenge. The mean clinical score of vaccinated pigs (4.895) was lower than that of control pigs (8.900), and the ADWG of vaccinated pigs (0.430 kg) was higher than the one of the control pigs (0.251 kg). Also, the mean lung lesion score at 14 DPC of vaccinated pigs (5.813) was lower than the one of the control pigs (46.780), resulting in a mitigated fraction of 0.937. Finally, the mean cumulative viral loads in sera (sum at 7 and 14 DPC) were lower in vaccinated pigs (14.178 $\log_{10}$) than in the control pigs (15.335 $\log_{10}$). Similarly, the mean viral loads in BAL fluids were lower in vaccinated pigs (6.476 $\log_{10}$) than in control pigs (7.798 $\log_{10}$)

Conclusion
The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, weight loss, lung lesions, and virus replication in the blood and lungs following a challenge with PRRSV-2 lineage 1A strain NC174.

Keywords: Cross-protection, Efficacy, Heterologous challenge, PRRSV, Vaccine.

SAFETY OF A SINGLE DOSE, A TENFOLD OVERDOSE, AND A REPEATED DOSE OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE

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Introduction and Objectives
Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the safety of a single dose, a tenfold overdose, and a repeated dose of that vaccine (Prevacent® PRRS) in two-week-old pigs.
Materials and Methods
Eighty four two-week-old pigs were allocated to seven groups of twelve pigs each. The pigs of group 1 were injected with a single dose of the vaccine. The pigs of groups 2 - 4 were injected with a tenfold overdose of the vaccine (each with another batch). The pigs of group 5 were injected with the vaccine diluent, serving as control group for groups 1 - 4. The pigs of group 6 were injected twice at a two-week interval with a single dose of the vaccine, serving as the repeated dose group. The pigs of group 7 were injected twice at a two-week interval with the vaccine diluent, serving as control group for group 6. All injections were done by intramuscular route. Clinical signs, rectal temperatures, injection site reactions, and body weights (for calculation of the average daily weight gain [ADWG]) were recorded up to 14 days after the last injection.
Results and Discussion
Except for one pig having a slightly increased respiratory rate at 14 days after its injection with a tenfold overdose of the vaccine, no clinical signs were observed. Using a threshold of ³39.6°C, most pigs showed transient fever for at least one day, but with no differences between the vaccinated groups and the respective control groups (12/12, 10/12, 10/12, 9/12, 9/12, 12/12, and 12/12 pigs in groups 1 - 7, respectively). None of the 84 pigs developed an injection site reaction following their single or double injection. Finally, there were no differences in ADWG between the vaccinated groups and the respective control groups.
Conclusion
The safety of a single dose, a tenfold overdose, and a repeated dose of Prevacent® PRRS was demonstrated by the absence of differences in the incidence of systemic and injection site reactions and ADWG between vaccinated pigs and the respective control pigs.
Keywords: Local reactions, PRRSV, Safety, Systemic reactions, Vaccine.

CROSS-PROTECTIVE EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST A PRRSV RFLP 1-4-4 LINEAGE 1C VARIANT STRAIN

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the efficacy of that vaccine (Prevacent® PRRS) against a PRRSV restriction fragment length polymorphism (RFLP) 1-4-4 lineage 1C variant strain when administered to two-week-old pigs.

Materials and Methods

A total of 40 two-week-old pigs were allocated to two groups of 20 pigs each and were injected by intramuscular route with either Prevacent® PRRS (Elanco) or a placebo. At 28 days post-vaccination (DPV), all pigs were challenged by intranasal and intramuscular routes with PRRSV RFLP 1-4-4 lineage 1C variant strain XY/JC 6-29-21. Efficacy was assessed by determining clinical scores (sum of scores for depression, respiratory distress, and loss of body condition), average daily weight gain (ADWG), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion

One out of the 20 vaccinated pigs died 16 days before the challenge, leaving 19 pigs for the challenge. The mean clinical score of the vaccinated pigs (2.105) was lower than the one of the controls (3.400), and the ADWG of the vaccinated pigs (0.386 kg) was higher than the one of the controls (0.267 kg). Also, the mean lung lesion score at 14 DPC of the vaccinated pigs (1.792) was lower than the one of the controls (4.125), resulting in a mitigated fraction of 0.361. Finally, the mean cumulative viral load in the sera (sum of viral loads at 3, 7, 10, and 14 DPC) was lower in the vaccinated pigs (28.126 $\log_{10}$) than in the controls (29.222 log10). Similarly, the mean viral load in the BAL fluids was lower in the vaccinated pigs (5.572 $\log_{10}$) than in the controls (7.052 $\log_{10}$).

Conclusion

The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, weight loss, lung lesions, and virus replication in the blood and lungs following a challenge with a PRRSV-RFLP 1-4-4 lineage 1C variant strain.

Keywords: Cross-protection, Efficacy, Heterologous challenge, PRRSV, Vaccine.

CROSS-PROTECTIVE EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST A TAIWANESE LINEAGE 3 STRAIN

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the cross-protective efficacy of that vaccine (Prevacent® PRRS) against a Taiwanese highly virulent PRRSV-2 strain belonging to lineage 3 when administered to two-week-old pigs.

Materials and Methods

A total of twenty-two-week-old specific pathogen-free (SPF) pigs were allocated to two groups of ten pigs each and were injected by intramuscular route with either Prevacent® PRRS (Elanco) or the diluent of the vaccine. Similarly, a total of ten conventional two-week-old pigs were allocated to two groups of five pigs each and were injected at a commercial Taiwanese farm by intramuscular route with either the vaccine or the diluent of the vaccine. At 21 days post-vaccination (DPV), all pigs were challenged by intranasal and intramuscular routes with the Taiwanese PRRSV-2 lineage 3 strain TSYM-142575. Efficacy was assessed by determining the mortality rate up to 14 days post-challenge (DPC).

Results and Discussion

None of the vaccinated pigs died, whereas eight out of the ten SPF challenge control pigs and two out of the five conventional challenge control pigs died between 8 and 13 DPC. Because of this high mortality rate in the non-vaccinated challenge control pigs, other efficacy parameters that were recorded, such as clinical scores, rectal temperatures, average daily weight gain, lung lesion scores, and viral loads in serum samples and broncho-alveolar lavage fluids, could not be analyzed, but the results were always in favor of the vaccinated pigs.

Conclusion

The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce the mortality rate following a severe lethal challenge with a Taiwanese PRRSV-2 lineage 3 strain, suggesting that Prevacent® PRRS can provide broad cross-protection against PRRSV-2 lineage 3 strains in pigs, which circulate widely in Taiwan.

Keywords: Cross-protection, Efficacy, Heterologous challenge, PRRSV, Vaccine.

SAFETY AND EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE UNDER JAPANESE FIELD CONDITIONS

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Introduction and Objectives
Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the attenuated PRRSV-2 lineage 1 strain SD 11 - 21. This study aimed to evaluate the safety and efficacy of Prevacent® PRRS under Japanese field conditions when administered to two-week-old pigs.
Materials and Methods
The trial was conducted on three Japanese farms where PRRSV-2 was circulating: cluster IV (lineage 1) on farms 1 and 2, and cluster III (lineage 4) on farm 3. On each farm, 50 two-week-old pigs were vaccinated with Prevacent® PRRS, and another 50 two-week-old pigs were treated with its diluent. Safety was evaluated by assessing local and systemic reactions. Efficacy was evaluated by comparing clinical scores, antibiotic treatment incidence, removal rates (mortality and culling), average daily weight gain (ADWG), and viremia detection rates. Observations continued from day 0 post-vaccination (DPV) to 126 DPV for ADWG and viremia, or until the end of the fattening period for other parameters.
Results and Discussion
None of the 150 vaccinated and 150 control pigs developed injection site and systemic reactions following their treatment. Clinical score of the vaccinated pigs was lower than that of the control pigs on all three farms (1.40 vs 4.42; 4.40 vs 6.62; 0.62 vs1.72 for farms 1–3). Similarly, fewer vaccinated pigs required antibiotic treatment than control pigs (12% vs. 22%; 8% vs. 16%; 4% vs. 10%). Fewer vaccinated pigs died or had to be culled than control pigs on two out of the three farms (6% vs. 16%; 2% vs. 2%; 0% vs. 2%). ADWG was higher in vaccinated pigs (0.577 vs. 0.561 kg; 0.634 vs. 0.601 kg; 0.623 vs. 0.603 kg). Finally, the viremia detection rate was lower in vaccinated pigs than in control pigs across all three farms (40.0% vs. 83.3%; 33.3% vs. 93.3%; 3.3% vs. 50.0%).
Conclusion
Vaccination of two-week-old pigs with Prevacent® PRRS proved to be safe and efficacious under Japanese field conditions, as evidenced by the complete absence of systemic and local reactions, and consistently better results of the vaccinated pigs compared to the control pigs across all three farms for all efficacy parameters assessed.
Keywords: Efficacy, Japan, PRRSV, Safety, Vaccine.

EPIDEMIOLOGY OF INFLUENZA A VIRUS IN SWISS PIG HERDS: SUBCLINICAL CIRCULATION AND ASSOCIATED RISK FACTORS

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Introduction and Objectives

The epidemiology of Influenza A viruses (IAVs) in Swiss pig herds was poorly understood, also because former studies only examined herds suffering from respiratory diseases but not unaffected herds (Lechmann et al. 2025). Therefore, we conducted a nationwide case–control study to investigate IAV occurrence, associated risk and protective factors, and genetic characteristics.

Materials and Methods

125 herds were examined during 2023 and 2025, including 40 with clinical respiratory disease and 85 without obvious signs. Caretakers completed semi-structured interviews on management, biosecurity, and human health. The pig herd was clinically examined, and nasal swabs were taken, with sampling designed to detect infection in at least one individual with 95% confidence at assumed within-herd prevalences of ≥ 50% (clinical) and ≥ 15% (subclinical). Samples were analyzed by pan-IAV qPCR (Nagy et al., 2021), and whole-genome sequencing was performed on positive samples (Mwanga et al., 2025).

Results and Discussion

Overall, 51 herds (40.8%) and 11.8% of sampled pigs tested positive for IAV. Most study sequences belonged to the H1N1 Eurasian avian-like subtype and formed a monophyletic cluster within clade 1C.2.2. Other genomes clustered within clade 1C.2.1, and less segments belonged to the H1N1pdm09 lineage Notably, 60.8% of positive herds showed no clinical signs. Questionnaire analysis revealed non-significant but consistent trends toward higher IAV detection in herds with higher production intensity and/or biosecurity gaps. Viral sequences clustered within the European avian-like H1N1 lineage (1C.2.2), forming a monophyletic group with previous Swiss strains, suggesting continued viral circulation largely isolated from neighboring countries.

Conclusion

IAV is a common but often subclinical infection in Swiss pig herds, with epidemiological patterns resembling those reported elsewhere in Europe. Despite smaller herd sizes and a largely closed production system, risk factors such as biosecurity shortcomings and higher production intensity appear to facilitate viral circulation. Strengthened surveillance and biosecurity measures are needed to mitigate the impact of IAV on swine health and to reduce zoonotic risk at the pig-human interface.

Keywords: Influenza A Virus, Prevalence, Surveillance, Subclinical infection.

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RECOMBINATION EVENTS OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV) IN USA FARMS

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Introduction and Objective

Recombination is an important evolutionary mechanism in RNA viruses, and this study is an attempt to understand those evolutionary patterns in PRRSV and identify eventual recombination events between vaccine strains and field isolates of PRRSV 2.

Material and Methods

Forty-seven isolates of PRRSV collected during the period 2007 - 2021 were sequenced. The library preparation was performed using the Nextera XT DNA Library Prep kit, and 150 bp paired-end sequencing was performed on an Illumina MiSeq instrument. Sequences from six vaccine strains (Ingelvac MLV, Ingelvac ATP, Fostera PRRS, Prime Pac PRRS RR, Prevacent PRRS, and PRRSGard) were retrieved from NCBI and other laboratories. Bioinformatics analysis was primarily conducted using CLC Genomics Workbench 25.0.1. Following the removal of adapters, short reads, and low-quality sequences, reads were mapped to PRRSV 1 (NCBI Reference Sequence: NC_001961) and PRRSV 2 (NCBI Reference Sequence: NC_038291) reference genomes. After the multiple sequence alignment and phylogenetic analysis of all the samples, vaccines, and some representative PRRSV sequences from NCBI, the samples were assessed for recombination using Simplot++ v1.3 and GARD from Datamonkey v2.0 based on the insights from the phylogenetic tree.

Results and Discussion

Most field isolates were found within PRRSV 2 strain correlating with geographic region and sample collection times. One clade corresponded to samples from Colorado, with sub-clades corresponding to different collection times. Two other distinct clades were observed, both corresponding to Kansas and adjacent Nebraska regions, again with sub-clades corresponding to different collection times. Two novel recombination events were identified during the present investigation, one between a vaccine and a previously sequenced field isolate found in NCBI, and another between two of the field isolates sequenced in this study. The two novel recombinants included GenBank ID-KT257984 - a recombinant between Sample-33 and Sample-45 with a single recombination breakpoint in the ORF3 region (occurred in the USA) and GenBank ID-PQ31610, a recombinant between GenBank ID-OP866751 and Fostera Vaccine with two recombination breakpoints in the region of ORF1a and one each in the regions of ORF1b and ORF2 (occurred in China).

Conclusion

Monitoring PRRSV sequencing in the field is very important.

Keywords: PRRSV, Recombination and field infection, Swine.
Acknowledgements: KVDL- NGS Section, Virology Section and USDA NIFA funding.

META-ANALYSIS OF AVERAGE DAILY GAIN(ADG) FOR PCV2 VACCINES BASED ON 9 FIELD TRIALS IN CHINA

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Introduction and Objectives

Vaccination is key in controlling PCV2. Over 60 commercial PCV2 vaccines are available in China, but their effects on improving ADG vary in the field. Suishot® Circo-One, an inactivated PCV2 vaccine, was assessed via a meta-analysis of data from 9 pig farms, which can be used to guide vaccine selection for farmers.

Materials and Methods

Side-by-side trials were conducted across nine pig farms from 2024 to 2025. The pigs in the trials were healthy, grow-finishing pigs, with no significant difference in initial body weight ($P > 0.05$). Group 1 (124, 52, 600, 480, 1071, 520, 763, 512, 470 pigs chosen in each farm, totaling 4592 pigs) received Suishot® Circo-One (1 dose per pig) at 21 to 28 days of age; Group 2 (117, 50, 840, 480, 1131, 530, 745, 505, 480 pigs chosen in each farm, totaling 4878 pigs) received other commercial PCV2 vaccines (1 dose per pig) at the same time. The trial lasted 160 - 180 days, and the mean ADG, standard deviation (SD), and sample size were recorded. Meta-analysis was performed using RevMan 5.4 with a random-effects model; effect sizes were expressed as Weighted Mean Difference (WMD) and 95% Confidence Interval (95% CI). Significance was set at $P < 0.05$.

Results and Discussion

Pooled analysis showed significantly higher ADG in the Group 1 compared with Group 2 (pooled WMD = 13.28 g/d, 95% CI [1.96, 24.61], Z=2.30, $P = 0.02$). High heterogeneity was observed in this study (Tau^2 = 286.12; Chi^2 = 243.22, df = 8, $P < 0.00001$; I^2 = 97%). This may be attributed to the small sample size (only 9 pig farms) and the concentrated trial duration. Future multi-regional, large-sample trials are needed to verify the generalizability of results.

Conclusion

A meta-analysis of data from 9 field trials revealed that Suishot® Circo-One significantly increases ADG (pooled WMD = 13.28 g/d, $P = 0.02$).

Keywords: Average daily gain (ADG), Feed conversion rate (FCR), Meta-analysis, PCV2.

Acknowledgements: Gratitude is extended to all pig farms involved in this field trial and Dr. Vet Testing Laboratory.

EFFECTS OF PCV3 AFTER VACCINATION INTERRUPTION

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Introduction and Objectives

Porcine circovirus type 3 (PCV3) has been associated with multisystemic wasting and reproductive failure since its detection in Canada in 2019. Following vaccine approval, uptake increased, but a temporary production interruption provided an opportunity to examine the effects of vaccination cessation and reintroduction on herd stability, clinical disease and viral load.

Materials and Methods

Internal MSD vaccine sales records (January 2021 - December 2023; July 2024 - August 2025) were analyzed to estimate vaccine coverage and reorder frequency. Concurrently, laboratory monitoring data (PCV3 PCR/ORF2 sequencing) and veterinarian-reported clinical observations from commercial herds were reviewed to assess detection of PCV3, clinical presentations, and changes in viral load in processing and oral fluid samples before, during and after the vaccine interruption. Regional patterns were evaluated with attention to co-infection status (notably PRRSV and *Mycoplasma hyopneumoniae* prevalence).

Results and Discussion

Between 2021 and 2023, 840,900 PCV3 vaccine doses were ordered, and an estimated 162,440 sows were vaccinated, with 59% of orders representing reorders. Following the production interruption (Dec 2023–Jul 2024), demand rebounded: 654,000 doses were ordered in the subsequent year, 86% as reorders. Herds vaccinated prior to the interruption typically exhibited clinical instability attributable to PCV3 within 6–8 months of vaccine cessation. Clinical presentations during unstable periods included multisystemic wasting and reproductive failure, accompanied by increased PCV3 viral loads detectable in processing and oral fluid samples. Regions in Western Canada - where PRRSV and *M. hyopneumoniae* prevalence is comparatively low - reported clearer detection of PCV3-associated disease. After the reintroduction of the vaccine and the implementation of pre-farrow sow vaccination, the affected herds achieved clinical and virological stabilization within approximately 2 - 3 production cycles.

Conclusion

Real-world data indicate that PCV3 vaccination contributes to herd health and production stability in affected Canadian herds. Interruption of vaccination is associated with resurgence of PCV3 clinical disease and rising viral loads, particularly in herds with low prevalence of confounding co-infections. Reinstatement of vaccination and targeted pre-farrow programs were effective in restoring herd stability. Prospective and controlled studies are warranted to quantify vaccine-attributable benefits and to define optimal vaccination strategies in different herd health contexts.

Keywords: PCV3, Production, Vaccination, Vtabilization.

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FIELD STUDY ON THE EFFICACY OF TWO PCV2 VACCINES

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Introduction and Objectives

Porcine Circovirus Type 2 (PCV2) is a major pathogen impacting the economics of pig farming. Vaccination remains the most widely used method for controlling PCV2 in China. A pig farm in Jilin Province, with 2,000 sows and a single-site production system, conducted a comparative study between a newly launched PCV2 vaccine (Suishot® Circo-One) and an existing commercial vaccine (Vaccine C) to evaluate their efficacy.

Materials and Methods

Weaning piglets from the same batch of sows vaccinated with Vaccine C 3 times per year (April, Aug, Dec) were randomly assigned to two groups. Group 1 (749 piglets) and Group 2 (732 piglets) were vaccinated with Suishot® Circo-One and Vaccine C separately. Both groups received a single dose at 3 weeks of age due to the label recommended in June. Serum samples were collected at 3, 6, 10, 14, 18, and 24 weeks of age for PCR and ELISA detection. Production parameters including Average Daily Gain (ADG), Feed Conversion Ratio (FCR), and mortality were also assessed.

Results and Discussion

Group 1 tested PCR-negative at 3, 6, 10, 14, 18 weeks of age, with 6.7% (1/15; Ct = 32.48) positive at 24 weeks of age. Group 2 tested PCR-negative at 3, 6, 10 weeks of age, with positivity thereafter: 6.7% (1/15; Ct = 32.48) at 14 weeks, 13.3% (2/15; Ct = 31.12, 33.89) at 18 weeks, 33.3% (5/15; Ct = 34.38, 32.95, 34.00, 34.94, 30.64) at 24 weeks of age. The average ELISA S/P values and positive rate of Group 1 showed 1.22 (100%), 1.12 (100%), 1.04 (100%), 0.66 (100%), 0.58 (87%), 1.26 (93%) at 3, 6, 10, 14, 18, 24 weeks of age, while that of Group 2 showed 1.37 (100%), 1.37 (100%), 1.25 (100%), 0.62 (73.3%), 0.45 (60%), 1.17 (100%). From weaning to finishing, Group 1 showed 38.83 grams higher ADG than Group 2, a better FCR with a difference of 0.23, and a significantly lower mortality rate (4.07% less), confirmed by Chi-square analysis.

Conclusion

Suishot® Circo-One provided longer-lasting protection than Vaccine C, delaying viremia by approximately 4 weeks and maintaining a lower PCV2 positivity rate at 24 weeks. Additionally, Group 1 showed improved production performance in terms of ADG, FCR, and mortality.

Keywords: Efficacy, PCV2, Vaccine, Viremia.

MOLECULAR DETECTION RATE OF PORCINE CIRCOVIRUS TYPE 2 IN DIFFERENT AGE HERDS

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is highly prevalent, inducing multiple clinical symptoms, causing economic losses. The objective of this study is to elucidate the infection rate of PCV2 from suckling piglets to finishers. Consequently, the detection rates and viral loads of PCV2 across six different age phases.

Materials and Methods

This study is a retrospective, active surveillance-based cross-sectional investigation. A total of 2,427 samples were procured from 46 PCV2 vaccinated commercial pig farms during the second half of 2024 and the first half of 2025. The samples were classified by week-age into six groups. PCV2 PCR detection of all samples was carried out using a commercial real-time polymerase chain reaction kit (Lijian Biotechnology Co., Ltd., Qingdao, China). A positive result was defined as a Ct value below 40. All detection procedures were carried out at the Vetcome Laboratory. Kruskal-Wallis H test and Dunn's test with Holm correction method were employed for statistical analysis. Different letters indicate there was a statistical difference between groups with P values less than 0.05.

Results and Discussion

This study detected PCV2 infection in 6 pig age groups (in weeks), with a total of 2,427 samples. The number of samples and positive rates for each age group were as follows: 489 samples (23.7%) in the 0 - 4 week group, 694 samples (29.5%) in the 4 - 10 week group, 378 samples (22.0%) in the 10 - 14 week group, 361 samples (19.7%) in the 14 - 18 week group, 311 samples (15.4%) in the 18 - 22 week group, and 194 samples (25.3%) in the ≥ 22 week group. Among these, the 4 - 10-week group had the highest positive rate, while the 18 - 22-week group had the lowest. In terms of the average Ct value, the 14 - 18-week group had a value of 31.6 ($P < 0.05$), which was significantly lower than that of the other groups (ranging from 33.7 to 35.3, with no statistical differences). This indicates that this age group had the highest PCV2 viral load.

Conclusion

The highest detection rate was in 4- to 10-week-old piglets, and the herds with the highest infection titer were from 18- to 22-week-old.

Keywords: Epidemiology, Porcine circovirus type 2, Productive phase.

MOLECULAR DETECTION RATE OF PORCINE CIRCOVIRUS TYPE 2 IN DIFFERENT SAMPLE TYPES

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Introduction and Objectives

Porcine circovirus type 2(PCV2) is widespread and highly prevalent within pig herds. It induces multiple diseases, thereby inflicting substantial economic losses. In contemporary field production practices, a diverse range of sample types, including oral fluid, processing fluid, etc., can be employed for the surveillance of pathogens. The objective of this study aims to compare the detection rates and viral loads of PCV2 across four different sample types, thereby offering guidance for sample selection in field surveillance.

Materials and Methods

This study is a retrospective, active surveillance-based cross-sectional investigation. A total of 2,491 samples were taken from 46 commercial pig farms (PCV2 vaccination status unshared) during the second half of 2024 and the first half of 2025. The four types of samples incorporated in this research were defined and collected as described below. Umbilical Blood (UB), sampled from newborn piglets; Processing Fluid (PF), obtained as castration fluid from male piglets aged 3 to 5 days; Oral Fluid (OF) and Serum samples were collected from wean to finish herds. PCV2 molecular detection of all samples was carried out using a commercial real-time polymerase chain reaction kit (Lijian Biotechnology Co., Ltd., Qingdao, China). A positive result was defined as a Ct value below 40. All detection procedures were carried out at the Vetcome Laboratory. The chi-square method was employed for statistical analysis of the detection rate. Inter-group differences were considered significant when the P value was less than 0.05.

Results and Discussion

The overall detection rate is 23.0%. Detection rate of the OF samples of PCV2 was 66.1%, with 160 positive samples out of 242 tested, followed by PF samples (34.9%, 60/172), serum samples (17.3%, 340/1970), and UB samples (11.2%, 12/107). In weaned to finish herd, the detection rate in OF was higher than in serum ($P < 0.001$). Likewise, in the suckling piglets, the detection rate of PF was significantly higher than UB ($P < 0.001$).

Conclusion

The findings indicate that the detection rates of the sample type based on the population (OF, PF samples) in suckling and weaning to finisher production phases are higher than those of the individual sampling method (serum, PF samples).

Keywords: Molecular detection, Porcine circovirus type 2, Population-based sampling, Sample type.

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META-ANALYSIS OF MORTALITY REDUCTION: SUISHOT® CIRCO-ONE VERSUS OTHER PCV2 VACCINES IN NINE CHINESE FIELD TRIALS

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Introduction and Objectives
Porcine circovirus type 2 (PCV2) is a major pathogen causing PCV2-associated diseases (PCVAD), leading to significant economic losses in pig production worldwide due to increased mortality. Vaccination remains the most effective strategy for PCVAD control. This study evaluated the efficacy of Suishot® Circo-one, an inactivated whole-virus PCV2 vaccine launched in 2024, through a meta-analysis of mortality data from nine commercial farms to provide evidence for its application.

Materials and Methods
Side-by-side trials were conducted on nine pig farms between 2024 and 2025. Healthy grow-finish pigs with similar initial body weights ($P > 0.05$) were enrolled. The trial group received a single dose of Suishot® Circo-one at 21 - 28 days of age, while the control group received other PCV2 vaccines (inactivated or subunit) at the same age and dose. Mortality data (sample size, n) were collected for both groups. A meta-analysis was performed using RevMan 5.4 with the Mantel-Haenszel random-effects model. Effect sizes were expressed as odds ratios (OR) with 95% confidence intervals (CI), and statistical significance was set at $P < 0.05$.

Results and Discussion
Meta-analysis of nine farms (4,878 pigs) showed significantly lower mortality in the Suishot® Circo-one group (OR = 0.73; 95% CI: 0.55 - 0.98; $P = 0.04$). The mortality rate was 4.92% (226/ 4,592) in the test group, compared to about 6.48% (316/4,878) in the control group. Most farms favored Suishot® Circo-one, though moderate heterogeneity ($Tau^2 = 0.10$; $Chi^2 = 16.67$, df = 7 ($P = 0.02$; $I^2 = 97\%$) suggests regional and management differences.

Conclusion
Suishot® Circo-one significantly reduced mortality compared with other PCV2 vaccines across nine commercial farms, demonstrating consistent protective effects under diverse field conditions. These findings support its use as a practical option for PCVAD control and highlight the value of evidence-based vaccine selection.

Keywords: Meta-analysis, Mortality, Porcine Circovirus Type 2, Vaccines.

META-ANALYSIS OF MARKET-QUALIFIED PIG RATES: SUISHOT® CIRCO-ONE VERSUS OTHER PCV2 VACCINES IN NINE CHINESE FIELD TRIALS

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) infection reduces the proportion of market-qualified pigs, causing significant economic losses in swine production. Vaccination is essential for PCV2-associated diseases (PCVAD) control. This study evaluated Suishot® Circo-one, an inactivated whole-virus PCV2 vaccine launched in 2024, through a meta-analysis of qualified pig ratio data from nine farms to provide evidence for its application.

Materials and Methods

Side-by-side trials were conducted on nine pig farms from 2024 to 2025. Healthy grow-finish pigs with similar initial body weights ($P > 0.05$) were included. The trial group received one dose of Suishot® Circo-one at 21 - 28 days of age, while the control group received other PCV2 vaccines (inactivated or subunit) at the same age and dose. The number of market-qualified pigs and total sample size (n) were recorded for both groups. A meta-analysis was performed using RevMan 5.4 with the Mantel-Haenszel random-effects model. Effect sizes were expressed as odds ratios (OR) with 95% confidence intervals (CI), and statistical significance was set at $P < 0.05$.

Results and Discussion

Meta-analysis showed a trend toward a higher qualified pig ratio in the Suishot® Circo-one group (OR = 1.60; 95% CI: 1.01 - 2.53; Z = 2.00; $P = 0.05$). The qualification rate was 97.76% (4,489/4,592) in the trial group, while it was about 96.60% (4,712/4,878) in the control group. Moderate heterogeneity was observed ($Tau^2 = 0.24$; $Chi^2 = 17.62$, df = 7, $P = 0.01$; $I^2 = 60\%$), suggesting variability likely due to regional management and environmental differences. Despite this, most farms showed improved qualification rates, indicating the vaccine's potential to enhance growth performance and market readiness.

Conclusion

Suishot® Circo-one demonstrated a significant advantage in improving the qualified pig ratio compared with other PCV2 vaccines, despite moderate heterogeneity among farms. These findings support its potential role in enhancing growth performance and market readiness under diverse field conditions.

Keywords: Meta-analysis, Porcine Circovirus Type 2, Qualified pig ratio, Vaccines.

Acknowledgements: Gratitude is extended to all pig farms involved in this field trial and colleagues participated in the trials.

COMPARISON OF TWO MEDICATION TREATMENTS IN PRRSV INFECTED FARMS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) negatively impacts sow and piglet performance. Macrolides such as tilmicosin and tylvalosin have demonstrated efficacy in reducing PRRSV replication in vitro. This study aimed to compare the effects of tilmicosin and tylvalosin on pre-weaning mortality and production performance in PRRSV-infected sow herds.

Materials and Methods

Side-by-side trials were conducted on three PRRSV-positive farms in China in 2025. Farm A (1,200 sows, PRRS-inactivated-vaccinated) and Farm B (2,400 sows, PRRS-unvaccinated) each had one production line, with sows randomly assigned to two treatment groups. Farm C (5,000 sows, PRRS-unvaccinated) had multiple production lines; two were selected for comparison. In Farm B, treatment was applied to sows at 85 - 109 days of gestation, while Farms A and C treated entire sow herds within the designated lines. Group TI received tilmicosin (Pulmotil®, Elanco) at 2 kg/ton feed (400ppm), and Group TY received tylvalosin at 1 kg/ton feed (200ppm) for 15 consecutive days, alongside routine farm medications. Outcomes included PRRSV positivity in processing fluid (PF) samples, pre-weaning mortality, average weaning weight, and sow performance indicators.

Results and Discussion

Post-treatment data showed consistent advantages for tilmicosin. In Farm A, pre-weaning mortality was 2.17% in Group TI versus 14.97% in Group TY; farrowing rate increased from 80% to 91.9% in Group TI, with no change in Group TY. In Farm B, pre-weaning mortality was 4.57% (TI) versus 6.89% (TY), and average weaning weight was 7.5 kg (TI) versus 7.0 kg (TY). In Farm C, pre-weaning mortality was 2.33% (TI) versus 5.02% (TY); the incidence of mummified, weak, and stillborn piglets decreased by 4.74% in TI but increased by 0.8% in TY. Breeding rate within 7 days post-weaning was 92% (TI) versus 91.25% (TY). PF PRRSV positivity dropped from 100 to 0% in TI and from 100 to 16.7% in TY.

Conclusion

Tilmicosin (Pulmotil®) consistently outperformed tylvalosin in reducing pre-weaning mortality, improving sow reproductive performance, and lowering PRRSV positivity across all three farms. The marked reduction in PRRSV detection and better production metrics suggest that tilmicosin may play a critical role in integrated PRRS control strategies for commercial sow herds.

Keywords: Pre-weaning Mortality, PRRSV, Pulmotil, Tilmicosin, Tylvalosin.

DETERMINING FARM SURFACE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS CONTAMINATION THROUGH VIABILITY RT-QPCR

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Introduction and Objectives

Biosecurity plays a crucial role in the swine industry (Alarcón et al., 2021). As most growing pig sites lack shower-in/shower-out facilities there is an opportunity for contaminated personnel to play a role in PRRSV indirect transmission (Harlow et al., 2024). Identifying viable PRRSV on frequently touched surfaces may offer additional insight for biosecurity protocols. This study aimed to 1) determine whether viable PRRSV can be detected on frequently touched surfaces by farm personnel; 2) assess whether the number of PRRSV detections from oral fluids in a population are associated with viable PRRSV detections on farm surfaces; and 3) explore the agreement between standard and viability RT-qPCR.

Materials and Methods

Ten PRRSV-positive growing pig farms were enrolled in this cross-sectional study. A total of 20 samples per farm from different surfaces were collected by swiping with a media moistened pad, placed in a resealable bag, squeezed, and poured into a tube. A set of 8 ropes (16 pens) per barn was hung to collect oral fluids. Samples were tested for PRRSV RT-PCR. Positive environmental samples were tested via viability RT-qPCR.

Results and Discussion

The virus' RNA was mostly detected on non-porous surfaces, with 80 out of 200 environmental samples testing positive. Viable virus was detected in 48 samples across six farms, with non-porous materials testing positively more frequently. A GLMM suggested a negative association (OR = 0.005; 95% CI 0.00, 6.82; $P = 0.18$) between the proportion of positive oral fluids and detecting viable virus from sampled surfaces. Agreement between the detection of RNA and viable PRRSV from surface samples using Cohen's kappa yielded perfect agreement ($\kappa = 1.00$) to low agreement ($\kappa = 0.29$) depending on the surfaces. These results indicate the presence of viable virus on surfaces that are frequently touched by the farm's personnel.

Conclusion

This study highlights the importance of biosecurity measures applied to the personnel and their potential role in environmental contamination and PRRSV dissemination. The use of viability RT-qPCR to detect viable PRRSV offers a practical tool in field settings to improve biosecurity protocols to reduce indirect transmission of PRRSV in swine production systems.

Keywords: Environmental contamination, Indirect transmission, Porcine reproductive and respiratory syndrome, Viability.

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FEASIBILITY OF PORCINE ENTEROIDS AS AN ALTERNATIVE TO CELL CULTURE AND PIG BIOASSAY FOR ASSESSING PORCINE DELTACORONAVIRUS VIABILITY

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Introduction and Objectives

Molecular detection of viral RNA on environmental surfaces following disinfection is highly sensitive but does not distinguish between infectious and non-infectious virus. Although pig bioassays can demonstrate viral viability, their routine use is limited by cost, logistics, and ethical constraints. This study evaluated porcine enteroids cultured on transwell inserts (PETCs) as an *ex vivo* diagnostic platform to assess the infectivity of porcine deltacoronavirus (PDCoV). The objectives were to (i) determine the minimum infectious dose of PDCoV required to establish infection in PETCs compared to swine testicular (ST) cells, and (ii) evaluate the infectivity of PCR-positive field samples using *ex vivo* (PETCs), *in vitro* (ST cells), and *in vivo* (neonatal piglet) models.

Materials and Methods

PDCoV (Michigan/8977/2014; 3.16×10^5 $TCID_{50}$/mL) was two-fold serially diluted (2^1 - 2^{14}) and inoculated into PETCs derived from duodenum, jejunum, and ileum of 7-day-old piglets (n = 3) and ST cells. Infection was assessed using cytopathic effect (CPE), immunofluorescence assay (IFA), and RT-qPCR targeting the nucleocapsid gene. Environmental samples (feeders, rubber teats, pen floor, and sewage) collected from a PDCoV-affected farm after disinfection (Cq 30 - 34) were inoculated into jejunum-derived PETCs, ST cells, and neonatal piglets. Cell cultures were evaluated by CPE, IFA, and RT-qPCR, while piglets were monitored for clinical signs, histopathology, and viral shedding.

Results and Discussion

In PETCs, CPE and IFA were minimal/absent, whereas RT-qPCR detected PDCoV RNA from 2^1 to 2^{10} (Cq 24 - 35). Unlike transformed *in vitro* cell lines, PETCs preserve epithelial polarity, differentiated intestinal cell populations, and native host-factor expression, enabling biologically relevant assessment of viral entry and replication and providing a practical *ex vivo* alternative to pig bioassay for infectivity evaluation. ST cells exhibited pronounced CPE and IFA across dilutions; however, no evidence of productive infection was detected in PETCs, ST cells, or piglets following inoculation with PCR-positive field samples.

Conclusion

While further optimization is required to enhance analytical sensitivity, PETCs represent a promising *ex vivo* platform that bridges with conventional cell culture and animal bioassays, aligns with the 3R principles, and supports infectivity assessment of enteric viruses relevant to swine health.

Keywords: Enteroids, Ex *vivo* culture, Porcine Deltacoronavirus, Porcine enteric coronavirus, Viability.

MONITORING PORCINE CIRCOVIRUS TYPE-2 VIREMIA BY QPCR IN PIGS

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Introduction and Objectives

Porcine circovirus type 2 (PCV-2) remains one of the most economically significant pathogens in swine production. Vaccination is a highly effective strategy for disease control, as it reduces viremia, viral shedding, lesion severity, and production losses (Segalés et al., 2012; Opriessnig et al., 2018). However, viral persistence in vaccinated populations may lead to subclinical infections, resulting in considerable economic impact. The objective of this study was to monitor PCV-2 viremia dynamics using real-time quantitative PCR (qPCR) in pigs from commercial production systems.

Materials and Methods

Monitoring was performed on eight commercial farms in Argentina, all vaccinating pigs against PCV-2 at 21 days of age. Three farms were evaluated longitudinally and five through cross-sectional sampling. Blood samples were collected at 21, 42, 63, 84, 105, 126, and 147 days of age, selecting 10 animals per age group (Martin et al., 1987). In the longitudinal evaluation, animals were individually identified with ear tags at the beginning of the study for follow-up. Samples were divided into two pools per age and analyzed using a validated commercial qPCR kit. Results were expressed as viral copies/mL and classified according to international criteria: < 5 $\log_{10}$ copies/mL (minimal or no clinical relevance), ≈ 6 $\log_{10}$ (active subclinical infection), and > 6 $\log_{10}$ (clinical circovirosis).

Results and Discussion

No viremia was detected at the time of vaccination in any of the farms. Between weeks 9 and 21, some farms showed low to moderate PCV-2 viral loads, consistent with controlled subclinical infection. Vaccination reduces the magnitude and duration of viremia but does not prevent infection or transient viral replication. These findings highlight the importance of identifying and mitigating predisposing factors that may favor viral circulation.

Conclusion

qPCR is a sensitive and reproducible method for monitoring PCV-2 in vaccinated farms. When integrated into a multifactorial diagnostic approach, it enables early detection of deviations, supports optimization of herd health programs, and helps reduce the productive impact associated with PCV-2.

Keywords: Molecular diagnosis, PCV-2, Subclinical disease, Viremia.

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THE LNCRNA HCG4 REGULATES THE RIG-I-MEDIATED IFN PRODUCTION TO FACILITATE H1N1 SWINE INFLUENZA VIRUS REPLICATION

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Introduction and Objectives

The influenza A virus nonstructural protein 1 (NS1) is a multifunctional protein that plays an important role in virus replication, virulence and inhibition of the host antiviral immune response. Previously, we rescued the NS1 mutant (S42P) of the A/swine/Shanghai/3/2014(H1N1) strain and found the mutant virus reduced the capability of NS1 to antagonize IFN-β expression. In this study, we focused on the different expression profiles of host long noncoding RNAs (lncRNAs) in cells upon infection with H1N1 SIV and its NS1 mutant, and revealed the underlying regulatory mechanisms of lncRNAs in the innate immune response.

Materials and Methods

By lncRNA-seq, we identified different expressed lncRNAs in cells and lncRNA HCG4 was selected due to its significantly higher expression with NS1 S42P mutant virus infection. To investigate the effect of HCG4 on viral replication and IFN expression, cells were transfected with plasmids encoding HCG4 or siRNA and subsequently infected with the strain A/swine/Shanghai/3/2014. We detected virus replication and IFN-β expression by TCID50 and Western blotting assay.

Results and Discussion

KEGG pathway analysis showed that JAK-STAT pathway was highly enriched by NS1mutant virus infection. Next, we found that in HCG4 overexpressed cells, SIV infection increased the expression of RIG-I, p-IRF3, and p-STAT1/2, and the IFN-β level was also significantly increased compared to that in the control cell. The TCID50 value showed that overexpression of HCG4 inhibited viral replication of SH/2014. Meanwhile, Silencing HCG4 in vitro attenuated RIG-I-triggered IFN-β expression and promoted SIV replication. We supposed that the HCG4 served as a positive feedback regulator in IFN signaling during SIV infection, thus exerting anti-viral effects on SIV.

Conclusion

In conclusion, our findings suggested that lncRNA HCG4 significantly elevated after SIV NS1 mutant infection, and this is the first study to describe the role of lncRNA HCG4 for NS1 function in SIV infection. This work reveals lncRNA HCG4 as a positive regulator in antiviral interferon response, which provides new insights into roles of lncRNAs in virus-host interactions.

Keywords: IFN, LncRNA, NS1 protein, Swine influenza virus.

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EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST A KOREAN LINEAGE 1 STRAIN

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11-21. The objective of this study was to evaluate the efficacy of that vaccine (Prevacent® PRRS) against a Korean PRRSV-2 lineage 1 strain when administered to two-week-old pigs.

Materials and Methods

Twenty four two-week-old pigs were allocated to three groups of eight pigs each. The pigs of one group were injected intramuscularly with Prevacent® PRRS (Elanco), whereas the pigs of the two other groups were injected intramuscularly with a placebo and included as positive and negative controls, respectively. At 28 days post-vaccination, the vaccinated pigs and the positive controls were challenged intranasally with the Korean PRRSV-2 lineage 1 strain SNUVR090851. The negative controls remained unchallenged. Efficacy was assessed by determining clinical scores, average daily weight gain (ADWG), lung lesion scores, and viral loads in sera up to 14 days post-challenge (DPC).

Results and Discussion

The negative controls remained virus-negative, and despite a mild dyspnea in some pigs resulting in a mean clinical score of 0.125, they had no lung lesions and showed a normal growth with an ADWG of 0.330 kg. The results of the pigs that were challenged were less good, but with clear differences in favor of the vaccinated pigs. Indeed, the mean clinical score of the vaccinated pigs (1.250) was lower than the one of the positive controls (2.313) and the ADWG of the vaccinated pigs (0.309 kg) was higher than the one of the positive controls (0.279 kg). Also, the mean lung lesion score of the vaccinated pigs (14.125) was lower than the one of the positive controls (27.188). Finally, the mean cumulative viral load in the sera (sum of viral loads at 7 and 14 DPC) was lower in the vaccinated pigs (3.872 $\log_{10}$) than in the positive controls (7.144 $\log_{10}$).

Conclusion

The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, weight loss, lung lesions, and virus replication in blood following a challenge with a Korean PRRSV-2 lineage 1 strain.

Keywords: Challenge, Efficacy, Korea, PRRSV, Vaccine.

SAFETY AND EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE IN PIGLETS UNDER KOREAN FIELD CONDITIONS

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the safety and efficacy of that vaccine (Prevacent® PRRS) under Korean field conditions when administered to two-week-old pigs.

Materials and Methods

On each of three Korean farms with circulation of PRRSV-2 lineage 5 strains, 20 two-week-old pigs were vaccinated with Prevacent® PRRS (Elanco), and another 20 two-week-old pigs were treated with its diluent. The safety was evaluated by assessing local reactions and rectal temperatures. The efficacy was evaluated by comparing clinical scores, mortality rates, average daily weight gain (ADWG), lung lesion scores, and detection rates of viremia between the vaccinated pigs and the control pigs from 0 days post-vaccination until the end of the fattening period.

Results and Discussion

Apart from nine vaccinated and four control pigs that showed a transient mild swelling at the injection site within two days following their treatment, no local reactions were observed. Further, there were no differences in rectal temperatures within the seven-day observation period following the treatment between both groups. The clinical scores of the vaccinated pigs were lower than the ones of the control pigs on all three farms (0.967 vs. 1.923, 0.833 vs. 1.710, 0.834 vs. 1.464), which was also reflected in lower mortality rates (5 vs. 10%, 5 vs. 15%, 5 vs. 10%), higher ADWG (0.625 vs. 0.590 kg, 0.637 vs. 0.604 kg, 0.632 vs. 0.605 kg), and lower lung lesion scores (11.6 vs. 27.1, 17.8 vs. 32.5, 13.3 vs. 29.1). Also, the detection rates of viremia were lower in the vaccinated pigs than in the control pigs on all three farms (58.9 vs. 77.5%, 56.2 vs. 81.4%, 56.8 vs. 77.5%).

Conclusion

A vaccination of two-week-old pigs with Prevacent® PRRS proved to be safe and efficacious under Korean field conditions, as evidenced by the low incidence of systemic and local reactions, and consistently better results of the vaccinated pigs compared to the control pigs across all three farms for all efficacy parameters assessed.

Keywords: Efficacy, Korea, PRRSV, Safety, Vaccine.

SAFETY AND EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE IN BREEDING PIGS UNDER KOREAN FIELD CONDITIONS

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the safety and efficacy of that vaccine (Prevacent® PRRS) under Korean field conditions when administered to sows at six weeks prior to breeding.

Materials and Methods

On each of three Korean farms with circulation of PRRSV-2 lineage 5 strains, 20 sows were vaccinated with Prevacent® PRRS (Elanco), and another 20 sows were treated with its diluent six weeks prior to their breeding. The safety was evaluated by assessing local reactions and rectal temperatures. The efficacy was evaluated by comparing percentages of weaned piglets, detection rates of viremia in the sows, and viral loads in the sera of two newborn piglets from each sow between the vaccinated sows and the control sows.

Results and Discussion

None of the vaccinated sows and control sows developed injection site reactions following their treatment. Further, there were no differences in rectal temperatures within the seven-day observation period following the treatment between both groups. The percentages of piglets weaned from the vaccinated sows were higher than the ones from the control sows on all three farms (90.1 vs. 81.5%, 90.1 vs. 81.8%, 93.2 vs. 85.7%). Further, the detection rates of viremia were lower in the vaccinated sows than in the control sows on all three farms (47.5 vs. 57.5%, 40.0 vs. 65.0%, 22.5 vs. 40.0%). Finally, the mean viral loads were lower in the sera of the newborn piglets from the vaccinated sows than in the ones from the control sows on all three farms (0.68 vs 1.13 $\log_{10}$, 0.86 vs 1.30 $\log_{10}$, 0.46 vs 1.03 $\log_{10}$).

Conclusion

A vaccination of sows with Prevacent® PRRS proved to be safe and efficacious under Korean field conditions, as evidenced by the absence of systemic and local reactions following the vaccination, and higher piglet viabilities, lower detection rates of viremia, and lower viral loads in the sera of newborn piglets in the vaccinated sows than in the control sows across all three farms.

Keywords: Efficacy, Korea, PRRSV, Safety, Vaccine.

COMPARATIVE STUDY WITH THE USE OF A NOVEL APATHOGENIC PRRS VACCINE OR AN MLV VACCINE ON REPRODUCTIVE PERFORMANCE IN A PRRSV-POSITIVE SOW HERD

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) causes significant reproductive losses, including fetal death, abortions, stillbirths, and mummified fetuses, thus, modified-live virus (MLV) vaccines are widely used, but their efficacy greatly varies under field conditions. A novel vaccine derived from the naturally apathogenic G16X strain has shown promising results, inducing protective immunity against pathogenic PRRSV, experimentally and in commercial conditions. The objective of this study was to compare the reproductive performance in a PRRSV-positive sow herd vaccinated with either a commercial MLV vaccine or with the G16X apathogenic strain.

Materials and Methods

A Site 1 production unit located in Tepatitlan, Jalisco, Mexico with 4,200 PRRSV-positive sows, confirmed by ELISA and qPCR, was monitored under two vaccination protocols: MLV or G16X vaccines, following the manufacturers´ recommendations of use in a period of 15 months with MLV vaccine, plus 4-months of transition, and 11 months with G16X vaccine. Reproductive parameters were computed and analyzed using Welch's t-test (GraphPad Prism v10.4.1).

Results and Discussion

Significant improvements were observed with the use of the G16X strain vaccine when compared with the use of the MLV vaccine:

- Live born piglets per litter increased by +0.44 ($P = 0.0161$)
- Stillbirth rate decreased by -1.65% ($P = 0.0006$)
- Mummified fetuses decreased by -0.94% ($P = 0.0496$)
- Sow mortality decreased by -1.79% ($P = 0.0276$)
- Piglets weaned per sow per year increased +1.11 ($P = 0.0337$)

The sows vaccinated with the G16X strain vaccine outperformed those vaccinated with MLV vaccine in key reproductive metrics, resulting in an estimated annual gain of 4,662 piglets, which represents a direct extra economic benefit of approximately $132,988.00 USD

Conclusion

The results obtained in this field study have been consistent with other trials conducted with the G16X strain, which support the use of it as a strategic alternative for controlling the disease and associated economic losses.

Keywords: Economic benefit, G16X, Naturally apathogenic, Porcine Reproductive and Respiratory Syndrome Virus, Reproductive losses.

BENEFIT OF INGELVAC® PRRS MLV VACCINATION ON A FARM SITE 2 IN MEXICO

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) has been one of the most economically important viral diseases worldwide for more than two decades. PRRS is characterized by reproductive failure in sows and respiratory distress in growing pigs (Moura et al., 2023). In nursery and finishing pigs, the economic impact attributable to PRRSV infection results from increased morbidity and mortality rates, reduced feed efficiency and growth rates, and an increase in unmarketable pigs (Holtkamp et al., 2023). The objective of this study was to evaluate the ratio of pigs sent to finishing from Site 2 to a population vaccinated with an MLV vaccine against PRRS in a highly challenged area.

Materials and Methods

The farm where the study was conducted is positive for PRRSV, *M. hyo*, IAV-S, PED, and PCV2. During the trial, the farm's historical mortality rate (G1) was analyzed over a period without application of any PRRSV vaccination schedule. During this period, the farm comprised a total of 26,210 pigs distributed across 23 production lots without any PRRSV vaccination schedule. This was compared with the mortality rate of the vaccinated population (G2) in the same farm, which received 2 ml of the Ingelvac® PRRS MLV vaccine (Boehringer Ingelheim AH) intramuscularly at an average age of 14 days in site 1 and the weaning was at 25 days. The total number of vaccinated piglets sent to site 2 was 32,875, distributed across 27 production lots, where they were housed for a period of 7 weeks. A Student's t-test was performed for independent samples ($P < 0.05$).

Results and Discussion

The analysis shows a statistical difference in the number of animals sent to feedlots, given that G2 had a value ($P = 0.00000008$) compared to G1.

Conclusion

Based on this field study, we can observe that vaccination with Ingelvac® PRRS MLV helps increase the number of pigs sent to fattening, resulting in a decrease in the farm's mortality rate.

Keywords: Mortality, PRRS, Vaccination.

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MOLECULAR AND SEROLOGICAL MONITORING OF INFLUENZA A VIRUS IN WILD BOAR IN SLOVENIA

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Introduction and Objectives

Influenza A viruses (IAV) in wild boars may pose a risk to domestic pigs and humans. Surveillance of IAV circulation in wild boar is therefore important for monitoring potential viral circulation. The aim of this study was to monitor IAV infections in wild boar using molecular and serological surveillance and to provide initial data relevant to One Health considerations.

Materials and Methods

Sampling was conducted in Slovenia between January 2024 and July 2025. A total of 229 wild boars found dead or road-killed were sampled (nasopharyngeal, brain, and lung swabs). IAV RNA was detected by real-time RT-PCR (Slomka et al., 2010), followed by real-time RT-PCR subtyping (Hofman et al., 2016). Serological surveillance included 471 serum samples from hunted wild boars and 37 body fluid samples, analyzed using commercial multi-species ELISA kits for IAV (Influenza An Antibody Competition Multi-Species, ID.Vet, Grabels, France; Batch. No. O84) and H5 antibodies (Influenza H5 Antibody Competition 3.0 Multi-Species, ID.Vet, Grabels, France; Batch No. P157), following manufacturer-recommended cut-off values (S/N 40 - 50%).

Results and Discussion

Influenza A virus (IAV) RNA was identified in upper respiratory tract samples from 3/135 wild boars (2.2%). Two specimens with matrix (M) gene Ct values of 28.85 and 28.05 were subtyped as swine IAV H1N1, while one sample (Ct = 34.54) remained unsubtyped due to low viral RNA load. IAV antibodies were detected in 3.2% of samples (19/508), with S/N values ranging from 7 to 38 (mean 16.7). Among seropositive samples, H5 antibodies were confirmed in one case (S/N 4%). These sporadic detections indicate ongoing viral circulation, but given the small number of positive samples, cross-reactivity or false positives cannot be excluded. The data suggests potential viral presence in wildlife populations, highlighting the need for continued surveillance.

Conclusion

Molecular and serological surveillance indicates low-level circulation of IAV in wild boar. Although prevalence was low, the findings are consistent with previous European reports and suggest that wild boar may occasionally contribute to interspecies transmission. Due to limited sample size and low prevalence, the study cannot definitively quantify spillover risk, but it emphasizes the epidemiological relevance of ongoing monitoring for public and animal health.

Keywords: Influenza A viruses, Spillover, Wild boar, Zoonotic potential

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PREVALENCE OF PORCINE CIRCOVIRUS GENOTYPES ON COMMERCIAL FARMS IN MEXICO

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Introduction and Objectives

The global evolution of PCV2 genotypes reflects the virus's high capacity to mutate and generate new variants. This genetic plasticity supports the emergence and spreads of different genotypes over time, influencing epidemiology, virulence, and vaccine performance. Understanding this dynamic is essential for effective control and prevention strategies. The objective of this study was to estimate the occurrence of different genotypes on Mexican farms.

Material and Methods

During the year 2025, 22 farms located in Central, Western, and Southern Mexico were sampled. Serum was collected from piglets aged 1 to 23 weeks of age. 203 serum samples were pooled in groups of 5, with 1015 piglets sampled. DNA was extracted by the IndiMag Pathogen Kit (Indical Bioscience) and subjected to the PCV2 genotyping assay by the Kylt® PCV-2 Typing Kit (AniCon Labor GmbH) to differentiate between PCV2 genotypes.

Results and Discussion

The results of the 203 samples analyzed, 72 were positive for PCV2 by PCR. 52 samples were typification and 62% of them were PCV2d, 36% were PCV2a, and 2% were PCV2a+d. And the results from the 22 farms sampled, 14 farms (63%) were positive for PCV2 PCR: 4 of those farms (28.5%) were positive for PCV2a, 6 farms (43%) for PCV2d, 4 farms (28.5%) for PCV2a+d. The data of this study reinforce that PCV2d remains the most prevalent genotype in the swine populations analyzed. This predominance is consistent with recent research from Mexico and other countries which also reported high detection rates of this genotype.

Conclusion

These data highlight the ongoing evolution of PCV2 and the need for continuous genetic monitoring to guide effective control strategies.

Keywords: Genotypes, Porcine Circovirus.

THE DIAGNOSTIC PERFORMANCE OF COMMERCIAL PRRSV RT-QPCR ASSAYS USING ORAL FLUID SAMPLES OF KNOWN STATUS

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Introduction and Objectives

Diagnostic performance of RT-qPCR protocols is often evaluated using raw quantification cycle (Cq) values. However, Cqs lack a defined quantitative scale, are affected by assay-specific factors, and do not support statistically valid comparisons among laboratories or diagnostic cutoffs. To address these limitations, Armenta-Leyva et al. (2024) proposed normalizing RT-qPCR responses by re-expressing them as efficiency standardized Cqs ("ECqs", calculated ECq = $E^{-\Delta Cq}$ relative to vaccine-derived PRRSV reference standards). Normalization accounts for amplification efficiency, enables valid inter-assay and inter-laboratory comparisons, and supports the calculation of statistically valid cutoffs.

Materials and Methods

We used ECqs to assess the diagnostic performance of 9 combinations of commercial nucleic extraction kits and RT-qPCR assays for PRRSV RNA detection in swine oral fluids. The 3 × 3 full factorial design included 3 extraction kits: (1) Applied Biosystems MagMAX™ Pathogen RNA/DNA, (2) Indical Bioscience IndiMag® Pathogen, and (3) Tetracore VetAlert™ MagBead Total Nucleic Acid Extraction; and 3 RT-qPCR assays: (A) Applied Biosystems VetMAX™ PRRSV EU & NA, (B) Indical Bioscience virotype® PRRSV RT-PCR, and (C) Tetracore EZ-PRRSV™ Real-Time PCR. Each unique extraction × PCR combination was labeled using a 2-character label (e.g., 1A = extraction 1 with PCR A), resulting in 9 protocols (1A through 3C).

Results and Discussion

We tested 308 pen-based oral fluid samples, including 96 negative and 212 positive samples, from pigs experimentally inoculated with various PRRSV-2 isolates. ECqs responses were calculated relative to 4 replicates of PRRSV-specific reference standards run in every plate. ECqs were evaluated by ROC analysis. For specific protocols, area under the curve (AUC) estimates derived from ROC analyses ranged from 0.916 (95% CI: 0.882, 0.959) to 0.986 (95% CI: 0.974, 1.000); AUC pairwise comparisons identified significant differences (p value < 0.05) between protocols. At optimal ECq cutoffs (Youden's index), diagnostic sensitivities ranged from 83% to 98.1%, with diagnostic specificities consistently at 100%.

Conclusion

Our findings showed that both extraction and amplification impacted RT-qPCR performance. Thus, PCRs need to be evaluated as an integrated system rather than as standalone components. Importantly, ROC analysis of ECqs provided a statistically valid approach for estimating diagnostic performance and comparing PCR-based testing.

Keywords: Diagnostic performance, Oral fluids, PRRSV, RT-qPCR.

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FIELD EVALUATION OF A PCV2D/MHYO BASED VACCINE (RTU) IN A PCV2 SUBCLINICAL CHALLENGE HERD IN BRAZIL

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) remains widely distributed and continuous viral evolution, particularly the emergence and predominance of PCV2d genotypes, has become increasingly evident in recent years (Sibila et al., 2021; Calveyra et al., 2024). The objective of this study was to evaluate the efficacy of two PCV2/Mhyo (RTU) vaccination protocols on PCV2 viremia and seroconversion under field conditions.

Material and Methods

The field trial started on a commercial farm located in Santa Catarina State (Brazil) with a previous confirmed history of PCV2d circulation. A total of 1470 Piglets at 3 weeks of age (WOA) were allocated into two treatment groups: Group 1: one shot, 2 mL, IM of PCV2d/Mhyo RTU - CIRBLOC® M Hyo, Ceva Animal Health and Group 2: one shot, 2 mL IM of PCV2a subunit vaccine + Mhyo RTU. Both groups were maintained under identical housing and environmental conditions throughout the experiment period. ELISA (BioChek®) and qPCR analyses were performed at 3, 5, 7, 9, 16, 22 WOA. At slaughterhouse, 30 samples of lymphatic and lung tissues from each group were sampled for PCV2 detection by qPCR. The ELISA means data were analyzed using T-test. The qPCR means data were analyzed by Mann-Whitney test.

Results and Discussion

Animals in Group 1 showed a significant difference in seroconversion compared to Group 2 (2.21 vs. 1.77) at 5 WOA and (3.18 vs. 2.58) at 7 WOA, $P < 0.05$. Group 1 presented lower viremia levels compared to Group 2, with no significant difference (Log_{10} 2 vs. 4) at 7 WOA (Log_{10} 2.6 vs.3.2) at 9 WOA and (Neg vs. Log_{10} 7) at 16 WOA, $P > 0.05$. Group G1 showed lower viral loads compared to Group G2 in lymphatic tissues (Log_{10} 6.8 vs. 9, $P < 0.01$) and in the lungs (Log_{10} 5.3 vs. 6.2, $P < 0.10$).

Conclusion

Animals in Group 1 showed a significantly stronger serological response against PCV2. Furthermore, there was a marked reduction in viral load over time, where, from 16 WOA onwards, all vaccinated animals were negative for PCV2, while Group 2 was strongly viremic. The Group 1 protocol demonstrated superior efficacy in controlling PCV2 infection compared to a PCV2a-based vaccine.

Keywords: Porcine Circovirus, Vaccine.

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APPETITE REGULATION IN PIGS INFECTED WITH PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS

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Introduction and Objective

Porcine reproductive and respiratory syndrome virus (PRRSV) infection commonly reduces feed intake by approximately 30% (Helm et al., 2019), however, little is known about how this disease regulates appetite. Our objective was to evaluate the effect of PRRSV on pig feed intake, neuroinflammation, and orexigenic and anorexigenic neuropeptides within the thalamic-hypothalamic region.

Materials and Methods

Thirty two mixed-sex pigs (27 ± 2.3 kg) were randomly allotted to individual pens, 16 pigs were inoculated with a PRRSV-2 L1C.2 variant receiving 0.5 mL (approx. 6,236 genomic copies/mL) intramuscularly and 0.5 ml intranasally, and 16 pigs served as sham-inoculated controls. Over 12 days post-inoculation (dpi), body temperature, feed intake and body weights were recorded, after which all pigs were euthanized, and heads were sectioned to collect thalamus-hypothalamus tissue for histopathology. Hematoxylin and eosin-stained sections were evaluated by a veterinary pathologist for evidence of inflammation and scored on a 0-3 scale corresponding to none, mild, moderate, or severe inflammation. Thalamic-hypothalamic sections were analyzed for transcriptional abundance of anorexigenic [cocaine and amphetamine regulated transcript (CART) and proopiomelanocortin (POMC)] and orexigenic [neuropeptide Y (NPY) and agouti-related protein (AgRP)] neuropeptides using RNAscope in situ hybridization.

Results and Discussion

Throughout the challenge period, PRRSV-infected pigs exhibited increased body temperatures (40.1°C vs. 39.1°C; $P < 0.0001$), reduced average daily feed intake (0.99 vs. 1.84 kg/d; $P < 0.0001$), and reduced average daily gain ($P < 0.0001$) compared with controls. PRRSV pigs exhibited greater inflammation within the thalamic-hypothalamic region ($P < 0.0001$). At 12 dpi, viral load, as measured by serum PRRSV PCR Ct value, was significantly correlated with thalamic-hypothalamic inflammation, such that higher viral load was associated with increased inflammation ($P < 0.0001$). Localized transcriptional abundance of the orexigenic neuropeptides NPY and AgRP was increased in PRRSV pigs relative to controls ($P = 0.006$), with no differences observed in anorexigenic transcripts.

Conclusion

PRRSV-2 L1C.2 reduced feed intake and growth performance while inducing fever and neuroinflammation in pigs. Despite pronounced anorexia, PRRSV pigs exhibited increased thalamic-hypothalamic transcriptional abundance of NPY and AgRP. These findings indicate that PRRSV-associated anorexia occurs despite upregulation of orexigenic signaling at the transcriptional level. Neuroinflammatory signaling may contribute to altered appetite control during PRRSV infection.

Keywords: Appetite regulation, Feed intake, Porcine reproductive and respiratory syndrome virus.

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PCV2D BASED VACCINE PERFORMANCE UNDER FIELD CONDITIONS IN BRAZILIAN FARMS: SEROCONVERSION AND VIREMIA

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Introduction and Objectives

Even with the outstanding results given by PCV-2 vaccination of piglets, immunizing this specific age group of animals has been shown to change the dynamic of infection of this virus (Segalés et al., 2025). Continuous viral mutations, the emergence and predominance of PCV2d genotype, have become evident in recent years (Segalés et al., 2022; Calveyra et al., 2024). This study aimed to evaluate PCV2 protection by comparing two PCV2/Mhyo RTU vaccination protocols, under field conditions in a herd with confirmed PCV2d circulation.

Material and Methods

The field trial started on a commercial farm located in Paraná State (Brazil) with a previous confirmed history of PCV2 b + d circulation. A total of 1050 Piglets (28 DOA) were allocated into two treatment groups: Group1: PCV2d/Mhyo vaccine RTU-CIRBLOC® M Hyo, Ceva Animal Health, and RTU PCV2 a, b + *M. hyo*. Both groups were maintained under identical housing and environmental conditions during the experimental period. Serology (ELISA BioChek®) and qPCR analyses were performed at 3, 6, 9, 12, 16, and 22 weeks to assess antibody response and viremia levels. The data were analyzed using t-test.

Results and Discussion

Animals from Group 1 showed a significantly stronger serological response against PCV2 especially five weeks post vaccination when compared with the other group (S/P 2,88 and 0,70, respectively, $P < 0.05$). No viral load was detected in both groups during the trial. The serological response to vaccination, especially in herds with low infection challenge, can provide important insight into the actual effectiveness of the vaccination program.

Conclusion

CIRBLOC® M Hyo displayed higher seroconversion rates which suggests a stronger potency compared with a PCV2a/b-based vaccine.

Keywords: Porcine Circovirus, Vaccine.

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DURATION OF IMMUNITY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AFTER FIELD VACCINATION AND LABORATORY CHALLENGE

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Introduction and Objectives

Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to confirm the duration of immunity (DoI) of that vaccine (Prevacent® PRRS) by vaccinating pigs under field conditions and challenging them 25 weeks later under laboratory conditions.

Materials and Methods

At a conventional pig unit, each 24 two- to three-week-old pigs were injected intramuscularly with either Prevacent® PRRS (Elanco) (three groups, each with a different vaccine batch) or a placebo. Sixteen pigs from each group were moved 25 weeks later to a BSL-2 facility for a combined intranasal and intramuscular challenge with PRRSV-2 lineage 8 strain NADC20. Efficacy was assessed by determining clinical scores (sum of scores for depression, respiratory distress, and loss of body condition), average daily weight gain (ADWG), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion

The mean clinical scores of the vaccinated groups (1.625, 0.438, and 0.063) were lower than the one of the controls (2.125), and the ADWG of the vaccinated groups (0.046, 0.216, and 0.237 kg) were higher than the one of the controls (-0.264 kg). Also, the mean lung lesion scores at 14 DPC of the vaccinated groups (0.634, 0.881, and 1.134) were lower than the one of the controls (6.447). Finally, the mean cumulative viral loads in the sera (sum of viral loads at 7 and 14 DPC) were lower in the vaccinated groups (4.173, 2.856, and 3.825 $\log_{10}$) than in the controls (11.159 $\log_{10}$). Similarly, the mean viral loads in the BAL fluids were lower in the vaccinated groups (1.812, 2.069, and 2.602 $\log_{10}$) than in the controls (6.134 $\log_{10}$).

Conclusion

The results of this study demonstrate that a vaccination of two- to three-week-old pigs with Prevacent® PRRS under field conditions is able to reduce clinical signs, weight loss, lung lesions, and virus replication in blood and lungs following an experimental challenge 25 weeks later, supporting a DoI until the end of the fattening period.

Keywords: Duration of immunity, Efficacy, Heterologous challenge, PRRSV, Vaccine.

MOLECULAR CHARACTERIZATION OF AFRICAN SWINE FEVER VIRUS RECOMBINANT STRAINS CIRCULATING IN PIGS IN SOUTHERN VIETNAM

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Introduction and Objectives

African swine fever (ASF) is a major threat to pig production. While genotype II has been the dominant circulating strain since its introduction in Vietnam in 2019, recently emergence of recombinant strain combining genetic material from genotypes I and II (rASFV I/II) raised new concern. This study aimed to detect and determine some molecular characters including 5 key genetic regions: B646L (p72), E183L (p54), EP402R (CD2v), B602L (containing Central Variable Region - CVR which is highly variable in number and composition of the tetrameric tandem repeat (TRS), thus highly sensitive to small genomic changes) of rASFV I/II circulating in pigs in Southern Vietnam.

Materials and Methods

Five genes (B646L, E183L, EP402R, B602L and IGR) of five recombinant strains (rASFV) (PY25/rASF1/BenTre, PY25/rASF2/TraVinh, PY25/rASF3/DongNai, PY25/rASF4/LamDong, PY25/rASF5/DakNong) were sequenced and edited with Sequencher 5.4.6 and aligned by BioEdit 7.2.6. Phylogenetic trees were constructed by MEGA 12.0 using the Neighbor-Joining method (1000 bootstrap replicates) to assess genetic relationships with previously reported ASFV genotypes I, II and rASF I/II strains.

Result and Discussion

Sequencing revealed the B646L (p72) gene belongs to genotype I, E183L (p54) to genotype II, and EP402R (CD2v) corresponds to serotype VIII with 100% identity to other reported recombinant strains from northern Vietnam, China and Russia. These isolates showed high genetic identity to rASFV strains from Northern Vietnam, China, and Russia, suggesting north-to-south dissemination. Notably, the CVR showed significant variation in tetrameric repeats, indicating evolution during its spread. The IGR was identified as group II, consistent with Vietnam dominant genotype II backbone. The emergence of these rASFV strains, which evade immunity from genotype II-based vaccines (Diep et al., 2024), is a serious problem for pig production.

Conclusion

New rASFV strains share strong genetic relations with previously reported recombinant strains but show significant mutations within the CVR. These findings indicate the need for updated diagnostic protocols, enhanced molecular surveillance, and urgently efficient vaccines to control these emerging rASFV strains.

Keywords: African swine fever virus, Recombinant ASFV, Southern Vietnam.

Acknowledgements: The authors thank P&Y Livestock Services Company Limited, Vietnam for providing testing facilities.

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PORCINE HEMAGGLUTINATING ENCEPHALOMYELITIS VIRUS AND A NOVEL ASTROVIRUS CO-INFECTION IN PIGLETS WITH RESPIRATORY DISEASE

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Introduction and Objectives

Respiratory disease in pigs is common worldwide. Traditionally, disease has been associated with single pathogens. Multiple microorganisms are now increasingly thought to contribute to disease in what is known as the porcine respiratory disease complex (PRDC). With the increasing availability of sophisticated diagnostic methods, such as whole-genome sequencing, previously undetected microorganisms can now be identified. The study aims to describe novel viruses detected in Swedish pigs with respiratory disease.

Materials and Methods

Clinical samples (n = 4) were submitted to the Swedish Veterinary Agency for diagnostics as part of routine veterinary herd health management from a Swedish pig farm with three- and eight-week-old piglets showing clinical signs of respiratory disease. Two snout samples from each age group were collected with eSwabs and initially tested with qPCR for several respiratory pathogens included in the routine diagnostic workflow: *Actinobacillus pleuropneumonia* (APP), *Glaesserella parasuis* (Gps), *Mesomycoplasma hyorhinis* (Mhr), *Mesomycoplasma hyopneumoniae* (Mhy), *Pasteurella multocida* (Pm), porcine respirovirus 1 (PRV-1), and swine influenza A (SIV). In addition, Illumina sequencing (2 x 75 nt) was performed. The Illumina reads were quality trimmed and assembled using SPAdes v. 3.15.4. The resulting contigs were then classified using DIAMOND v. 2.0.9.

Results and Discussion

All four pigs were PCR-positive for Mhr and Gps. Three pigs were also PCR-positive for APP, two for Mhy and Pm, and one for SIV. Deep sequencing revealed that several pigs were co-infected with a variant of the betacoronavirus Porcine Hemagglutinating Encephalomyelitis Virus (PHEV), a virus previously not found in Sweden, and a novel astrovirus 4. Astroviruses are well known for being associated with enteric disease or asymptomatic infection. However, the astrovirus detected in this study had the closest sequence similarity to recently characterized porcine astrovirus 4, which displayed respiratory epitheliotropic infection in young pigs in the USA (Rahe et al., 2023).

Conclusion

This is the first detection of an astrovirus 4 with respiratory tropism and the Betacoronavirus PHEV in Sweden. This, together with the recent detection of a swine Orthopneumovirus, previously not detected in Sweden, further adds to the complexity of PRDC. However, their contribution to clinical disease remains to be verified.

Keywords: Astrovirus, Porcine Hemagglutinating Encephalomyelitis Virus, Respiratory disease.

Acknowledgements: The CoVetLab consortium (project CVL2324_04) funded the sample analysis.

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CHARACTERIZING DYNAMICS OF PRRSV RNA POSITIVITY OVER TIME AND ASSOCIATED RISK FACTORS IN 275 SOWS POST LIVE VIRUS EXPOSURE BASED ON TOSC SAMPLES

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Introduction and Objectives

Sows are a major source of porcine reproductive and respiratory syndrome virus (PRRSV) infection for piglets, and undetected infection in sows remains a major barrier to PRRSV management. Characterization of PRRSV persistence at the individual sow level has been limited by the lack of practical sampling tools. Tonsil-oral-scrubbing (TOSc) is a rapid, non-invasive method for detecting PRRSV in crated sows without snaring (Li et al., 2024). This study aimed to characterize PRRSV RNA positivity dynamics and associated risk factors in sows over 24 weeks following live virus inoculation (LVI).

Materials and Methods

A prospective observational study was conducted in a previously PRRSV-negative breed-to-wean herd undergoing elimination after an outbreak with a L1C.5 strain using herd closure and whole-herd LVI. TOSc samples were collected every four weeks from 2-days pre- to 24-weeks post LVI from the same 275 sows and tested by real-time RT-PCR (VetMAX PRRSV 3.0). Sows were evenly distributed by parity (P0, P1 - P2, P3+) and production phase. PRRSV RNA positivity was analyzed using Probit regression, including time, parity, production phase, and interactions.

Results and Discussion

PRRSV RNA positivity declined over time, reaching 4.43% at 16 weeks post-LVI and remaining below the < 10% low-prevalence threshold following AASV guidelines, with a rebound to 8.00% at 24 weeks. Under high-prevalence conditions, P0 and P1 - P2 sows had higher positivity than P3+ sows ($P < 0.05$). At low prevalence, farrowing sows showed markedly higher positivity (28.56% at 20 weeks and 34.49% at 24 weeks), while other phases remained < 5% ($P < 0.05$).

Conclusion

PRRSV RNA detection in sows decreased to low prevalence by 16 weeks post-LVI. Lower parity and farrowing (possibly due to PRRSV activation after farrowing stress) were key risk factors at low prevalence, and rebound detection suggests persistent carrier sows, supporting targeted interventions such as test-and-removal or segregation to accelerate herd stability.

Keywords: Parity, Production phase, PRRSV dynamics, Sows, TOSc.

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CROSS-PROTECTIVE EFFICACY OF A TYPE 2 LINEAGE 1 MODIFIED-LIVE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS VACCINE AGAINST THE NADC20 STRAIN

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Introduction and Objectives
Elanco developed a modified-live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine containing the live attenuated PRRSV-2 lineage 1 strain SD 11 - 21. The objective of this study was to evaluate the efficacy of that vaccine (Prevacent® PRRS) against PRRSV-2 lineage 8 strain NADC20 when administered to two-week-old pigs.

Materials and Methods
Sixty two-week-old pigs were allocated to four groups of 15 pigs each and were injected by intramuscular route with either Prevacent® PRRS (Elanco) (three groups, each with a different vaccine batch) or a placebo. At 28 days post-vaccination, all pigs were challenged by intranasal and intramuscular route with PRRSV-2 lineage 8 strain NADC20. Efficacy was assessed by determining clinical scores (sum of scores for depression, respiratory distress, and loss of body condition), average daily weight gain (ADWG), lung lesion scores, and viral loads in sera and broncho-alveolar lavage (BAL) fluids up to 14 days post-challenge (DPC).

Results and Discussion
The mean clinical scores of the vaccinated groups (2.267, 3.000, and 2.267, respectively) were lower than the one of the controls (10.600) and the ADWG of the vaccinated groups (0.388 kg, 0.396 kg, and 0.388 kg, respectively) were higher than the one of the controls (0.149 kg). Also, the mean lung lesion score at 14 DPC of the vaccinated groups (0.577, 1.413, and 3.683, respectively) was lower than the one of the controls (20.093), resulting in a mitigated fraction of 0.80, 0.74, and 0.64, respectively. Finally, the mean cumulative viral loads in the sera (sum of viral loads at 3, 7, 10, and 14 DPC) were lower in the vaccinated groups (28.163, 29.896, and 28.645 $\log_{10}$, respectively) than in the controls (31.238 $\log_{10}$). Similarly, the mean viral loads in the BAL fluids were lower in the vaccinated groups (6.547, 6.177, and 6.598 $\log_{10}$, respectively) than in the controls (8.424 $\log_{10}$).

Conclusion
The results of this study demonstrate that a vaccination of two-week-old pigs with Prevacent® PRRS is able to reduce clinical signs, weight loss, lung lesions, and virus replication in blood and lungs following a challenge with PRRSV-2 lineage 8 strain NADC20.

Keywords: Cross-protection, Efficacy, Heterologous challenge, PRRSV, Vaccine.

OCCURRENCE AND GENETIC DIVERSITY OF PORCINE ROTAVIRUSES IN RUSSIAN PIG FARMS

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Introduction and Objectives

Enteric diseases are major causes of porcine health issues, especially in suckling and weaning classes. Rotavirus (RV) is one of the most severe pathogens responsible for diarrheal outbreaks in pigs (Vlasova et al., 2017). Currently, works introducing the molecular epidemiology of RVs in Russia are primarily dedicated to infections in humans, while those in pigs are not well documented. The research aim was to clarify the situation regarding RVA, RVB, and RVC in 22 large-scale pig farms across eleven Russian regions.

Materials and Methods

We tested 774 rectal swabs collected during 2023-2025 for the presence of three RV species. Diarrheal outbreaks were reported at all farms, mainly among suckling (1 - 10 days), pre-weaned (11 - 20 days), and weaned piglets (22 - 36 days), while fattening pigs (66 - 80 days) were mostly clinically healthy. To reveal G/P combinations, Sanger sequencing was applied. Additionally, two isolates (RVA and RVC) were completely characterized through nanopore sequencing.

Results and Discussion

We found that at least one RV species was circulating on each farm, and the overall detection rate was 44.96%. The highest total detection rate was observed in post-weaning piglets (75.2%), followed by suckling (42%), fattening (36.8%), and pre-weaned (31.2%) groups. RVA was detected in 32.43%, RVB in 13.18%, and RVC in 13.95% of cases, respectively. Genetic characterization of RVA exhibited a variety of G/P genotypes, including G3, G4, G5, and G9, as well as P[6], P[13], and P[23]. The most common combinations were G4P[23], G4P[6], and G3P[13]. Phylogenetic analysis of RVA revealed clades with human isolates in G4, G9, and P[6]. By contrast, RVC isolates showed modest genetic diversity, G6 for VP7 and P[5] and P[6] for VP4, and the G6P[5] combination was predominant. Whole genome sequencing of the RVA isolate revealed G2 and P[27] with a typical porcine backbone constellation I5-R1-C1-M1-A8-N1-T7-E1-H1. The first complete porcine RVC genome from Russia is characterized by a constellation G6-P[5]-I14-R1-C1-M1-A7-N9-T6-E1-H1, including a putative novel VP6 genotype - I14.

Conclusion

These findings contribute to our understanding of the molecular epidemiology of porcine RVs in Russia, demonstrating the presence of three species and underscoring the extensive genotype diversity of RVA and RVC.

Keywords: Diarrhea, Genotyping, Porcine rotaviruses, Phylogenetic analysis, Zoonotic potential.

Acknowledgements: We acknowledge veterinary specialists on farms for their willingness to provide specimens for this research.

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PREVALENCE OF PORCINE CIRCOVIRUS TYPE 2 (PCV2) GENOTYPES IN RUSSIA

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) remains one of most important pathogens for industrial swine production in the world. Intensive use of vaccines to PCV2 control has contributed to changes in genome of PCV2 circulating in the field. Several genotypes can be found in industrial and wild pigs. The aim of the study was to assess genetic diversity of PCV2 circulating in commercial pig populations in Russian Federation.

Materials and Methods

Between January and September 2025, 1,850 samples of blood sera from 10 regions were collected. Sizes of farm/herd varied from 3500 up to 5500 sows. The blood sera were sampled from industrial pigs (different ages) with PCV2-assotiated clinical signs: reproductive failures, increased mortality, poor growth, etc. The samples were pooled into 374 pools. Illumina NextSeq 2000 and MGI DNBSEQ G-400 next-generation sequencing platforms were used. Genome assembly and consensus sequence generation were performed using BWA-MEM2, Samtools and iVAR. IQ-TREE2 was used for phylogenetic analysis, custom scripts in R were used for phylogenetic tree visualization.

Results and Discussion

Thirty-six tested pools were positive for PCV2 in Realtime PCR, of which 22 samples underwent whole-genome amplification and sequencing. All positive sera were collected from fattening pigs (120 - 163 d.o.) originating from the south of Russia (Krasnodar, Belgorod). A protocol for whole-genome amplification and sequencing of PCV2 based on NGS technology has been implemented. 22 complete PCV2 genomes from Russia have been obtained in 2025. All (100%) sequences belong to the 2d genotype of PCV2. The detection of exclusively PCV2d indicates the widespread prevalence of this PCV2 genotype among commercial pigs in Russia in 2025. The PCV2d sequences are being prepared for submission to GenBank.

Conclusion

This report on prevalence of PCV2 genotypes in commercial pigs in Russia provides valuable information on the global distribution of this virus variant. The obtained data agrees with global tendency. The detection of PCV2d in affected herds highlights its role in the development of PCV2-associated diseases in commercial pigs. These results confirm the importance of continued research and possibly the need to modify existing vaccination protocols to improve the epizootic situation in modern pig farms.

Keywords: Genotype prevalence, NGS sequencing, Porcine circovirus type 2, Russia.

Acknowledgements: The authors thank swine producers for participation in this study and Research Institute of Influenza, for providing testing facilities and realization of sequence process.

DISTRIBUTION AND DIVERSITY OF PORCINE CIRCOVIRUS TYPE 2 AND 3 IN THE WILD BOAR POPULATION OF RUSSIA

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Introduction and Objectives

Industrial pig farming is a leading sector of Russian agriculture; however, infectious swine diseases can cause significant economic losses. Porcine circovirus (PCV) infection is a multisystem disease affecting animals of all ages and sexes. Among these, porcine circovirus type 2 (PCV-2) and porcine circovirus type 3 (PCV-3) are the most significant for veterinary medicine. Control of swine pathogens in the wild boar population is a critical component of veterinary surveillance, particularly in the context of potential cross-border transmission.

Materials and Methods

Samples of 476 free-living European wild boars were collected during 2021 - 2025 from 23 regions, including both the European and Asian parts of Russia. In the study, the study type of samples was pieces of organs such as the spleen, lymph node, and lung. PCR testing was conducted to detect DNA of pathogens. Positive samples were sequenced by the Sanger method. Genetic diversity of detected viruses was analyzed using MEGA7 software. A detailed protocol of the study is described in a previous publication (Krasnikov et al., 2024).

Results and Discussion

We found high detection rates for PCV2 (34.9%) and PCV3 (35.5%). For PCV2, co-circulation of two genotypes, PCV2b (5/53) and PCV2d (48/53), was demonstrated. Comparative analysis of the capsid protein sequences revealed amino acid substitutions between the PCV2a vaccine strain and the studied isolates across all four known antibody recognition domains (A–D). All 29 PCV3 sequences belonged to the PCV3a genotype, but significant variation within this genotype was detected. The extensive geographical scope of this study provides valuable data for our national context and also offers a unique opportunity to investigate the potential for cross-border viral transmission. Genomes of PCV2 and PCV3 were detected in all studying regions associated with pork production. The highest detection rate of PCV2 (76.0%) was detected in Belgorod, known as an intensive pig-farming region.

Conclusion

This is the first comprehensive study of the distribution and diversity of PCV2 and PCV3 in Russian wild boar herds.

Keywords: Genetic diversity, Porcine circoviruses types 2 and 3, Wild boar.

Acknowledgements: The authors thank the Russian Science Foundation for financial support, grant number 23-76-10055.

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FIELD STUDY ON THE EFFICACY OF TWO PCV2 VACCINES IN SOWS

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Introduction and Objectives

Porcine Circovirus Type 2 (PCV2) is a ubiquitous pathogen in pig farms, associated with reproductive disorders in sows and vertical transmission to piglets. Vaccination remains the primary strategy for PCV2 control. This study evaluated the efficacy of a new PCV2 vaccine (Suishot® Circo-One) compared with an existing commercial vaccine (Vaccine B) in sows on a single-site farm in Jilin Province, China, housing 1,200 sows. Recently, the pregnant sows in the farm experienced abortion, and the mixed umbilical cord blood of aborted fetuses tested positive for PCV2, with Ct value of 27.67, no other pathogens were detected. The sows were immunized twice a year with PCV2 vaccine.

Materials and Methods

Sows were divided into two groups: Group 1 (n = 559) received Suishot® Circo-One, and Group 2 (n = 389) received Vaccine B, both vaccinated once one month before farrowing under identical management. Serum from 10 sows per group was collected at 1 and 3 months post-vaccination. Additionally, ≥ 1 month post-vaccination, 25 pooled testicular fluid and 20 pooled umbilical cord blood samples from piglets were collected. PCV2 antigen was detected by qPCR, and positivity rates were calculated. Reproductive performance - average healthy and weaned piglets per litter, stillbirths, and mummies - was compared between groups using Chi-square tests.

Results and Discussion

All tested sow serum samples (10 per group) were PCV2-negative at both time points, though other sows may have carried the virus. In piglets, Group 2 showed PCV2 positivity in 40% of testicular fluid pools (mean Ct = 32.79) and 10% of umbilical cord blood pools (mean Ct = 34.33); Group 1 was negative in both. The difference in testicular fluid positivity was significant ($P < 0.05$), but not in cord blood ($P > 0.05$). Group 1 also had better reproductive performance: 0.27 more healthy piglets per litter, 0.1% lower stillbirth/mummy rate, and 0.39 more weaned piglets per litter than Group 2.

Conclusion

Suishot® Circo-One provided enhanced protection against PCV2, effectively preventing vertical transmission and improving reproductive performance compared to Vaccine B.

Keywords: Efficacy, PCV2, Sows, Vaccine.

IMPACT OF NEONATAL PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS STATUS ON FARROWING ROOM PRODUCTION PERFORMANCE IN SOW HERDS IN THE NETHERLANDS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) type 1 is endemic in the Netherlands, with over 90% of sow herds vaccinated. Previous studies have highlighted significant economic losses due to PRRSV, yet many farmers remain unaware of its negative impact on farrowing room production. This retrospective study aimed to analyze the relationship between neonatal PRRSV status and farrowing room production parameters.

Materials and Methods

Four conventional sow herds (average 1,500 sows each) were monitored for neonatal PRRSV status using PCR testing of processing fluids (Vilalta et al., 2019) or tongue fluids from neonatal dead piglets (Baliellas et al., 2018). Samples were categorized by sow parity: first parity (P1), second parity and older (P2+), or mixed (x). Farrowing batch data were matched with production records from farm management systems (Pig Expert, Agrovision, Netherlands). Statistical analyses included Chi-square and Wilcoxon signed rank tests.

Results and Discussion

Out of 323 farrowing batches analyzed, 22.3% were PRRSV positive, with higher rates in first parity sows (25.6%) than older sows (15.2%). PRRSV-positive batches had up to 5.2% lower farrowing rates in first parity sows ($P < 0.005$), up to 0.41 fewer live-born piglets, and up to 0.54 fewer weaned piglets per litter. On average, these batches weaned 1.1 fewer piglets per litter. For an average 1,500-sow herd, this results in about 857 fewer piglets marketed annually and an estimated € 45,000 economic loss. These findings highlight the significant production impact of PRRSV, especially in first parity sows, and emphasize the need for better farmer awareness and management, as 65% of farmers are unaware of PRRSV's negative effects (Hendrickx et al., 2024).

Conclusion

Neonatal PRRSV status significantly affects farrowing room production outcomes. First parity sows are especially susceptible, with notable reductions in farrowing rate and piglet weaning.

Keywords: Economic impact, Farrowing room, PRRSV, Production performance, Sow parity.

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TIMING THE REGIONAL SPREAD OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS 2 (PRRSV-2) VARIANTS ACROSS THE UNITED STATES

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Introduction and Objectives

PRRSV-2 threatens the swine industry and is classified into lineages, sub-lineages, and variants based on ORF5 genetic distances. New genetic variants emerge every year, some of which spread widely in the U.S. via animal movements. To better understand the spatiotemporal dynamics of emergence and inform preparedness, our objective was to estimate the average time between the emergence of a given variant in its region of origin and its dispersal to a new region.

Material and Methods

We analyzed 14,835 ORF5 sequences obtained between 2015 and 2024 from the Morrison Swine Health Monitoring Program (MSHMP), representing 158 variants defined by a mean pairwise genetic distance of ~ 2.5%. Samples were collected from five major U.S. swine regions: the Upper Midwest (UM), Lower Midwest (LM), Atlantic Seaboard (AS), Northeast (NE), and Great Plains (GP). Survival analysis and structured coalescent models estimated the time between variant emergence and spread to new regions, and variant diversity was measured using Hill numbers.

Results and Discussion

The UM presented the highest number of variants (n = 123), which was approximately 2.5 to 3.5 times more than any other region. The UM region also represents a diversification center for PRRSV variants, with 50% of the variants detected in the region emerging locally as opposed from imported from elsewhere. In addition, UM functions as a central hub in the PRRSV-2 dissemination network, acting both as the main source of dispersal and as a sink, receiving the highest number of variant introductions from other regions. At the other extreme, we observed regions with asymmetric connectivity, such as NE, which receives more variants than it exports, and AS, which exports more variants than it receives. Overall, the LM showed the shortest dispersal time-lags around 1 year, followed by NE and UM with approximately 1.6 years, GP and AS with dispersal times of about 2 years. Estimates of the time-lag between variant emergence and regional dispersal were consistent across both estimation methods.

Conclusions

Results provide important information for implementing more targeted viral dispersal containment strategies by highlighting the risk of regions connected to those that exhibit accelerated dispersal patterns.

Keywords: Diversity, PRRSV-2, Space-temporal dynamics, Spread waiting time.

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PHYLOGENETIC LINEAGES OF PRRSV-2 FROM CANADA AND THE USA REVEAL BIDIRECTIONAL TRANSBOUNDARY SPREAD AND TWO NOVEL SUB-LINEAGES IN NORTH AMERICA

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Introduction and Objectives

In Canada, PRRSV-2 causes annual losses of approximately USD 150 million, and ~6.4 million live pigs are exported annually to the USA. Although Canada has been suggested as a source of some PRRSV-2 sub-lineages introduced into the USA, these inferences rely on outdated or a limited number of contemporary sequences, limiting our understanding of viral genetic diversity and dispersal patterns. Here, we characterize the diversity of PRRSV-2 in Canada and infer dispersal events between Canada and the USA.

Material and Methods

We analyzed 3,573 PRRSV-2 ORF5 sequences from Canada (2000 - 2024) across five provinces. Sub-lineages were assigned using PRRS-Loom, genetic distances estimated with SDTv1.2, and spatiotemporal dynamics inferred in BEAST v10.5.0 using > 40,000 USA sequences.

Results and Discussion

In total, we identified 13 PRRSV-2 sub-lineages in Canada (1A–1C, 1E–1I, 5A, 7, 8A, 8C, and 9A), along with four highly divergent monophyletic clades with strong bootstrap support (above 99%) that did not belong to any previously described sub-lineage. These four clades exhibit more than 9.5% dissimilarity relative to known sub-lineages. Two of these clades were small and last detected in 2021, whereas two remained in circulation. Thus, we propose two new sub-lineages, 1K and 1L. Phylogeographic reconstruction of sub-lineages between Canada and the USA indicates that sub-lineages 1C, 1H, 1I, 1K, and 1L likely originated in Canada, whereas 1A, 1B, 1E, and 1F likely originated in the USA. Sub-lineages 1C, 1H, and 1K exhibited unidirectional spread from Canada to the USA, with 1C and 1H showing strong geographic structure, suggesting independent diversification trajectories and limited dispersal between the two countries. In contrast, 1B and 1F showed unidirectional movement from the USA into Canada, whereas 1E and 1I exhibited bidirectional transmission. Sub-lineage 1L remains restricted to Canada.

Conclusions

Our results expand the understanding of PRRSV-2 diversity in North America, revealing two previously undocumented variants. We observed geographic structuring consistent with local differentiation for some sub-lineages, whereas others exhibited more frequent dispersal. These findings provide valuable insights to support efforts aimed at preventing the introduction of PRRSV-2 sub-lineages and variants not yet detected in a given region.

Keywords: Diversity, New sub-lineages, PRRVS-2, Space-temporal dynamics.

Acknowledgements: This study was developed at the Department of Veterinary Population Medicine, University of Minnesota, in the Veterinary Epidemiology and Informatics Laboratory. We thank Demeter Services Vétérinaires Inc. and Morrison Swine Health Monitoring Program (MSHMP) for providing access to data for this study.

PRRSV SEROCONVERSION DYNAMICS AND IMMUNO-MODULATING PROPERTIES OF TILMICOSIN DURING NAÏVE GILT EXPOSURE TO PRRS LVI

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Introduction and Objectives

PRRS live virus inoculation (LVI) of naïve gilts is a common practice in the U.S. swine industry to provide consistent exposure during acclimation strategies (Linhares et al., 2014). LVI is also used to manage PRRS in breeding herds despite the availability of modified live virus vaccines. However, LVI exposure is associated with mortality and abortions. Tilmicosin penetrates porcine alveolar macrophages, inhibiting PRRSV replication (Puntawee et al., 2017; O'Sullivan et al., 2016). Therefore, this study evaluated the effects of tilmicosin on PRRSV viremia and shedding in naïve gilts exposed to LVI and compared mortality and immunologic responses between tilmicosin-treated and non-treated gilts.

Materials and Methods

In this field-controlled study, 80 seven-week-old gilts naïve to PRRSV and *Mycoplasma hyopneumoniae* were assigned to treatment and control groups, housed separately. All pigs were exposed to PRRS LVI one week after study initiation. The treatment group received in-water tilmicosin 7 days before to 14 days after LVI. LVI was administered intramuscularly using 2 mL serum from weaned pigs. Serum and oral fluids were collected twice weekly for 5 weeks. PRRSV RNA detection used RT-qPCR, and immunologic responses were assessed using ELISA and Luminex immunoassays. Time to PRRSV RNA positivity was compared using Kaplan-Meier analysis. Logistic regression evaluated RNA positivity, while cytokines, Ct values, and viral load were analyzed using linear mixed models with repeated measures and Tukey–Kramer post hoc tests.

Results and Discussion

PRRSV RNA and antibody responses showed similar temporal patterns between groups. Treatment group exhibited earlier and higher cumulative PCR positivity. Peak RNA detection in oral fluids was delayed in treatment group. No significant difference in viremia was observed between groups ($P = 0.8$), however, 8% of animals remained PCR-negative throughout the study. Control group had threefold higher mortality compared with treatment group ($P = 0.09$). Tilmicosin reduced systemic IL-1β, TNF-α, and IL-12p40 concentrations 4 days post-administration and sustained through 14 days post-LVI ($P < 0.05$).

Conclusion

PRRS LVI exposure in naïve gilts resulted in inconsistent infection dynamics. Tilmicosin use was associated with a trend towards reduced mortality and modulation of PRRSV-induced systemic inflammatory responses, indicating mitigation of clinical impact post-LVI.

Keywords: Inconsistency, Immune modulators, LVI, PRRSV, Tilmicosin.

Acknowledgements: The authors thank HANOR production system and Elanco Animal Health for their collaboration and funding respectively.

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IMPACT OF MASS VACCINATION AGAINST PORCINE CIRCOVIRUS TYPE 2 ON REPRODUCTIVE PERFORMANCE IN A COMMERCIAL SOW HERD

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Introduction and Objective

Porcine circovirus type 2 (PCV2) is a major pathogen that plays a significant role in the swine industry. Reproductive failure associated with PCV2 is typically characterized by the occurrence of mummified, stillborn, and weak-born piglets, accompanied by gross pathological lesions such as cardiomyopathy, pulmonary edema, hepatomegaly, and ascites (West et al., 1999; O'Connor et al., 2001). This study evaluated the efficacy of sow PCV2 vaccination on farms experiencing a high rate of fetal mummification associated with PCV2 infection.

Materials and Methods

From mid-February to mid-March 2025, a markedly increased incidence of fetal mummification (MM) was identified in a 500 farrow-to-finish sow farm. Weekly MM rate was 4.7, 8.8, 4.5, and 3.2%, respectively, from 16 February to 15 March, compared to the average MM rate of 1.5% in 2024. PCV2-infected mummified fetuses were identified by PCR in litters that farrowed from February 16 to 22. In response to these diagnostic findings, mass vaccination of sows with Ingelvac CiroFLEX® was implemented twice at one-month intervals. Reproductive parameters were evaluated before (January 19 to February 15) and after the PCV2 infection (February 16 to March 15), as well as following the implementation of sow vaccination (March 16 to April 12).

Results and Discussion

Prior to PCV2 infection, reproductive performance in sows showed the following averages: total born piglets (TB) at 14.0, born alive (BA) at 13.1, still born (SB) at 5.2%, and MM at 1.5%. After PCV2 infection, TB slightly decreased to 13.9, BA dropped to 12.4, SB remained similar at 5.0%, while MM increased significantly to 5.3%. Following the administration of Ingelvac CircoFLEX® to sows, reproductive parameters improved markedly: TB increased to 15.2, BA to 14.3, SB decreased to 4.8%, and MM dropped substantially to 1.0%. This represents a statistically significant improvement in TB, BA and MM rates, confirmed by least squares statistical analysis ($P < 0.05$) compared to the post-infection period.

Conclusion

These results suggest that Ingelvac CiroFLEX® may be an effective tool for reducing or preventing reproductive PCV2 associated failure in affected sow herds.

Keywords: Ingelvac CiroFLEX®, Mummified fetuses, PCV2, Reproductive disorder.

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COMPARATIVE FIELD EFFICACY TRIAL BETWEEN INGELVAC PRRS MLV AND PRIMEPAC PRRS IN KOREAN COMMERCIAL SWINE FARM

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) is a major cause of productivity loss in modern swine production. The use of PRRS vaccination as a pivotal tool for disease management has been a long-established practice, with substantial evidence supporting its safety and efficacy. This study aimed to evaluate the effectiveness of Ingelvac PRRS® MLV and PrimePac® PRRS vaccines in piglets under the Lineage 1C PRRS virus exposure on a PRRS-positive farm in Korea.

Materials and Methods

The trial was conducted on a commercial farm with 700 sows confirmed Lineage 1C (NADC30-like) PRRSV infection. Piglets were divided into three groups: Ingelvac PRRS® MLV (n = 118), PrimePac® PRRS (n = 107), and unvaccinated control (n = 110). Vaccination and saline injection occurred at 4 weeks of age, one day post-weaning. Body weight was measured at 4, 13, and 23 weeks of age. Blood sampling and temperature checks were performed at 4, 6, 8, 10, and 15 weeks. The PRRSV ELISA and quantitative PCR were used to assess antibody levels and viremia. The mortality, medication usage, and treatment costs were recorded.

Results and Discussion

Ingelvac PRRS® MLV group showed significantly higher average body weight (89.77 vs 87.26 vs 85.23 kg) and daily weight gain compared to the control group ($P < 0.05$). PrimePac® PRRS group did not show statistically significant improvement. The genomic copies of PRRS in the serum (Log $TCID_{50}$/ml) and IDEXX PRRS X3 ELISA s/p ratio differed significantly between the Ingelvac PRRS® MLV-vaccinated groups and the control group, particularly at 10 and 8 weeks ($P < 0.05$), with no difference observed in the PrimePac® PRRS group. Treatment frequency and cost per pig were lowest in the Ingelvac PRRS® MLV group (2.51 treatments/pig, $1.02), compared to PrimePac® PRRS (4.21 treatments/pig, $1.51) and control (3.21 treatments/pig, $1.79). No significant differences were observed in mortality rates among groups.

Conclusion

Vaccination with Ingelvac PRRS® MLV in piglets prior to Lineage 1C PRRSV exposure was an effective strategy to mitigate PRRS-related productivity losses in Korean swine farms. When selecting a PRRS vaccine, it is recommended to consider criteria such as improvement in daily weight gain, reduction in viremia, and antibody response.

Keywords: Ingelvac PRRS® MLV, PRRS, Piglet vaccination, PrimePac® PRRS, Viremia

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FIELD EFFICACY OF INGELVAC PRRS MLV VACCINE AGAINST NADC34-LIKE PRRSV IN A KOREAN COMMERCIAL SWINE FARM

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) continues to be a major challenge in swine production, particularly with the emergence of highly pathogenic variants such as the NADC34-like strain (1). This study aimed to evaluate the field efficacy of Ingelvac PRRS® MLV vaccine in piglets exposed to NADC34-like PRRSV under commercial farm conditions.

Materials and Methods

The trial was conducted on a farrow-to-finish farm with 1,200 sows. The farm experienced a NADC34-like PRRS outbreak. Piglets were divided into two groups and vaccinated at 3 weeks of age: Ingelvac PRRS® MLV (n = 412), and unvaccinated control (n = 413). The mortality rate, number of underweight animals (UWA) at 120 days old and respiratory health status (ReHS) in nursery were recorded. The number of UWA refers to those weighing less than 80% of the average weight at 120 days of age. The PRRSV specific ELISA and PCR were performed to assess antibody levels and viremia at 30, 60, 90 and 120 days old.

Results and Discussion

Ingelvac PRRS® MLV group showed significantly lower number of dead animals (39 vs 57) compared to the control group (Chi-square, $P < 0.05$). The number of UWA was lower in Ingelvac PRRS® MLV group (73/412, 19.5%) compared to control (86/413, 24.1%). The diagnostic results confirmed the presence of NADC 34 like PRRSV in blood samples taken from 60-day-old pigs. The ReHS is a numerical value from 0 to 100 that indicates the respiratory health of pigs, was monitored using SoundTalks® between 49 and 93 days old in separate rooms by each group. The control group showed yellow alarm from 63 days old and worsening to red alarm from 81 days old. The ReHS of the two groups demonstrated statistically significant differences of 92.5 and 66.4, respectively. (Paired t-test, $P < 0.01$). No significant differences were found in ELISA, and PCR testing detected Type 2 PRRSv in both groups.

Conclusion

Vaccination with Ingelvac PRRS® MLV in piglets prior to NADC34-like PRRSV exposure significantly improved mortality rate and ReHS compared to unvaccinated controls. These findings support the use of Ingelvac PRRS® MLV as an effective strategy to mitigate L1A PRRS-related productivity losses.

Keywords: Ingelvac PRRS® MLV, NADC-34 like PRRSv, PRRS, piglet vaccination, SoundTalk.

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COMPARATIVE EFFICACY EVALUATION OF TWO MODIFIED-LIVE PRRS VACCINES AGAINST A NADC34-LIKE STRAIN OF PRRS VIRUS IN SOUTH KOREA

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) has a significant threat to the global swine industry since its detection in the late 1980s. Recently, PRRSV strains belonging to NADC30-like and NADC34-like groups have been identified as the predominant variants circulating across South Korea (Kim et al., 2023; Jeong et al., 2025). This study aimed to evaluate the efficacy of Ingelvac PRRS® MLV (Boehringer Ingelheim, Germany) and Prevacent® PRRS (Elanco, USA) vaccines in piglets under NADC34-like PRRS virus exposure on a PRRS-positive farm in Korea.

Materials and Methods

This study was conducted in March 2025 at a commercial farm with 200 sows infected with a NADC34-like PRRSV strain that caused high mortality and abortion rates. The farm had three-week management system, with consecutive batches sequentially divided into Ingelvac PRRS® MLV (n = 205) and Prevacent® PRRS (n = 201). Vaccination occurred at 4 weeks of age immediately after weaning. Body weight was measured at 4, 10, and 19 weeks of age. Blood sampling for PRRSV ELISA and quantitative PCR was performed at 4, 7, 10, 13, and 19 weeks.

Results and Discussion

Ingelvac PRRS® MLV batch showed significantly higher average body weight at 19 weeks of age (64.7 ± 3.4 kg vs 63.3 ± 3.5 kg) and daily weight gain from 4 to 19 weeks of age (552 ± 26 g/d vs 540 ± 28 g/d) compared to the Prevacent® batches (unpaired t-test, $P < 0.0001$). The mortality rate and laboratory tests did not show statistically significant differences. The mortality rate was 6.8% (14/205) and 6.5% (13/201) in Ingelvac PRRS® MLV and Prevacent® batch, respectively. NADC34-like strain was confirmed in both batches at 4 and 7 weeks of age, respectively. Also, EU type PRRSV was confirmed in both batches at 19 weeks of age.

Conclusion

Ingelvac PRRS® MLV-vaccinated piglets originating from PRRSV unstable sow herds demonstrated significantly enhanced growth performances in comparison with the Prevacent®-vaccinated piglets in the context of NADC34-like PRRSV infection. These results suggest that Ingelvac PRRS® MLV can serve as an effective approach to reduce productivity losses associated with Lineage1 PRRSV in Korean pig farms. It also indicates that the recommendation of PRRS vaccines based on the ORF 5 sequencing is not advised.

Keywords: Ingelvac PRRS® MLV, PRRS, piglet vaccination, Prevacent® PRRS, positive unstable herd.

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A STUDY OF THE PREVALENCE OF PORCINE CIRCOVIRUS TYPE 2 IN PROCESSING FLUIDS AND THE EFFECTS OF SOW VACCINATION ON ITS PREVALENCE

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Introduction and Objectives

Porcine circovirus-associated disease (PCVAD) has been significantly reduced since porcine circovirus type 2 (PCV2) vaccines; however, PCV2 remains prevalent in commercial pig populations worldwide. Vertical transmission is considered an important route contributing to virus persistence within sow herds. The study aimed to evaluate PCV2 shedding status of sow herds using processing fluids and to assess the impact of sow PCV2 vaccination on PCV2-positive rate in processing fluids collected from their offspring.

Materials and Methods

Between June 2023 to May 2025, a total of 1,011 processing fluids were collected from 216 sow herds and tested by PCV2 using quantitative PCR (qPCR). Among these herds, 185 implemented PCV2 vaccination programs (mass vaccination two to four times per year or rolling vaccination against PCV2), while 31 herds did not use PCV2 vaccines. The proportions of PCV2-positive sow herds and samples were calculated. PCV2-positive rates in processing fluids from vaccinated and non-vaccinated sow herds were compared using Chi-square test.

Results and Discussion

Overall, 26.85% of sow herds and 15.73% of processing fluid samples tested positive for PCV2. The proportion of vaccinated sow herds with PCV2-positive processing fluids (24.86%) was significantly lower than that observed in non- vaccinated sow herds (38.71%) (P = 0.0325). Among vaccinated herds, the proportions of herds with 100% positive, high positive (50 - 100%), low positive (< 50%), and negative processing fluids were 4.86, 2.70, 17.3 and 75.14%, respectively. In contrast, corresponding proportions in non-vaccinated herds were 19.35, 3.23, 16.13, and 61.29%, respectively. These findings indicate that sow vaccination substantially reduces PCV2 detection in processing fluids, supporting its role in mitigating vertical transmission.

Conclusion

Processing fluids provide a useful population-level surveillance matrix for monitoring PCV2 circulation in sow herds. Sow herd vaccination against PCV2 significantly reduces the PCV2 qPCR- positive rate in processing fluids collected from their offsprings. Further investigation is warranted to elucidate the factors contributing to persistent high PCV2 detection in a subset of vaccinated sow herds.

Keywords: Porcine circovirus type 2, Prevalence, Processing fluid, qPCR testing, Vaccination.

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ENVIRONMENTAL MONITORING AND ANALYSIS OF PORCINE EPIDEMIC DIARRHEA VIRUS IN TRANSPORT VEHICLES FOLLOWING ENHANCED DISINFECTION AT TAINAN CITY MEAT MARKETS

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Introduction and Objectives

This study aims to analyze the seasonal occurrence trends of Porcine Epidemic Diarrhea (PED) in Tainan and evaluate effective prevention strategies to eliminate Porcine Epidemic Diarrhea Virus (PEDV). Since October 2013, Taiwan has experienced a severe outbreak of PED, resulting in nearly 100% mortality of piglets under seven days old in infected farms. This outbreak caused significant economic losses to the swine industry and led to a supply-demand imbalance and an increase in domestic pork prices. Between 2022 and 2024, sporadic PED cases in Tainan were submitted to our office.

Materials and Methods

To monitor the epidemic status, veterinarians and animal health inspectors from our office conducted monthly random sampling at meat markets in Tainan, collecting anal swabs from market-bound pigs, samples from transport vehicles (steering wheels, foot mats, and vehicle surfaces), and environmental samples from pens. These samples were analyzed to assess the prevalence of PED in the region and to strengthen biosecurity and disease prevention measures for pig farms in Tainan. This study employed the POCKIT Central automated nucleic acid analyzer for magnetic bead-based nucleic acid extraction and insulated isothermal polymerase chain reaction (iiPCR) to detect PEDV.

Results and Discussion

We collected 198 samples from transport vehicles before and after disinfection. Results showed that 11 samples tested positive for the virus before disinfection. After disinfection, only 2 samples tested positive. The overall risk of virus detection decreased by approximately 82%, and the zero-virus detection rate after disinfection reached 98.0%. Fisher's exact test analysis showed that the difference in virus detection rate before and after disinfection was statistically significant ($P \approx 0.013$), indicating that disinfection can effectively reduce the risk of virus contamination on pig transport vehicles.

Conclusion

According to the analysis, PED outbreaks in Tainan were most prevalent during seasonal transitions, specifically in March–April and September-November. This finding suggests that PEDV is not a winter-season disease but is also influenced by temperature fluctuations. Based on these researches, our office has been regularly issuing disease warnings to pig farmers in Tainan, urging them to enhance biosecurity measures to minimize the impact of PED on the swine industry.

Keywords: Meat market, Porcine Epidemic diarrhea, Transport vehicles.

EFFECTS OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME MODIFIED LIVE VIRUS VACCINE AND IMMUNOSTIMULANT ON OXIDATIVE STRESS PARAMETERS IN INFECTED NURSERY PIGS

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Introduction and Objectives

Oxidative stress is an imbalance between production of free radicals and activity of antioxidants caused by heat stress or infections (Hao et al., 2021). Porcine reproductive and respiratory syndrome (PRRS) is a major disease that has negative performances in pigs and can cause oxidative stress (Zimmerman et al., 2019). PRRS vaccination and immunostimulants are provided as control strategies for PRRS. This study investigates how vaccine and immunostimulants can affect oxidative stress status.

Materials and Methods

22 pigs (5-week-old) were divided into 3 groups of positive control (POS), vaccination (VAC) and vaccination with immunostimulant (VSA). VAC and VSA groups were injected with PrevacentTM PRRS MLV vaccines at 5 and 7 weeks old. At 9 weeks old, all pigs were infected with PRRS virus meanwhile VSA pigs were fed Swine AwakeTM from 9 to 11 weeks old. Blood samples were collected at 0- and 7-day post-infection then processed and tested for concentration of malondialdehyde (MDA), superoxide dismutase (SOD) and glutathione peroxidase (GPX) via ELISA test kits. Each parameter results were compared between groups by one-way ANOVA.

Results and Discussion

MDA concentration between 0DPI and 7DPI from VAC and VSA groups decreased (-9.69 and -33.81 ng/mL) while POS group increased (59.25 ng/mL). Moreover, difference MDA concentration of POS group was significantly higher than the other two treatments (P = 0.005). Results showed that vaccination can decrease free radical production by PRRS infection especially with immunostimulant feeding. Meanwhile, SOD and GPX concentrations between groups were not significantly different.

Conclusion

As PRRS infection causes oxidative stress, the uses of PRRS MLV vaccine and immunostimulant not only lessen the chance of infection but can decrease MDA level in serum thus reducing lipid peroxidation from oxidative stress.

Keywords: Immunostimulant, Oxidative stress, Porcine reproductive and respiratory syndrome, Vaccination.

Acknowledgements: The authors thank Elanco (Thailand) Ltd for the funding support.

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PHYLOGENETIC ANALYSIS OF OPEN READING FRAME 5 SEQUENCES OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS IN TAIWAN BETWEEN 2024 AND 2025

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) caused by Betaarterivirus suid (PRRSV), leading to severe economic loss in the global swine industry. In previous surveys, the dominant viral strains circulating in Taiwan belong to the type II PRRSV (PRRSV II) lineage (L) 3 with several L1 NADC-like strains identified since the first report in 2018. To investigate the PRRSV variants currently circulating in Taiwan, sequences covering ORF5 of Taiwan PRRSV isolates collected between 2024 and 2025 were analyzed.

Materials and Methods

A total of 412 PRRSV multiplex real-time RT-PCR-positive cases collected during 2024 - 2025 from the Animal Disease Diagnosis Center, Yunlin Division, National Taiwan University, were used in this study. The samples included serum and homogenized tissues. Among these, 303 cases with Ct values lower than 30 were selected for subsequent analysis. ORF5 genes were amplified by the primer set described in previous study. Sequence alignment and phylogenetic analyses were conducted in MEGA 12 using the maximum likelihood method with the Kimura 2-parameter model and 1,000 bootstrap replicates.

Results and Discussion

All of the cases collected in the present study belong to PRRSV II. The amplicons covering the whole ORF5 gene were successfully amplified in 132 samples. The nucleotide sequence identities among these strains range from 77.446 - 100%. There are amino acid variations identified at the regions of B cell and T cell epitopes. Phylogenetic analysis illustrated that while most of the Taiwan clinical samples belong to the L3, the detection rate of the L1 strains increased yearly, and all of them were grouped with the NADC-34 strain, which belongs to the L1A sub-lineage.

Conclusion

This study demonstrates the phylogenetic diversity of PRRSV-II circulating in Taiwan during 2024 - 2025. Increased detection of L1A strains indicates expansion of L1 viruses, whereas L3 strains remain closely related to historical Taiwanese lineages. The identification of co-circulating L1 and L3 PRRSV II in Taiwan and unique substitutions in B- or T-cell epitopes revealed in the present study suggest that ongoing viral evolution may undermine vaccine efficacy, facilitate immune escape, and necessitate continuous molecular surveillance and periodic updating of PRRSV control and immunization strategies.

Keywords: Lineage 1, Lineage 3, Porcine reproductive and respiratory syndrome virus, Taiwan.

HUMAN-SEASONAL H3 INFLUENZA A VIRUSES DETECTED IN NORTH AMERICAN SWINE IN 2025

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Introduction and Objectives

Influenza A virus is a key component of the swine respiratory disease complex, with interspecies transmission from humans regularly introducing novel genetic diversity. Since 2022, multiple H3 human-to-swine spillover events have been detected through surveillance at the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL). The objective of this study was to determine if cases with human-like detections in 2025 provided evidence of establishment in the swine population.

Materials and Methods

Twenty-one suspected spillover cases were compared with human strains using BLAST and classified using Nextstrain. A subset of samples was selected for whole-genome sequencing on the Illumina MiSeq platform. Assembled contigs were classified using octoFLU. Hemagglutinin (HA) gene sequences were collated with contemporary human and swine reference sequences, aligned, and used to construct a phylogenetic tree.

Results and Discussion

North American cases were classified within the G.1.1, J.2, or J.2.5 H3 human seasonal clades (formerly 2a.1 and 3a.1). Six G.1.1 cases were detected in Iowa and Illinois. HA sequences from these cases differed by 25nt on average from the closest human sequence in GenBank, reflecting considerable genetic divergence. All six cases had reassorted, acquiring endemic swine genes, including the swine N2.2002B neuraminidase (NA) and swine-origin internal gene segments. Since 2024, repeated spillovers of J.2 and J.2.5 subclades into swine have been observed. In 2025, 15 sequences from 12 cases were submitted to the ISU VDL, with the most recent detection in November 2025. HA genes from these cases remain highly similar to contemporary human strains, consistent with recent spillovers. Three of the seven recovered whole genomes consisted entirely of human-origin gene segments.

Conclusion

Genetic divergence, reassortment, and detection at multiple locations across the country indicate the G clade human-seasonal H3 has become regionally endemic in the swine population. In contrast, there is currently no substantive evidence of onward transmission of J-clade viruses within swine populations. These findings demonstrate that recurrent spillovers can lead to establishment in swine, increase viral diversity and drive swine influenza evolution, may retain human transmissibility, and hinder zoonotic risk prediction by expanding the diversity of circulating swine lineages.

Keywords: Establishment, Influenza A, Spillover, Reassortment, Zoonosis.

Acknowledgements: The authors thank the producers and veterinarians who have submitted their sequences to the Iowa State University Veterinary Diagnostic Laboratory.

ASSESSING THE EFFECT OF POOLING VERSUS NOT POOLING COMMONLY USED SAMPLE TYPES ON THE PROBABILITY OF INFLUENZA A VIRUS SEQUENCING

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Introduction and Objectives

This abstract summarizes findings from two studies. The first evaluated how pooling different sample types influences the probability of obtaining full IAV hemagglutinin (HA) sequences. The second assessed the probability of successful HA and neuraminidase (NA) Sanger sequencing across various porcine sample types submitted to the Iowa State University Veterinary Diagnostic Laboratory from 2018 to 2024.

Materials and Methods

For the first study, 36 PCR-positive IAV samples (12 family oral fluids (FOF) x 12 udder wipes (UW) x 12 nasal wipes (NW)) were selected from an endemically infected breeding herd. These samples were pooled with PCR-negative samples at three dilution levels: undiluted, 1:3, and 1:5. For each sample type, six samples were tested at each dilution level, resulting in 18 samples by cycle threshold (Ct) category A- Ct 26-30 and B- Ct between 30 - 34. The second study targeted samples previously tested for IAV by RT-rtPCR and followed by Sanger sequencing of the HA and NA genes. Using RT-rtPCR, positive Ct values representing different sample types were assessed to determine the 95% probability of successful sequencing.

Results and Discussion

The pooled study showed 14/18 FOF with complete sequences in category A and 2/18 undiluted in category B. Udder wipes had 7/18 in A and 2/18 undiluted in B. NW showed 11/18 in A and 2 undiluted in B across all tested sample types that were assessed. Regarding the retrospective study, the 3 most common sample types submitted for IAV sequencing were lung tissues, nasal swabs, and oral fluids with maximum Ct values corresponding to successful HA sequencing of 25.7, 27.8, and 27.3, and NA of 21.5, 23.6, and 22.1, respectively.

Conclusion

Full sequences were recovered from FOF and NW on both Ct categories, while for UW, full sequences were only recovered when Ct was lower than 30 in the pooled study. The second study determined that nasal swabs and lung tissue had the highest probability of IAV HA and NA sequencing success, while oral fluids, a common swine diagnostic sample type, can be effective for gene sequencing when using lower IAV RT-rtPCR Ct values, i.e. ≤ 22.1.

Keywords: Diagnostics, Influenza A virus, Sanger sequencing, Swine.

AN UPDATE OF INFLUENZA A IN AUSTRALIAN COMMERCIAL PIGGERIES

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Introduction and Objectives

Influenza A virus (IAV) is understudied in Australian commercial piggeries. Multiple transmission pathways for swine IAV infection exist, including pig-to-pig, human-to-pig, and pig-to-human (1,2). From the limited studies conducted, IAV in Australia is genetically distinct from viruses collected internationally. Viruses collected on the west and east coasts of Australia also show independent circulation. Pro-active IAV monitoring and characterization (genomic and antigenic) are warranted to inform epidemiological assessments of circulating strains1. In this study, we utilized serum samples from abattoir collections in 2025 and historical genomic data since 2017, to inform future diagnostic / characterization approaches, providing an update on IAV in Australian commercial piggeries.

Materials and Methods

Serology testing of 420 serum samples collected in October 2025 from healthy fit-to-load market progeny (22 - 24 weeks) or culled sows, was undertaken using the IDEXX Influenza A ELISA. Serum samples were collected from seven farms in southeastern Australia. Phylogenomic analysis was performed on IAV historical genome sequences in swine across Australia from almost a decade of passive surveillance periods.

Results and Discussion

IAV seropositivity was detected in samples from healthy fit-to-load market progeny, with culled sows sampled within the same production flows also seropositive. Genomic analysis of IAV detected since 2017 indicated H1 and H3 viruses have continued to co-circulate in Australian commercial piggeries.

Conclusion

This study provides unique insight into IAV in Australian piggeries, enabling industry to elucidate the role of IAV in Australian pork production. In addition, this information informs One-Health approaches to understanding IAV epidemiology and provides an IAV serological baseline in swine in preparation for a potential incursion of highly pathogenetic avian influenza A virus (HPAIV) H5N1 clade 2.3.4.4b into Australia.

Keywords: Diagnostics, genomics, Influenza A, seroprevalence.

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EVALUATION OF PRRS VACCINE AGAINST A NOVEL PRRSV LINEAGE 1 STRAIN IN TAIWAN

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is classified into two distinct species: Betaarterivirus suid 1 (PRRSV-1) and Betaarterivirus suid 2 (PRRSV-2). Both species have been identified in Taiwan; however, PRRSV-2 remains the dominant strain and is associated with substantial economic losses. Among PRRSV-2 strains, lineage 3 was initially the prototype in Taiwan, whereas lineage 1 strains have recently become the most prevalent (Kuo et al., 2025). This study investigates the cross-protection efficacy of a lineage 5 vaccine against a novel PRRSV-2 lineage 1 isolate in Taiwan.

Materials and Methods

Sixteen PRRSV-free pigs (IACUC, NPUST; Approval No. NPUST-114-081) were randomly divided into two groups. The vaccinated group consisted of eight pigs and was vaccinated intramuscularly with Ingelvac PRRS® MLV at 4 weeks of age. The control group, also consisting of eight pigs, was sham-vaccinated with 2 mL of normal saline. All pigs were challenged intranasally and intramuscularly with 2 mL of PRRSV-2/NPUST7408 (lineage 1 strain) at 10^3 TCID50/mL at 8 weeks of age (Chan et al., 2025). Body weights and body temperatures were measured at 0 and 14 days post-inoculation (DPI) and monitored daily, respectively. Serum and nasal swab samples were collected at 0, 3, 7, 10, and 14 DPI to evaluate PRRSV-specific antibodies and viral loads using the IDEXX PRRS X3 Ab Test kit (IDEXX, Westbrook, ME, USA) and RT-qPCR, respectively. RT-qPCR data were analyzed using one-way ANOVA.

Results and Discussion

During this study, fever (> 40.5℃) was observed post-challenge in the control group. Regarding PRRSV-specific antibodies, all pigs in the vaccinated group were seropositive at 0 DPI. In the vaccinated group, the average viral titers in serum were significantly lower than those of the control group at 7, 10, and 14 DPI ($P < 0.05$). In contrast, the average viral titers in nasal swabs were significantly higher in the control group than in the vaccinated group at 3 DPI ($P < 0.05$).

Conclusion

This study demonstrates that vaccination significantly reduces post-challenge viremia and nasal viral shedding, supporting the protective efficacy of the Ingelvac PRRS® MLV vaccine against the novel PRRSV-2 lineage 1 strain in Taiwan.

Keywords: Cross protection, Lineage 1, PRRSV-2, Vaccines.

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NO SIGNIFICANT ASSOCIATIONS BETWEEN PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS PREVALENCE AND WEATHER, MANURE TRANSPORT, OR PIG PRICES IN DUTCH SOW HERDS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) remain endemic in the Netherlands, with over 90% of sow herds vaccinated. Despite extensive monitoring, the factors influencing variation in neonatal PCR positivity rates are unclear. This study aimed to identify correlations between PRRSV prevalence in neonatal piglets and external variables such as weather conditions, manure transport, and pig prices.

Materials and Methods

From 2022 to 2025, 176 sow herds participated in weekly monitoring. Neonatal piglets were sampled using processing fluids, tongue fluids, or umbilical cords, and pooled samples were tested by PCR. Only PRRSV-positive farms were included. Monthly PRRSV positivity rates were compared to pig prices, weather data, and manure transport records using correlation matrices. Correlation strengths were categorized as very weak (0 - 0.19), weak (0.20 - 0.39), moderate (0.40 - 0.59), strong (0.60 - 0.79), and very strong (0.80 - 1.0) (BMJ).

Results and Discussion

Serafini 2025 related manure processing to PRRSV-outbreaks. We hypothesized that manure transport would be a useful proxy for manure processing. However, no strong or consistent correlations were found between PRRSV prevalence and manure transport, or pig prices, or weather. Correlation values for manure transport and pig prices were -0.04 to 0.35. Weather showed a moderate correlation only with average wind speed per day (0.45), independent from the season and likely to reflect barn climate effects rather than direct causation. Other weather conditions like temperature, wind speed, hours of sunshine, air pressure, relative humidity and precipitation variables had weak correlations (-0.25 to 0.38). Study limitations included incomplete sequence data and above all the lack of continuous monitoring, creating a rotating subsample of farms over time.

Conclusion

In an PRRSV endemic environment outbreaks are more difficult to recognize. Continuous monitoring is recommended to better identify outbreak patterns and optimize sampling for sequencing.

Keywords: Manure transport, Pig prices, PRRSV, Sow herds, Wind speed.

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SFV REPLICON VECTOR HARBORING PORCINE EPIDEMIC DIARRHEA VIRUS IMMUNOGENS DELIVERED BY ATTENUATED *SALMONELLA TYPHIMURIUM* INDUCES PROTECTIVE IMMUNE RESPONSES AND LACTOGENIC IMMUNITY

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) is a highly contagious pathogen causing severe diarrhea and high mortality in neonatal piglets.

Materials and Methods

In this study, consensus sequences encoding the N-terminal domain of spike subunit 1 (S1-NTD) and nucleocapsid (N) protein of PEDV were cloned into a eukaryotic expression vector pJHL204 and transformed into an attenuated Salmonella Typhimurium strain JOL2500. Antigen expression was confirmed by Western blot and immunofluorescence analyses. The recombinant strains were evaluated in vivo for safety, persistence and immunogenicity. Immunogenicity was characterized by measuring antibody response, virus neutralizing assays, cytokine profiling, and flow cytometric analysis of T cell subpopulation. Protective efficacy against salmonellosis and passive transfer of neutralizing antibodies to suckling mice were evaluated.

Results and Discussion

Vaccinated mice exhibited no adverse effects or bacterial persistence in major organs, confirming the vaccine's safety. Immunization elicited robust humoral and cell-mediated immune responses against PEDV and Salmonella antigens. Upon Salmonella challenge, vaccinated mice showed significantly reduced bacterial loads in splenic tissues. Furthermore, vaccinated dams and their offspring induced detectable anti-PEDV neutralizing antibodies, indicating successful passive antibody transfer.

Conclusion

Our findings suggest that the designed vaccine constructs provide a promising platform for inducing multifaceted immune protectivity against PEDV and salmonellosis in swine.

Keywords: Humoral and cell-mediated immunity, Neutralizing antibodies, PED virus, Salmonella Typhimurium.

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FIELD EVALUATION AND ECONOMIC IMPACT OF A NEW READY-TO-USE VACCINE CONTAINING *MYCOPLASMA HYOPNEUMONIAE* AND PCV2D IN A FATTENING FARM WITH SEVERE RESPIRATORY DISEASE

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Introduction and Objectives

Porcine Circovirus Type 2 (PCV2) and *Mesomycoplasma hyopneumoniae* (*M. hyo*) are pathogens within Porcine Respiratory Disease Complex (PRDC). Vaccination against M. hyo and PCV2 is key prophylaxis to stabilize respiratory health. This field investigation evaluated the impact of switching to CIRBLOC® M Hyo (VAC2) in a fattening herd suffering from severe respiratory disease and compromised performance.

Materials and Methods

The evaluation was carried out on a 1,280-finishing farm. Piglets were vaccinated at 3 weeks with a ready-to-use M. hyo/PCV2 combination (VAC1) and PRRSV MLV. In September 2024, the farm experienced intense coughing and 7% mortality rate. A slaughter lung assessment (Ceva Lung Program/CLP®) (nVAC1 = 170) was performed. Altered lung (Lu), serum (S) and oral fluid (OF) samples of VAC1 were examined in the laboratory (All samples: PRRSV EU/NA-, PCV2/3-PCR; Lu and OF: swIAV-PCR; Lu: M. hyo-, App-PCR; S: ApxIV-ELISA;). Based on the findings, the producer switched to VAC2. To assess the efficacy of VAC2, another CLP®, including altered lung sampling, was conducted in September 2025 (nVAC2 = 77).

Results and Discussion

Lab results revealed in VAC1: Lung samples were positive for *M. hyo* (Ct 27), PRRSV EU (Ct 28), PCV2 (Ct 32), PCV3 (Ct 31), serum samples for PCV2 (Ct 36), PRRSV EU (Ct 31) and oral fluids for PCV2 (Ct 27.5), PCV3 (Ct 36). Sequencing demonstrated PCV2d circulation. Lung samples of VAC2 revealed: *M. hyo* (Ct 31), PCV3 (33.5). Lung scoring showed a decreasing EP index (4.24 (VAC1) vs 1.75 (VAC2)) and bronchopneumonia prevalence (73.83% (VAC1) vs. 36.36% (VAC2)). Performance improved with VAC2: mortality decreased by 5.3%, ADG increased by 129 g, fattening duration shortened by 15 days, and antimicrobial use reduced from therapy index 10.5 to 1.2. Using the Respinomics® economic calculator, the overall benefit per pig was calculated as the difference in profit (selling price minus production costs) attributable mostly to higher average daily weight gain and reduced mortality. This comparison resulted in an overall benefit of € 21.1 per pig.

Conclusion

VAC2 improved respiratory health, normalized mortality, and suppressed PCV2d circulation. Overall, VAC2 effectively stabilized the PRDC situation and improved economic outcomes under field conditions.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Performance parameters, Vaccination.

COMPARISON OF TWO COMMERCIAL PORCINE CIRCOVIRUS TYPE 2 AND *MYCOPLASMA HYOPNEUMONIAE* COMBINED VACCINE ON PERFORMANCE PARAMETERS AND ECONOMIC IMPACT

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Introduction and Objectives

For convenience and animal welfare reasons, some farmers prefer to use PCV2/M.hyo combination vaccines. The objective of this study was to evaluate the efficacy of a new PCV2d subunit-based and M.hyo combination vaccine by comparing the growth performance between pigs vaccinated with this vaccine and with a well-established PCV2/M.hyo competitor combination vaccine.

Materials and Methods

In a commercial Belgian farm positive for Mycoplasma hyopneumoniae (M.hyo) and PCV2, piglets were vaccinated at 4,5 weeks of age. 504 pigs vaccinated with CIRBLOC® M Hyo (2 ml, I.M.) (group A) and 505 pigs vaccinated with a PCV2a-based ready-to-use PCV2/M.hyo combination vaccine (2 ml, I.M.) (group B) were followed in the fattening phase. Each group had an equal number of females and males. The presence of *M.hyo* and PCV2 was confirmed by serology. Piglets of each treatment group were housed in similar conditions but kept separate. Pigs were weighed by pen at the beginning and end of the fattening phase, according to routine farm procedures. Feed consumption was measured per treatment group. Statistical analysis was performed using the statistical software SAS 9.4.

Results and Discussion

Pigs in groups A and B had an average weight upon entry in the fattening unit of 32,46 and 32,57 kg respectively and an end weight of 127,58 and 126 kg. The average daily gain in group A was 16 g/day higher than in group B, respectively 897 and 881 g/day. The weight differences observed were not significant (Wilcoxon rank sum test, $P = 0.21$), probably associated with the fact that the pigs were weighed by pen and not individually. The feed conversion rate in group A was 0,011 lower than in group B (2,345 vs 2,356). In none of the treatment groups there was mortality caused by respiratory distress or waste. The overall benefit per pig was calculated considering the higher average daily weight gain and reduced feed conversion rate. In the farm studied, this comparison resulted in an overall benefit of €1.6 per pig.

Conclusion

In this study, vaccine A performed numerically better in ADG and feed conversion rate over the PCV2a-based ready-to-use PCV2/M.hyo combination vaccine.

Keywords: Economic impact, *Mycoplasma hyopneumoniae*, PCV2, Performance parameters, Vaccination.

COMPARISON OF TWO PCV2/MHYO RTU VACCINE PROTOCOLS ON PERFORMANCE EFFECTS AND ECONOMIC BENEFITS

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Introduction and Objectives

Two of the main pathogens in swine production are PCV2 and *Mycoplasma hyopneumoniae (M.hyo)*. Present worldwide, they are responsible for significant losses on farms, making efficient control essential. The objective of this study was to compare two PCV2/Mhyo RTU vaccination protocols using zootechnical data from a commercial farm in Brazil.

Materials and Methods

In a farm located in the state of Santa Catarina, with 2300 sows, 1470 animals were divided into two groups: Group 1: animals vaccinated with CIRBLOC® M Hyo: PCV2d subunit /M Hyo RTU vaccine, 1 shot, 2 mL, IM at 3 weeks of age (WOA), N = 765 and Group 2: animals vaccinated with PCV2a/Mhyo RTU subunit vaccine, 1 shot, 2 mL, IM at 3 WOA, N = 705. The animals were distributed in the same room, under the same management and facility conditions. The animals were weighed individually at 3, 10 and 22 WOA. Feed consumption was measured per pen during all weeks of study. The data were evaluated using Mann-Whitney test. The financial calculation was made using market data (website: https://www.accs.org.br/cotacoes/bolsa-de-suinos/).

Results and Discussion

The initial weight of G1 and G2 was 5.269 vs 5.275 kg ($P > 0.05$). Weight gain in group 1 was 1.032 kg higher than in group 2 (129.470 vs. 128.438 kg), $P < 0.10$. Feed conversion ratio of groups G1 and G2 was 1.963 vs 2.004, $P > 0.05$. The calculated economic benefit for Group 1 was US$ 2.35 compared to Group 2.

Conclusion

The difference in weight gain of 1.032 kg and the 0.041-point reduction in feed conversion ratio in G1 implies a substantial economic impact per animal. These results demonstrate that CIRBLOC® M Hyo vaccine can be an excellent tool for controlling the pathogens involved and contributing to improved farm productivity and profitability.

Keywords: Economic impact, *Mycoplasma hyopneumoniae,* PCV2, Performance parameters, Vaccination.

DETECTION AND HISTOPATHOLOGICAL CHARACTERIZATION OF PORCINE CIRCOVIRUS TYPES 2 AND 3 IN TWO ARGENTINE PIG FARMS

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Introduction and Objectives

Porcine circovirus type 3 (PCV3) and type 2 (PCV2) are major pathogens affecting swine health worldwide. While PCV3 is an emerging threat in Argentina, PCV2 remains a constant challenge. The objective of this study was to investigate the presence of both PCV2 and PCV3 and to correlate molecular detection with histopathological lesions in two farms with a prior history of viral circulation.

Material and Methods

Between 2022 and 2025, 15 clinical cases (Farm A: n = 9; Farm B: n = 6) were studied; rule-in criteria for these cases were animals found dead with previous clinical history of respiratory or systemic disease. For histopathology, formalin-fixed samples of kidney, heart, lung, liver, and lymph nodes were collected. For molecular analysis, these same organs were kept fresh. Additionally, 112 sera (14 per category: pre-weaning, nursery, growing-finishing, and sows) were collected per farm (n = 224). PCV3 was detected via qPCR (Palinski protocol) using 48 pools (each consisting of 5 sera or tissue samples grouped by category); Ct values > 35 were negative. For PCV2 detection, conventional PCR was employed using primers targeting a fragment of the ORF2 gene. PCV2 was detected via conventional PCR (ORF2 gene) in tissue homogenates.

Results and Discussion

PCV3 DNA was detected in three serum pools per farm (piglets, nursery, and sows). Among the 15 tissue homogenates, three from Farm A were PCV3-positive (Ct: 29.28 - 34.69). PCV2 was identified in three growing-finishing homogenates from Farm B. Tissues corresponding to PCV2-positive animals showed multifocal non-suppurative nephritis and hepatitis. Lymph nodes displayed subtle lesions with slight secondary follicle predominance but lacked lymphoid depletion. In contrast, PCV3-positive cases showed non-specific histopathological findings, reinforcing that PCV3 can occur in subclinical infections with low viral loads (Ct > 32). These results highlight that while PCV2 remains associated with classic lesions, PCV3 detection requires strict clinical-pathological correlation to determine its pathogenic role.

Conclusion

Both PCV2 and PCV3 circulate in Argentine farms, often in subclinical forms. This study confirms that PCV2 is still associated with systemic lesions in finishing pigs, whereas PCV3 findings in these cases were non-specific, suggesting a need for further diagnostic tools like in situ hybridization to clarify its pathogenicity.

Keywords: Histopathological lesions, Molecular study, PCV2, PCV3.

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EPIDEMIOLOGICAL INVESTIGATION OF INFLUENZA A IN JAPANESE PIG FARMS USING ELISA KITS

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Introduction and Objectives

Influenza A virus is a key pathogen in porcine respiratory disease complex and imposes substantial economic burdens on pig production, with potential zoonotic risks (Li et al., 2021). This study aimed to investigate farm-level Influenza A occurrence in Japan and evaluated factors associated with positivity, including geographic distribution, seasonality trends, sow herd size, and production system characteristics (farrow-to-finish versus finishing-only), to support targeted control strategies.

Materials and Methods

From December 2022 to November 2024, ELISA results (IDEXX) generated by the Zoetis Japan laboratory were aggregated at farm level. In accordance with national diagnostic guidance issued by Ministry of Agriculture, Forestry and Fisheries in Japan and the expected decline of maternally derived antibodies, a farm was classified positive if at least one finisher pig aged ≥ 90 days had an ELISA S/N ratio ≤ 0.6 (Tse et al., 2012). Sow samples were excluded due to uncertain origin. Regional and seasonal distributions and associations with herd size and production system were assessed using chi-square tests with significance defined as $\alpha = 0.05$.

Results and Discussion

Influenza A-positive farms were detected across all regions. Seropositivity was significantly higher in high-density pig areas including Kanto (91.7%), Shikoku (78.9%), Kyushu (89.9%), while lower rates were observed in Chubu and Kinki combined (18.5%), and Chugoku (27.6%). No significant seasonal differences were observed. Larger sow herd sizes were correlated with higher positivity: farms with > 1,000 sows showed a positivity rate of 91.3%, whereas farms with < 1,000 sows had an average positivity rate of 69.7 %. Farrow-to-finish farms showed significantly higher positivity (73.3%) compared with finishing-only farms (54.5%) ($P < 0.05$). These findings indicate that farm structure and regional pig density are important determinants of Influenza A circulation and support prioritizing surveillance and biosecurity interventions toward large-scale, farrow-to-finish operations in high-density regions.

Conclusion

Influenza A is widely distributed across Japanese pig farms without clear evidence of seasonality, while regional density and farm characteristics substantially influence infection risk. Targeted surveillance and strengthened biosecurity in large herds and farrow-to-finish systems may reduce Influenza A burden and contribute to improved control of porcine respiratory disease complex.

Keywords: Biosecurity, Epidemiology, Influenza A, Pig Farms, Surveillance.

Acknowledgements: We thank participating farms and laboratory personnel for sample collection and testing support.

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A COMPARATIVE STUDY ON THE EFFECTS OF PORCINE CIRCOVIRUS 2 (PCV2) SOW VACCINATION IN A PCV2 SUBCLINICALLY INFECTED FARM

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Introduction and Objectives

Sows infected with Porcine circovirus 2 (PCV2) can experience returns to estrus, abortion, stillbirth, mummification, as well as reduced vitality in newborn piglets (Unterweger *et al*., 2021). This study aimed to evaluate the effect of sow vaccination with different PCV2 vaccines on serological, virological and reproductive parameters of sows and their offspring in a subclinically infected farm.

Materials and Methods

A total of 140 pregnant sows with similar parity distributions were selected for both groups. Sows from Group A were vaccinated with Circovac® (Ceva Hangzhou, 2 mL/sow, I.M.) at 70 days and 91 days of pregnancy. Sows from Group B were vaccinated with a PCV2 subunit vaccine according to the manufacturer's instructions. 20 serum samples from sows one day before farrowing and 30 serum samples from weaned piglets (before PCV2 vaccination) were collected and sent to the laboratory for PCV2 antibody (INgezim CIRCO IgG ELISA) and PCV2 nucleic acid testing (5 in 1 pooled, LSI Real PCR). The data were analyzed using t-test.

Results and Discussion

The positivity rate of PCV2 DNA qPCR for sows was 0% in Group A vs 25% in Group B (with a Ct value above 35, data not shown, indicating subclinical circulation of PCV2 on the farm). Weaned piglets were negative in both groups. The birth weight of piglets in Group A was significantly higher than that in Group B ($P < 0.01$). Group A had a smaller percentage of low-birth-weight piglets (< 1.2 kg) but a larger percentage of high-birth-weight piglets (> 1.5 kg) compared to Group B. Similarly, the antibody S/P ratio of weaned piglets in Group A was significantly higher than that in Group B ($P < 0.05$). Although weaned piglets in Group A were 0.14 kg heavier and exhibited 1.38% lower mortality compared to Group B, these differences were not statistically significant.

Conclusion

PCV2 remains widespread and continues to cause economic losses in pig production. This study demonstrated that even on farms with subclinical PCV2 infection, vaccinating sows with Circovac® could improve birth weight than the control group. This may be beneficial for hyperprolific sow's management.

Keywords: Birth, Porcine Circovirus 2 (PCV2), Subclinical, Vaccination.

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INFECTION STATUS OF SOWS AND PIGLETS FROM DIFFERENT FARMS OF A CHINESE GROUP COMPANY FOLLOWING ROUTINE PCV2 VACCINATION

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Introduction and Objectives

Post-vaccination PCV2-SD can occur due to late vaccination (infection prior to/during vaccination), early vaccination (MDA interference), or concurrent immunomodulatory infections (Joaquim et al., 2022). Sow vaccination is recommended to prevent PCV2-reproductive disease and improve reproductive performance (Pejsak et al., 2018). This study evaluated PCV2 infection status in sows and piglets following routine vaccination across 10 farms in a Chinese group company.

Materials and Methods

This study was conducted on 10 farms across four southern Chinese provinces (Guizhou, Sichuan, Jiangxi, Hunan). All farms followed a routine PCV2 vaccination protocol: piglets (21 days old) and sows received simultaneous vaccination (Circovac®, 2 mL/sow, 0.5 mL/piglet) at weaning starting in 2023. In March 2025, 20 serum samples were collected from sows of varying parities per farm, and 10 - 20 serum samples were taken from weaned piglets (one per litter). Samples were tested for PCV2 DNA via pooled (5-in-1) qPCR and for IgG antibodies using INgezim CIRCO ELISA.

Results and Discussion

A total of 197 sow and 179 weaned piglet serum samples were collected. PCV2 qPCR positivity in sows was 67% in parity 1, 33% in parity 2, and 33% in parity ≥ 3. No samples showed CT < 30 (i.e., $>10^5$ copies/mL). Weaning piglets ELISA positivity was 86% (mean S/P 0.65). Piglets in farms 2, 3, and 4 showed qPCR positive rates of 25, 25, and 50%, respectively, all with CT > 35. The other 7 farms were negative for qPCR. In PRRSV-unstable farms (1, 2, 7, 9), parity 1 sows exhibited higher qPCR positivity, with some low CT values (31.94). Piglet's optimal vaccination strategy needs to balance the levels of passive immunity and timing of infection (Martelli et al., 2016). From this study, maternal antibodies persisted until weaning but not too high to interfere piglet's vaccination during the time. The low PCV2 viremia in piglets suggested sow's vaccination reduced vertical transmission.

Conclusion

The combination of PCV2 vaccination in sows and piglets at weaning was effective for controlling natural infection. It's necessary to enhance PCV2 vaccination in gilts and close monitoring of PRRSV infection to mitigate immunosuppression and maintain vaccine efficacy.

Keywords: ELISA, Porcine Circovirus 2 (PCV2), Parity, qPCR, Vaccination.

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ASSESSMENT OF SOW HERD PCV-2 STABILITY UTILIZING UMBILICAL CORD SERUM IN 18 HERDS IN BRAZIL

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Introduction and Objectives

A prevalence assessment of porcine circovirus type 2 (PCV-2) infection in the early life of piglets is essential to clarify the infection dynamics in a herd. A high number of pre-suckle early infected piglets has been associated with a higher chance of horizontal transmission of PCV-2 between littermates (Madson et al., 2009). The aim of this study was to assess sow herd PCV-2 stability using umbilical cord serum in 18 herds in Brazil.

Materials and Methods

Eighteen farms (A-R) from four Brazilian companies were selected for the study. The selection criteria included: herd size ≥ 1000 sows; not vaccinated the sows for PCV-2 for at least two years prior to the study; not having a historical of PCV-2 clinical disease in the last 12 months; and having maximum of two sites (sow farm or sow farm plus nursery). Umbilical cord blood was collected directly from the placenta or directly from the umbilical cord of piglets. A total of 3 - 4 umbilical cords from each litter were sampled, yielding at least 3 mL of serum (UCS). A qPCR for PCV-2 was performed.

Results and Discussion

A total of 17.6% (96/545) of the UCS was positive. PCV-2 DNA was detected in UCS from almost all farms (17/18), with a prevalence ranging from 3,3 to 87.1%. The average Ct was 33.73, and farms O (25.62) and J (31.65) had the lowest Ct values. These results indicate very unstable herds, which contrasts with previous literature from other countries describing lower prevalence (Dieste-Pérez et al., 2018; Eddicks et al., 2016).

Conclusion

Almost all farms had at least one positive sample, and 17.6% of the UCS were positive for PCV-2, despite the herds show no clinical signs of PCV-2 associated disease.

Keywords: Porcine circovirus type 2, Prevalence, Umbilical cord.

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ENHANCED PORCINE CIRCOVIRUS 3 REPLICATION IN MESENCHYMAL CELLS ASSOCIATED WITH A SINGLE CAPSID PROTEIN SUBSTITUTION

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Introduction and Objectives

Porcine circovirus 3 (PCV3) was first reported in the United States in 2016; this virus is thought to be involved in diverse pathologies, such as multisystem inflammation, porcine dermatitis and nephropathy syndrome, and reproductive disorders. We previously established a system for isolating PCV3 using primary porcine bone marrow-derived mesenchymal cells and obtained a persistent isolate (the bm isolate) from PCV3-infected miniature pig organ homogenates. In this system, PCV3 persistently infects and replicates, and during long-term culture, viral genetic variation emerged. In this study, we analyzed the properties of the bm isolate and the strain obtained at passage 11 (bm-P11).

Materials and Methods

Bone marrow-derived mesenchymal cells were persistently infected with the bm isolate and passaged weekly for long-term culture. At passage 11, we obtained the bm-P11 strain, which showed > 10^{11} viral genome copies/mL in the supernatant, and full-length genome sequencing was performed. To compare proliferative capacity, newly seeded bone marrow cells were infected with the bm isolate or the bm-P11 strain and subsequently passaged. To assess the structural impact of the capsid protein substitution, a structural model was generated with AlphaFold3 and analyzed in PyMOL.

Results and Discussion

The bm-P11 strain exhibited a single nonsynonymous substitution in the capsid protein compared with the bm isolate. When newly inoculated into bone marrow-derived mesenchymal cells, the bm-P11 strain showed significantly higher viral copy numbers than the bm isolate, suggesting enhanced proliferative capacity in these cells. Structural prediction indicated that the substitution is located on the capsid surface. The local solvent-accessible surface area values around the substitution site were higher in the bm-P11 model than in the bm isolate model, suggesting that the substitution might increase solvent exposure of this region. This structural alteration could potentially modify local chemical properties, potentially influencing viral replication efficiency.

Conclusion

In summary, a single nonsynonymous substitution in the capsid protein was predicted to increase the surface exposure of the affected residue, which may in turn be associated with the enhanced proliferative capacity of PCV3 in bone marrow-derived mesenchymal cells. Further studies, including reverse genetics, are required to validate this hypothesis.

Keywords: Capsid protein substitution, Porcine circovirus 3, Viral replication.

A COMPARATIVE STUDY ON THE INFLUENCE OF LONG-TERM VACCINATION OF A BREEDING HERD AGAINST PCV2 IN A SUBCLINICALLY INFECTED FARM

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Introduction and Objectives

Previous studies have shown that vaccinating sows against Porcine circovirus type 2 (PCV2) in subclinically infected herds has positive effects on sow reproductive performance and offspring vitality (Olier et al., 2018). This study aims to compare the long-term efficacy of different vaccines against PCV2 in a herd with subclinical infection.

Materials and Methods

The trial was conducted in a Danish genetic breeding farm with 6,000 sows, practicing 18-day batch management system. The PCV2 positivity by qPCR testing in gilts was 40%, while sows showed no obvious clinical signs related to PCVD. From the same batch, 116 sows were selected randomly and divided into two groups (with same parity distribution) to be vaccinated with either Circovac® (Ceva) or PCV2 vaccine M. Record the ear tags of all selected sows for identification. In the first reproduction cycle, sows were vaccinated twice on day 70 and day 91 of gestation. During the second reproduction cycle, sows were vaccinated on day 91 of gestation. Reproductive data were collected and analyzed using T-tests.

Results and Discussion

After first cycle of vaccination, the qualified born (defined as total born excluding those classified as weak born (< 0.8 kg body weight), stillbirths, or mummified fetuses), qualified born rate, weak born rate and stillbirth rate from two groups were 13.88 - 14.00, 87.50 - 89.30, 6.99 - 7.03, 3.61 - 5.21%, respectively. Compared with vaccine M, primiparous sows vaccinated with Circovac after the first cycle showed numerical improvement. Same trend was observed after the second vaccination cycle for the same cohort of sows (including all parities) in the Circovac group. Compared to vaccine M, sows vaccinated with Circovac showed a 4.11% higher qualified born rate ($P = 0.04$). A limitation of this study was the lack of non-vaccinated control group for comparing differences between the vaccinated and unvaccinated. No PCV2 nucleic acid was detected by qPCR in offsprings (20 weaning piglets from each group after the second vaccination cycle). It is necessary to expand sampling to verify the vertical transmission blocking of PCV2 by vaccination.

Conclusion

The study demonstrated that in subclinically infected herds, continuous vaccination with Circovac could improve the reproductive performance of the sow herd compared to Vaccine M.

Keywords: Porcine Circovirus 2 (PCV2), Qualified Piglet, Subclinical, Vaccination.

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ENVIRONMENTAL PRRSV SURVEILLANCE IN SOW HERDS: AN INNOVATIVE MONITORING ALTERNATIVE

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Introduction and Objectives

Due to the importance of understanding the dynamics of PRRS infection in sow herds, different diagnostic methods have been developed (Holtkamp et al., 2021). These mainly involve sampling serum, familiar oral fluids, processing fluids and tongue fluids (Baliellas et al., 2021; Almeida et al., 2024). Producers are interested in developing sampling methods that provide accurate information at a reasonable labor and economic cost (Linhares et al., 2012). The objective of this study was to determine whether surface sampling can be a reliable alternative method to existing ones, to monitor PRRSV infection dynamics on farms.

Materials and Methods

The study was conducted between June 2025 and November 2025 on a commercial herd producing 20 kg piglets with 2,200 Iberian sows. An outbreak of PRRSV occurred two months earlier and 10 surface samples were taken by a swabbing method. Eight surface samples were taken monthly in the farrowing room: four from the mat, two from the room fans, one from the worker's clothing, one from the worker's boots, one from the processing trolley, and one from the treatment needle. Simultaneously, 15 serum samples were taken from due to wean piglets and analyzed in pools of 5 and between 2 and 7 weekly tongue tips from stillborn piglets. All the samples were tested using VetMAX PRRS EU/NA 3.0 kit (Thermofisher)

Results and Discussion

Between June and August, all serum and tongue samples tested positive, and all surface samples - except for the syringe and the processing trolley - tested positive. In September, 5 out of 7 tongue samples from stillborn piglets tested positive, and 3 of the surface samples (2 from the Mat and the boots) tested positive. In October, all serum and tongue samples from stillborn piglets were negative, but 3 mat samples were positive. From November onwards, all samples were negative

Conclusions

Under the conditions of this study, the performance of surface samples compared to serum from due to wean piglets and tongue tip samples was very similar, therefore, considering the ease of sampling, which reduces labor costs and the non-impact on animal welfare, environmental surveillance could be considered a good tool to assess the dynamics of PRRSV infection.

Keywords: Monitoring, PRRSV, Surveillance, Surfaces.

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GENERATION AND INVESTIGATION OF ECTODOMAINS OF BETAARTERIVIRUS SUID 2 MINOR ENVELOPE GLYCOPROTEINS AND THE CD163 CELLULAR RECEPTOR PROTEIN

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Introduction and Objectives

Betaarterivirus suid virus causes porcine reproductive and respiratory syndrome (PRRS), a major swine disease characterized by high genetic diversity and partial vaccine cross-protection. Interactions between PRRSV-2 minor envelope glycoproteins GP2a, GP3, and GP4 and the host receptor CD163 are critical for viral entry and represent key targets for PRRSV subunit vaccine development. This study aimed to generate PRRSV GP2, GP3, GP4, and CD163 for investigating virus-host interactions for future rational PRRSV vaccine design.

Materials and Methods

The coding sequences of PRRSV minor envelope glycoproteins GP2, GP3, and GP4 from the Taiwan SW2018001 strain were synthesized. The ectodomain sequences of GP2 and GP4 were amplified by PCR. The GP3 coding sequence and the ectodomains of GP2 and GP4 were subsequently subcloned into the pcDNA™3.1/V5-His TOPO® vector using BamHI and NotI restriction enzymes. The truncated GP2a and GP4, and the GP3 were stably expressed in HEK293 cells following G418 selection. Protein expression was detected by immunocytochemistry and Western blotting and purified by cobalt-based affinity chromatography. In parallel, untruncated porcine CD163 was subcloned into the EGFP-pcDNA™3.1 vector and stably expressed in HEK293 and MARC-145 cells, with expression verified by fluorescence microscopy and Western blot analysis.

Results and Discussion

All minor envelope glycoproteins were successfully detected by immunocytochemistry staining (ICC) and western blot. Under ICC, intracytoplasmic signals were noted in about 30 - 80% of transfected HEK293 cells. Under the western blotting detection of the cell lysate and culture medium, the sizes of GP3, and the ectodomains of GP2 and GP4 ectodomains were approximately 37 kDa, 26 kDa, and 18 kDa, respectively. The expression of CD163-EGFP was successfully in HEK293 cells and MARC145 cells and was approximately 140 kDa.

Conclusion

The ectodomains of PRRSV-2 minor envelope proteins and their attachment protein CD163 were successfully expressed. These proteins could serve as tools for systematic approach to investigate the interactions between PRRSV envelope glycoproteins and the host receptor CD163 as well as the novel antigens for developing subunit vaccines against PRRSV.

Keywords: Betaarterivirus suid 2, Minor envelope glycoproteins, Porcine CD163, PRRS.

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THE FIRST MOLECULAR CHARACTERIZATION OF PORCINE CIRCOVIRUS TYPE 2 IN CAMBODIA SWINE HERDS

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Introduction and Objectives

Porcine Circovirus Type 2 (PCV2) is a key agent of PCV-associated diseases (PCVAD), including post-weaning multisystemic wasting syndrome (PMWS), porcine dermatitis and nephropathy syndrome (PDNS), reproductive failure, and respiratory disorders (Segalés et al., 2013). Genotyping PCV2 is vital for understanding its epidemiological patterns and guiding effective vaccine strategies (Xiao et al., 2015). While PCV2 has been studied extensively in Southeast Asia, no molecular data have been previously reported from Cambodia. This study provides the first molecular characterization of PCV2 in Cambodian swine herds to support national surveillance efforts.

Materials and Methods

Eleven blood samples were collected between October and December 2024 from clinically suspected PCVAD cases in central Cambodia (n = 11 farms), including growing pigs (n = 7) and sows (n = 4). DNA was extracted and analyzed using conventional PCR targeting the ORF2 region (442 bp), a standard genotyping marker (Xiao et al., 2015). Positive samples were sequenced and aligned using BLASTn. Phylogenetic trees were constructed using the Neighbor-Joining method with 1,000 bootstrap replicates (Segura-Alabar et al., 2023).

Results and Discussion

PCV2 was detected in 8 of 11 samples (72.7%). Positive cases included growers (5/7) and sows (3/4). One PCR-positive sample could not be sequenced due to poor DNA quality. Among the seven sequenced samples, five were 100% identical and clustered with PCV2d-2 reference strains (JX535296, HM038017). Sample #1 showed 97.94% similarity to this cluster. Sample #2 grouped with PCV2b, with 98.63 - 99.32% similarity to reference strains HQ713495 and AY4844092.

Conclusion

This study provides the first molecular evidence of PCV2 genotypes circulating in Cambodian swine farms. The predominance of PCV2d-2 supports global trends showing its increasing dominance, which may be associated with higher virulence and reduced vaccine efficacy (Xiao et al., 2015). The presence of PCV2b suggests co-circulation of multiple genotypes. These findings emphasize the need for continued molecular surveillance and vaccine evaluation in Cambodia. Although limited by sample size, the data establish a baseline for future PCV2 epidemiological research.

Keywords: Cambodia, Genotype, Molecular surveillance, PCV2, Prevalence.

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DEVELOPMENT OF A MOTIF-BASED CLASSIFICATION PLATFORM FOR PORCINE EPIDEMIC DIARRHEA VIRUS

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) is a highly pathogenic enteric coronavirus threatening the swine industry. Rapid mutation and frequent recombination within PEDV populations have led to marked changes in virulence and immune evasion, posing challenges to viral classification and vaccine development. N-glycosylation plays multiple important biological roles, and polymorphism of N-glycosylation sites within specific motifs may reflect antigenic variation. Here, we propose a motif-based PEDV classification system focusing on antigenic diversity in the spike (S) protein, together with a user-friendly online platform.

Materials and Methods

A total of 3,229 PEDV S gene sequences available in the NCBI database as of September 2025 were collected. Sequence translation and alignment were performed, and N-glycosylation sites were predicted using NetNGlyc 1.0. The genotyping platform was developed in R, integrating Biostrings for sequence processing and DECIPHER for codon-aware alignment and motif detection. Data processing and visualization were implemented using dplyr, tidyr, and DT, and the platform was deployed on shinyapp.io.

Results and Discussion

Glycosylation analysis revealed multiple sites in the S protein with distinct population frequencies, including several polymorphic sites with intermediate prevalence (10 - 90%), suggesting ongoing evolutionary diversification. Three glycosylation sites located in different domains of the S protein have previously been identified and proposed to be related to virulence or immune evasion. In addition, a G1158S substitution was identified and found to be associated with geographic shifts in circulating PEDV populations. Based on combined patterns of three glycosylation motifs and the G1158S mutation, 17 main motif-types with population frequencies exceeding 1% were detected and named. Under the proposed nomenclature, G2c L4 and G2c L10 represent the dominant motif-types in China and the United States, respectively. Additionally, our platform allows flexible incorporation of motif-based classification rules and provides definitions and references for each motif-type.

Conclusions

We propose a motif-based PEDV classification framework and present an online web tool for automated sequence classification (http://raysapp.shinyapps.io/pedvmotiffinder_v2), providing a practical resource for studying viral evolution and PEDV molecular epidemiological surveillance.

Keywords: Online platform, PEDV, Spike gene, Viral classification.

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PRELIMINARY STUDY ON PORCINE VIRUS TYPE 3 IN PIG FARMS IN SAXONY (GERMANY) WITH DIFFERENT CLINICAL SYMPTOMS

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Introduction and Objectives

Porcine Circovirus type 3 was first detected in pigs in the USA in 2015 and has then been detected in several European, Asian and American countries (Palinski et al., 2017; Fux et al., 2018; Zou et al., 2018). Its clinical relevance remains debated: while some studies link PCV3 to reproductive failure, porcine dermatitis and nephropathy syndrome (PDNS), and respiratory issues (Palinski et al., 2016; Fux et al., 2018), the virus also occurs in healthy sows (Zou et al., 2018). As PCV3 data from pig farms in Saxony are limited, this study aimed to determine the prevalence of PCV3 and correlate the findings to clinical symptoms and co-infections.

Material and Methods

Sixty samples (blood, carcasses, fetal tissue and testicular fluid) from fourteen farms were collected, of which eight were PCV3-positive, identified by real-time PCR (Fux et al., 2018). Three of the PCV3-positive samples, representing diverse tissues (lung, brain, lymph node), were selected for molecular characterization. These samples were subjected to a subsequent circovirus-family-specific conventional PCR targeting the replication-associated region (Halami et al., 2008). The resulting amplicons were characterized using Sanger and Nanopore sequencing to distinguish between PCV3 field viruses and to enable phylogenetic analysis.

Results and Discussion

PCV3 was detected in eight samples and six different pig farms, including testicular fluid, fetal material and carcasses from various age groups (sow, weaner and fattening pig). Affected animals exhibited abortion, pneumonia or PDNS. Co-infections with Picornavirus, Acinetobacter Lwoffii, PCV2 as well as pathogenic *E. coli* were identified.

Conclusion

PCV3 is present in Saxon pig farms, associated with various clinical symptoms. Veterinarians and farmers should consider PCV3 in cases of reproductive failure, porcine dermatitis and nephropathy syndrome, respiratory symptoms, post-weaning multisystemic wasting syndrome or unexplained causes of illness. Further research is required to evaluate the prevalence, symptoms, co-infections and economic impacts of PCV3 in pigs.

Keywords: PDNS, Pig, Porcine circovirus type 3, Reproductive failure

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PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS-2 LINEAGE 1 VACCINATION IN A NAÏVE HERD CHALLENGED BY A LINEAGE 5 VACCINE - LIKE STRAIN: A CASE REPORT ON PERFORMANCE

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Introduction and Objectives

In the Philippine swine industry, the most challenging disease to solve by farmers and veterinarians is swine respiratory disease (SRD). One of the main pathogens to consider is Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) that can have a significant impact in farm production performance (Philippine College of Swine Practitioners, 2023).

Materials and Methods

A naïve swine breeding herd weans non-PRRS vaccinated grower pigs into off-site grower-finisher farms located in a high pig-dense area. In May to June 2024, the grower-finisher farm experienced poor performance due to increased incidence of SRD. Blood samples showed positive PRRSV-2 (North American, NA strain) revealed to be a Lineage 5A strain with 98.7% homology to available L5 vaccine strain (Ferrer et al., 2025).

Results and Discussion

Farm mapping and interviews with farm operators revealed that nearby farms were vaccinating may be a source of infection. PRRSV can be transmitted via aerosols, with the risk significantly increased by farm proximity and passing pig transport vehicles. The performance parameters of the swine herd across three distinct production cycles. Cycle 1 represents the initial operational period in 2023, during which the farm was naive for PRRSV. Key performance metrics were recorded as: morbidity (10 - 20%), mortality (7.5%), ADG (669 grams), and FCR (2.72). Cycle 2 includes the period where the infection happened, characterized by the detection of the PRRSV-2 strain and a drop in production performance: morbidity (20 to 30%), mortality (11.1%), ADG (573 grams), and FCR (3.30). Cycle 3 (2024 - 2025) represents the period following the first implementation of PRRS MLV (NA, L1D)* administered 2 days post-placement (72 days old). Cycle 3 exhibited improved Morbidity of 5 to 10% (66.7 to 75.0%), Mortality of 4.18 (62.3%), Average Daily Gain (ADG) of 794 grams (38.6%) and a more favorable Feed Conversion Ratio (FCR) of 2.72 (17.3%).

Conclusion

In this scenario, a lineage 1 PRRSV-2 vaccine was able to address and improved production parameters despite an infection caused by the PRRSV-2 lineage 5 virus strain.

Keywords: Lineage 5, Lineage 1, North American strain/PRRSV-2, *Prevacent™ PRRS MLV, (NA L1D)

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ALTERNATIVE SAMPLE MATRICES FOR THE DETECTION OF ANTIBODIES AGAINST CLASSICAL SWINE FEVER VIRUS

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Introduction and Objectives

Classical swine fever (CSF) is a severe systemic disease of domestic pigs and wild boar worldwide. Affected wild boar populations have often maintained the infection over months or even years and threatened domestic pig holdings. Therefore, passive surveillance of fallen wild boar plays an important role in early detection of disease introduction. As CSF shows comparable pathological findings to African swine fever (ASF), which nowadays affects many countries worldwide, differential diagnosis is performed. Especially, if no serum sample can be collected from wild suids, blood swabs represent an alternative matrix for ASF diagnosis. Based on this, the present study focused on the evaluation of different sample matrices for the detection of antibodies against CSF virus (CSFV).

Materials and Methods

Quick-drying swabs were soaked with EDTA blood, which was collected from domestic pigs infected with CSFV, as well as from non-infected animals. Pieces of the swab were taken up in sample dilution buffer or cell culture medium and were analyzed in CSF antibody ELISAs or virus neutralization assay (VNT). To assess potential species effects, antibody negative EDTA blood samples from wild suids were spiked with CSFV antibody positive serum. Moreover, organ homogenates were included in the study.

Results and Discussion

By comparing serum and blood swabs (n = 15) in a CSF antibody ELISA, a moderate loss of sensitivity (~ 9%) was observed, but this had no impact on sample classification when the material was collected 21 dpi. In addition, 2 out of 3 swab samples collected on 14 dpi were tested positive. No species effects were observed using blood swabs of various wild suids (wild boar, warthog, red river hog). When using the VNT, neutralizing antibodies are detected in all samples collected during the convalescent phase of the infection. Moreover, the use of organ homogenates, a second matrix tested, showed lower sensitivity compared to blood swabs.

Conclusion

Taken together, blood swabs and organ homogenates represent an alternative sample matrix for serological testing when serum is not available. Blood swabs facilitate sampling of fallen wild boar during CSF surveillance and are applicable for both, CSFV- and ASFV diagnoses.

Keywords: Classical swine fever, Differential diagnosis, Serology, Wild suids

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MATERNAL ANTIBODIES SHAPE HEPATITIS E VIRUS INFECTION DYNAMICS IN PIGS: INSIGHTS INTO AGE-DEPENDENT SUSCEPTIBILITY

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Introduction and Objectives

Hepatitis E virus (HEV) is an emerging zoonotic pathogen widely circulating in pig herds, posing risks to public health. Maternal antibodies may modulate HEV infection dynamics, yet field evidence remains limited. This study investigated HEV shedding and maternal antibody levels and antibody responses in piglets during the first 130 days on farms in Northeast China.

Materials and Methods

A longitudinal study was conducted on two farrow-to-finish farms (Farm-1: 67 piglets, 6 sows; Farm-2: 87 piglets, 6 sows). Umbilical cord blood (day 0, pre-colostrum), milk (day 0), and testicular fluid (day 7) were collected, followed by monthly sampling of blood, rectal swabs, feces, and environmental swabs. HEV antibody was detected by ELISA, and viral RNA was detected and quantified by RT-qPCR.

Results and Discussion

In farm-1, 83.3% (95% CI 35.8 - 99.6%) of sows were seropositive. All piglets were seronegative at birth; 86.6% (95% CI 76.0 - 93.7%) became seropositive by day 27 via colostrum. Antibody titters declined post-weaning, with 80.4% (95% CI 67.7 - 90.8%) and 46.7% (95% CI 21.3 - 73.4%) positivity at 56 and 107 days, respectively. Three piglets seroconverted due to natural infection demonstrated at 56 days. HEV RNA was undetectable in all samples, suggesting low-level endemic circulation. In farm-2, 83.3% (95% CI 35.8 - 99.6%) of sows were seropositive. Piglets seropositivity was 0, 73.7% (95% CI 48.8 - 90.9%), 61.8% (95% CI 49.0 - 74.0%), 56.0% (95% CI, 41.3 - 70.0%), 64.3% (95% CI, 35.1 - 87.2%), and 100% (95% CI, 85.2 - 100%) at 0, 7, 27, 54, 96, and 125 days, respectively, with 19.5% (17/87; 95% CI, 11.8 - 29.4%) seroconversion between 54 and 125 days. Active antibody response was lower in piglets with maternal antibodies (13.46%; 7/52) than in naïve piglets (48.57%; 17/35), indicating partial protection against HEV infection. Fecal HEV RNA (~10^4 copies/g) was detected in 73.79% (107/145; 95% CI, 65.8 - 80.7%) of samples, confirming active herd circulation.

Conclusion

This study demonstrates maternal antibodies may be involved in piglet protection against HEV infection or disease, shaping age-dependent infection dynamics on farms. Natural infection and viral shedding predominantly occurred between 60 - 120 days, highlighting a critical window for biosecurity and vaccination strategies.

Keywords: Hepatitis E virus, Infection dynamics, Longitudinal study, Maternal antibodies.

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PROTECTIVE EFFICACY OF A MRNA VACCINE AGAINST HP-PRRSV CHALLENGE IN PIGLETS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a major threat to the swine industry, while current vaccines provide limited protection and raise safety concerns. Aiming to provide a scientific theoretical basis for the prevention and control of PRRS, this study developed a multiepitope mRNA-LNP vaccine for effective immune protection in piglets.

Materials and Methods

A HP-PRRSV strain was isolated from clinical lung tissue samples and characterized by ORF5, NSP2, and whole-genome sequencing. Key B-cell and T-cell epitopes from the structural proteins of HP-PRRSV (JXA1 strain), including GP2a, GP3, GP4, GP5, M, and N, were identified using immunoinformatics approaches and assembled into a multiepitope mRNA-LNP vaccine. Piglets were immunized twice and subsequently challenged with JX021, with a commercial inactivated vaccine used as a comparator. RT-qPCR, ELISA, histopathological analysis, and related methods were employed to evaluate immune responses, clinical signs, survival rates, viral loads, lung pathology, and inflammatory cytokine levels.

Results and Discussion

A HP-PRRSV strain belonging to Lineage 8, designated JX021, was successfully isolated and characterized. Pathogenicity experiments demonstrated that JX021 induced severe clinical symptoms in piglets. Based on immunoinformatics analyses, key B- and T-cell epitopes from major HP-PRRSV structural proteins were linked to construct a multiepitope mRNA vaccine. Pigs vaccinated with the mRNA vaccine developed significantly higher virus-neutralizing antibody titers (10.6 ± 0.84) than those receiving an inactivated vaccine (2.26 ± 0.75, $P < 0.01$). The challenge group developed fever (> 40 °C) by 5 days post-challenge, whereas the mRNA-vaccinated group maintained lower temperatures; both vaccine groups were significantly lower than the challenge group ($P < 0.05$). Viremia peaked at 7 d post-challenge, reaching $10^{7.10}$ copies/μL in the challenge group, $10^{5.24}$ copies/μL in the inactivated vaccine group, and $10^{3.98}$ copies/μL in the mRNA vaccine group. Viral loads were highest in lung and submandibular lymph nodes, with lower levels in mRNA-vaccinated piglets. Moreover, the mRNA vaccine conferred an 80% survival rate, compared with 60% in the inactivated vaccine and challenge control groups.

Conclusion

The multiepitope PRRS mRNA-LNP vaccine effectively protected against HP-PRRSV challenge, highlighting the potential of mRNA-based vaccines for PRRS control and providing new insights into the design and development of further PRRS vaccine research.

Keywords: Antigenic Epitopes, Immune protection, mRNA Vaccine, Pathogenicity Analysis, PRRSV.

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COMPARISON OF TWO COMMERCIAL PORCINE CIRCOVIRUS TYPE 2 AND *MYCOPLASMA HYOPNEUMONIAE* COMBINED VACCINE ON ANTIBODY RESPONSE AND MORTALITY IN NURSERY PIGS UNDER FIELD CONDITIONS

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* (MH) are major contributors to respiratory disease complexes and production losses in pig production systems. Differences in vaccine composition may influence immune responses and health outcomes under field conditions. This study aimed to compare PCV2 antibody responses and nursery mortality between two ready-to-use PCV2 and MH combined vaccines.

Materials and Methods

A field study was conducted in a farm vaccinating piglets with PCV2 and MH combined vaccines at 3 weeks of age (WOA). Group A included 776 piglets vaccinated with a PCV2d+MH vaccine (CIRBLOC® M Hyo, Ceva, France), while group B comprised 767 piglets vaccinated with a PCV2a/b+MH vaccine. Blood samples were collected from 10 pigs per group at 4, 6, 8, and 12 WOA to measure PCV2 antibody titers using a BioChek® PCV2 ELISA and to assess PCV2 viremia by PCR. Antibody titers were compared using the Wilcoxon rank-sum test. Mortality was compared using the chi-square test, and risk ratios (RR) were calculated.

Results and Discussion

No significant differences in PCV2 antibody titers were observed between groups at 4 and 6 WOA. In contrast, group A showed significantly higher antibody titers with reduced variability at 8 WOA (mean ± SD: 6,550.8 ± 1,212.5 vs 4,254.1 ± 1,706.0; $P = 0.007$) and 12 WOA (5,779.0 ± 337.1 vs. 1,993.0 ± 1,380.3; $P < 0.001$). PCV2 PCR results were negative at all sampling time points in both groups. Overall mortality from 4 - 12 WOA was significantly lower in group A (3.38%; 26/776) compared with group B (8.21%; 64/767) (chi-square test, $P < 0.001$), corresponding to an approximately 60% reduction in mortality risk (RR = 0.40). These findings indicate a more sustained immune response associated with the PCV2d-based vaccination strategy, accompanied by significantly improved survival under field conditions.

Conclusion

Vaccination with a PCV2d+MH combined vaccine resulted in higher PCV2 antibody titers at later nursery stages and a substantial reduction in nursery mortality compared with a PCV2a/b+MH vaccine, supporting its effectiveness in improving protection and health outcomes under commercial pig production.

Keywords: Antibody response, *Mycoplasma hyopneumoniae*, Nursery pigs, PCV2, Vaccination.

COMPARATIVE STUDY ON PRODUCTIVITY AND ECONOMIC IMPACT OF A FRESHLY MIXED VACCINE AGAINST PORCINE CIRCOVIRUS TYPE 2 AND *MYCOPLASMA HYOPNEUMONIAE*

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* (Mhyo) cause major economic losses in pig production. Vaccine choice affects immunity and productivity. Combination vaccines for PCV2 and Mhyo differ in adjuvant and antigen processing and are available as freshly mixed or ready-to-use (RTU). Previous Japanese studies suggest freshly mixed vaccines may improve productivity (Mori et al., 2022; Naito et al., 2022). This study compared these vaccine types under field conditions, including CSF vaccination.

Materials and Methods

The trial was conducted on a 500-sow integrated farm in Shikoku. Piglets received PCV2 + Mhyo vaccination at 21 days: control (RTU; 3,944 pigs, Sept 2023 - Feb 2024) and test (freshly mixed, Ingelvac® FLEXcombo Mix; 3,965 pigs, Aug 2024 - Jan 2025). Both groups were weaned at 24 days, vaccinated against CSF at 55 days, and moved to finishing at 75 days. There was no difference in birth weight between the two groups. Parameters included mortality, weights at weaning and transfer, nursery ADG, slaughter age, carcass weight (3,539 vs. 3,449 pigs). Statistical analysis used T-tests and Z-tests; economic impact combined productivity and slaughter data.

Results

Post-weaning mortality was higher in the test group (9.6 vs. 7.0%). However, all other performance indicators showed significant differences ($P < 0.05$) favoring the test group: higher weaning weight (7.85 vs. 7.24 kg), finishing transfer weight (34.33 kg vs. 31.36 kg), nursery ADG (540.38 vs. 492.30 g), and earlier slaughter age (165.8 vs. 167.7 days). Economic analysis indicated an additional 465 JPY (€2.6) per head.

Discussion

Although the freshly mixed vaccine group had higher post weaning mortality, significant improvements were observed in growth performance. The increased mortality may have been influenced by management factors such as water supply issues rather than vaccine effects. On this farm, a 3-day interval between vaccination and weaning likely affected feed intake via differences in reactogenicity related to antigen purification and adjuvant composition. According to staff, freshly mixed vaccine recipients showed fewer reactions and maintained intake, aligning with the observed weight metrics. Together with a gain of 465 JPY per head, this supports superior field applicability and overall economic benefit.

Keywords: *Mycoplasma hyopneumoniae,* Porcine circovirus type 2.

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ISOLATION AND BIOLOGICAL CHARACTERISTICS STUDY OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS GZ2022 STRAIN

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) remains a major threat to the global swine industry. In China, NADC30-like PRRSV2 strains have become predominant, marked by frequent recombination and immune evasion (Du et al., 2017; Ye et al., 2025). This study characterized a novel recombinant NADC30-like PRRSV2 strain, GZ2022 [GenBank: OR369723.1], and evaluated its genetic novelty and pathogenicity compared to ancestral lineages.

Materials and Methods

PRRSV-2 GZ2022 was isolated from clinical samples in Guizhou Province using PAMs and Marc-145 cells, identified by immunofluorescence, and purified by plaque cloning. The complete genome was sequenced, followed by phylogenetic analysis and recombination detection using SimPlot and RDP5. The one-step growth curve of GZ2022 in Marc-145 cells was determined. Pathogenicity was evaluated in piglets by assessing clinical symptoms and viral load, with highly pathogenic WUH3 [GenBank: HM853673] as control.

Results and Discussion

A PRRSV-2 strain, GZ2022, was successfully isolated. Phylogenetic analysis placed GZ2022 within Lineage 1 (NADC30-like), with its complete genome sharing the highest homology with the NADC30 reference strain. Recombination analysis identified GZ2022 as a recombinant virus with NADC30 as the major parental strain and HuN4 (GenBank: EF635006) as the minor contributor; recombination breakpoints were located in the ORF1a/b region. Consistent with NADC30-like strains, GZ2022 harbors a 131-amino acid discontinuous deletion in NSP2. In vitro, GZ2022 reached peak titers of $10^{7.1}$ $TCID_{50}$/mL at 72 hpi. In piglets, GZ2022 induced typical PRRS clinical signs, with 0% mortality compared to 80% in the WUH3 group. Serum viral loads were significantly lower in GZ2022-infected pigs than in WUH3-infected pigs ($P < 0.01$), with the highest viral burden detected in lung tissue and milder pathological changes. These results demonstrate that GZ2022 is a moderately pathogenic recombinant PRRSV-2 strain, exhibiting a "high replication, low pathogenicity" phenotype.

Conclusion

This study reports the isolation of a recombinant NADC30-like PRRSV-2 strain, GZ2022, which originated from recombination between NADC30 and the highly pathogenic strain HuN4. GZ2022 exhibits moderate pathogenicity in piglets, with lower mortality and milder pathological changes compared to highly pathogenic strains. These findings contribute to understanding PRRSV-2 evolution and diversity.

Keywords: complete genome sequencing, NADC30-like, PRRSV-2 GZ2022, pathogenicity.

Acknowledgements: Thank National Key Laboratory of Agricultural Microbiology Core Facility and the Cooperative Innovation Center for Sustainable Pig Production for assistance during the experiments.

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COMPARISON OF THE EFFICACY OF COMMERCIAL PORCINE CIRCOVIRUS TYPE 2 VACCINES BETWEEN SUBUNIT AND CHIMERIC VACCINE IN FATTENING PIGS FROM A FARM WITH SUBCLINICAL PCV2 INFECTION

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) remains a critical pathogen in swine production system, with subclinical infections adversely affecting herd performance (Segalés et al., 2013; Ferrando et al., 2016). This study aimed to compare the field efficacy of a commercial subunit vaccine and a chimeric vaccine in fattening pigs raised on a farm with confirmed subclinical PCV2 infection.

Materials and Methods

A total of 1,800 piglets were randomly assigned to a control group (Vaccine A, subunit) or a treatment group (Vaccine B, chimeric, Fostera® PCV Metastim). Vaccine A (2 ml) and Vaccine B (1 ml) were administered at 3 and 7 weeks of age. Previous farm batches had tested PCR-positive for PCV2 at 20 weeks despite no clinical signs. Sera were collected at 6, 10, 16, and 20 weeks to detect PCV2 DNA by real-time PCR (Ct > 38) and assess immune responses by PCV2 ELISA (Biocheck). Production parameters - including pigs marketed, market weight, total weight gain, mortality, ADG, and FCR - were recorded. Statistical analyses used independent t-tests for means and chi-square tests for proportions between groups.

Results and Discussion

Both vaccination protocols effectively controlled PCV2 infection, as PCR results were negative at all tested ages, indicating no detectable viremia under field conditions. Despite similar virological outcomes, pigs receiving the chimeric vaccine (Vaccine B) showed superior production performance compared with the subunit vaccine group (Vaccine A), including higher number of pigs marketed (869 vs. 832), greater market weight (111.12 vs. 105.37 kg), increased total weight gain (104.52 vs. 99.37 kg), higher ADG (768.53 vs. 736.07 g/day), and lower mortality (3.44 vs. 7.56%) ($P < 0.01$). FCR was comparable between groups (2.57 vs. 2.57). These differences are likely attributable to variation in the quality and duration of vaccine-induced immune responses, which may better control subclinical PCV2-associated effects beyond detectable viremia.

Conclusion

Both vaccines effectively prevented detectable PCV2 viremia under field conditions. However, the chimeric vaccine demonstrated superior production performance and lower mortality, suggesting enhanced control of subclinical PCV2 impacts.

Keywords: Chimeric vaccine, Fattening pigs, Porcine circovirus type 2 (PCV2), Subunit vaccine.

Acknowledgements: The authors gratefully acknowledge the support from the swine farm staff and Zoetis (Thailand) Limited technical team during this study.

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ASSESSMENT OF EARLY PCV2 INFECTION FROM SOWS TO PIGLETS AND THE IMPACT OF SOW VACCINATION IN SOUTHERN VIETNAM

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is an important pathogen in pigs, which can cause early infection from sows to piglets via multiple routes (Eddicks et al., 2022; Gerber et al., 2012). These transmission pathways pose risks to piglets' health and may reduce the efficacy of vaccination programs impacting the productivity. This survey aimed to describe the early infection of porcine circovirus type 2 in sows and offspring using different vaccination protocols across farms in Southern Vietnam.

Materials and Methods

Twelve commercial farrow-to-wean and farrow-to-finish swine farms located in Southern Vietnam were included in the study. Farm information, such as PCV2 vaccination program was documented, and a total of 66 samples were randomly collected, including 15 sow colostrum, 45 piglet serum, 3 piglet thymus, and 3 piglet lymph node samples. Sows were selected at random across different parity groups (P1, P2, and P ≥ 3), and piglets were randomly chosen from these sows. All samples were tested for PCV2 using the NK PCV2 Real-time PCR kit (NAM KHOA BIOTEK, Vietnam). Data analysis was performed using JMP 18 statistical software.

Results and Discussion

A total of 702 samples were analyzed, of which 23 (3.3%) tested positive. Six out of twelve farms (50%) had at least one positive sample. All farms vaccinated piglets, while two did not vaccinate sows and three vaccinated only P1 sows. Colostrum (4.4%) and serum (2.0%) showed lower detection rates compared to lymph nodes (11.5%) and thymus (11.0%). The highest positivity was observed in colostrum from P3 sows (7%) and lymph nodes from P1 piglets (4%). Farms vaccinating sows had significantly lower positivity compared to non-vaccinated farms (OR = 8.02, P = 0.049), though no difference was found among vaccination protocols.

Conclusion

PCV2 was detected in 3.3% of samples, with half of the farms surveyed showing positivity. Vaccination of sows was associated with significantly lower PCV2 prevalence in newborn piglet samples as a proxy for early infection, although differences among vaccination protocols were not observed. These findings highlight the importance of sow vaccination in reducing PCV2 circulation on swine farms in Southern Vietnam.

Keywords: Colostrum, Early infection, PCV2, Suckling piglets, Thymus.

Acknowledgements: The authors thank Boehringer Ingelheim, Faculty of Animal Husbandry and Veterinary Medicine of Nong Lam University and research partners for the support with providing testing facilities.

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CONFORMATIONAL EPITOPE MAPPING OF THE E2 GLYCOPROTEIN IN CLASSICAL SWINE FEVER VIRUS, BOVINE VIRAL DIARRHEA VIRUS, AND BORDER DISEASE VIRUS

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Introduction and Objectives

Classical swine fever virus (CSFV), bovine viral diarrhea virus (BVDV), and border disease virus (BDV) are closely related members of the genus *Pestivirus* within the family *Flaviviridae*. These viruses share high structural and antigenic similarity, particularly in the envelope glycoprotein E2, leading to serological cross-reactivity that complicates diagnosis and disease control. Importantly, all three viruses can infect pigs, further challenging serological surveillance. This study aimed to identify and characterize conformational antigenic determinants on the E2 proteins of these Pestiviruses, thereby supporting improved differential diagnostics and informing future vaccine development.

Materials and Methods

A panel of E2 glycoprotein constructs from CSFV, BVDV, and BDV was generated, including antigenic domains B/C, D/A, and full-length E2, as well as site-directed mutants targeting residues previously implicated in these domains (Huang et al., 2021, 2023). Recombinant E2 proteins were expressed using a baculovirus expression system and harvested for downstream analyses. Antibody reactivity was evaluated using E2-specific monoclonal antibodies by indirect fluorescent assay and Western blot.

Results and Discussion

The antigenic characterization of E2 proteins among pestiviruses revealed the presence of both virus-specific and pan-pestivirus epitopes. The domain B/C of the E2 harbors both virus-specific and pestivirus-conserved antigenic determinants, whereas the domain D/A primarily contains virus-specific antigenic determinants. The TSXXF motif in domain B/C is a critical conserved antigenic determinant across pestiviruses.

Conclusion

This antigenic analysis identified key conformational residues on the E2 glycoproteins of CSFV, BVDV, and BDV that determine monoclonal antibody binding, enhancing our understanding of pestivirus antigenic structure and supporting improved differential serological diagnostics and epitope-based vaccine design.

Keywords: Border disease virus, Bovine viral diarrhea virus, Classical swine fever virus, E2 glycoprotein, Epitope mapping.

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PRM AND E PROTEIN VIRULENCE SITES: PIVOTAL FACTORS ACROSS JAPANESE ENCEPHALITIS VIRUS GENOTYPES GIII AND GV

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Introduction and Objectives

Japanese encephalitis virus (JEV) can infect swine via mosquito-borne transmission or contact with oronasal secretions, resulting in reproductive disorders (Ricklin et al., 2016). Humans, serving as dead-end hosts for JEV, are at risk of developing permanent neurological sequelae post-infection. JEV exhibits global endemicity, with its dominant genotype transitioning from GIII to GI. In recent years, GV JEV has been sporadically identified in Korea (Lee et al., 2022). Identifying critical virulence sites among distinct genotypes and elucidating their regulatory mechanisms could provide a scientific basis for advancing prevention and control strategies against Japanese encephalitis.

Materials and Methods

Firstly, the differential residues among various genotypes of JEV were identified based on their aligned sequences. Subsequently, recombinant viruses with mutated sites were rescued through the reverse genetic techniques. Finally, the replication kinetics, neuroinvasiveness, and neurovirulence of these mutant viruses were evaluated and compared with those of wild-type (WT) viruses.

Results and Discussion

We found that amino acid 31 in prM and 389 in the E protein of JEV exhibit variation among GI, GIII, and GV JEV. Compared to the WT virus, the mutant prM-E31A and E-D389G both displayed decreased replication efficiency in BHK-21 cells while enhancing viral replicative capacity in PK-15 cells. Notably, this mutation resulted in significant attenuation of neuroinvasiveness in infected mice. However, the neurovirulence of JEV remained unaffected by this mutation. These findings suggest that the prM-E31 and E-D389 sites play a role in the replication and virulence of JEV, with this capability potentially varying across different host species.

Conclusion

The amino acid at position 31 in the prM and 389 in the E protein may represent a critical virulence site among different JEV genotypes. The significant attenuation of neuroinvasiveness observed in the mutant virus may be attributed to obstruction of viral maturation or Golgi stress after prM-E31A mutation, the enhanced accumulation of positive charges within the E protein domain, or the reduced affinity for glycosaminoglycans. These alterations potentially impair the virus's efficiency to invade the central nervous system, thereby disrupting its ability to induce cytokine storms and cause neurological injury.

Keywords: GIII, GV, Japanese encephalitis virus, Potential virulence sites

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FIELD EVALUATION OF A COMBINED PRRSV, PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE (3FLEX®) IN THAI SWINE PRODUCTION

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Introduction and Objectives

Porcine Respiratory Disease Complex (PRDC) is a cause of significant economic losses. Key pathogens include PRRSV, PCV2, and *Mycoplasma hyopneumoniae*. Vaccination is recognized as the most cost-effective approach. Using separate vaccines for PRRS and PCV2-M. hyo increases handling, time, and needle use, raising pathogen transmission risk. The concern about maternal antibody interference at weaning led to poor performance in fattening pigs (Hua et al., 2016). This study evaluated the field efficacy of a combined PRRSV, PCV2, and *M. hyo* vaccine (3FLEX®) in a large Thai farm with piglets from different breeder sources.

Materials and Methods

The study was conducted on a 20,000-fattening batch. The farm receives weaned piglets from two breeder farms: breeder1 and breeder2 (n = 10,000 pigs each). Previously, weaned piglets were vaccinated with PRRS and RTU PCV2-M. hyo vaccines as separate vaccines, and production results were below farm targets (ADG 730 g/day, FCR 2.5, and % loss < 5). Then the farm changed the vaccine to a combined vaccine (3FLEX®) with 2 ml intramuscularly in piglets. To evaluate vaccine efficacy, pig production performance data, including ADG, FCR, and % loss, were recorded. Serum was collected at 5, 9, 13, 17, and 23 weeks old (10 samples each) and analyzed for PCV2 ELISA (BioChek) antibody titers and PCR for PCV2 detection. Comparison of diagnostic and performance data between piglets from both breeders, which have different maternal antibody levels, was tested by Student's t-test; losses were analyzed by chi-square test.

Results and Discussion

Production performance from this batch vaccinated with 3FLEX® exceeded farm targets: ADG 750 g/day, FCR 2.5, and %loss 3.5%. Reduction of losses was significant ($P \leq 0.05$). Antibody titers between sources were not statistically different, although titers at week 5 were numerically higher for the breeder. PCV2 PCR results remained negative at all sampling points for both sources.

Conclusion

The study demonstrated ADG improvement and mortality reduction with a triple combined vaccine, translating into significant production performance gains. Pigs vaccinated with 3FLEX® remained PCR negative for PCV2 in endemic areas. Overall, the combined vaccine simplifies management, improves health, and achieves farm targets under field conditions.

Keywords: Maternal antibody, PCV2, Production performance, Triple combined vaccine.

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COMPARISON OF INFECTION DYNAMICS AND HOST FACTOR–MEDIATED REGULATORY MECHANISMS OF HISTORICAL AND NEWLY INVADING CLASSICAL SWINE FEVER VIRUSES

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Introduction and Objectives

In recent decades, classical swine fever virus (CSFV) genotype 2 (G2) has demonstrated a transmission advantage over genotypes 1 (G1) and 3 (G3) worldwide. In Taiwan, a rapid replacement of historical G3.4 by newly invading G2.1 was observed between 1994 and 1996. Previous studies have demonstrated that G2.1 exhibits superior replication efficiency and enhanced transmissibility (Liu et al., 2023). This study aims to investigate genotype-specific host factor dynamics in both cultured cells and tissue immune cells during infection, using immunofluorescence (IF) staining and the Co-Detection by Indexing (CODEX) technology.

Materials and Methods

PK-15 cells were separately infected with CSFV G2.1 or G3.4 and collected at sequential time points post-infection. IF staining followed by confocal microscopy was used to evaluate the colocalization of viral proteins with selected host factors. In parallel, tissue samples were obtained from pigs experimentally inoculated with G2.1 or G3.4. High-dimensional multiplex staining on tissue sections was enabled by the CODEX platform.

Results and Discussion

In the in vitro study, intracellular host proteins involved in viral attachment and endocytosis were examined, and their colocalization with CSFV signals was quantified, revealing genotype-dependent differences. For CODEX technical innovation, the staining panel incorporated CSFV antigens, immune lineage markers, and indicators of immune response. Spatial overlap between CSFV E2 and lineage markers (e.g., Iba-1 and CD3) revealed selective cellular tropism. In addition, immune checkpoint and cell–cell interaction markers were leveraged to characterize the genotype-specific phenotypic shifts and spatial immune dynamics driven by CSFV G2.1 and G3.4 within infected tissues.

Conclusion

Colocalization between host markers and viral signals highlights candidate host proteins that interact with CSFV, providing leads to dissecting the mechanisms of viral entry and intracellular trafficking. In vivo analyses further indicated that CSFV infection is associated with immune cell exhaustion and apoptosis, exhibiting genotype-dependent patterns.

Keywords: Classical swine fever, CODEX, Genotype shift, Host factor dynamics.

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IDENTIFICATION OF THE VIRULENCE SITES IN GI, GIII AND GV OF JAPANESE ENCEPHALITIS VIRUS

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Introduction and Objectives

Japanese encephalitis virus (JEV) can infect swine via mosquito-borne transmission or contact with oronasal secretions, resulting in reproductive disorders (Ricklin et al., 2016). Humans, serving as dead-end hosts for JEV, are at risk of developing permanent neurological sequelae post-infection. JEV exhibits global endemicity, with its dominant genotype transitioning from GIII to GI. In recent years, GV JEV has been sporadically identified in Korea (Lee et al., 2022). Identifying critical virulence sites among distinct genotypes and elucidating their regulatory mechanisms could provide a scientific basis for advancing prevention and control strategies against Japanese encephalitis.

Material and Method

Firstly, the differential residues among various genotypes of JEV were identified based on their aligned sequences. Subsequently, recombinant viruses with mutated sites were rescued through the reverse genetic techniques. Finally, the replication kinetics, neuroinvasiveness, and neurovirulence of these mutant viruses were evaluated and compared with those of wild-type (WT) viruses.

Results and Discussion

We found that amino acid 389 in the E protein of JEV exhibits variation among GI, GIII, and GV JEV. Compared to the WT virus, the mutant displayed decreased replication efficiency in BHK-21 cells while enhancing viral replicative capacity in PK-15 cells. Notably, this mutation resulted in significant attenuation of neuroinvasiveness in infected mice. However, the neurovirulence of JEV remained unaffected by this mutation. These findings suggest that the E-D389 site plays a role in the replication and virulence of JEV, with this capability potentially varying across different host species.

Conclusion

The amino acid at position 389 in the E protein may represent a critical virulence site among different JEV genotypes. The significant attenuation of neuroinvasiveness observed in the mutant virus may be attributed to either an enhanced accumulation of positive charge within this structural domain of the E protein or a reduced affinity for glycosaminoglycans. These alterations potentially impair the virus's efficiency to invade the central nervous system, thereby disrupting its ability to induce cytokine storms and cause neurological injury.

Keywords: GI, GIII, GV, Japanese encephalitis virus, Potential virulence sites.

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2. Lee, A et al., 2022. *Journal of microbiology and biotechnology* 32(8), 955-959.

MOLECULAR EPIDEMIOLOGY OF SWINE HEPATITIS E VIRUS IN TAIWAN

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Introduction and Objectives

Hepatitis E virus (HEV) is an important zoonotic pathogen, with swine serving as the primary natural reservoir. HEV infection in pigs is typically asymptomatic, yet infected animals can shed large amounts of virus in feces, posing a potential public health risk. In Taiwan, a previous study reported a 25.1% HEV RNA-positive rate in fecal samples from slaughter-age pigs in 2015 (Liao et al., 2020). Accordingly, this study aimed to investigate the current serological and virological prevalence of HEV on pig farms in Taiwan.

Materials and Methods

Samples were collected from pigs aged 16 - 24 weeks across multiple counties in Taiwan in 2022 and 2024. In 2022, 531 serum samples from 41 pig farms were screened using an HEV antibody ELISA to identify seropositive farms. Subsequently, 362 fecal samples were collected from the same individual pigs in 20 seropositive farms and analyzed by RT-nested PCR. ORF2 sequences were obtained from positive samples and subjected to genotyping and genetic analyses. In 2024, an additional 673 serum samples from 46 pig farms were screened by HEV antibody ELISA to assess serological prevalence.

Results and Discussion

High HEV ELISA seropositivity was observed at both the farm and animal levels in Taiwan. Farm-level seropositivity was 78% (32/41) in 2022 and 76% (35/46) in 2024, while animal-level seropositivity reached 50% (265/531) and 54% (364/673), respectively, indicating sustained HEV exposure during 2022–2024. Animal-level seroprevalence exceeded 60% in southern and eastern Taiwan in both years. HEV RNA was detected in 5.5% (20/362) of fecal samples, demonstrating active viral shedding. Genotyping identified three HEV subtypes (3a, 4b, and 4h), indicating substantial genetic diversity among circulating strains. These findings highlight ongoing HEV activity in swine populations and the relevance of HEV infection in market-age pigs to zoonotic transmission and food safety.

Conclusion

This study demonstrates widespread HEV exposure and ongoing viral circulation in Taiwanese pig farms, supported by high seropositivity rates and fecal HEV RNA detection. The presence of multiple HEV subtypes reflects considerable genetic diversity, suggesting continued viral circulation and evolution. These findings underscore continued surveillance and molecular characterization for zoonotic risk assessment and prevention.

Keywords: Genotyping, Hepatitis E Virus, Seroprevalence, Swine, Zoonotic Risk.

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INVESTIGATING HOST CELL GENE REGULATION DURING CLASSICAL SWINE FEVER VIRUS REPLICATION USING SIRNA AND CRISPR/CAS9

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Introduction and Objectives

Classical swine fever virus (CSFV) remains a major threat to the swine industry. The progressive replacement of genotype 3.4 (G3.4) by genotype 2.1 (G2.1) suggests that there are genotype-specific differences in viral fitness and host–virus interactions. Here, host regulators and immunomodulatory factors involved in CSFV infection were interrogated using complementary siRNA knockdown and CRISPR/Cas9 knockout approaches to compare the replication of CSFV G2.1 and G3.4.

Materials and Methods

PK-15 cells were transfected with siRNAs targeting Rab5A, Rab7, or a non-targeting control. At 48 hours post-transfection, cells were infected with CSFV G2.1 or G3.4. Viral replication was quantified at 24 hours post-infection by quantitative real-time PCR. For CRISPR/Cas9-mediated gene editing, sgRNA/Cas9 ribonucleoprotein complexes targeting Poly (rC)-binding protein 1 (PCBP1) (Qi et al., 2022) and S100A9 (Huang et al., 2025) were delivered into PK-15 cells to generate knockout cell lines. Following limiting dilution cloning, knockout clones were selected and expanded, and their susceptibility to CSFV G2.1 and G3.4 infection was evaluated.

Results and Discussion

siRNA-mediated knockdown of Rab5A and Rab7 significantly reduced CSFV replication, supporting a key role for endosomal trafficking in the early stages of infection. The stronger inhibition observed for genotype G3.4 than G2.1 suggests that G3.4 relies more heavily on canonical endosomal entry/maturation, whereas G2.1 may enter or traffic more efficiently through alternative routes, consistent with its higher fitness. In parallel, CRISPR/Cas9 knockout clones of PCBP1 and S100A9 were generated to enable follow-up analyses of genotype-specific host requirements, including potential immunomodulatory effects, during CSFV G2.1 and G3.4 infection.

Conclusion

This study demonstrates genotype-specific differences in host factor dependency during the early stages of CSFV infection. CSFV G3.4 depends more strongly on Rab5A/Rab7-mediated endosomal trafficking than G2.1, which may partly explain its reduced replication efficiency. In addition, the successful establishment and validation of CRISPR/Cas9 knockout strategies targeting PCBP1 and S100A9 provide a platform for future functional dissection of host determinants governing CSFV replication.

Keywords: Classical swine fever virus, CRISPR/Cas9, PCBP1, Rab, siRNA.

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EVALUATION OF A PCV2B VACCINES AGAINST PCV2D CHALLENGE IN PIGLETS WITH MATERNALLY DERIVED ANTIBODIES

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Introduction and Objectives

The efficacy of porcine circovirus 2 (PCV2) vaccines is challenged by genotype shifts and maternal-derived antibodies. The PCV2d sub-genotype has become predominant worldwide (Sirisereewan et al., 2023), raising concerns about cross-protection provided by commercial PCV2a- or PCV2b-based vaccines. This study aimed to evaluate the efficacy of a commercial PCV2b vaccine in seropositive piglets challenged with PCV2d.

Materials and Methods

A Thai PCV2d isolate was used for challenge at 10^7 copies/mL, as determined by real-time PCR. Forty piglets were allocated into four groups: Group 1 (n = 4), negative control; Group 2 (n = 12), positive control (unvaccinated/challenged); Group 3 (n = 12), vaccinated with a PCV2b vaccine (CircoGard®, Pharmgate Animal Health, USA); and Group 4 (n = 12), vaccinated with a PCV2b–*Mycoplasma hyopneumoniae* combination vaccine (CircoMycoGard®, Pharmgate Animal Health, USA). Vaccination was performed at three weeks of age, and PCV2 challenge was conducted 21 days post-vaccination. Clinical signs, serological responses, and PCV2 DNA loads were monitored up to 14 days post-inoculation (dpi).

Results and Discussion

No clinical signs were observed in any group throughout the study. All piglets were seropositive for PCV2 at vaccination, indicating the presence of maternal-derived antibodies. Antibody levels declined gradually in all groups but remained positive at the time of challenge, suggesting interference of maternal antibodies with humoral responses. PCV2 viremia was not detected prior to challenge. At 14 dpi, quantitative PCR showed mean PCV2 genomic copies in serum of 4.1, 2.8, and 3.6 $\log_{10}$ copies/mL in Groups 2 - 4, respectively. In superficial inguinal lymph nodes, mean PCV2 genomic copies were 7.7, 6.8, and 5.6 $\log_{10}$ copies/mL, respectively. Mean microscopic lymphoid depletion scores (range 0 - 3) were 1.9, 1.8, and 1.7, respectively.

Conclusion

Despite the absence of seroconversion, PCV2b-based vaccination of seropositive piglets partially limited viral replication and tissue damage following PCV2d challenge. These findings indicate that PCV2 vaccination can provide biological protection in the presence of maternal antibodies, even when humoral responses are not detectable.

Keywords: Maternal-derived antibody, Pig, Porcine circovirus 2, Vaccine.

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IMPACT OF NEEDLE-FREE VACCINATION ON PCV2 VIREMIA AND SEROLOGICAL RESPONSE IN PIGLETS UNDER FIELD CONDITIONS

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) transmission involves multiple routes, making its control essential. Although intramuscular (IM) vaccination is standard (Chae et al., 2012), it may increase the risk of iatrogenic transmission within herds (Otterson et al., 2002). Needle-free intradermal (ID) vaccination eliminates this specific risk factor. This study evaluated the impact of a needle-free PCV2 vaccine versus conventional IM vaccination on PCV2 viremia and serological responses under commercial farm conditions.

Materials and Methods

The trial utilized on a 1,000-sow farrow-to-nursery farm using a parallel design across four consecutive batches. Piglets were housed in separate barns. Group A received a needle-free ID PCV2 vaccine (Mhyosphere® PCV ID, HIPRA) at 3 weeks of age (WOA), while Group B received IM *M. hyopneumoniae* vaccination at 1 WOA and PCV2 vaccination at 3 WOA using needles without strict needle replacement between animals. Cross-sectional blood samples were collected from piglets aged 4, 5, 6, and 7 WOA (n = 3 per age group per treatment; total n = 24) for pooled PCV2 PCR and individual ELISA antibody testing.

Results and Discussion

No PCV2-positive PCR samples were detected in Group A. In contrast, Group B showed PCV2 viremia starting 2 weeks after weaning. However, the difference in PCR detection rates did not reach statistical significance (Fisher's exact test, $P = 0.1429$), likely due to the limited sample size. Seroconversion occurred earlier in Group B, which also showed slightly higher PCV2 ELISA antibody titers; however, the difference between groups was not statistically significant (Welch's T-test, $P = 0.372$). While PCV2 spreads via various routes, the absence of viremia in Group A suggests that eliminating needle-mediated transmission may have contributed to this favorable outcome, although other environmental factors cannot be fully excluded in this field design.

Conclusion

Needle-free ID vaccination was associated with an absence of detectable PCV2 viremia, whereas viremia was observed in the conventional IM group. Although the difference was not statistically significant, the results suggest that removing needles - a known mechanical vector - may aid in reducing iatrogenic transmission risks as part of a broader biosecurity strategy. Further studies with larger sample sizes are warranted to confirm these observations.

Keywords: Intradermal, Iatrogenic transmission, Needle-free vaccination, Porcine circovirus type 2.

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A RETROSPECTIVE STUDY OF PRRS-ASSOCIATED WITH CO-INFECTIONS PATTERNS IN NURSERY PIGS DURING 2023 - 2025

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) is a major viral disease in swine due to its clinical impact and immunosuppressive effects that predispose pigs to secondary infections. Under field conditions, PRRS-associated co-infections are linked to increased disease severity, complex lesions, and poor treatment response. However, information of co-infection patterns in diagnostic submissions remains limited. This study retrospectively analyzed the frequency and patterns of PRRS-associated co-infections in pigs submitted for necropsy and laboratory investigation between 2023 and 2025.

Materials and Methods

A retrospective review was conducted on 78 PRRS-positive cases from 68 farms, consisting of nursery pigs submitted for diagnostic investigation to the Kamphaeng Saen Veterinary Diagnostic Center (KVDC) between 2023 and 2025. PRRS virus was confirmed by RT-PCR, while concurrent bacterial pathogens were identified through routine bacteriological culture following the KVDC guideline.

Results and Discussion

Of the 78 PRRS-positive cases, PRRS infection alone was detected in 36 cases (46.2%), while 42 cases (53.8%) involved one or more concurrent pathogens. In PRRS co-infected cases, *Streptococcus* spp. was most frequently identified (73.8%), followed by *Glaeserella parasuis* (4.76%), *Actinobacillus pleuropneumoniae* (2.38%), and Porcine circovirus type 2 (PCV2) (2.38%). Mixed co-infections involving two or more pathogens were also observed (16.66%). These findings support that PRRS-associated respiratory disease is particularly problematic in nursery pigs due to bacterial–viral co-infections (Sun et al., 2022).

Conclusion

This retrospective analysis highlights the involvement of concurrent pathogens in PRRS-positive diagnostic cases, particularly in nursery pigs. The observed co-infection patterns emphasize the need for integrated diagnostic interpretation beyond PRRSV detection alone and support targeted antimicrobial selection, improved treatment strategies, and more effective herd health management in PRRS-affected farms.

Keywords: Co-infection, Diagnostic investigation, Nursery pigs, PRRS, *Streptococcus* spp.

Acknowledgements: The authors acknowledge the Kamphaeng Saen Veterinary Diagnostic Center (KVDC) for providing diagnostic data, laboratory support, and technical assistance.

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A CROSS-SECTIONAL STUDY OF SEROPREVALENCE OF HEPATITIS E VIRUS AMONG FATTENING PIGS IN TAIWAN

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Introduction and Objectives

Hepatitis E virus (HEV) is a major global cause of acute viral hepatitis and an important zoonotic foodborne pathogen. In Asia, an increasing number of studies have reported unexpectedly high seroprevalence of HEVs in pigs across all age groups. Previous studies in Taiwan indicate active HEV circulation in swine, highlighting potential food safety and occupational health risks and the need for updated epidemiological data.

Materials and Methods

A cross-sectional study was conducted to estimate the seroprevalence of hepatitis E virus (HEV) antibodies among fattening pigs in Taiwan. A total of 32 commercial pig farms were included in five different counties. Five serum samples were collected from each farm in 2024, resulting in a total of 160 serum samples. ELISA testing was conducted to evaluate serological anti-HEV antibody. Subsequently, statistical analyses were conducted to compare seroprevalence across different age groups, counties, and individual farms.

Results and Discussion

The overall seroprevalence of HEV IgG among sampled pigs was 52.5% (84/160). At the farm-level, 24 of 32 farms were tested positive for anti-HEV IgG, corresponding to a prevalence of 75%. The farm-level HEV seroprevalence across the counties was 75% (6/8) in Changhua, 71.4% (10/14) in Yunlin, 100% (1/1) in Chiayi, 100% (2/2) in Tainan, and 71.4% (5/7) in Pingtung. Anti-HEV IgG prevalence showed a progressive upward trend across the fattening period, rising from 41.4% (early stage) to 50.0% (mid-stage), and finally to 66.7% (late stage). Although HEV infection probability increases with production stage, the model's low AUC (0.62) highlights that additional environmental or management factors beyond age drive infection dynamics.

Conclusion

This study delineates the seroprevalence of Hepatitis E virus (HEV) in Taiwan's pig farms, identifying a progressive upward trend throughout the swine production cycle. These findings underscore a significant potential for zoonotic transmission to occupationally exposed individuals, particularly farm workers and veterinarians. Consequently, future research should prioritize seroprevalence among high-risk personnel and the establishment of robust public health interventions and preventive protocols.

Keywords: ELISA, Hepatitis E virus, Serological test, Zoonotic disease

Acknowledgements: This study was supported by the National Science and Technology Council (NSTC) of Taiwan.

POTENTIAL MECHANISMS OF IMMUNE MODULATION BY AFRICAN SWINE FEVER VIRUS CD2V VIA PROTEIN TRANSLOCATION

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Introduction and Objectives

African swine fever (ASF) is a hemorrhagic disease with a high mortality rate in domestic pigs, leading to significant economic losses in the swine industry. CD2v, a glycoprotein located on the outer viral envelope of ASFV, shares structural similarity with the T-lymphocyte surface antigen CD2. It mediates hemadsorption, thereby facilitating viral dissemination within the host, and also contributes to immune evasion, although the underlying mechanisms remain poorly understood, particularly its interaction with CD58, the cellular receptor of host CD2.

Materials and Methods

To explore the immune modulation mechanism and potential CD2v - CD58 interaction, two eGFP-tagged recombinant proteins, ectodomain of CD2v (CD2v-ecto) and full-length of CD2v (CD2v-FL), were constructed and expressed in HEK293 cells. Upon transfection, eGFP fluorescence was detected in HEK293 cells to confirm the successful expression. Moreover, 3D4 cells (a porcine alveolar macrophage cell line) transfected with CD2v-FL or a mock plasmid were subjected to differential gene expression analysis.

Results and Discussion

Compared with the mock-transfected cells, several cytokine-related genes were differentially expressed in CD2v-FL-transfected cells, demonstrating that CD2v-FL modulates host immune signaling pathways. Collectively, these findings reveal that CD2v may function as a key viral factor in modulating host immune responses, providing a foundation for further investigation into its interaction with CD58 and its contribution to ASFV immune evasion.

Conclusion

In this study, HEK293 cells efficiently expressed both types of eGFP-tagged fusion proteins, the full-length CD2v (CD2v-FL) and the CD2v ectodomain (CD2v-ecto). The CD2v-FL transfected HEK293 cells formed rosette hemabsorption, indicating that the expressed protein retains extracellular properties comparable to those of native ASFV CD2v. The transcriptomic analysis of CD2v-FL transfected 3D4 cells revealed that CD2v-FL modulated multiple signaling pathways related to cytokine secretion and receptor interactions. Finally, the soluble CD2v-ecto was purified to investigate the interactions with the CD2v and CD58.

Keywords: African Swine Fever Virus (ASFV), CD2v, CD58 interaction.

Acknowledgements: The project was supported by National Science and Technology Council (NSTC) of Taiwan with the grant numbers of NSTC-114-2313-B-005-048 and NSTC 112-2313-B-005-047-MY2.

MOLECULAR DETECTION OF ATYPICAL PORCINE PESTIVIRUS IN FREE-RANGING WILD BOARS IN EUROPEAN RUSSIA

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Introduction and Objectives

Atypical porcine pestivirus (APPeV), also known as Pestivirus scrofae, belongs to the genus *Pestivirus*, family *Flaviviridae*. The virus was first identified in 2015 in the USA and is currently widespread in many countries of Europe and Asia, as well as in North and South America. APPeV causes congenital tremor type A-II in piglets and persists in adult pigs (Hause et al., 2015; Postel et al., 2017). In this study, the first detection of APPeV in the wild boar population of Russia is reported.

Materials and Methods

From December 2021 through August 2025, a total of 445 tissue samples were collected from 236 free-ranging wild boars hunted across seven regions of European Russia: Moscow, Belgorod, Tver, Tula, Lipetsk, Ryazan, and Krasnodar Krai. For qRT-PCR, primers and probes targeting the 5'UTR region, and for sequencing, primers targeting the NS2-NS3 gene described by Kauffman et al. (2015) and Postel et al. (2016) were used, respectively. cDNA was synthesized using random primer and Superscript IV kit following the manufacturer's instructions. Phylogenetic analysis was carried out in MEGA 7.0.

Results and Discussion

The overall APPeV detection rate in investigated areas was estimated to be 9.7% (23/236). In total, APPeV was detected in wild boars of four regions: Moscow (10.5%), Tver (12.2%), Belgorod (12.0%), and Tula (33.3%). Our findings demonstrated that APPeV has circulated in the wild boar population of Russia since at least 2021. Infected wild boars were identified in all age groups, tissue species and sexes (p>0.05). Following phylogeny, Russian isolates constituted their own distinct clades differing from other strains. The nucleotide sequence identity between the Russian isolates varied from 86.1% to 99.1% and from 74.0% to 93.5% with APPeV strains from GenBank.

Conclusion

This study provides the first evidence of APPeV circulation in wild boars in Russia and determines its prevalence in the European part of the country. Further investigation is warranted to enhance our understanding of the infection epidemiology within the country and to explore the role of wild boars as a natural reservoir for APPeV transmission.

Keywords: Atypical porcine pestivirus, Infection, Pestiviruses, Phylogeny, Wild boars.
Acknowledgements: This research was funded by the Russian Science Foundation, grant number 23-76-10055.

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MGB PROBE-BASED QUADRUPLEX MGB-QRT-PCR ASSAY: A HIGH-THROUGHPUT SURVEILLANCE METHOD FOR JEV, WNV, AND CO-CIRCULATING MOSQUITO-BORNE FLAVIVIRUSES IN SWINE FARMS

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Introduction and Objectives

Global trade and climate change have intensified the threat of mosquito-borne flaviviruses to animal and public health. In pig farming, Japanese encephalitis virus (JEV) is a well-established pathogen, while the incursion risk of others like West Nile virus (WNV) is a growing concern. Co-circulation of flaviviruses such as Dengue (DENV) and Zika (ZIKV) can complicate diagnosis (Erlanger et al., 2009; Pejsak et al., 2025). To address the need for efficient, simultaneous pathogen surveillance, this study aimed to develop a sensitive and specific quadruplex quantitative RT-PCR (qRT-PCR) assay for the joint detection of JEV, WNV, DENV, and ZIKV, and to evaluate its applicability in porcine environmental monitoring.

Materials and Methods

A quadruplex one-step qRT-PCR assay was developed using Minor Groove Binder (MGB) probes (Kutyavin et al., 2000). Specific primers and probes were designed for conserved genomic regions of JEV, WNV, DENV, and ZIKV. The assay's analytical specificity and sensitivity were rigorously characterized and compared to conventional TaqMan probe-based assays. Validation was performed using RNA from virus-spiked cell cultures, laboratory-infected mosquitoes, and field-collected mosquitoes from peri-domestic environments near pig farms.

Results and Discussion

The MGB probe-based quadruplex assay demonstrated high specificity with no cross-reactivity among the four targets. It showed superior sensitivity compared to the conventional TaqMan probe method, with a detection limit of 1 RNA copies per reaction for all viruses and a linear dynamic range over 11 orders of magnitude ($R^2 > 0.99$). The assay successfully detected target viruses in all validation sample types, confirming its robustness for complex matrices.

Conclusion

We developed and validated a high-throughput, highly sensitive, and specific quadruplex MGB-qRT-PCR assay for the simultaneous detection of JEV, WNV, DENV, and ZIKV. This method significantly enhances the capability for multiplex surveillance of key mosquito-borne flaviviruses. It serves as a powerful tool for early warning of JEV and potential incursions of other flaviviruses like WNV in pig farm environments. Based on its reliability, this method provides a technical foundation for future implementation of integrated "environment-vector-host" monitoring strategies, contributing to proactive disease control in the pig industry within a "One Health" framework.

Keywords: Disease surveillance, Japanese encephalitis virus, MGB probe, Quadruplex quantification real-time PCR, Swine veterinarian.

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DEVELOPMENT AND APPLICATION OF A TRIPLE MGB-QPCR ASSAY FOR MONITORING SWINE VECTOR-BORNE VIRUSES

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Introduction and Objectives

The pig farming industry faces a growing threat from arthropod-borne viruses, exacerbated by global trade and climate change. Rift Valley fever virus (RVFV) and vesicular stomatitis virus (VSV) are established pathogens in swine, while evidence of Banna virus (BAV) infection in pigs indicates a potential risk (Lubisi et al., 2023; Liu et al., 2010). To improve the efficiency of multi-pathogen surveillance, this study aimed to establish a triplex real-time quantitative PCR method for the concurrent detection of RVFV, VSV, and BAV.

Materials and Methods

A triplex quantitative real-time PCR (qPCR) assay was developed using Minor Groove Binder (MGB) probes. Virus-specific primers and probes were designed to target conserved regions of the RVFV L segment, the VSV N gene, and the BAV Seg12 segment. The analytical specificity and sensitivity of the assay were rigorously evaluated. The assay was then validated using RNA extracted from Aedes and Culex mosquito pools collected from peri-domestic environments in endemic regions.

Results and Discussion

The developed assay demonstrated high specificity, with no cross-reactivity among the three target viruses or with other common porcine pathogens such as Japanese encephalitis virus, West Nile virus, and Dengue virus. It showed high sensitivity, with a limit of detection of 10 RNA copies per reaction for RVFV, VSV, and BAV. In application testing, the assay successfully identified 2 BAV-positive pools out of 100 field-collected mosquito samples, confirming its utility for environmental surveillance.

Conclusion

We developed a robust and sensitive triplex MGB-qPCR assay for the simultaneous detection of RVFV, VSV, and BAV. This method allows for efficient screening of three important pathogens in a single reaction, significantly enhancing monitoring throughput. It provides a practical molecular tool for the surveillance of these arthropod-borne viruses in pig farming contexts.

Keywords: Banna virus, Mosquito surveillance, Rift Valley fever virus, Triplex real-time PCR, Vesicular stomatitis virus.

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GENOMIC CHANGES IN VACCINE-LIKE AFRICAN SWINE FEVER VIRUS FIELD ISOLATES FROM SOUTHEAST ASIA

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Introduction and Objectives

African swine fever (ASF) is a highly contagious viral disease causing severe mortality in domestic pigs. ASFV was initially considered genetically stable, increasing genomic variants within the same genotype have been reported following prolonged field circulation. While ASF live-attenuated vaccine candidates have shown high experimental efficacy, concerns remain following reports of vaccine-like strains detected in Vietnam (Ambagala et al., 2024; Nguyen et al., 2025). This study aimed to compare genomic changes among vaccine-like ASF field isolates in Thailand and Vietnam.

Materials and Methods

Four WGSs of vaccine-like were analyzed, including two isolates detected in non-vaccinated pig herds in Thailand (2024 - 2025) and two vaccine-like field isolates from Vietnam: ASF-GUS-Vietnam (2021) and VN/Sows_32005/23 (2023). Comparative genomic analyses were performed using Geneious Prime with ASFV Georgia 2007 and ASFV-G-delta as the references to identify nucleotide substitutions, gene deletions, gene integrity, and structural changes affecting viral proteins.

Results and Discussion

All analyzed genomes shared a genomic backbone consistent with ASFV-G-delta. The Thailand isolates detected in 2024 predominantly exhibited silent mutations, whereas the isolate collected in 2025 showed multiple novel single nucleotide polymorphisms and a 688-bp deletion, resulting in premature stop codons and complete loss of EP153R, EP402R (CD2v), ACD_00120, and MGF_110-4L. Temporal genomic changes were also observed in Vietnam, with four large fragment deletions detected in the 2023 (VN/Sows_32005/23) isolate compared with the 2021 isolate (ASF-GUS-Vietnam). Partial or complete loss of function in virulence-associated proteins suggests adaptive trends that may enhance viral persistence under field conditions.

Conclusion

Together with previous reports from Vietnam, these findings suggest progressive accumulation of mutations and deletions in vaccine-like strains during field circulation. Continuous whole-genome surveillance is therefore essential to monitor evolutionary trajectories, assess genetic stability, and detect potential reversion to virulence or recombination with other field strains.

Keywords: African swine fever, Field isolates, Genomic changes, Vaccine-like strains.

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PARALLEL, RANDOMISED FIELD EFFICACY, AND RETURN-ON-INVESTMENT STUDY OF A NEXT GENERATION PRRSV2-MLV VACCINE COMPARED TO A CONVENTIONAL PRRSV1-MLV VACCINE IN A PRRSV1+2 ENDEMIC HERD

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a major challenge in global swine production. A next-generation PRRSV modified live virus (MLV) vaccine, developed by Synthetic Attenuated Virus Engineering (Coleman et al., 2008). Via targeted attenuation by codon pair deoptimization, a significantly reduced speed of NSP1 translation is achieved. The subsequent reduced viral replication and immune deviation are indicated to provide very high efficacy, cross-protective capacity, and safety (Park et al., 2021). This study aimed to compare the effectiveness of the CPD-PRRSV2-MLV with a conventional PRRSV1-MLV in reducing production losses and improving economic outcomes from vaccination at 2 weeks of age (woa) till slaughter under field conditions.

Materials and Methods

The trial was conducted on a 2,000-sow, 3-site production system in Thailand with a history of both PRRSV1 and PRRSV2 infections. PRRSV status was confirmed by longitudinal serum PCR; attempts at sequencing the field strain were unsuccessful. Piglets were assigned randomly into two groups housed in separate barns with similar management. The CPD-MLV group (n = 935) received a CPD-lineage 5 PRRSV2-MLV (PersoporcTM, Ceva, France), while the Con-MLV group (n = 929) received the conventional PRRSV1-MLV, already used at the farm, at 2 woa. Growth performance, mortality, and economic data were collected during nursery and finishing phases. Economic return was calculated using Gompertz standardization and current local prices. Number of dead and culled pigs were analysed using Fisher's exact test.

Results and Discussion

During nurseries, mortality was 0.22 vs. 1.08% ($P < 0.05$), and average daily growth (ADG) was 507 vs. 458 g/day, feed-conversion-ratio (FCR) was 1.40 vs 1.42 for the CPD-MLV and Con-MLV groups, respectively. During the finishing phase, mortality was 1.80 vs. 2.79% ($P < 0.05$), and ADG was 782 vs. 768 g/day, FCR was 2.50 vs 2.48. Economic analysis revealed a higher net profit per pig (54.4 vs. 46.1€), of 8.3€ in favor of the CPD-MLV group. Under endemic PRRSV1+2 conditions, the CPD-MLV vaccine demonstrated to be a superior alternative to a traditional MLV vaccine, shown on health, production, and economic outcomes.

Conclusion

These findings support the value of the next-generation CPD-MLV vaccine in PRRSV1+2 control programs, offering additional benefits for herd health, animal welfare, and profitability.

Keywords: Next-generation, Profitability, PRRSV2, Return-on-investment, Vaccine.

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PARALLEL, RANDOMISED FIELD EFFICACY, AND RETURN-ON-INVESTMENT STUDY OF A NEXT-GENERATION PRRSV2-MLV VACCINE COMPARED TO A CONVENTIONAL LINEAGE 1 BASED PRRSV2-MLV VACCINE IN A TYPE 1+2 ENDEMIC SWINE HERD

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Introduction and Objectives

Porcine reproductive and respiratory syndrome viruses (PRRSV) are major challenges in global swine production. A next-generation PRRSV modified live virus (MLV) vaccine providing significantly reduced speed of NSP1 translation via targeted attenuation by Codon Pair Deoptimization (Coleman et al., 2008). Subsequent reduced viral replication and immune deviation are indicated to provide high efficacy, cross-protective capacity, and safety (Park et al., 2021). This field study aimed to compare the effectiveness of the CPD-PRRSV2-MLV with conventional PRRSV2-MLV in improving productivity and profits.

Materials and Methods

In a Thai PRRSV1+2 endemic, stable 2,000-sow herd, 4,112, 2-week-old piglets were assigned randomly into two groups housed in separate barns with similar management and followed till slaughter. The CPD-MLV group (n = 2,136) received a CPD-lineage 5 PRRSV2-MLV (PersoporcTM, Ceva, France), while the Con-MLV group (n = 1,976) received the conventional lineage 1 PRRSV2-MLV. PRRSV status was monitored by longitudinal serum PCR; sequencing of the circulating field strain was not achievable during the study period. Growth performance, mortality, and economic data were collected during nursery and finishing phases. Differences in mortality rates between groups were analysed using Fisher's exact test. Economic return was calculated using Gompertz standardization and current local prices.

Results and Discussion

PRRSV viremia was detected in both groups, with PCR positivity for a PRRSV2 at 6 weeks of age and PRRSV1 at 12 weeks of age. In the nursery phase, mortality was 1.12% vs. 1.32% ($P = 0.047$), and average daily growth (ADG) was 309 vs. 280 g/day for the CPD-MLV and Con-MLV groups, respectively. During the finishing phase, mortality was 3.00% vs. 3.08% ($P = 0.092$), and ADG was 896 vs. 862 g/day. Economic analysis revealed a higher net profit per pig (48.27€ vs. 42.88€), of 5.39€ in favor of the CPD-MLV group. Under endemic PRRSV2 field conditions, the CPD-MLV vaccine demonstrated to be a valid alternative to a traditional MLV vaccine, shown on health, production, and economic outcomes compared to the conventional vaccine.

Conclusion

These findings support the value of the next-generation CPD-MLV vaccine in PRRSV2 control programs, offering benefits for herd health, animal welfare, and profitability.

Keywords: Next-generation, Profitability, PRRSV2, Return-on-investment, Vaccine.

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COMPARISON OF THREE PORCINE CIRCOVIRUS TYPE 2 VACCINES IN GROWING-FININSHING PIGS

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is one of the primary pathogens which leads to immunosuppression, secondary infections, growth retardation, causing substantial economic losses in pig production. Vaccination remains a key strategy for PCV2 control. This study aimed to compare the immune efficacy of three PCV2 vaccines in grower-finisher pigs under field conditions.

Materials and Methods

A total of 237 healthy 22-day-old piglets from the same farm were randomly assigned to three groups: Group A (n = 77) received Suishot® Circo-One; Group B (n = 78) received an imported PCV2 - *M. hyopneumoniae* combined vaccine; Group C (n = 82) received a domestic whole-virus inactivated PCV2 vaccine. Groups A and C also received a single dose of the imported *M. hyopneumoniae* vaccine at 14 days. All groups were vaccinated once at 22 days with 2.0 mL per piglet. Serum was collected at 10, 14, 18, and 22 weeks for PCV2 qPCR (TaqMan®). Body weights were recorded at 3, 10, and 27 weeks (slaughter), and ADG was calculated from weaning to slaughter. Data were analyzed using one-way ANOVA in SPSS.

Results and Discussion

Groups A and B were PCR-positive only at 18 weeks (13 and 10%, respectively), while Group C tested positive at 14, 18, and 22 weeks (10, 40, and 50%). Group A had the highest Ct values at all time points (37.3, 36.98, 38.45), followed by Group B (36.9, 34.89, 37.68) and Group C (36.8, 33.11, 33.76), indicating lower PCV2 viral loads in Groups A and B. At slaughter (27 weeks), Group A had the highest average weight (138.76 kg) vs. Group B (133.25 kg) and Group C (132.30 kg). ADG was significantly higher in Group A (798.09 ± 39.87 g/d) than in Groups B (762.73 ± 45.62 g/d) and C (758.94 ± 56.31 g/d) ($P < 0.05$).

Conclusion

Suishot® Circo-One showed the lowest PCV2 viral load, highest slaughter weight, and greatest ADG, making it a strong choice for PCV2 control in commercial herds. However, as these are field case studies with inherent uncontrolled variables, further controlled trials are needed to confirm the findings.

Keywords: Field trial, Growth performance, PCV2, Swine health, Vaccine comparison.

COMPARISON OF THREE COMBINED VACCINES AGAINST PCV2 + *M. HYOPNEUMONIAE* ON PERFORMANCE PARAMETERS IN PIGS UNDER FIELD CONDITIONS

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Introduction and Objectives

PCV2 is the ubiquitous and causative pathogen of Porcine Circovirus Diseases (PCVD). Besides clinical symptoms, PCV2 significantly affects fattening performance parameters e.g. daily gains. PCV2d is currently predominant PCV2 genotype worldwide. In the period preceding the study, clinical cases suggestive of PCV2-SD were observed. Combined vaccination against PCV2 + *M. hyo* was routinely administered due to the epizootic situation. The aim of the study was to compare the impact of new commercial vaccine containing PCV2d genotype + *M. hyo* for I.M. use CIRBLOC® M Hyo (Vaccine CMH) with 2 other vaccines containing PCV2a genotype + *M. hyo* for: 1) RTM I.M. administration (Vaccine A) and 2) intradermal administration (Vaccine B) on body weight performance in fatteners at the day of slaughter.

Materials and Methods

All compared groups of piglets were vaccinated in the 4th WOA. Observations were conducted on the sow farms: "Farm C" (4900 sows) and "Farm J" (3700 sows), which have nursery units. Nearly 2900 animals were included in the trials until slaughter. Individual groups of animals were marked with additional ear tags. Pigs were weighed in groups (Vaccine CMH, A or B). During fattening period, comparable groups were kept under the same conditions. Fatteners were weighed on the day of slaughter.

Results and Discussion

Fatteners from farm "C" vaccinated with CIRBLOC M Hyo® were heavier with a total gain of 3.1 and 3.2 kg (depending on the fattening unit) more than animals vaccinated with the intradermal product (Vaccine B). Fatteners from farm "J" vaccinated with CMH achieved 6.9 kg of total gain more than fatteners vaccinated with RTM product. On the final farm, the collected data allowed for the performance of economic analyses. Using the Respinomics® economic calculator, the overall economic benefit per pig was quantified as the difference in profit (selling price minus production costs) attributable to the increase in average daily weight gain and lower mortality. For Farm “J”, this analysis indicated an overall economic benefit of €7.80 per pig.

Conclusion

The resulting differences in body weight, confirmed by slaughterhouses, represent additional revenue for the breeder. Under the same conditions, the only variable was the vaccination with CMH.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Vaccination, Performance parameters.

EFFECTS OF SACCHAROMYCES CEREVISIAE VAR. BOULARDII CNCM I-1079 SUPPLEMENTATION ON PRRSV INCIDENCE, GROWTH PERFORMANCE AND ANTIOXIDANT STATUS IN WEANED PIGLETS

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is a major threat to swine production, causing severe economic losses due to high variability and limited vaccine efficacy (Zimmerman et al., 2019). This study evaluated the effect of Saccharomyces Cerevisiae var. Boulardii CNCM I-1079 (LSB) (Collier et al., 2011) supplementation on clinical outcomes, growth performance and viral shedding in weaned piglets experimentally challenged with PRRSV.

Materials and Methods

Thirty PRRSV-negative piglets (23 days old) were allocated to three groups:
- LSB group: Basal diet + LSB (200 gr/t); 2 x 10^6 CFU/g of feed) + PRRSV challenge.
- Challenge control (CC): Basal diet + PRRSV challenge.
- Negative control (NC): Basal diet, unchallenged.

Piglets received LSB for 21 days before PRRSV inoculation (1x105 TCID50 intranasal + intramuscular) and continued supplementation until 28 days post-infection. Parameters analyzed included survival rate, clinical scores, rectal temperature, growth performance (ADG, FCR) and oral viral shedding.

Results and Discussion

LSB supplementation improved early clinical outcomes, delaying symptom onset and reducing fever severity compared to CC ($P < 0{,}001$). Survival rates at 28 days post-infection were higher in LSB (30%) than CC (0%). Growth performance improved significantly in LSB vs. CC during the first week post-infection (ADG: 0,329 vs. 0,144 kg/day; $P < 0{,}01$) and Feed Conversion Ratio was lower (1,62 vs. 3,33). Oral viral shedding was significantly reduced in LSB compared to CC at 3 and 7 days post-infection ($P <$ 0,001). No differences were observed in tissue viral load or viremia.

Conclusion

Saccharomyces Cerevisiae var. Boulardii CNCM I-1079 supplementation mitigates early clinical signs, improves growth performance and reduces viral shedding in PRRSV-challenged piglets, suggesting its role as a supportive nutritional strategy.

Keywords: Feed efficiency, Growth performance, Live yeast, PRRSv, Viral shedding.

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LAURIC ACID GLYCERIDES MODULATE IMMUNE RESPONSE DURING PRRSV INFECTION IN VIVO AND EX VIVO

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSv) remains a major challenge in swine production, causing immunosuppression and economic losses. Lauric acid glycerides (GLA) exhibit antiviral properties and may enhance immune function. This study assessed the immunomodulatory effects of GLA supplementation on innate and adaptive immune responses to PRRSv infection using ex vivo and in vivo models.

Materials and Methods

In the ex vivo assay, porcine alveolar macrophages (PAMs) from healthy 4-week-old piglets were infected with PRRSv (strain 13V091) and treated with GLA at 0, 0.022, 0.044, and 0.088%. Viral titers and cytokine secretion were measured at multiple timepoints. In vivo, weaned piglets (~24 days) were allocated to three groups: Control (Ctrl), Challenged (Chal), and Challenged + GLA (Chal GLA, 3 - 4 kg/T). Challenged groups were inoculated with PRRSv on day 60 of age. Viremia, nasal shedding, and cytokine profiles were monitored for 14 days post-infection. Data were analyzed using one-way ANOVA.

Results and Discussion

Ex vivo, GLA pre-treated PAMs presented up to ~3.5 log -decrease in PRRSv titers compared to the control group ($P < 0.001$). A significantly enhanced activation was observed, characterized by increased IL-8 secretion and a significant correlation TNF-α secretion with GLA concentration *(*$P < 0.05$). In vivo, GLA supplementation lowered nasal shedding and viremia and increased TNF-α and IFN-γ levels in serum (TNF-α: 148 vs. 16 & 103 pg/mL; IFN-γ: 62.6 vs. 1.3 & 2.5 pg/mL in Chal GLA, Ctrl and Chal groups respectively; $P < 0.05$). TNF-α secretion in bronchoalveolar lavage fluids also tended to increase ($P = 0.056$). No significant differences were observed in zootechnical performance.

Conclusion

GLA supplementation mitigated PRRSv immunosuppressive effects by reducing viral replication and shedding while enhancing the activation of innate immune cells and Th1 lymphocytes. These effects likely induce indirect antiviral action through improved immune response.

Keywords: Glycerides of lauric acid, Immune modulation, PRRSV, Shedding, Viremia.

THE SURVEY ON THE CIRCULATION OF JAPANESE ENCEPHALITIS VIRUS IN VIETNAM IN 2025

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Introduction and Objectives

Japanese encephalitis virus (JEV) is a mosquito-borne flavivirus of major veterinary and public health importance in Asia, primarily transmitted by Culex mosquitoes. Although infection in pigs is often subclinical, JEV infection in sows may cause reproductive disorders such as abortions, stillbirths, mummified fetuses, premature farrowing, and weak-born piglets, leading to reduced reproductive performance. This study aimed to document the current circulation of JEV in pig herds in Vietnam by determining seroprevalence and detecting JEV in different clinical specimens.

Materials and Methods

A total of 136 specimens were collected from pig farms with reproductive disorders in five provinces of Vietnam. Samples were obtained from affected sows and their corresponding fetuses or piglets showing abnormalities such as abortions, stillbirths, or weak births. Serum samples (n = 86) were tested for anti-JEV antibodies using a commercial ELISA kit (VDPro® Japanese Encephalitis AB ELISA). In addition, 50 clinical samples, including fetal tissues, brain tissues, pooled sera (prepared from 50 out of the 86 antibody-tested serum samples), and anticoagulated blood, were analyzed for JEV RNA by real-time RT-PCR (TopSPEC® JEV RT-qPCR Kit). None of the sampled pigs had been vaccinated against JEV.

Results and Discussion

Anti-JEV antibodies were detected in 60.05% (52/86) of pig serum samples, indicating widespread exposure to JEV. This finding is consistent with the study by Lee et al. (2019), who reported a seroprevalence of 73.45% among unvaccinated pigs across ten provinces in Vietnam, confirming endemic circulation of JEV in swine populations. Molecular analysis detected JEV in 24% (12/50) of clinical samples. The highest detection rate was observed in stillborn and aborted fetuses (8/15), followed by brain tissues (3/7). No viral RNA was detected in pooled serum or anticoagulated blood samples. These results are in agreement with Thu et al. (2022), who identified JEV and specific antibodies in abnormal swine litters associated with reproductive failure.

Conclusion

These findings indicate that JEV is still widely circulating in pig populations, particularly in sows, where infection is associated with reproductive disorders and reduced productivity. For molecular diagnosis of JEV, stillborn fetuses, aborted fetuses, and brain tissues are the most appropriate sample types.

Keywords: Japanese encephalitis virus, Pig, Reproductive disorder, Seroprevalence.

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STUDY ON THE BENEFITS OF AN EARLY VACCINATION PROGRAM USING A PRRS MLV VACCINE (STRAIN 96V198) IN PIGLETS UNDER FIELD CONDITIONS ON A FARM INFECTED WITH THE PRRS STRAIN "ROSALÍA"

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Introduction and Objectives

This study aimed to assess the potential positive effects of early piglet immunization, with a vaccine that is able to overcome maternal immunity (Balasch et al., 2018), comparing the results of vaccinated groups against the historical data of unvaccinated groups during the post-weaning phase.

Materials and Methods

The study was conducted in a commercial farm in Spain, comprising Site 1 and Site 2, several kilometers away. While the breeding herd has shown some level of stability (no viremic born alive from week 21), viremic piglets are still detected at Site 2 (week-24, weaned piglets detected positive PRRSV-1, Ct 20). The farm's PRRSV-1 strain (ORF-5) was sequenced at GSP Laboratory, Lleida, showing > 97% homology to the highly virulent Rosalia variant. Given the active circulation in nursery, in addition to mass vaccination of sows we included piglet vaccination around 5 days of age, in week 26. 82124 piglets were included in the evaluation. DIVA PCR PRRS specific for Suvaxyn ® PRRS was used to monitor post-weaning stability, which discriminates vaccine and field viruses. For monitoring purposes, piglets of different ages are bled every 3 - 8 weeks during the post-weaning period, with samples grouped into pools of three. In the farrowing unit, weekly analysis is performed using processing fluids. Nursery mortality was evaluated before implementation (weeks 1 - 28, unvaccinated control group, C) and after (weeks 29 - 49, vaccinated group, V). Statistical analyses were performed using Mann-Whitney U and Student's T-test.

Results and Discussion

Post-weaning Wild-Type PRRSV-1 viremia was delayed, with three consecutive (W40, W48, W49) negative samplings (at least 30 samples/week) observed via DIVA PCR, viremia in piglets disappears in 11 weeks and they remain negative until the end of the study (W49). Mortality rate analysis revealed a significant reduction in V, decreasing by 4.95% (from 15.86% to 10.91%, $P < 0.05$), equating to approximately 83 additional piglets per week, 1700 more piglets produced in period analyzed.

Conclusion

Under the conditions of this study, early vaccination with Suvaxyn ® PRRS MLV resulted in statistically significant improvements in both, health and productivity, as demonstrated by reduced WT-PRRSV viremia level showing negative results and decrease in mortality.

Keywords: DIVA PRRS PCR, Mortality, Non-viremic piglets, PRRSV-1 strain "Rosalia".

Acknowledgements: The authors thank ICPOR for providing the data that made this study possible.

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INDENTIFICATION OF SWINE INFLUENZA VIRUS (SIV) BY REAL-TIME PCR IN VIET NAM FROM 2024 TO 2025

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Introduction and Objectives

Swine influenza virus (SIV) is a primary respiratory pathogen that inflicts substantial economic losses on the global porcine industry while presenting a persistent zoonotic risk for human pandemics. Although various diagnostic modalities exist, including virus isolation, Hemagglutination Inhibition (HI), and ELISA, Real-time PCR is currently regarded as the gold standard for diagnosis due to its superior sensitivity and specificity (Truong et al., 2025; Wang et al., 2025). This study was undertaken to evaluate the prevalence of SIV within Vietnam utilizing Real-time RT-PCR technology.

Materials and Methods

Surveillance was conducted across 12 provinces located in Northern and Central Vietnam. A total of 92 pools clinical samples were collected for analysis including 36 samples of swabs and oral fluids, 34 samples of serum and whole blood, and 22 organ samples (lung, lymph node, brain, kidney, and aborted fetuses). Diagnostic testing utilized the Real-time PCR Influenza RNA Mix (IDEXX) performed on the AriaMx 96-well system, employing specific fluorescence channels for target detection (FAM) and internal control (IC) (HEX).

Results and Discussion

Among the 92 clinical samples analyzed, SIV was detected in 13 pools, yielding an overall prevalence rate of 14.13%. Analysis of sample matrices revealed that viral detection was most effective in swab and oral fluid samples, which accounted for 69.23% of the positive results, followed by organ samples at 30.77%. No positive cases were identified in serum or whole blood samples. Temporally, the detection rate observed in 2024 was found to be higher than that in 2025. These findings place the current SIV prevalence in Vietnam within a comparable range to recent epidemiological studies. Specifically, the 14.13% positivity rate aligns closely with the 11.27% prevalence reported in Vietnam (Truong et al., 2025), while indicating a higher incidence compared to the 2.7% positivity rate observed in China (Wang et al., 2025).

Conclusion

The study demonstrates that the IDEXX Real-time PCR Influenza RNA Mix serves as an accurate, rapid, and convenient tool for the identification of SIV. The adoption of this diagnostic protocol offers significant potential to reduce the time and effort required for pathogen surveillance in Vietnam's industrial pig farming.

Keywords: Swine influenza virus (SIV), Realtime PCR, Indentification

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ESTABLISHMENT OF IMMORTALIZED PORCINE LUNG-DERIVED VASCULAR ENDOTHELIAL CELLS

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Introduction and Objectives

Viruses such as porcine reproductive and respiratory syndrome virus and influenza A virus in swine (IAV-S) are believed to cause porcine respiratory complex diseases. While these viruses primarily target alveolar macrophages and airway epithelial cells, recent studies suggest pulmonary microvascular endothelial cells are also involved in viral infection and disease progression. However, there are very few immortalized porcine lung-derived vascular endothelial cell lines available for research. Here, we report the establishment and characterization of an immortalized vascular endothelia cell line from porcine lung tissue.

Materials and Methods

A two-week-old pig that had undergone a hysterectomy and was deprived of colostrum was used to prepare the primary lung cell cultures. Lenti-SV40 (tsA58) was used to immortalize the cells. To obtain a population of cells derived from the progeny of a single cell, 200 cells were seeded in a 100-mm dish. Individual colonies showing cobblestone morphology were encircled with cloning cylinders in the dish, and the cells within the cylinders were harvested and passaged several times. Then, we characterized the cloned cell line by immunofluorescence cytochemistry and Western blot analysis for several cell markers. We also tested the susceptibility of the cell line to IAV-S.

Results and Discussion

The established cell line expressed vimentin, a typical marker of the mesenchymal stromal cell lineage, and did not express cytokeratin, a typical marker of the epithelial cell lineage. These cells expressed PECAM-1, a marker representative of vascular endothelial cells. They also expressed occludin and ZO-1, indicating the presence of tight junction structures. This cell line was much less susceptible to IAV-S than the porcine alveolar epithelial cell line that we had previously established.

Conclusion

To our knowledge, this is the first report demonstrating the establishment of an immortalized porcine vascular endothelial cell line. Although this cell line (designated iPLVEC) exhibits typical vascular endothelial cell characteristics, its susceptibility to various respiratory viruses has not yet been fully evaluated. Nevertheless, iPLVEC could be a useful tool for elucidating interactions with respiratory viruses and analyzing the relationship between primary target cells (e.g., airway epithelial cells for IAV-S) and vascular endothelial cells.

Keywords: Porcine endothelial cell line, Porcine respiratory viruses, Tight junction, Vascular barrier function.

ISOLATION AND IDENTIFICATION OF PORCINE HEMAGGLUTINATING ENCEPHALOMYELITIS VIRUS STRAIN JS-2025 AND ANALYSIS OF ITS GENETIC CHARACTERISTICS

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Introduction and Objectives

Porcine hemagglutinating encephalomyelitis virus (PHEV), a member of the Betacoronavirus genus, is widespread in swine herds and the only known coronavirus causing neurological diseases in pigs (Mora-Díaz et al., 2019). A deep understanding of the virus's genetic and biological characteristics is of great significance for prevention and control efforts. This study conducted the isolation, identification, and genetic characterization of a PHEV strain isolated in the Jiangsu region, aiming to provide a scientific basis for the prevention and control of PHEV in China.

Materials and Methods

RT-PCR detection was performed on suspected PHEV-positive samples collected from a large pig farm in Jiangsu Province, China, followed by virus isolation. The isolated virus was validated by indirect immunofluorescence assay (IFA), transmission electron microscopy (TEM), and whole genome sequencing. Phylogenetic analysis was performed based on the complete genome, S gene, HE gene, and NS2 gene.

Results and Discussion

A PHEV strain, designated as PHEV JS-2025, was successfully isolated from the brain tissue sample. IFA showed strong red fluorescence signals in the cytoplasm, and TEM revealed typical coronavirus particles with a diameter of approximate 150 nm. The strain showed vigorous propagation in HRT-18 cells, reaching the peak viral titer at 72 h. Whole genome sequencing revealed that the strain shared over 94.9% nucleotide sequence identity with 14 reference PHEV strains, clustering within the rvPHEV-L-1 lineage. Of note, a mutation in the NS2 gene caused a premature termination at amino acid 19, resulting in the functional loss of the NS2 protein.

Conclusion

This study successfully isolated and identified a novel PHEV strain, JS-2025, from the Jiangsu region. The strain possesses unique cellular tropism and genetic characteristics. The ability of the virus to infect human-origin cells suggests that attention should be paid to its potential for cross-species transmission. The results provide an important scientific basis for further understanding the genetic evolutionary characteristics of PHEV and formulating control strategies.

Keywords: Isolation and identification; Genetic evolutionary analysis, PHEV.

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DETECTION OF PORCINE PARVOVIRUS GENOTYPE 4 IN A SOW FARM FOLLOWING VACCINATION AND FEEDBACK PRACTICES

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Introduction and Objectives

Porcine parvovirus (PPV) is a major cause of reproductive failure in swine herds, commonly associated with mummified fetuses, stillbirths, and reduced litter size. Immunization programs are commonly based on commercial vaccines or feedback practices, which involve the oral administration of macerated PPV-infected mummified fetuses to stimulate immunity. The present study evaluated seroconversion induced by feedback and commercial vaccination in a commercial sow farm located in Sonora, Mexico, experiencing reproductive problems.

Materials and Methods

Replacement gilts (n = 30 per group) were allocated into two treatment groups: T1, receiving feedback at 24 weeks of age, and T2, vaccinated with a commercial PPV vaccine at 24 and 27 weeks of age. Multiparous sows (n = 80 per group) were divided into T3, receiving feedback at weaning, and T4, vaccinated with a commercial PPV vaccine two weeks before farrowing. Serum samples were collected one week before treatment administration (T0) and three weeks post-treatment to evaluate the immune response using the hemagglutination inhibition (HI) test (Beta method) with 0.5% guinea pig erythrocytes and parvovirus antigen adjusted to 4 hemagglutination units. The presence of PPV was evaluated by endpoint PCR using genotype-specific primers targeting PPV genotypes 1 through 6, and selected samples were analyzed by next-generation sequencing (NGS).

Results and Discussion

Seroconversion rates were 90% in T1, 83% in T2, 78% in T3, and 50% in T4. Antibody titers were higher in animals receiving feedback (T1 and T3) compared with vaccinated groups (T2 and T4). Approximately 80% of samples in T1 and T3 presented antibody titers ≥ 1:3840, suggesting previous exposure to PPV. PPV4 was detected by PCR in samples from T1, T2, and T4. NGS confirmed the presence of PPV4 and revealed additional viral, bacterial, fungal, and parasitic agents, highlighting the complexity of pathogen circulation under field conditions.

Conclusion

PPV4 detection highlights the need to critically evaluate preventive medicine strategies under farm-specific conditions. Commercial vaccines may not protect against all circulating PPV genotypes, while feedback practices may facilitate dissemination of additional pathogens, emphasizing the need for tailored immunization and biosecurity programs.

Keywords: Parvovirus, PPV4, Sequencing

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WHOLE GENOME SEQUENCES OF AFRICAN SWINE FEVER VIRUS FROM 2024 OUTBREAKS IN THE PHILIPPINES REVEAL ONGOING DIVERSIFICATION

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Introduction and Objectives

Molecular epidemiology is recognized as the most important tool for African swine fever (ASF) prevention and control by enabling the tracking of potential transmission routes and identification of novel variants of the causative ASF virus (ASFV). In as early as September 2019, B646L gene sequencing has been employed to characterize ASFV in the Philippines. Following the report of the first ASFV whole-genome sequence in 2022, 19 more strains have been locally sequenced which came from samples collected in 2019 to 2023. Whole genome sequencing (WGS) has also been used for non-clinical samples such as meat juice, raw meat and other pork products. To continue the efforts on ASFV monitoring in the Philippines, the present study reports on the WGS of ASFV from outbreaks in several farms in Luzon in 2024.

Materials and Methods

Whole blood, serum and organ samples were submitted by concerned farm veterinarians from ASF outbreaks in the provinces of Albay, Batangas and Bulacan in 2024. Following molecular detection of ASFV in the samples, whole-genome sequencing via virus genome amplification was performed.

Results and Discussion

Five whole genome sequences of ASFV (strains BA25-0103 to BA25-0107) were generated through nanopore sequencing. All sequenced strains belong to p72 genotype II, CD2v serogroup 8 and genotype II CVR variant 1. Database comparison showed that the strains were most related to Asian and European p72 genotype II strains. Philippine-specific phylogenomic analysis revealed that strain BA25-0104 clusters with strains from 2023 samples of Negros Occidental and Oriental Mindoro provinces, forming a monophyletic clade. Strains BA25-0103 and BA25-0107, meanwhile, seem to form a nascent monophyletic clade though more sequences are warranted to support it.

Conclusion

The study provides an update on the genetic characteristics of ASFV strains causing local epidemics in swine farms in the Philippines in 2024. Based on phylogenomics and known variable loci in the ASFV genome, it appears that the circulating ASFV strains in the Philippines are continuously changing. Further, we report a potential transmission of ASFV from the 2023 Negros Occidental and Oriental Mindoro outbreaks to Bulacan, emphasizing the need for strict biosecurity and continued molecular surveillance.

Keywords: African swine fever virus, CD2v, CVR, Phylogenomic analysis, Whole-genome sequencing.

Acknowledgements: We would like to thank the concerned farm veterinarians who submitted the clinical samples and granted us permission to share the research findings.

SOW PERFORMANCE ASSOCIATED WITH THE CHANGE OF VACCINE AGAINST PRRS VIRUS IN A COMMERCIAL FARM

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome virus (PRRSv) causes reproductive failure and respiratory issues, leading to significant economic impact in swine production (Osemeke et al., 2024). In Mexico, Lineage 1 (L1) is the most prevalent, accounting for 76% of isolates in a sample representing over 30% of Mexican pig farming (Arceo et al., 2024). This analysis aimed to evaluate sow performance on a Site I farm after transitioning the PRRS vaccine from Lineage 8 (VL8) to Lineage 1 (VL1).

Material and Methods

A before/after comparison study was implemented in a commercial farm setting, 2,500-sow Site I farm in Mexico, which had been using Fostera® PRRS (Zoetis) VL8 (sows vaccinated every 3 months) from July 2022 to August 2024, exhibited variable sow performance. Following a positive laboratory diagnosis for wild PRRSv L1 in sow serum samples, the farm transitioned to Prevacent® PRRS (Elanco) VL1 vaccine in Sept. 2024. Sow performance parameters (SPP) were compared across two one-year periods: one using VL8 (Sept. 2023-to-August 2024) and another using VL1 (Sept. 2024-to-August 2025). Performance data were obtained from PigCHAMP monitoring reports. The SPP included farrowing rate (FR), abortion percentage (A%), total birth (TB), mummies percentage (M%), born alive (BA), weaned pigs per sow (WP), weaned pigs per sow per year (WPSY), and interval days between farrows (IBF). Statistical analyses considered parity effects, with weekly data serving as the experimental unit. Differences were evaluated using Student's t-test and Dunnett's test for least squares means, with significance set at $P < 0.05$.

Results and Discussion

Transition to VL1 vaccine significantly improved sow performance compared to VL8 vaccine across all evaluated parameters. FR: 87.11 vs 80.22% ($P < 0.0001$), A%: 3.18 vs 5.92% ($P < 0.005$), TB: 14.64 vs 13.39 ($P < 0.0001$), M%: 4.03 vs 6.72% ($P = 0.0004$), BA: 13.09 vs 11.79 ($P = 0.0001$), WP: 11.02 vs 10.31 ($P < 0.0001$), WPSY: 25.93 vs 23.42 ($P < 0.0001$) and IBF: 155.3 vs 161.3 ($P < 0.0001$).

Conclusion

Under these conditions, transitioning from VL8 to VL1 vaccine in the presence of wild PRRSv L1 improved sow performance, and the study shows the benefits of using the appropriate vaccine as an additional PRRS control tool. No other factors such as mycotoxins in grain/feed, seasonal variables were recorded. No major changes were made on diets or management.

Keywords: Born alive, Farrowing Rate, Interval between farrow, Lineage 1, Weaned Pigs.

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PREDOMINANCE OF PCV2D AMONG PORCINE CIRCOVIRUS TYPE 2 FIELD STRAINS IN VIETNAM FROM 2024 TO 2025

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is a genetically diverse virus and a major pathogen of swine in Vietnam. Recent molecular surveillance studies have reported a predominance of PCV2d, suggesting an ongoing genotype shift in circulating field strains. Routine real-time PCR assays enable PCV2 detection but do not provide genotype-level information. Therefore, PCV2 genotyping is essential for monitoring viral evolution and genotype dynamics in swine populations. This study aimed to investigate the distribution of PCV2 genotypes in swine herds in Vietnam from 2024 to 2025.

Materials and Methods

From 2024 to 2025, a total of 85 PCV2-positive field samples, including organ tissues (lymph node, spleen, lung, kidney, liver, and heart), blood, and serum, were collected from 12 provinces of Vietnam and analyzed at VETLATECH Joint Stock Company. PCV2 DNA was detected by real-time PCR by RealPCR PCV2/PCV3 DNA (IDEXX) and genotyping was performed using a commercial genotype-specific real-time PCR kit (Kylt® PCV-2 Typing, Kylt®, Germany). Amplification and fluorescence detection were carried out on an AriaMx 96 real-time PCR system, targeting PCV2a, PCV2b, and PCV2d genotypes via the FAM, Cy5, and TXR channels, respectively.

Results and Discussion

Among the 85 PCV2-positive samples, PCV2d was the predominant genotype, detected in 75 samples (88.2%). PCV2b was identified in only 2 samples (2.4%), while 8 samples (9.4%) were PCV2-positive but could not be assigned to a specific genotype. These findings are consistent with recent molecular surveillance conducted in Vietnam during 2022 - 2023, which reported a high prevalence of PCV2d (80.9%) (Lai et al., 2024), indicating the sustained dominance of this genotype over time. The presence of untyped PCV2-positive samples may reflect low viral loads or genetic variability beyond the target regions of the assay, given that PCV2 is currently classified into multiple genotypes ranging from PCV2a to PCV2h (Franzo and Segalés, 2018).

Conclusion

This study demonstrates a clear predominance of PCV2d among PCV2 field strains circulating in Vietnam from 2024 to 2025. The results highlight the importance of PCV2 genotyping as a tool for molecular surveillance and provide updated epidemiological evidence on the current genotype distribution of PCV2 in Vietnam.

Keywords: molecular surveillance, Northern Vietnam, PCV2 genotyping, PCV2d.

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SOW PERFORMANCE IMPROVEMENT ASSOCIATED WITH THE CHANGE OF PRRS VIRUS LINAGE 5 VACCINE TO A PRRS VIRUS LINAGE 1 VIRUS VACCINE AGAINST PRRS VIRUS IN A COMMERCIAL FARM

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome virus (PRRSv) causes reproductive failure and respiratory issues, leading to significant economic impact in swine production (Osemeke et al., 2024). In Mexico, Lineage 1 (L1) is the most prevalent, accounting for 76% of isolates in a sample representing over 30% of Mexican pig farming (Arceo et al., 2024). This analysis aimed to evaluate sow performance on a Site I farm after transitioning the PRRS vaccine from Lineage 5 (VL5) to Lineage 1 (VL1).

Material and Methods

This was a pre-post quasi-experimental study. A comparison performance was developed in a Site I farm with 3,150 sows in Mexico, in a 3-weeks batch production system. Over a 3-year period (September 2022 to August 2025), two different PRRSV vaccines were used. VL5 was administered during the first 1.5-years, and Prevacent® PRRS (Elanco) during the following 1.5-years (VL1). Throughout both periods, sows were vaccinated every 3 months. During the use of VL5, some reproductive performance issues associated with a positive laboratory diagnosis of wild PRRSV L1 detected in sow serum samples were observed. A sow performance parameter (SPP) comparison was developed across 2 time periods. Performance data were obtained from PIGKNOWS performance monitor reports. The SPP used were farrowing rate (FR), abortion% (A%), mummies% (M%), weaned pig/litter (WP), average weight of weaned pig (AWP), % of weaned sows inseminated in 7 days (%SI7D), and interval wean-to-service (IWS). Statistical analyses considering parity and year effects, using 3-weeks batch production system data as experimental unit. Differences were evaluated using Student's t-test and Dunnett's test for least squares means, $P < 0.05$ (JMP 18.1.0).

Results and Discussion

Transition to VL1 vaccine significantly improved sow performance compared to VL5 vaccine across all evaluated parameters. FR: 92.9 vs 87.3% (P = 0.016), A:1.9 vs 8.0% ($P = 0.0343$), M: 3.7 vs 2.3% ($P = 0.0144$), WP: 13.64 vs 12.83 ($P = 0.0161$), AWP: 6.815 vs 6.250 kg; ($P < 0.0015$), SI7D: 90.0 vs 86.0% ($P < 0.0004$) and IWS: 5.7d vs 7.3d ($P < 0.0001$).

Conclusion

Under commercial farm conditions, transitioning from VL5 to VL1 vaccine in the presence of wild PRRSv L1 improved sow performance; however, no other factors such as mycotoxins in grain/feed, seasonal variables were recorded. No major changes were made on diets or management.

Keywords: Homologous vaccination, PRRSv, Sow performance.

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PSEUDORABIES VIRUS TEGUMENT PROTEIN UL16 HIJACKS GTPBP2 TO FACILITATE HOST PROTEIN CROTONYLATION AND ENHANCE VIRAL PROLIFERATION

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Introduction and Objectives

Pseudorabies virus (PRV) is a neurotropic Alphaherpesvirus. While traditionally a swine pathogen, recent reports of human encephalitis caused by PRV indicate a significant zoonotic risk. The mechanisms allowing PRV to cross species barriers and manipulate host machinery remain unclear. This study aimed to identify host dependency factors required for PRV infection in human cells and to elucidate the molecular mechanisms used by the virus to evade host immune responses.

Materials and Methods

We conducted a genome-wide CRISPR-Cas9 knockout screen in human microglial cells (HMC3) using a gD-deleted PRV strain. We validated candidate genes via siRNA knockdown and assessed viral replication using qPCR and TCID50 assays. Protein interactions were mapped using Co-Immunoprecipitation and affinity purification-mass spectrometry. We monitored autophagy flux through immunoblotting and confocal microscopy. Finally, we evaluated the therapeutic potential of the crotonylation inhibitor C646 in a murine infection model.

Results and Discussion

The screen identified GTP-binding protein 2 (GTPBP2) as a key host factor. Deletion of GTPBP2 significantly impaired viral replication. Mechanistically, the viral tegument protein UL16 interacts with the C-terminus of GTPBP2. Under normal conditions, GTPBP2 binds the chaperone YWHAE and HSPA8 to regulate chaperone-mediated autophagy (CMA). However, PRV infection induces specific crotonylation of GTPBP2 at lysine residues K546 and K561. This modification acts as a molecular switch that detaches YWHAE from GTPBP2. Consequently, the virus blocks the CMA pathway to prevent degradation and facilitate replication. In mice, treatment with the p300/CBP inhibitor C646 reduced global crotonylation and significantly improved survival rates against PRV infection.

Conclusion

PRV exploits the host factor GTPBP2 to promote viral entry and replication. The virus uses the tegument protein UL16 to induce GTPBP2 crotonylation, which subsequently disrupts cellular autophagy. These findings define a novel immune evasion strategy and suggest that targeting the UL16-GTPBP2 axis or inhibiting protein crotonylation offers a promising therapeutic approach for neurotropic herpesvirus infections.

Keywords: Crotonylation, Chaperone-mediated autophagy, GTPBP2, Pseudorabies virusUL16.

Acknowledgements: We acknowledge the support of the National Key Laboratory of Agricultural Microbiology Core Facility for their aid in confocal microscopy.

ADAPTING RFLP AND LINEAGE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS-2 (PRRSV-2) CLASSIFICATIONS TO CANADIAN HERDS

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Introduction and Objectives

As PRRS virus continues to evolve, historical restriction fragment length polymorphism (RFLP) classification systems cannot accurately describe the relatedness of sequences, leading to confusion amongst practitioners. New classification systems have been developed in the United States, to better name viruses based on phylogenetic relatedness, rather than ORF5 comparisons alone. The objective was to understand lineage prevalence in sequences generated by a private swine-focused clinic in Ontario, Canada.

Materials and Methods

Sequences derived from field-strain PRRSV-2 outbreaks in commercial sow herds between 2022 and 2025 were input into the PRRSLoom tool (Makau, 2025). Sequences were classified into lineages, sub-lineages and variants and compared to pre-existing RFLP classifications. PRRSV-2 seasons were categorized, beginning in October and ending in September of the following year.

Results and Discussion

When assessing lineages, most sequences were classified as Lineage 1H (59%, n = 167), followed by Lineage 1K (29%, n = 83) and Lineage 1E (12%, n = 34). Within this, various sub-lineages and variants were detected. Lineage 1H.48 was the most common sub-lineage variant (33%, n = 93), followed by 1K.1, 1H.46, and 1E.12. Other lineages included 1H.47, 1H-unclassified, 1E.10, 1E-unclassified, 1H.38, and 1K-unclassified. The most common RFLP categories were 1-4-2 (27%, n = 78), 1-1-1 (22%, n = 63) and 1-8-4 (14%, n = 42). Other RFLP categories included 1-30-1, 1- 3-1, 1-3-2, 1-4-1, 1-4-4 and 1-8-3. Although trends exist, there is not a distinct comparison between lineage and RFLP. An example of this is Lineage 1H.48 as not all sequences are 1-4-2 RFLP, but most are. When looking at outlier RFLP groups, such as 1-8-3 compared to 1-8-4, these closely related sequences will be classified in the same lineage, which allows for easier comparison.

Conclusion

When comparing RFLP and lineage classifications across PRRSV-2 strains, even though the system was developed in the United States, it can be applied to PRRSV-2 sequences across North America. This allows veterinarians to discuss health status of herds across international borders, as well as gain information about phylogenetic relationships across various sequences. The lineage classification system allows for greater information to be collected for strain comparison as part of ongoing surveillance programs.

Keywords: Lineage, PRRSV, RFLP, Sequencing.

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PROTEOMIC ANALYSIS OF THE NONSTRUCTURAL PROTEIN 2-HOST PROTEIN INTERACTOME REVEALS A NOVEL REGULATORY ROLE OF SH3 DOMAIN-CONTAINING KINASE-BINDING PROTEIN 1 IN PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS REPLICATION AND APOPTOSIS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) nonstructural protein 2 (NSP2) is a multifunctional protein critical for viral replication and pathogenesis. This study aimed to comprehensively map the NSP2-host protein interactome to elucidate its functional roles and identify potential antiviral targets.

Materials and Methods

A recombinant PRRSV (rJXA1R-NSP2C-HA) expressing HA-tagged NSP2 was constructed using reverse genetics. Host proteins interacting with NSP2 were identified in infected Marc-145 cells (1moi) via co-immunoprecipitation coupled with liquid chromatography-tandem mass spectrometry (LC-MS/MS). Bioinformatics analyses (GO, KEGG, STRING) were performed. Interactions with selected host proteins (CtBP1, CtBP2, HSPA2, PPP1CA, SH3KBIP1) were validated by co-IP and confocal microscopy. Functional impacts on viral replication were assessed using siRNA knockdown and overexpression assays.

Results and Discussion

A total of 120 host proteins were identified as NSP2 interactors, primarily involved in translation, metabolism, signal transduction, and innate immunity pathways. Validation confirmed interactions between NSP2 and five selected proteins. Knockdown of SH3KBIP1 enhanced PRRSV replication, while its overexpression inhibited it, identifying SH3KBIP1 as a host restriction factor. Notably, NSP2 interacts with and cleaves SH3KBIP1 at residues G585/G586 via its N-terminal protease domain, thereby antagonizing SH3KBIP1's pro-apoptotic activity. This cleavage promotes SH3KBIP1 degradation and is likely to facilitate viral replication by suppressing host cell apoptosis.

Conclusion

This study provides a comprehensive NSP2-host protein interaction network, revealing novel insights into PRRSV replication mechanisms. The cleavage of SH3KBIP1 by NSP2 represents a novel viral strategy to counteract host apoptosis, highlighting SH3KBIP1 as a potential target for antiviral intervention.

Keywords: Apoptosis, Porcine reproductive and respiratory syndrome virus NSP2, SH3KBP1, Virus-host protein interactions, Virus replication.

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TRANSITION OF PSEUDORABIES VIRUS FROM LATENCY TO REACTIVATION STATE SELECTIVELY TRIGGERED BY PATHOGENIC BACTERIA

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Introduction and Objectives

Pseudorabies virus (PRV) remains a formidable challenge to the global swine industry. Alarmingly, it has emerged as a significant zoonotic pathogen, evidenced by increasing human infections in China (Liu et al., 2021). Although PRV establishes lifelong latency in swine, the precise triggers for reactivation - particularly during co-infections remain poorly understood (Smith et al., 2012). Here, we investigated whether common porcine bacterial pathogens, specifically Extraintestinal pathogenic *Escherichia coli* (ExPEC) and *Streptococcus suis* (*S. suis*), facilitate PRV reactivation and elucidated the underlying molecular mechanisms.

Materials and Methods

A recombinant PRV strain expressing mCherry was utilized to establish latency and reactivation models both *in vitro* (Neuro-2a cells) and *in vivo* (mice and pigs). PRV reactivation was assessed using fluorescence microscopy, RT-qPCR, and Western blotting to evaluate the capacity of ExPEC, *S. suis*, *Glaesserella parasuis* (*G. parasuis*), and enterotoxigenic *E. coli* (ETEC) to induce viral reactivation. Furthermore, RNA-seq was integrated to systematically identify host target genes and signaling pathways involved in ExPEC-mediated PRV reactivation.

Results and Discussion

PRV latency was defined by the loss of mCherry fluorescence, high-level latency-associated transcript expression, and lytic gene silencing in Neuro-2a, alongside the absence of clinical signs and viral shedding *in vivo*. ExPEC consistently triggered PRV reactivation, whereas *S. suis* exhibited strain-dependent effects, evidenced by mCherry re-emergence and increased viral genome loads. Conversely, *G. parasuis* and ETEC failed to induce reactivation. *In vivo*, bacterial challenge precipitated renewed shedding and elevated viral burdens in trigeminal ganglia. Notably, booster immunization significantly reduced reactivation rates in pigs, highlighting vaccine-induced immunity as a critical defense against bacterium-triggered viral recrudescence. Mechanistically, ExPEC infection up-regulated *CXCL1* (~130-fold at the mRNA level), promoting STAT3 phosphorylation and nuclear translocation. This signaling axis directly transactivated the early viral genes *IE180* and *EP0*, thereby initiating the PRV productive replication cycle.

Conclusion

Common clinical bacteria selectively trigger latent PRV reactivation. Notably, ExPEC drives viral recrudescence via the CXCL1-STAT3 axis, escalating outbreak risks under mixed-infection conditions. These findings underscore the necessity of integrated bacterial control strategies mitigate economic losses in the swine industry and safeguard public health against emerging zoonotic threats.

Keywords: Bacterial pathogens, Co-infection, Latency and reactivation, Pseudorabies virus.

Acknowledgements: The authors thank Huazhong Agricultural University for the support with providing testing facilities and research resources.

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NON-VESICULAR CHOLESTEROL TRANSPORTER GRAMD1C AS A PAN-CORONAVIRUS ANTIVIRAL TARGET

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Introduction and Objectives

Coronaviruses (CoVs) heavily rely on host lipid metabolism for efficient replication. Cholesterol is crucial for the biogenesis of double-membrane vesicles (DMVs), which serve as viral replication organelles[1]. GRAMD1C is an ER-localized protein mediating non-vesicular cholesterol transport, yet its role in viral replication remains undefined. This study aimed to investigate the function and mechanism of GRAMD1C in the replication of multiple coronaviruses and evaluate its potential as a broad-spectrum antiviral target.

Materials and Methods

CRISPR/Cas9-generated GRAMD1C-knockout cell lines were infected with multiple coronaviruses (TGEV, SARS-CoV-2, PEDV, PDCoV, MHV). Mechanisms were probed via Co-IP, TEM, confocal imaging, domain rescue, and inhibitor (20α-HC) assays. GRAMD1C$^{+/-}$ mice and inhibitor-treated models assessed in vivo relevance.

Results and Discussion

GRAMD1C is essential for multiple coronaviruses, as its knockout blocks coronavirus replication. It promotes DMV biogenesis by interacting with viral protein nsp4 and recruiting cholesterol via its GRAM and ASTER domains. Inhibiting GRAMD1C with 20_{α}-HC disrupts DMV formation and suppresses replication in vitro, while in vivo, its deficiency or inhibition reduces disease severity and viral load. No compensatory upregulation of GRAMD1A or GRAMD1B was observed in our study cells. These findings reveal a conserved mechanism where coronaviruses hijack GRAMD1C-mediated cholesterol transport, highlighting it as a broad-spectrum antiviral target.

Conclusion

GRAMD1C is a critical host factor supporting coronavirus replication through cholesterol transport to DMVs. Its inhibition represents a promising strategy for developing pan-coronavirus antivirals.

Keywords: coronavirus, double-membrane vesicles, GRAMD1C, replication, virus entry.

Acknowledgements: The authors thank the Huazhong Agricultural University, Wuhan for the support with providing testing facilities.

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A NOVEL PPP2R5B/HSF1/ANPEP PATHWAY CONTROLS HOST CELL ENTRY OF PORCINE CORONAVIRUS TGEV

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Introduction and Objectives

Porcine transmissible gastroenteritis virus (TGEV) is a significant pathogen that severely threatens the swine industry. Its high mortality rate and complex relationships with other coronaviruses pose a potential threat to public health security (Turlewicz-Podbielska and Pomorska-Mól 2021). Elucidating virus-host interaction mechanisms is fundamental for developing novel control strategies. Protein phosphorylation plays a central role in regulating cellular processes and pathogen infections. PPP2R5B, a key regulatory subunit of protein phosphatase 2A (PP2A), is primarily involved in insulin signaling and cell cycle regulation, but its function in viral biology remains poorly understood (Singh, et al., 2017). This study aimed to determine if and how PPP2R5B regulates TGEV infection in PK-15 cells, focusing on the infection stage and mechanism.

Materials and Methods

PPP2R5B was knocked out in PK-15 cells using CRISPR/Cas9. TGEV infection was assessed by IFA and RT-qPCR. Viral entry stage was defined via time-of-addition and temperature-shift assays. HSF1 phosphorylation and ANPEP expression were analyzed by Western blot and RT-qPCR.

Results and Discussion

PPP2R5B knockout significantly inhibited TGEV infection by specifically blocking viral entry. Mechanistically, PPP2R5B knockout increased phosphorylation of HSF1 at Ser304/Ser308, leading to downregulation of the TGEV receptor ANPEP. This effect was independent of PP2A phosphatase activity, revealing a novel PPP2R5B-HSF1-ANPEP axis.

Conclusion

This study identified PPP2R5B as a key host restriction factor regulating TGEV entry. Its absence suppresses viral entry by inducing HSF1 phosphorylation at Ser304/Ser308, leading to the downregulation of the viral receptor ANPEP.

Keywords: Aminopeptidase N (ANPEP), Heat Shock Factor 1 (HSF1), PPP2R5B, Phosphorylation, TGEV, Viral Entry

Acknowledgements: The authors thank the Huazhong Agricultural University, Wuhan for the support with providing testing facilities.

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TUNNELING NANOTUBES INDUCED BY PSEUDORABIES VIRUS FACILITATE VIRAL TRANSMISSION UNDER NETRALIZING ANTIBODIES IN SK-N-SH CELL

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Introduction and Objectives

Pseudorabies virus (PRV), a swine-endemic alphaherpesvirus, has recently caused fatal human encephalitis, yet its neuropathogenic mechanisms remain elusive. Tunneling nanotubes (TNTs), actin-rich intercellular membrane extensions, mediate cell-to-cell viral transmission. Here, we investigated whether PRV induces TNTs in human neurons, identified the viral factors governing this process, and explored TNTs' role in the differential neuropathogenicity of classical and emergent hypervirulent PRV strains.

Materials and Methods

SK-N-SH cells (Cat. No. GDC0047; CCTCC) were cultured in Minimal Essential Medium supplemented with 10% fetal bovine serum. The PRV strain Ea was isolated from an infected pig in China in 1998 and the PRV strain hSD-1/2019 was isolated from the cerebrospinal fluid of a PRV-infected patient in China in 2019, which are isolated and preserved in our lab. SK-N-SH cells were infected with PRV strains at a dose of 0.01 multiplicity of Infection. Using immunofluorescence, confocal imaging, and time-lapse microscopy, we characterized PRV-induced TNTs in human neurons. A compartmentalized co-culture model was established to compare TNT morphology and viral transmission efficiency under immune pressure from neutralizing antibodies across PRV strains. Additionally, US3 overexpression and gene-deleted virus assays were used to verify US3's role in TNT biogenesis.

Results and Discussion

PRV infection robustly induced TNT formation in SK-N-SH cells, which widely serve as a commonly used in vitro model in neurobiology and related disease studies; these structures served as shielded conduits for efficient cell-to-cell transmission, enabling antibody evasion. Notably, the human-isolate hSD-1/2019 strain triggered significantly more and longer TNTs than the classical strain, enhancing viral spread under immune pressure from neutralizing antibodies and explaining its hypervirulence. Viral protein US3 was essential for neuronal TNT formation, but TNTs induced by full viral infection differed morphologically from those induced by US3 overexpression alone, indicating that additional viral factors regulate TNT maturation and structure.

Conclusion

Our findings provide novel insights into PRV neuropathogenesis from the perspective of viral transport dynamics and identify virus-induced intercellular conduits as a potential therapeutic target against infections of PRV and similar neuroinvasive viruses.

Keywords: Intercellular viral transmission, Immune evasion, Neuropathogenic mechanism, Pseudorabies virus, Tunneling nanotubes.

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PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS-2 (PRRSV-2) ELIMINATION STRATEGY IMPACTS ON DIAGNOSTIC TIMELINES IN CANADIAN SOW SITE OUTBREAKS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) outbreaks significantly impact sow herd productivity and economic outcomes. Understanding diagnostic timelines to establish when piglets are born negative and the number of weeks until weaned pigs test negative is important to predict impacts of various strains. In addition, understanding the difference in time required to return to baseline production levels across strains can help veterinarians make decisions regarding elimination strategies.

Materials and Methods

A surveillance program (2022 - present) enrolls independent sow herds showing clinical signs alongside PRRS sequencing results. Time to born negative (TTBN) is defined as number of weeks to reach three consecutive weeks of PRRS PCR negative processing fluids (~5-days). Time to negative weaned pigs (TTWN) is defined as number of weeks to reach three consecutive weeks of PRRS PCR negative serum (~20-days). Production data is retrieved 42-weeks pre-/post-sequencing. Baseline is defined 21-weeks before sequencing, immediate post-outbreak period is 8-weeks after sequencing and the number of weeks to return to baseline (TTBP) for variables of interest are calculated for each herd.

Results and Discussion

Diagnostics data were available for 68 herds attempting elimination. Elimination was successful in 64% (18% MLV, 18% MLV and serum, 32% serum, 32% depopulation). New virus introduction occurred in 6, 22% failed to eliminate, and 7% had incomplete diagnostics. Mean TTBN (weeks) across all successful elimination strategies was 34 (range 22 - 49, n = 24). TTBN for MLV (30, 26 - 42, n = 7), serum (38, 26 - 49, n = 9), MLV and serum (36, 22 - 50, n =12). Mean TTWN (weeks) across all successful elimination strategies was 38 (range 20 - 64, n = 32). TTWN for MLV (33, 20 - 42, n = 8), serum (42, 32 - 64, n = 12), and MLV and serum (40, 30 - 50, n = 12). A further 25 herds are undergoing elimination. Complete production data was retrieved for a total of 158 sow herds, comparison across outbreaks is underway.

Conclusion

Comparing successful elimination strategies, TTBN and TTWN were fastest in herds that used MLV. Results should be interpreted with caution, due to small sample size. As more herds complete elimination, timelines will be compared across PRRS lineages and strategies. Future analyses will incorporate production data to evaluate TTBP across strategies and lineages.

Keywords: Diagnostics, PRRSV, Timelines.

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BROAD-SPECTRUM PEDV DETECTION USING MONOCLONAL ANTIBODIES AGAINST CONSERVED NUCLEOCAPSID PROTEIN DOMAINS

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) causes severe enteric disease and high mortality in neonatal piglets. Although the nucleocapsid (N) protein is commonly targeted in antigen-based diagnostics, previous studies have shown that amino acid variation in the PEDV N protein can affect antibody recognition and reduce detection sensitivity across genotypes and subgenotypes. This study aimed to develop monoclonal antibodies (mAbs) targeting conserved regions of the PEDV N protein and to establish a broad-spectrum sandwich ELISA for improved antigen detection.

Materials and Methods

A recombinant PEDV N protein containing conserved N-terminal and C-terminal domains was expressed using an Escherichia coli system and purified for immunization. Mice were immunized to generate monoclonal antibodies, and rabbits were immunized to produce polyclonal antibodies. Two mAb clones (4C7 and 2E5) were selected and characterized. A double-antibody sandwich ELISA was established using mAbs as capture antibodies and an in-house HRP-labeled rabbit polyclonal antibody as the detection antibody. Analytical performance was evaluated using PEDV strains from Vietnam (V2, G2a) and Korea (Q1401, G2b). Clinical validation was conducted using 20 intestinal and fecal samples from diarrheic piglets in Vietnam, including RT-qPCR-confirmed PEDV-positive and negative samples. Cross-reactivity was assessed against ASFV, PCV2, and PRRSV. The in-house HRP-labeled polyclonal antibody was also compared with a commercial antibody.

Results and Discussion

Both mAbs showed strong binding, with detection limits of 0.027 nM (4C7) and 0.083 nM (2E5). The sandwich ELISA detected PEDV at viral titers as low as $10^{3.364}$ - $10^{4.799}$ $TCID_{50}$/mL for both G2a and G2b strains, demonstrating broad genotype coverage. Clinical testing showed high concordance with RT-qPCR results. No cross-reactivity with ASFV, PCV2, or PRRSV was observed. The in-house HRP-labeled polyclonal antibody produced higher signal-to-background ratios than the commercial antibody, indicating improved analytical sensitivity.

Conclusion

Targeting conserved domains of the PEDV N protein enables sensitive and genotype-inclusive antigen detection. The developed sandwich ELISA provides an improved PEDV antigen detection platform with enhanced sensitivity and broader strain coverage for laboratory and field surveillance.

Keywords: Antigen detection, Diagnostic sensitivity, Monoclonal antibody, PEDV, Recombinant N protein.

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A CROSS-SPECIES FRAMEWORK FOR CLUSTERING H3NX INFLUENZA A HEMAGGLUTININ NUCLEOTIDE SEQUENCES

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Introduction and Objectives

Influenza A viruses (IAVs) frequently cross species barriers, complicating surveillance. H3 viruses are particularly widespread, circulating among multiple host species. This broad host range highlights the need for a standardized, host-agnostic grouping system. Such consistency is increasingly important as machine learning (ML) methods are applied to nucleotide sequences. Existing systems for classifying H3 nucleotide sequences typically focus on a single host species (1,2), limiting their utility for genomic surveillance and real-time risk assessment. Therefore, this study aims to develop a preliminary grouping system for the HA of H3NX IAVs using publicly available sequences up to 2024 to support ML model development.

Materials and Methods

Whole genome H3 IAV nucleotide sequence data were retrieved from public repositories, assessed for quality and duplicates within species, and label information was used as metadata and investigated. Sequences from the HA segment were used to infer a maximum likelihood phylogenetic tree with 1000 ultra-fast bootstrap replicates using IQ-TREE v 3.0.1, which was used to identify clusters using TreeCluster (3) with the max-clade method and a range of patristic distance threshold values of 0.01 - 0.05 subs/site. The number of clusters, singletons, and maximum cluster size were then compared across threshold values, and agreement between generated groups and established lineages was assessed.

Results and Discussion

Of the 21,427 whole genome sequences, 72.8% were found to originate from North America (n =15596), 9.6% from Oceania (n = 2054), and 9.4% from Asia (n = 2011). Most sequences were collected in recent years with 59.7% from the 2010s (n = 12798), 21.5% from the 2020s (n = 4599), and 14% from the 2000s (n = 2998). After clustering sequences using TreeCluster, the number of clusters excluding singletons ranged from 467 to 1,347, and the number of singletons ranged from 217 to 1149, with both decreasing as threshold values increased. In contrast, maximum phylogenetic cluster size ranged from 1139 - 4604, increasing as threshold values increased. Preliminary analyses identified 0.02 subs/site as a suitable clustering threshold.

Conclusion

Grouping of H3 HA IAV sequences into clusters using this methodology will allow for phylogenetically informed model validation in future studies involving host prediction and investigation of between-species transmission using ML.

Keywords: Influenza A virus, H3Nx, classification, phylogenetics

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GENETIC DIVERSITY OF PORCINE CIRCOVIRUS TYPE 2 IN DENMARK IN 2014-2025

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) has been a major infection in modern pig production worldwide since its emergence in the early 2000s. It has been extensively studied due to its association with a range of clinical syndromes collectively referred to as porcine circovirus diseases, including PCV2 systemic disease, porcine dermatitis and nephropathy syndrome, and reproductive disorders. PCV2 is notable for its high evolutionary rate, which has driven the development of multiple genetically distinct variants. These variants are classified into genotypes, currently designated PCV2a - PCV2h, of which PCV2a, PCV2b, and PCV2d are considered the major genotypes due to their global distribution and long-term persistence. The aim of this study was to investigate the genetic diversity of PCV2 in Danish pig populations between 2014 and 2025.

Materials and Methods

The samples originated from previous research projects, diagnostic submissions, and screening activities. Screening samples were collected from herds without any specific clinical signs associated with PCV2. Diagnostic samples were submitted for laboratory investigation from herds experiencing health issues. All samples were collected from pigs in conventional herds in Denmark. Initially, the samples were tested for the presence of PCV2 by qPCR and selected positive samples were subsequently genotyped by Sanger sequencing.

Results and Discussion

A total of 117 PCV2-positive samples collected between 2014 and 2025 (1 - 36 per year) were sequenced and genotyped. Two sequences were classified as PCV2a, while 52 belonged to PCV2b and 63 to PCV2d. From 2014 - 2016, only PCV2b was detected. In 2017, both PCV2b (64%) and PCV2d (36%) were present, and in 2018 the distribution was equal (47% each). By 2019, PCV2d (76%) had become dominant, and since then PCV2b has appeared only sporadically, with PCV2d remaining the prevailing genotype. Analysis of the capsid protein sequences revealed amino acid substitutions within the conformational epitope regions in the Danish sequences - PCV2a (T47A, T63S, A68S, M72L, L185M), PCV2b (T63K/R, S190A/T) and PCV2d (S169G/R).

Conclusion

Up to 2018, PCV2b was the predominant genotype in Danish pigs, however, since 2019, PCV2d has emerged as the dominant type. Genotyping represents a valuable tool for guiding the selection of appropriate vaccines.

Keywords: Denmark, Genetic diversity, Porcine circovirus type 2.

ASSESSING SOW MILK AS A POTENTIAL TRANSMISSION ROUTE OF INFLUENZA A VIRUS

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Introduction and Objectives

High pathogenicity avian influenza virus (HPAIV) H5N1 clade 2.3.4.4b was detected in dairy cattle in the US in 2024. High viral titers were detected in the milk, and influenza A virus (IAV) tropism for mammary glands might not be limited to cattle. A key host barrier is the IAV receptor distribution. IAVs adapted to pigs prefer α2,6-linked glycans (pig receptor), whereas IAVs isolated from birds prefer α2,3-linked glycans (avian receptor). This study aimed to assess the risk of sow milk as a potential transmission route for IAV in sow herds.

Materials and Methods

Mammary glands from lactating sows were collected, formalin-fixed, and paraffin-embedded (FFPE). The pig IAV receptor distribution was examined using SNA lectin and viral attachment patterns using pseudotyped HIV Gag-based virus-like particles (VLPs) with the glycoproteins from H1N1pdm pig origin on FFPE tissues. Similarly, the avian IAV receptor was detected using MAA-I and MAA-II lectins and VLPs with glycoproteins of H5N1 avian origin. Additionally, sow milk was obtained from four Danish sow herds with known circulation of IAV and tested for IAV RNA using reverse-transcriptase real-time PCR.

Results and Discussion

H1N1pdm VLPs showed strong tissue attachment in 2/3 sows, corresponding to the pig receptor, which showed the highest expression, particularly on milk-filled mammary gland alveoli. H5N1 VLPs bound sparsely in 2/3 sows, corresponding to lower expression of the avian receptor. Of 85 milk samples from sows with IAV-positive piglets, one tested positive (Ct = 35.19 in 16-fold dilution) for IAV RNA, but no viable virus could be isolated from this sample.

Conclusion

Receptor expression and binding of both pig and avian IAV indicate that sow udders may support IAV replication. Low detection of IAV RNA and lack of viable virus from sow milk, however, suggest limited transmission risk via sow milk in these herds. The risk of environmental contamination of the one IAV-positive sow milk sample cannot be excluded. Further studies, including nasal swabs from sows, are needed to clarify whether IAV replicates in the sow mammary glands of infected sows and to relate these results to the presence of IAV antibodies in sow milk.

Keywords: Influenza A virus, Mammary glands, Receptor, Transmission, Viral attachment.

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SURVEILLANCE OF SWINE PATHOGENS IN NORTHERN VIETNAM IN 2025

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Introduction and Objectives

Pig production in Northern Viet Nam faces increasing pressure from transboundary, endemic, and emerging infectious diseases, resulting in significant economic losses and complex disease patterns. This study aimed to describe the prevalence and distribution of major viral and bacterial pathogens detected through routine molecular diagnostics in swine samples in Northern Viet Nam over a one-year period, providing practical insights into current disease circulation and diagnostic demand.

Materials and Methods

A retrospective analysis was conducted on 7,957 clinical samples collected from pig farms in Northern Viet Nam and tested between January and December, 2025. Samples submitted for routine disease investigation. Molecular diagnostics were performed to detect 28 pathogens, including African swine fever virus (ASFV), PRRS virus (US, CH, EU genotypes), porcine circoviruses (PCV2, PCV3), classical swine fever virus (CSFV), porcine epidemic diarrhea virus (PEDV), and key bacterial pathogens. Detection rates were calculated as the proportion of positive samples among tested samples for each pathogen.

Results and Discussion

Overall, 2,043 samples (25.7%) tested positive for at least one pathogen. ASFV remained the most frequently detected pathogen, reflecting its continued endemicity and high diagnostic demand. PRRS virus was widely detected, predominantly the US genotype, followed by CH and EU genotypes, highlighting ongoing viral diversity. PCV2 and PCV3 were consistently identified, while PEDV and FMDV were also detected at notable levels. Among bacterial pathogens, Mycoplasma suis showed a relatively high detection rate, followed by *Streptococcus suis*, *Actinobacillus pleuropneumoniae*, and *Glaesserella parasuis*, emphasizing the importance of bacterial co-infections in respiratory and systemic disease complexes. Several pathogens, including CSFV and JEV, were not detected during the study period, suggesting effective control or limited circulation.

Conclusion

This surveillance provides a practical overview of major swine pathogens currently circulating in Northern Viet Nam. The findings underscore the continued dominance of ASFV, the complexity of PRRS and PCV-associated infections, and the significant contribution of bacterial pathogens to disease burden. Strengthening integrated surveillance and data sharing is essential for early warning, targeted control strategies

Keywords: Molecular diagnostics, PRRS, Surveillance, Swine diseases, Viet Nam.

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IMPACT OF LARGE-SCALE DEPOPULATION AND REPOPULATION ON PCV2 PREVALENCE AND GENOTYPE DIVERSITY WITHIN AN INTEGRATED PRODUCTION SYSTEM

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Introduction and Objectives

This observational-epidemiology-study, carried out in 2023 - 2024, was used to measure PCV2 prevalence and genotype diversity prior/following a massive depopulation-repopulation effort underway to eradicate specific viral and bacterial agents. The whole process included a rigorous decontamination of the sow facilities, pig-flow downstream site depopulation along with cleaning-disinfection efforts. The production system includes 1-nucleus site, 2-multipliers and 8-commercial flows having PCV2a genotype as the predominant genotype prior to depopulation.

Materials and Methods

Samples were collected in the multiplier flows and 3 out of 8 commercial flows. Processing-fluids from all piglets were collected for 3 consecutive months (1 PF/month) and tested by PCV2 qPCR genotyped (a, b, d or e). Oral-fluids were collected from 4 pens from 3 different nurseries (8 - 10 weeks-of-age) and three different finishers (14 - 18 weeks-of-age) tested individually by PCV2 qPCR/genotyped. Total of 207 PCV2-3 qPCRs were analyzed and 17 sequences were obtained.

Results and Discussion

Considering results from the flows tested (n = 157), 43% of samples were positive prior depopulation and 70% were positive following repopulation. Processing-fluids were positive in 28% of samples (CtMdn = 39.0; 31.4-39.0) prior to depopulation and in 21% (M = 39.0;19.4 - 39.0) following repopulation. Nursery oral-fluids were positive in 44% of samples (M = 39.0;19.7-39.0) prior to depopulation and in 85% (M = 33.5; 25.7 - 39.0) after repopulation. Finisher oral fluids were positive in 54% of samples (M = 35.2; 19.6 - 39.0) prior to depopulation and in 79% (M = 27.2;11.6 - 39.0) after repopulation. Genotypes identified prior to the depopulation in descending frequency order were 2a, 2d, 2e and 2a-2b. The new order following repopulation shifted to 2d, 2a - 2d, 2b - 2d, 2b, 2e, 2a. PCV2 genotype co-infections were identified in 3% of the samples prior to depopulation and in 25% of the samples following repopulation.

Conclusion

This study highlighted the possibility that PCV2 prevalence and genotype diversity could be influenced by production practices targeting health management, such as Depop-Repop, where parity distribution structure of sow herds, and changes in replacement gilts source may represent potential epidemiology changes in the whole production system population with potential implications on diseases control effectiveness, emphasizing the importance of monitoring breeding herd PCV2-stability along with active surveillance to understand PCV2 infection dynamics and possible genotype shifts and/or genotypes co-infections.

Keywords: Breeding herd stability, Genotype co-infections, PCV2, Surveillance.

RISK FACTORS ASSOCIATED WITH INTRODUCTION OF WILD-TYPE PRRSV INTO GROWING PIGS IN THE MIDWESTERN US

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a leading cause of economic losses in swine production, especially in growing pigs (Osemeke et al., 2025). Despite advances in breeding herd biosecurity, the introduction of wild-type PRRSV (WT-PRRSV) into growing pigs remains a significant challenge (Angulo et al., 2023). This study aimed to identify risk factors related to production practices and herd characteristics associated with WT-PRRSV introduction in wean-to-finish (WTF) herds in the Midwestern US, with the goal of informing biosecurity improvements.

Materials and Methods

A prospective cohort study was conducted in 63-WTF herds across 10-production companies in Iowa and Minnesota. Site-level data were collected via two structured electronic surveys: an enrollment survey capturing herd demographics, source herd PRRSV status, and vaccination protocols, and a site characteristics survey detailing barn structure, pig flow, biosecurity practices, and management routines. Additionally, a daily checklist was maintained at each site to document key activities such as mass treatments, movement of pigs, visitor entry, maintenance events, and mortality management. Monthly oral fluid samples (eight-per-sampling event) were collected at pre-determined intervals (3, 8, 12, 16, 20, and 25 weeks post-placement) and tested for PRRSV using RT-PCR. PRRSV ORF-5 sequencing was performed for virus characterization. Logistic regression was performed to assess associations between management practices, specific events, and the detection of WT-PRRSV, adjusting for season and local pig density.

Results and Discussion

Outsourcing trucks for mortality removal (OR = 7.08, $P = 0.03$) and the presence of external maintenance crews (OR = 7.14, $P = 0.03$) were significantly associated with increased risk of WT-PRRSV infection. Practices such as sourcing pigs from a single sow farm, all-in/all-out pig flow, and using dedicated equipment for dead pig removal had a protective effect but were not statistically significant in the multivariate analysis. The findings underscore the importance of mechanical transmission and highlight gaps in biosecurity protocols during the growing phase. Enhanced protocols for mortality management and maintenance crew entry are recommended.

Conclusion

Mechanical transmission via outsourced mortality trucks and external maintenance crews are key risk factors for WT-PRRSV introduction into growing pigs. Strengthening biosecurity around these activities is critical for PRRSV control and the mitigation of PRRS economic impact in this production phase.

Keywords: biosecurity, growing pigs, mortality management, PRRSV, risk factors.

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IMMUNE ONTOGENY AND HUMORAL CORRELATES OF PROTECTION FOLLOWING SENECAVIRUS A INFECTION IN SOWS AND GILTS

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Introduction and Objectives

Senecavirus A (SVA) causes vesicular disease in swine and poses a diagnostic and biosecurity concern due to its clinical similarity to other vesicular diseases. While antibody responses to SVA have been described, comparative characterization of immune ontogeny between replacement gilts and breeding sows remains limited. This study aimed to compare antibody responses to SVA infection in gilts and sows at different gestation stages and to evaluate protective immunity by previous infection against homologous re-challenge in gilts.

Materials and Methods

SVA-naïve sows and gilts were experimentally inoculated intranasally with a contemporary SVA isolate and monitored for clinical signs, viremia, and antibody responses. The sows consisted of crossbred white pigs of various parities and included pre-farrowing sows between 3 and 18 days before farrowing (n = 5) and post-farrowing sows between 1 and 14 days after farrowing (n = 5). Gilts were approximately 8-month-old crossbred white pigs (n = 15). SVA-specific IgG and virus-neutralizing (VN) antibodies were measured using indirect fluorescent antibody and virus neutralization assays. Viral protein-specific IgG responses were evaluated in gilts using Western immunoblot. A subset of gilts was re-challenged with homologous SVA to assess protection against reinfection.

Results and Discussion

Following primary inoculation, vesicular disease was observed in only one post-farrowing sow, which developed a single snout vesicle at 5 days post-inoculation (PI) that resolved within one week. No vesicular lesions occurred in the remaining sows. Piglets born to the inoculated sows exhibited mild, self-limiting diarrhea in two litters, and no piglets developed vesicular lesions. In contrast, all gilts developed vesicular lesions following primary inoculation. Both sows and gilts developed detectable SVAspecific IgG and VN antibodies. In gilts, homologous re-challenge at 140 - 153 days PI did not result in clinical disease or viremia. Viral protein-specific IgG analysis identified VP2 as the dominant antigen associated with SVN activity.

Conclusion

SVA infection caused limited vesicular disease in sows and consistent lesions in gilts, while both groups developed comparable antibody responses. VP2-specific IgG was associated with protection in gilts against homologous re-challenge 5 months PI, supporting the relevance of VP2-targeted antibody responses for SVA vaccine and diagnostic development.

Keywords: Immunity, Neutralizing Antibody, Senecavirus A, Swine, VP2.

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STRUCTURAL PROTEIN REQUIREMENTS FOR SENECAVIRUS A VIRUS-LIKE PARTICLE ASSEMBLY WITH IMPLICATIONS FOR VACCINE

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Introduction and Objectives

Senecavirus A (SVA) causes vesicular disease in pigs that is clinically indistinguishable from foot-and-mouth disease and other high-consequence vesicular diseases in pigs, posing a major biosecurity and diagnostic challenge for the swine industry. Vaccination may serve as a mitigation tool in specific situations; however, no commercial vaccines for SVA are currently available. Virus-like particles (VLPs) represent a safe, non-infectious platform for vaccine and antigen development for many viruses, as they mimic native structure. Such a platform can also be applicable to an SVA vaccine since experimental killed virus vaccines have demonstrated their efficacy against SVA infection. Yet, the structural requirements for SVA capsid assembly are not fully understood, although SVA virions have been reported to contain four structural proteins (VP1, VP2, VP3, and VP4). This study compared different SVA structural protein compositions to identify conditions that support efficient VLP assembly.

Materials and Methods

Structural protein genes were amplified from a contemporary SVA isolate and cloned into an expression vector for the production of recombinant protein in Escherichia coli. Individual proteins were expressed, purified, and confirmed by Western immunoblot. Defined mixtures of structural proteins (VP0, VP1, and VP3 or VP1, VP2, VP3, and VP4) were subjected to density gradient centrifugation to evaluate particle assembly. Virus-like particle formation was assessed by transmission electron microscopy.

Results and Discussion

Recombinant expression and purification of individual SVA structural proteins were successfully achieved. Icosahedral particles consistent with SVA-like morphology were observed only in mixtures containing VP0, VP1, and VP3, confirming successful VLP assembly. In contrast, such particles were not detected in mixtures containing VP1, VP2, VP3, and VP4. These findings suggest that the presence of VP0, without cleavage into VP2 and VP4, is critical for SVA VLP assembly. Understanding capsid assembly requirements is essential for designing stable and reliable non-infectious antigens or immunogens.

Conclusion

This study demonstrates that SVA VLP assembly depends on structural protein composition and identifies VP0 as a key component in virion formation. These findings offer practical insights for the development of VLP-based vaccines or diagnostic antigens for SVA, supporting biosecurity preparedness and disease mitigation efforts in swine production systems.

Keywords: Immunogenicity, Senecavirus A, Vaccine, Virus-like Particles, Vesicular Disease.

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RE-EMERGING SWINE VIRAL PATHOGENS: EPIDEMIOLOGICAL DRIVERS, EVOLUTIONARY DYNAMICS, AND CONTROL CHALLENGES IN MODERN PIG PRODUCTION

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Introduction and Objectives
Re-emerging viral diseases continue to represent a major constraint to sustainable pig production worldwide. Despite long-standing control efforts, several swine viruses have re-established or expanded their epidemiological impact due to viral evolution, intensification of production systems, global trade, and wildlife reservoirs. Notably, African swine fever virus (ASFV), porcine reproductive and respiratory syndrome virus (PRRSV), swine influenza A virus, porcine epidemic diarrhea virus, and porcine circoviruses remain responsible for significant economic losses and animal health challenges. The objective of this study was to review and synthesize current knowledge on the epidemiology, evolutionary dynamics, and control challenges associated with major re-emerging swine viral pathogens, with emphasis on factors driving their persistence and resurgence.

Materials and Methods
A narrative review of peer-reviewed scientific literature published between 2000 and 2025 was conducted using international databases. Publications focusing on epidemiology, molecular evolution, pathogenesis, surveillance, and control strategies of re-emerging swine viral pathogens were analyzed. Emphasis was placed on recent outbreaks, emerging variants, vaccine performance, and the role of biosecurity and wildlife reservoirs in disease spread.

Results and Discussion
Re-emerging swine viral pathogens exhibit diverse biological and epidemiological characteristics but share common drivers of persistence. RNA viruses such as PRRSV and swine influenza A virus demonstrate high mutation and recombination rates, enabling immune escape and reduced vaccine efficacy. In contrast, ASFV, a large DNA virus, shows remarkable environmental stability and complex immune evasion mechanisms, complicating eradication efforts. Global animal movement, high farm densities, and incomplete biosecurity were consistently identified as key risk factors for re-emergence. Additionally, the increasing role of wild swine in maintaining and spreading infections presents significant challenges for control. Advances in molecular diagnostics and genomic surveillance have improved outbreak detection and strain characterization, yet effective vaccines remain unavailable or insufficient for several major pathogens.

Conclusion
Re-emerging swine viral pathogens remain a persistent threat to global pig health and production. Effective mitigation requires integrated control strategies combining enhanced biosecurity, continuous genomic surveillance, improved vaccine development, and coordinated international disease monitoring. A deeper understanding of viral evolution and transmission dynamics is essential to reduce the impact of future re-emergence events.

Keywords: Epidemiological drivers, Pig production, Re-emerging viral pathogens, Swine.

TRAILER CONTAMINATION AT THE HARVEST PLANT: THE RISK OF UNLOADING PIGS

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Introduction and Objectives

Unloading market hogs at the harvest facility is a risky event, as trailers can become contaminated. Only one study has been done assessing contamination at the harvest facilities (Lowe et al, 2014), highlighting that PEDV trailer contamination occurred and could lead to virus dissemination. However, there is no data on the frequency of contamination and factors associated. To address this gap, a study investigating trailer contamination when unloading market hogs at the harvest facility throughout the year was conducted.

Materials and Methods

A total of 389 docks and trailers were sampled every other week at a Midwestern United States harvest plant throughout one year. In total, 45 environmental samples were collected at each visit: dock (n = 15), trailer before unloading (n = 15), and trailer after unloading (n = 15). Samples were RT-PCR tested for PRRSV, PEDV, PDCoV, TGE and SVA at the University of Minnesota Diagnostic Lab.

Results and Discussion

The harvest facility dock samples tested positive for PRRSV, PDCoV, PEDV, and SVA in 51.7, 71.2, 61.9 and 48.1%, respectively. Before unloading, trailers were testing positive for the above-mentioned pathogens in 34.9, 27.2, 41.1, and 21.8%, respectively, while after-unloading positivity rate increased to 44.5, 51.0, 61.9, and 39.4%. Season was significantly associated with detection of viruses, $\chi^2(3)$ values ($P < 0.001$) at the dock, before and after unload were respectively 34.3, 4.87 ($P = 0.182$), and 31 for PRRSV; 24.4, 10.3, and 23.8 for PDCoV; 52.5, 16.2, and 60.4, for PEDV, and, 111.8, 20.4, and 88.3 for SVA. The median Ct values observed were 34.2923 (25.1057 - 39.8042) for PRRSV, 33.9037 (14.4456 - 37.9675) for PDCoV, 34.0000 (24.9977 - 37.9900) for PEDV, and 31.9494 (17.7813 - 39.9508) for SVA.

Conclusion

The study demonstrates that the harvest facility serves as a critical point of trailer contamination during unloading. Contamination at the dock level and on the trailers was observed throughout the year, with an increase in contamination of trailers after unloading. Seasonality significantly influenced contamination levels for all the viruses. These findings highlight the need for targeted biosecurity measures, including improved cleaning and disinfection protocols and seasonal risk mitigation strategies, to reduce the spread of viruses during the unloading process.

Keywords: Biosecurity, harvest facilities, market hogs, trailer contamination.

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TIMING MATTERS: MODELLING THE INTERPLAY AMONG MATERNALLY DERIVED ANTIBODIES, PREVALENCE OF INFECTION AND PCV2 VACCINATION IN SWINE

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Introduction and Objectives

Porcine circovirus 2 (PCV2) remains one of the most impactful endemic pathogens in global swine production. Although piglet vaccination is widely implemented, its effectiveness is influenced by maternally derived antibodies (MDA) and the timing of natural infection. This study aimed to develop a model to explore how MDA levels and infection pressure shape PCV2 transmission dynamics and to identify optimal vaccination timing under different epidemiological contexts.

Materials and Methods

A stochastic individual-based model was developed using the EMULSION framework to simulate a single batch production in a farrow-to-finish production system. The model integrates horizontal transmission, age-dependent MDA decay, vaccine-induced humoral immunity, and clinical outcomes, including PCV2 subclinical infection (PCV2-SI), systemic disease (PCV2-SD), and their consequences on growth performance. Four MDA distributions at weaning (low, medium, high and very high, which are < 0.5, 0.5 - 1.0, 1.0 - 2.0 and > 2.0, respectively, with PCV2 Ingezim Circovirus IgG ELISA test) and three PCV2 prevalence levels at nursery entry (1, 5 and 10%) were combined with six intervention strategies: no vaccination (NV) and vaccination at 14, 21, 28, 35, or 42 days of age. 72 epidemiological scenarios were simulated (10 replicates each). Model parameterization was based on published literature. Outputs included PCV2-SI and PCV2-SD prevalence, viraemia dynamics, growth performance and economic indicators. Model robustness was supported by two-phase sensitivity analysis (one-at-a-time screening and full factorial design).

Results and Discussion

Under NV conditions, higher MDA levels delayed PCV2 infection onset, whereas higher PCV2 prevalence at weaning accelerated viral circulation. Vaccination performance was MDA-dependent. In farms with low to high MDA levels, early vaccination (14 - 21 days of age) minimized PCV2-SI and maximized growth, reducing PCV2-SI and PCV2-SD by up to 94% and 97%, respectively. In contrast, very high MDA levels required delayed vaccination (28 - 42 days of age) to avoid immune interference. NV pigs showed 5 kg lower finishing BW, while optimal vaccination increased economic margin by 0.05 - 0.10 €/kg live weight.

Conclusion

This modelling approach provides a robust framework to support data-driven optimization of PCV2 vaccination timing. Integrating serological (MDA) and virological (PCV2 prevalence at weaning) information enables tailored vaccination strategies adapted to farm-specific epidemiological conditions.

Keywords: Maternal derived antibodies, PCV2, Stochastic modelling, Vaccination timing.
Acknowledgements: We are grateful to the INRAE MIGALE bioinformatics facility (MIGALE, INRAE, 2020. Migale bioinformatics Facility, doi: 10.15454/1.5572390655343293E12) for providing computing resources.

WHOLE-GENOME SEQUENCE ANALYSIS OF VACCINE-LIKE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS 2 STRAINS IN A CLINICAL OUTBREAK ON A PIG FARM IN THE PHILIPPINES

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Introduction and Objectives

A previously porcine reproductive and respiratory syndrome virus (PRRSV)-naïve, high-health swine herd maintained under strict biosecurity and remote location experienced an outbreak of swine respiratory disease (SRD) in May to June 2024. Piglets were reared in on-site nurseries and transferred at 10 weeks to off-site grower-finisher farms in Tarlac, Philippines. The farms were surrounded by multiple neighboring operations within two kilometers and at risk from indirect exposure via shared transport routes and wash-water runoff. The present study aims to characterize the pathogen associated with the outbreak.

Materials and Methods

Twenty-four blood samples were collected from clinically affected pigs and submitted for molecular detection of suspected pathogens. All tested negative for porcine circovirus type 2 but 19 were positive for PRRSV-2. Four PRRSV-2-positive samples (Ct < 25) were subjected to whole-genome sequencing (WGS) by nanopore sequencing and subsequently analyzed.

Results and Discussion

WGS produced three partially complete and one coding-complete PRRSV-2 genomes which were highly identical (> 99%), suggesting a single dominant strain. All sequences shared 98.7% ORF5-nucleotide identity with the L5A modified live vaccine, effectively classifying the sequenced strains as L5A vaccine-like. Furthermore, virulence-associated markers in viral proteins nsp1β, nsp10, GP2, GP5 and GP6 were detected in strain BA24-05-01, indicating that the PRRSV-2 strains may be virulent.

Conclusion

This study reports the first Philippine case of L5A vaccine-like strains associated with SRD outbreak in a pig herd with no history of L5A vaccination, underscoring the importance of strict biosecurity and routine molecular surveillance. It is recommended that surrounding pig farms be investigated for potential use of the L5A vaccine.

Keywords: PRRSV-2, Swine respiratory disease, Vaccine-like, Whole-genome sequencing.

CHOLESTEROL SYNTHESIS INHIBITORS EFFECTIVELY INHIBIT THE REPLICATION OF AFRICAN SWINE FEVER VIRUS *IN VITRO*

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Introduction and Objectives

African swine fever (ASF) is a globally significant animal health threat caused by African swine fever virus (ASFV). Currently, the development of commercial vaccines remains hampered, while no specific antiviral agents targeting ASFV are clinically available. Previous researchers found that cholesterol metabolism is a significant pathway in ASFV infection and replication in host cells. It is not only a core component of lipid rafts essential for viral entry but also influences viral release from endosomes. Accordingly, this study targets central regulators of cholesterol synthesis, using small-molecule inhibitors to assess the effects and stage-specific actions on ASFV. The goal is to identify novel targets for ASFV drug development.

Materials and Methods

Porcine alveolar macrophages (PAMs) were isolated from 2-week-old pigs. Cells were treated with small molecule compounds and infected with ASFV simultaneously. Subsequently, the cells were collected for the detection of the antiviral effect of the compound, and its stage of action on virus reproduction was explored, and the mechanism of action of the compound was verified by exogenous supplementation of cholesterol.

Results and Discussion

We chose two cholesterol biosynthesis inhibitors AM580 and Simvastatin, they potentially inhibit ASFV replication at non-cytotoxic concentrations in vitro. Mechanism investigations indicated that these compounds primarily exert antiviral effects by disrupting the post-entry stages of the viral life cycle. Furthermore, exogenous cholesterol supplementation partially reversed the ASFV suppression elicited by both inhibitors. Collectively, these findings support that AM580 and Simvastatin inhibit ASFV replication in vitro through reducing intracellular cholesterol levels. However, considering the complexity of the internal environment, animal experiments will be conducted to confirm efficacy and safety.

Conclusion

In this study, we revealed that AM580 and Simvastatin inhibit ASFV in PAM, primarily targeting the post-entry and replication stages of the viral lifecycle. Additionally, exogenous cholesterol supplementation reversed the inhibitory effects of both inhibitors, suggesting that suppressing intracellular cholesterol levels is an important pathway for its antiviral mechanism. Together, cholesterol synthesis inhibitors have shown potential to inhibit ASFV in vitro. Future work will include in vivo validation in animal models to evaluate the efficacy and safety of the drugs.

Keywords: African swine fever virus, Antiviral, Cholesterol synthesis, Lipid metabolism, Viral replication.

EFFECTS OF PORCINE EPIDEMIC DIARRHEA VIRUS VACCINATION TIMING AND ROUTE OF ADMINISTRATION ON COLOSTRUM ANTIBODY LEVELS AND CLINICAL PROTECTION OF PIGLETS UNDER FIELD CONDITIONS

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Introduction and Objective

Porcine epidemic diarrhea virus (PEDV) causes severe diarrhea and high mortality in neonatal piglets. Because maternal antibodies are not transferred transplacentally in pigs, protection of suckling piglets depends on lactogenic immunity acquired through colostrum, particularly secretory immunoglobulin A (sIgA). This study compared colostral antibody responses induced by different PEDV vaccination programs and their association with piglet protection on a PEDV-endemic commercial farm.

Materials and Methods

The study was conducted on a 400-sow farrow-to-wean farm in Korea with continuous PEDV circulation and no PEDV vaccination history for two years. PEDV infection in diarrheic piglets was confirmed by quantitative RT-PCR, rapid antigen detection, and partial spike gene sequencing. Sows were assigned to five vaccination groups combining intramuscular inactivated and oral live PEDV vaccines. The live attenuated vaccine and the inactivated vaccine were prepared from a genotype 2b strain. PEDV-specific IgA and IgG levels in colostrum were measured using commercial ELISA kits (VDPro® PEDV IgA/IgG ELISA), and virus-neutralizing antibody titers (VNT) were determined using a cell culture-based assay. Piglet diarrhea occurrence and average weaning weight were recorded.

Results and Discussion

Oral administration of the live attenuated PEDV vaccine 1 week before farrowing significantly increased colostral IgA levels. Mean IgA S/P values were 2.39 ± 0.71 in unvaccinated controls and 3.60 ± 0.26, 3.41 ± 0.62, and 4.27 ± 0.81 in sows receiving oral live vaccination at 1 week before farrowing with or without intramuscular priming ($P < 0.001$). IgG S/P values showed limited variation among groups. Log_2-transformed VNTs differed significantly, with the highest titers observed in sows receiving repeated intramuscular priming followed by an oral live booster (7.00 ± 0.67). Clinically, PEDV-associated diarrhea and growth retardation observed before vaccination were eliminated in piglets born to sows receiving intramuscular priming and an oral live booster. Average weaning weight increased markedly from approximately 4.1 kg before vaccination to about 7.0 kg after vaccination.

Conclusion

An oral live PEDV vaccine 1 week pre-farrowing, combined with prior intramuscular priming, most effectively enhanced colostral IgA and lactogenic protection. Optimizing vaccination timing and route depending on the PED occurrence situation at the farm based on the colostral antibody profiles is critical for protective immunity in PEDV-endemic farms.

Keywords: Colostrum IgA & IgG, Live oral vaccine, Porcine epidemic diarrhea; PEDV vaccination.

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MODIFIED LIVE PRRS VACCINATION AS A CONTROL STRATEGY IN A MALAYSIAN FARM EXPERIENCING PRSS OUTBREAK WITH EU AND US STRAINS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) remain endemic in Malaysia, causing significant economic losses through impaired reproduction and increased mortality in pigs (Kuiek et al., 2015). In early 2024, a commercial farm experienced a severe PRRS outbreak involving both EU and US strains. This study aimed to evaluate the impact of implementing a mass modified live PRRS vaccination strategy on sow during the outbreak.

Materials and Methods

The case occurred in a 200-sow farrow-to-finish farm. Prior to the outbreak, sows were vaccinated against Aujeszky's disease and classical swine fever but not PRRS. Between March and May 2024, abortion rates surged to 35%, and return-to-service rates reached 60%. Diagnostic testing (serology and qPCR) confirmed PRRS infection with EU and US strains. A mass vaccination program using Ingelvac PRRS MLV vaccine was implemented, followed by a booster dose after four weeks. Performance indicators (abortion rate, return to service, pre-weaning mortality, and weaner mortality) were compared before and after vaccination.

Results and Discussion

Two mass vaccinations in sows markedly improved herd performance. Abortion rate decreased by 97.1%, and return-to-service rate improved by 90%. Piglet mortality declined from 50% during the outbreak to 10%, while weaner mortality decreased from 50 to 5%. These findings highlight the effectiveness of modified live PRRS vaccination in stabilizing sow and piglet performance during outbreaks involving multiple PRRS strains. As with any disease control program, vaccination must be integrated with strict biosecurity and proper gilt acclimation to prevent reinfection and maintain herd stability. This case also reinforces that vaccine type does not dictate vaccine choice, as cross-protection was achieved against both EU and US strains.

Conclusion

Mass vaccination with Ingelvac PRRS MLV successfully mitigated the impact of a severe PRRS outbreak and restored productivity. A structured PRRS control program, such as the 5-Steps PRRS Control approach, combined with continuous monitoring, is essential for long-term herd health.

Keywords: Abortion, Blanket vaccination, PRRS, Sow performance, Weaner mortality

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INTEGRATING ALGAE BETA GLUCAN WITH PRRS VACCINATION A STRATEGY FOR ENHANCED SURVIVAL IN NURSERY PIGS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) is a significant disease affecting the global swine industry, with estimated annual losses to 3 billion USD. This study evaluated the efficacy of combining Algae Beta Glucan (ABG) with PRRS vaccination in nursery pigs challenged with a highly virulent PRRS virus strain.

Materials and Methods

Thirty-two PRRSV-seronegative, 4-week-old pigs were randomly assigned to four groups: T1 (n = 10): PRRS vaccination + ABG (200 g/t); T2 (n = 9): PRRS vaccination only; T3 (n = 10): PRRSV challenge only (blank: no treatment, no vaccination); T4 (n = 3): Negative control (no challenge or treatment). Product ABG is dried algae containing 50% of β-1,3glucan provided by Kemin. Fostera® (PRRS Modified Live Virus from Zoetis) was given at 4-week-old. In groups T1 - T3, five pigs were intranasally inoculated with PRRSV strain 108 - 929 (10^3 TCID50/mL), with 1 mL administered into each nasal cavity at 8-week-old. The remaining five pigs in T1 - T3 were co-habited with inoculated pigs as contact infection. Parameters for evaluating were: body weight, antibody, survival rate, serum viral load, cortisol and cytokines (IL-6, IL-12, TNF-alpha, INF-alpha)

Results and Discussion

At 21 days post challenge, T3 exhibited the highest viral loads in serum (2 x 10^6) and highest mortality (90%). T2 provided limited protection (viral load 1.5x 10^3, mortality 70%), whereas T1 (combining vaccine with ABG) significantly increased the survival rate (mortality 40%) and reduced viral load (4.8 x 10^2). Comparison between the treated groups versus T3, revealed that i) the ADG in T3 was significantly lowest than treated groups; ii) the serum PRRSV load in T3 was significantly higher than T1 and T2; iii) the survival rate of T3 was significantly lower than T1 and T2.

Conclusion

The results provide evidence that vaccine plus ABG (200 g/t) was able to reduce the mortality and PRRSV load in weaned pigs, supporting AGP-free production. With a market value of USD 133 per pig, T1 group saved four additional pigs (USD 532) compared with T2, yielding an ROI of 222:1. These findings indicate potential biological and economic advantages that may contribute to improved PRRSV control and herd productivity.

Keywords: β-glucan supplementation, Economic ROI, Immunomodulation, Porcine Reproductive and Respiratory Syndrome Virus (PRRSV).

Acknowledgements: The authors thank NPUST, Taiwan for its support with providing testing facilities.

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IMPACT OF A MODIFIED LIVE PRRS VACCINATION (LINEAGE 5) ON SOW PERFORMANCE DURING A PRRS LINEAGE 1 STRAIN OUTBREAK IN A MALAYSIAN COMMERCIAL FARM

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) remains endemic in Malaysia, causing significant economic losses through impaired reproduction and increased piglet mortality (1). PRRS impairs the reproductive performance of sows and boars, it also causes respiratory disease in wean-to-finish (2). In early 2025, a commercial farm vaccinating with Ingelvac PRRS MLV vaccine (Lineage 5) experienced PRRS outbreak associated with Lineage 1. This study aimed to evaluate the impact of implementing blanket vaccination with Ingelvac PRRS MLV on sow performance during the outbreak.

Materials and Methods

The case occurred in an 800-sow farrow-to-finish farm in Malaysia. In December 2024, purebred gilts of unknown PRRS status were introduced and kept in a quarantine area located near production units. Between February and April 2025, late-term abortions, increased returns to service, reduced farrowing rates, and elevated pre-weaning mortality were observed. Diagnostic testing (serology and qPCR) confirmed PRRS infection with the EU & US strain, sequencing identified Lineage 1. Subsequently, two blanket vaccinations with Ingelvac PRRS MLV, four weeks apart were carried out. Farm performance indicators (abortion rate, return to service, farrowing rate, pre-weaning mortality) were compared before and after vaccination.

Results and Discussion

After vaccination, abortion storm ceased, return-to-service rate decreased by 75%, farrowing rate improved by 28.7%, and pre-weaning mortality declined by 35.9%. This demonstrates that Ingelvac PRRS MLV effectively controlled outbreaks caused by Lineage 1 strains, even when the vaccine lineage differs from the circulating virus. These findings provide real-world evidence of cross-protection, which is critical given the genetic diversity of PRRS viruses. However, vaccination alone is not sufficient for sustainable control. Success depends on integrating vaccination with strict biosecurity measures and proper gilt acclimation to minimize pathogen introduction and transmission. This holistic approach ensures long-term herd stability and productivity.

Conclusions

Ingelvac PRRS MLV demonstrated strong efficacy in controlling a PRRS Lineage 1 outbreak and restoring sow performance. Importantly, this case confirms that vaccine lineage does not dictate vaccine choice, as cross-protection was achieved against a newly circulating strain. A holistic 5-Steps PRRS Control program remains a critical systemic approach for managing PRRS outbreaks.

Keywords: PRRS, Outbreak, Reproductive failure.

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EVALUATING THE ANTIVIRAL ACTIVITY OF FINIO AGAINST PEDV AND PRRSV USING VIABILITY RT-QPCR

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Introduction and Objectives

Anitox offers the commercial product Finio for the control of microbial contamination in feed. Finio was launched in 2017 in the EU and is under registration process in the U.S. as a non-formaldehyde solution containing patent protected formulation of novel phytochemical and carboxylic acids. Recently Finio has shown a log reduction of 4.5 log10 units of viable viral particles against the megavirus Emiliania huxylei virus (EhV), a surrogate for African swine fever virus (ASFV) (Palowski et al., 2025). To date, Finio has yet to be tested for its potential antiviral activity, if any, against common swine viruses such as porcine epidemic diarrhea virus (PEDV) and porcine reproductive and respiratory syndrome virus (PRRSV). We previously conducted a Finio dose response analysis using the ASFV-like surrogate, EhV (Palowski et al., 2025). Therefore, the objective of this study was to evaluate any antiviral properties of Finio at 0.3% final concentration against PEDV and PRRSV after 24 hours exposure.

Materials and Methods

Samples of PEDV and PRRSV L1C (6 log10 copies) in biological triplicates were treated with Finio at a 0.3% for 24 hours at 20°C. Samples were then evaluated for virus viability using viability RT-qPCR methods optimized by Balestreri et al. 2024. Briefly, the QuantiNova SYBR Green RT-qPCR kit (Qiagen, CA, US) was used at the following conditions: 10 min at 50 and 10 min at 95°C followed by 40 cycles of 15 s at 95°C and 60 s at 60°C for both viruses.

Results and Discussion

After 24 hours exposure, 0.3% Finio significantly reduced viable virus particles of both PEDV and PRRSV (P = 0.0064 and 0.0004, respectively). We observed a reduction of 4.5 $\log_{10}$ units of viable PEDV particles and a reduction of 4.7 log10 units of viable PRRSV particles.

Conclusion

Finio show promising potential as an antiviral chemical mitigation tool against swine viruses by degrading the virus particle itself. Additional research is needed, particularly in feedstuffs using viability RT-qPCR methods to determine further potential of Finio as a biosecurity tool in the swine industry.

Keywords: Porcine epidemic diarrhea virus, Porcine reproductive and respiratory syndrome virus, Viral inactivation, Viability RT-qPCR.

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SWIAV GENOTYPING RESULTS IN FRENCH PIG FARMS FROM 2023 TO 2025

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Introduction and Objectives

Swine influenza A virus (swIAV) causes respiratory and reproductive disorders in swine herds and harbors a potential zoonotic risk. Characterization of circulating strains is now routinely available in French veterinary diagnostic laboratories by whole genome sequencing (WGS) (Moalic et al., 2025). The aim of this investigation is to share the genotyping results of a private hold passive surveillance on swIAV performed in France from late 2023 to end of 2025.

Materials and Methods

In 491 farms facing flu evocative clinical signs, between 1 and 30 samples (nasal swabs, broncho-tracheal mucus, lungs or oral fluids) were collected by veterinary practitioners. Presence of swIAV was assessed by RT-qPCR targeting the M gene on pooled samples (up to 5 samples/pool). WGS was performed on pools with a Cq < 30. An automated bioinformatics pipeline was used to generate consensus sequences for swIAV genotyping. These sequences were aligned to a curated French NRL database to assign segment lineages, and results were confirmed by phylogenetic analysis of viral subtype and genotype.

Results and Discussion

SwIAV was detected in 35.2% of the investigated farms. Weaned piglets below 12 weeks of age were the most frequently sampled age group (48.2% of the sampled animals) and showed a positivity rate of 37.8 %. Additional samples were collected from fatteners (21.3%), breeders (15.9%) and suckling piglets (12.6%) with positivity rates of 21.5%, 34% and 29.8%, respectively. Genotyping was successful on 74 pools. Nine different genotypes were identified. The highly predominant genotype was H1avN2#E (HA-clade 1C.2.4, N2-Gent lineage, Internal Genes (IG) clade EA-DK) (52/74), followed by H1avN1#A (HA-clade 1C.2.1, N1-clade EA, IG-clade EA) (5/74), H1N1pdm#A (HA-clade 1A.3.3.2, N1-clade pdm09, IG-clade pdm09) (4/74) and H1avN1#C (HA-clade 1C.2.2, N1- clade EA, IG-clade EA) (3/74). Three genotyped swIAV without HA-clade 1A.3.3.2 or N1-clade pdm09 hid IG-clade pdm09. In addition, seven genotyped swIAV presented unexpected IG according to their lineage.

Conclusion

This passive surveillance provides initial insight into the genetic diversity of swIAV in French domestic swine. Further results are needed to confirm that genotype diversity is increasing, as the comparison with Moalic et al. data tends to show.

Keywords: Influenza A virus, flu, genotype, respiratory disease, whole genome sequencing.

Acknowledgements: We thank Labocea, Labofarm-Bio Chêne Vert and the French NRL for the performed analyses and the shared knowledge on swIAV. We thank the veterinarians, farmers, and colleagues whose dedicated support for farm sampling was essential to this work.

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COMPARATIVE EFFECTIVENESS OF TWO VACCINES IN A TAIWANESS SWINE HERD WITH PCV2D SUBCLINICAL INFECTION

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is a major swine pathogen with substantial genetic diversity. Ongoing PCV2 evolution raises concerns regarding vaccine breadth and field effectiveness (Bandrick et al., 2020). This study compared the effectiveness of a trivalent PCV2a/ PCV2b/ *Mycoplasma hyopneumoniae* (MHP) vaccine with a bivalent PCV2a/MHP vaccine in a commercial Taiwanese herd with subclinical PCV2d infection.

Materials and Methods

The trial was conducted on a 4,000-sow farrow-to-finish farm in Taiwan. Piglets were allocated into two groups: Group Z received the trivalent vaccine Fostera® Gold PCV MH, while Group M received a bivalent vaccine (VacA). Survival from weaning to market was assessed across 45 batches between March 2023 and May 2024. For epidemiological evaluation, one representative batch per group was selected. Blood samples were collected from 10 piglets at 3 weeks old (pre-vaccination), and at 7, 11, 15, and 20 weeks of age. Serum samples were tested for PCV2 viremia and PCV2-specific antibodies using a commercial ELISA (BioChek). Additionally, T-cell epitope content (EpiCC) of both vaccines was analyzed by CircoMatch™ (EpiVax Inc.).

Results and Discussion

All PCV2 isolates from the farm belonged to PCV2d genotype. CircoMatch™ analysis demonstrated that trivalent vaccine provided 34% higher T-cell epitope coverage than the bivalent VacA. At 3, 7, and 11 weeks of age, the PCV2 viremia positive rate in Group M was 13.3%, whereas Group Z remained negative. Group M seroconverted between 7 and 11 weeks, whereas Group Z seroconverted between 11 and 15 weeks. These results suggest more pronounced early natural exposure in Group M. Among over 55,000 pigs from 45 batches, survival from weaning to market was higher in Group Z (95%) than Group M (94%); the difference was not statistically significant ($P > 0.05$). These results suggest including a dual PCV2 genotype in the vaccination program may improve coverage in herds with circulation of heterologous or PCV2 co-infections with multiple genotypes.

Conclusion

Fostera® Gold PCV MH provided broader immunological coverage and improved field performance compared with a bivalent PCV2a-based vaccine in a herd with subclinical PCV2d infection, resulting in improved pig survival from weaning to market.

Keywords: Porcine circovirus type 2, Trivalent vaccine, Vaccine effectiveness

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COMPARATIVE FIELD EVALUATION OF TWO VACCINES AGAINST LINEAGE 1 AND LINEAGE 3 PRRSV-2 IN A TAIWANESE SWINE FARM

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) is a major challenge for global swine production. The co-circulation of PRRSV-2 Lineages 1 and 3 in Taiwan complicates disease control (Kuo et al., 2025). Vaccination with Modified Live Virus (MLVs) vaccines is a cornerstone for PRRS control; however, comparative field data for different lineages are limited. This study evaluated two PRRS MLV vaccines on a commercial Taiwanese farm, assessing nursery mortality, growth, and herd stability using Statistical Process Control (SPC).

Materials and Methods

The study was conducted in a 700-sow farrow-to-finish farm in Taiwan under endemic PRRS. The breeding herd received quarterly vaccination, and piglets were vaccinated at 7 - 10 days. From June 2021 to March 2022, a PRRSV-2 Lineage 5.1 MLV vaccine (Ingelvac PRRS® MLV, Boehringer Ingelheim) was used, then switched to PRRSV-2 Lineage 8 MLV (Fostera® PRRS, Zoetis) from April 2022. Data collection (June 2021–July 2025) and monitoring were supported by the farm staff under routine production conditions. Nursery mortality and average daily gain (ADG) were compared, and mortality trends were analyzed using Shewhart individual control charts (Minitab 20.1.1).

Results and Discussion

Routine molecular monitoring indicated PRRSV-2 Lineage 3 predominated prior to April 2025, while Lineage 1 was detected thereafter. Viral sequence analyses revealed ongoing introduction of wild-type strains and persistent biosecurity gaps. Nursery mortality was significantly lower during the Lineage 8 MLV period than the Lineage 5.1 (9.8% vs. 16.1%; $P < 0.01$). SPC analysis demonstrated improved stability and reduced variability in nursery mortality following adoption of the Lineage 8 PRRS MLV vaccine. Nursery ADG was significantly higher in the Lineage 8 MLV period compared with the Lineage 5.1 (318.5 vs. 248.1 g/day; $P < 0.01$). The observed benefits of Fostera® PRRS are based on numerical outcome differences under field conditions; strict experimental control was not possible.

Conclusion

Under conditions where PRRSV-2 Lineage 1 emerged following Lineage 3 in Taiwan, use of Fostera® PRRS was associated with lower nursery mortality, enhanced growth performance, and greater production stability compared to the Lineage 5.1 PRRS MLV vaccine. These findings support the use of vaccination in PRRS control programs under dynamic viral epidemiology.

Keywords: Growth performance, Lineage 1, Lineage 3, Nursery mortality, Porcine reproductive and respiratory syndrome.

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DETECTION OF PORCINE SAPOVIRUS IN NATURALLY INFECTED PIGS AND ITS ASSOCIATION WITH OTHER PATHOGENS

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Introduction and Objectives

Porcine Sapovirus virus genotype III (PSaV) is an emerging swine enteric pathogen. Pigs experimentally challenged with PSaV develop intestinal lesions of villus atrophy and blunting and diarrhea, but evidence linking sapovirus detection to intestinal lesions in naturally infected pigs and association of PSaV with other common swine pathogens is poorly documented. The objective of this study was to characterize the demography of PSaV in naturally infected pigs and identify co-occurrences among PSaV and other prevalent swine pathogens.

Materials and Methods

Data from cases submitted to the UMN Veterinary Diagnostic Laboratory for diagnostic investigation of diarrhea from November 2022 to November 2025 were obtained for analysis. The original dataset consisted of all pigs evaluated for PSaV by real-time PCR, and the results of all other diagnostic tests performed on these pigs. RStudio was used for correlation analysis.

Results and Discussion

From the 2541 cases selected, 2230 were PSaV positive (87.8% prevalence). The prevalence by age group was: 77.4% in pigs from 0 - 7 days old, 90.2% in pigs from 8 - 21 days, 96% in pigs from 22 - 50 days, and 71.5% in pigs older than 50 days. The prevalence by year was: 92.7 ± 1.73% in 2022, 89.5 ± 7.48% in 2023, 89.0 ± 4.96% in 2024, and 82.3 ± 19.68% in 2025. Out of the initial 42 pathogens included in the correlation analysis, 9 [*E. coli, G. parasuis, M. hyopneumoniae*, Parvovirus type 2, PRRSv, Rotavirus, and *S. suis*] were identified as possibly co-occurring with PSaV ($P < 0.2$) and were included in further evaluations. Of all PSaV positive pigs, 60.7% were also positive for rotaviruses A, B, and C. Weak to moderate correlations were found between PSaV and rotavirus A (OR = 5.04, $P < 0.0001$), B (OR = 2.19, $P < 0.0001$), and C (OR = 0.30, $P < 0.0001$). A strong, positive correlation was found between PSaV and β-haemolytic *Escherichia coli* (OR = 349.13, $P < 0.0001$).

Conclusion

The preliminary results of this study indicate a high prevalence of PSaV in naturally infected pigs with diarrhea and demonstrate an association between PSaV, rotavirus, and β-haemolytic Escherichia coli infections.

Keywords: Co-infection, Diagnostic Surveillance, Diarrhea, Intestinal Disease, PSaV.

Acknowledgements: University Veterinary Diagnostic Laboratory for providing the dataset.

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MORPHOLOGICAL CHANGES IN THE ENDOMETRIUM OF GILTS INFECTED WITH PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a primary driver of reproductive failure in swine. In pregnant sows, PRRSV infection is characterized by severe lesions at the maternal-fetal interface during late gestation, including localized apoptosis, lymphohistiocytic endometritis, vasculitis, and placental detachment. While these late-gestation lesions in mature sows are widely recognized, the specific pathological effects of PRRSV on the endometrium of replacement gilts, which plays a crucial role in implantation and pregnancy maintenance, remain poorly understood. The present study aims to evaluate the morphological changes in the endometrium of replacement gilts infected with PRRSV.

Materials and Methods

Genital organs were evaluated from a selected cohort of 64 gilts culled for reproductive failure. To ensure definitive classification, inclusion in this study required consistent diagnostic results; therefore, only gilts testing positive on both ELISA (S/P > 0.4) and immunohistochemistry (IHC) (PRRSV-infected group; n = 20), or negative on both assays (non-infected group; n = 44), were selected for examination. The uterine horns were dissected, preserved and cut according to routinely histological procedures and stained with hematoxylin & eosin (H&E). The endometrium samples were evaluated by histological and histomorphometric studies under light microscope.

Results and Discussion

The results revealed that the increasing of the immune cell infiltration within the subepithelial layer and in the epithelial surface including the sloughing of uterine epithelium was significantly ($P < 0.05$) observed in the PRRSV-infected gilts. Besides, the heights of uterine epithelium, the density of subepithelial blood vessels and the estimated edematous scores were significantly elevated in the infected group ($P < 0.05$) compared to the non-infected group. Dense infiltration of lymphocytes, macrophages, and plasma cells, particularly around uterine glands and blood vessels, were consistently observed in infected samples, indicating chronic endometritis.

Conclusion

These findings suggested that the PRRSV-infected gilts exhibit deteriorative morphological changes leading to endometritis. Although the impact of untested co-infecting agents cannot be excluded, the results provided a possible pathological explanation for the high culling rates due to anestrus and repeat breeding in PRRSV-positive herds; hence, highlight the importance of monitoring PRRSV status in replacement gilts and maintaining strict biosecurity and herd-level disease control measures to prevent reproductive losses.

Keywords: Endometrium, Morphology, Gilt, PRRSV.

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EVALUATION OF A NANOSCALE HIGH-THROUGHPUT SMARTCHIP REAL-TIME PCR PLATFORM FOR PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV) DETECTION

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a major and evolving threat to the U.S. swine industry, with estimated annual losses of $1.2 billion. Although reverse-transcription quantitative real-time PCR (RT-qPCR) in a 96 wells format is the current diagnostic standard, its limited throughput and high reagent costs constrain large-scale surveillance. High-throughput nanoscale PCR platforms, such as the SmartChip Real-Time PCR System (SCRPS), miniaturize reactions and enable thousands of parallel RT-qPCR assays. This study evaluated the performance of the commercial VetMAX™ PRRSV 3.0 assay on the SCRPS platform compared with the ABI 7500 Fast Real-Time PCR system (ABI).

Materials and Methods

Samples included synthetic PRRSV controls, PRRSV-positive sera from an experimental study (n = 145), and PRRSV-negative diagnostic specimens spiked with MN184 and 1-7-4 L1A isolates at low, medium, and high concentrations. Viral RNA was extracted using the KingFisher™ Apex system with the MagMAX™ Pathogen RNA/DNA Kit. The VetMAX™ PRRSV 3.0 assay was performed as a multiplex assay on ABI and as a custom singleplex FAM-labeled assay on SCRPS using 4× TaqMan™ Fast Virus 1-Step Master Mix, with four technical replicates per sample under manufacturer-recommended cycling conditions.

Results and Discussion

All negative samples remained negative on both platforms. Quantification cycles (Cq) values were comparable between SCRPS and ABI up to the SCRPS cutoff (Cq = 31). However, SCRPS showed reduced analytical sensitivity (100 copies/µL; Cq 32.5 ± 1) compared with ABI (10 copies/µL; Cq 34 ± 0.6). Among positive sera, the mean Cq bias (ABI-SCRPS) was −0.88, with 95% limits of agreement from -1.91 to -0.15 and an overall %CV < 4%. In spiked samples, mean Cq values at high, medium, and low concentrations were 18.52, 24.83, and 30.35 on SCRPS, versus 16.64, 23.40, and 30.04 on ABI, with %CVs of 7.42, 4.16, and 0.80, respectively. Intra- and inter-assay variability on SCRPS were < 7 and < 10%, respectively.

Conclusion

Although SCRPS showed high precision and reproducibility, reduced analytical sensitivity may limit its use for routine PRRSV diagnostics, particularly in low–viral load samples. Ongoing work focuses on improving sensitivity and evaluating cost-effective, high-throughput differentiation of wild-type and vaccine strains.

Keywords: Diagnostics, High-throughput qPCR, PRRS virus, SmartChip Real-Time PCR system.

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AUTOMATED HIGH-THROUGHPUT TESTING FOR PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS DETECTION USING 384-WELL RT-QPCR ASSAY

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Introduction and Objectives

Reverse-transcription quantitative real-time PCR (RT-qPCR) is the standard diagnostic method for detecting porcine reproductive and respiratory syndrome virus (PRRSV), one of the most economically significant diseases affecting the U.S. swine industry (Osemeke et al., 2025). Testing nearly 400,000 PRRSV samples in 2023 using a 96-well RT-qPCR format underscored the need for higher-throughput diagnostics at the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL). The objective of this study was to evaluate the performance of a 384-well RT-qPCR assay integrated into a fully automated workflow using the QuantStudio™ 7 Pro (QS 7 Pro) system and to compare its performance with the routinely used 96-well ABI 7500 Fast Real-Time PCR system.

Materials and Methods

Samples included synthetic PRRSV controls, PRRSV isolates MN184 and 1-7-4 L1A, and diagnostic specimens submitted to ISU-VDL. Viral RNA was extracted using the MagMAX™ Pathogen RNA/DNA Kit on the KingFisher™ Apex system. The VetMAX™ PRRSV 3.0 assay was performed in 20 µL (96-well) and 10 µL (384-well) reaction formats. For the 384-well automated workflow, automated liquid handling (Bravo, Agilent Technologies), plate sealing, incubation, and transfer to the QS 7 Pro system was performed using integrated robotic instrumentation (4 °C automated Cytomat incubator, Orbitor-RS2 plate mover) and scheduling software (Momentum). A continuous 13-hour automated workflow was evaluated across five sequential 384-well runs using the same diagnostic samples. Data analysis was performed using GraphPad Prism.

Results and Discussion

The 384-well QS 7 Pro platform produced Cq values comparable to those of the 96-well ABI platform, with a Cq cutoff of 37. Intra- and inter-assay variability on the 384-well platform were low, with CVs of 1.4% and 0.4%, respectively, and variability between platforms was < 3% across multiple runs. The automated workflow reliably transferred 384-well plates sequentially without delays, with run-to-run variability below 5% and stable positive control performance with repeatable Cq values of 29 ± 1.

Conclusion

The automated 384-well RT-qPCR workflow demonstrated equivalent analytical performance to the conventional 96-well format while substantially increasing throughput and efficiency. This system enables processing of approximately 4,000 samples within a 12-hour operation, supporting rapid, cost-effective PRRSV diagnostics and timely disease control efforts.

Keywords: 384-well RT-qPCR, Automation, Diagnostics, High-throughput qPCR, PRRS virus.

Acknowledgements: The authors thank the ISU-VDL molecular section for providing the samples. The project is partly funded by the United States Department of Agriculture (USDA) - Animal and Plant Health Inspection Service (APHIS) and National Animal Health Laboratory Network (NAHLN) Farm Bill grants.

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STRAIN-DEPENDENT VIRULENCE AND INTESTINAL MICROBIOTA DYNAMICS OF PORCINE AND BOVINE ROTAVIRUS A IN NEONATAL BALB/C MICE

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Introduction and Objectives

Rotavirus A (RVA) is a major cause of neonatal diarrhea in livestock, resulting in significant economic losses worldwide. Although porcine and bovine RVA strains differ genetically and antigenically, direct in vivo comparisons of their relative virulence and effects on intestinal microbial homeostasis remain limited. Understanding strain-dependent differences in replication dynamics and host-microbiota interactions is critical for clarifying disease severity and informing control strategies. This study aimed to compare the virulence of porcine RVA G9P[23] and bovine RVA G6P[1] in neonatal BALB/c mice using integrated clinical, virological, histopathological, and longitudinal microbiota analyses.

Materials and Methods

Six timed-pregnant BALB/c dams (7 ± 1 pups/dam) were allocated to three groups (two dams/group; ~14 - 16 pups/group). Neonates were orally inoculated with 1×10^5 $TCID_{50}$ virus; mock controls received MEM. Diarrhea incidence was recorded from 12 - 96 hpi. Small intestinal viral load was quantified using a VP6-specific RT-qPCR assay at 24, 48, and 72 hpi. At 3 dpi, three mice per group were examined histologically and by immunohistochemistry. Colonic microbiota were analyzed longitudinally at 1, 2, and 3 dpi (n = 3/timepoint) using 16S rRNA sequencing.

Results and Discussion:

Diarrhea peaked at 24 hpi in 58.3% (7/12) of porcine-infected mice and 33.3% (4/12) of bovine-infected mice, while mock mice remained asymptomatic. Viral RNA was detected in all infected animals, with significantly higher VP6 genome copy numbers in the porcine group at 24 and 48 hpi, followed by decline at 72 hpi. Histopathology at 3 dpi revealed villous atrophy in 3/3 infected mice per group, with more pronounced epithelial damage in porcine infection. Longitudinal microbiota profiling demonstrated dysbiosis in all infected mice, characterized by Lactobacillus depletion and Proteobacteria expansion. Notably, porcine infection induced earlier loss of microbial diversity and greater community instability. These findings suggest that enhanced viral replication correlates with aggravated mucosal injury and accelerated disruption of intestinal microbial succession.

Conclusion:

The neonatal BALB/c model discriminates strain-dependent RVA virulence. Porcine G9P[23] exhibits enhanced replication, higher diarrhea incidence, more severe intestinal pathology, and accelerated microbiota destabilization compared with bovine G6P[1], highlighting links between viral replication kinetics and intestinal ecosystem imbalance.

Keywords: Intestinal pathology, Gut microbiota dynamics, Neonatal BALB/c mouse model, Rotavirus A, Strain-dependent virulence, VP6 RT-qPCR.

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GENETIC DIVERSITY DEPENDING ON PRRSV INFECTION STATUS IN PIG HERDS IN VIETNAM FROM 2023 TO 2025

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Introduction and Objectives

PRRS is one of the most important diseases affecting the global pig industry, and vaccination is considered one of the most effective tools for PRRS control. In Vietnam, Nguyen et al. (2022) first reported the emergence of PRRSV lineage 1. The infection status and genetic variability of PRRSV can influence protective immunity (Labarque et al., 2004). This study aimed to clarify the genetic diversity of PRRSV and the stage of active PRRSV infection so that contribute to more effective PRRS control strategies, particularly vaccination-based programs.

Materials and Methods

A total of 332 serum samples collected from sows, suckling piglets, and growing pigs from 14 farms with subclinical PRRSV infection, along with 310 PRRSV-positive samples (VDx® HP-PRRSV qRT-PCR Ver 1.1 kit, Median Diagnostics), were obtained over a three-year period (2023 - 2025) for analysis. Among these, 289 ORF5 sequences of PRRSV-2 were analyzed to determine lineage or sublineage according to Yim-Im et al. (2023), and RFLP patterns were identified using the RFLP Tool (Iowa State University).

Results and Discussion

The results showed that all 14 PRRSV-vaccinated farms had subclinical PRRSV infections, with higher viral activity observed during the growing stage. Most farms (92.9%) were infected with PRRSV genotype 2. Overall, one lineage of genotype 1 and seven lineages of genotype 2 (L1, L4, L5, L7, L8, L10, and L11) were detected. Over time, the prevalence of genotype 1 decreased, whereas genotype 2 increased. For genotype 1, sublineage L1.11 consistently showed the highest prevalence, ranging from 72.23% to 88.89%. Regarding genotype 2, lineages 1, 5, and 10 were predominant across all three years, with prevalence ranging from 29.88 to 51.43% for L1, 10 to 32.31% for L5, and 12.31 to 30.52% for L10. RFLP analysis revealed substantial genetic diversity, with 24 distinct RFLP patterns. The most prevalent patterns were 2-5-2, 1-4-3, 1-39-4, 1-16-3, 1-7-4, and 1-7-3. Differences in genotype distribution and RFLP patterns were observed between subclinical and clinical PRRSV infections.

Conclusion

This study demonstrated considerable genetic diversity of PRRSV in Vietnam, as characterized by lineage classification and RFLP patterns, depending on the infection status of pig herds.

Keywords: Genotype, Lineage, PRRSV infection status, RFLP.

Acknowledgements: The authors thank the Elanco Vietnam for the financial support and P&Y Livestock Services Company Limited, Vietnam with providing testing facilities.

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DIAGNOSTIC SURVEY OF PORCINE CIRCOVIRUS TYPE 2 IN VIETNAMESE PIG FARMS, 2018 - 2022

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is the causative agent of porcine circovirus-associated diseases (PCVAD), which cause major economic losses in swine production worldwide. This study aimed to update information on the presence of PCV2 in diagnostic samples collected from Vietnamese pig farms between 2018 and 2022, providing baseline data to support vaccination and biosecurity programs.

Materials and Methods

Between 2018 and 2022, a total of 1,961 diagnostic samples - including blood/serum, pooled tissues, oral fluids, aborted fetuses, semen, saliva, and DNA/RNA extracts - were submitted from healthy and clinically affected pigs across Vietnamese farms. PCV2 detection was performed by PCR assays targeting the conserved ORF2 region.

Results and Discussion

Overall, 579/1,961 samples (29.53%) tested positive for PCV2. Positivity rates were highest in 2018 (52.41%) and 2020 (45.39%), followed by a marked decline in 2021 (15.45%) and 2022 (11.81%). Oral fluid (63.01%) and pooled tissue samples (53.67%) showed higher detection rates than blood/serum (24.26%). Age-specific analysis revealed nursery pigs (32.25%) and grower/finisher pigs (30.70%) as the most affected groups, while sows (19.37%) and boars (6.72%) had lower rates. The decline after 2020 likely reflects improved vaccination and biosecurity, though persistent detection in certain samples indicates ongoing viral circulation.

Conclusion

This diagnostic survey highlights dynamic fluctuations in PCV2 positivity in Vietnam from 2018 to 2022, with a clear downward trend. Oral fluid and tissue samples proved more sensitive than blood, and nursery/grower pigs were the most vulnerable age group. These findings provide updated baseline data to guide vaccination strategies, biosecurity measures, and continuous surveillance of PCV2 circulation in Vietnamese pig production systems.

Keywords: Positivity, Porcine circovirus type 2, PCVAD, PCR, Vietnam.

Acknowledgements: The authors thank Nong Lam University HCMC, Vietnam for the support with providing testing facilities.

PRRSV-2 RECOMBINATION: THE INTERPLAY OF VIRAL FIDELITY, REPLICATION EFFICIENCY, AND BACKBONE FITNESS SHAPING THE "RECOMBINATION ENGINE" AND "FITNESS TRAP"

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Introduction and Objectives

Recombination drives porcine reproductive and respiratory syndrome virus (PRRSV) evolution. Currently, PRRSV-2 lineage 1C NADC30-like (L1C) and lineage 8E (L8E) modified live vaccine revertant recombinants dominate in China. Conversely, lineage 5A (L5A) recombinants are rarely detected despite widespread L5A vaccines use. We investigated the interplay of replicase fidelity, viral fitness, and strain-specific phenotypes to elucidate this disparity.

Materials and Methods

Primary porcine alveolar macrophages (PAMs) were co-infected with representative strains CHsx1401 (L1C), BJ-4 (L5A), and JXwn06 P80 (L8E) at a multiplicity of infection of 0.5 per strain. At 24 h post-inoculation, supernatants were analyzed via direct next-generation sequencing. To assess viable recombinants, the progeny viruses collected from PAMs were isolated by plaque purification on MARC-145 cells and characterized via whole-genome sequencing.

Results and Discussion

Sequencing revealed that the L5A replicase is intrinsically error-prone, generating high-frequency junctions similar to L1C. However, a stark disconnect exists between molecular events and viable progeny survival. L1C/L8E co-infection yielded 100% recombinants, whereas L5A/L8E produced less than 20%. L5A-backbone recombinants were eliminated via competitive exclusion, revealing a "fitness trap". Conversely, L1C acted as a potent "recombination engine", leveraging robust replication and a fit backbone to ensure progeny survival. Notably, even when utilizing the fit L1C backbone, co-infection with L5A generated a lower recombinant rate (75%) compared to L8E (100%), indicating L5A genetic sequences confer a competitive disadvantage.

Conclusion

PRRSV recombination is a complex outcome governed by multi-dimensional phenotypic profiles. The dominance of L1C and scarcity of L5A recombinants result from an intricate interplay of replication efficiency, template abundance, and backbone fitness. Viral evolution is shaped by strict biological constraints, where specific phenotypic weaknesses prevent certain lineages from diversifying the viral population.

Keywords: Co-infection, Fitness trap, NADC30-like, PRRSV, Recombination.

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ISOLATION AND IN VITRO CHARACTERIZATION OF A PORCINE EPIDEMIC DIARRHEA VIRUS VARIANT STRAIN ASSOCIATED WITH THE RECENT OUTBREAKS IN ILLINOIS AND IOWA

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) remains a major threat to the U.S. swine industry. Beginning in June 2024, multiple sow farms in Illinois and Iowa experienced PEDV outbreaks and the previously used control strategies were not effective. This study aimed to characterize the PEDV associated with these recent outbreaks.

Materials and Methods

Sixty-nine samples from seven outbreak sow farms (two in Illinois and five in Iowa) between June 2024 and December 2024 were first tested by a PEDV screening PCR targeting the conserved nucleocapsid gene. Fifteen PCR-positive samples were selected for spike (S1) gene sequencing and virus isolation attempts in Vero cells. Whole-genome sequencing was performed on one clinical sample and three cell culture isolates. Comparative sequence and phylogenetic analyses were conducted. Additionally, sera collected 28 days post-inoculation from pigs inoculated with a 2013 non-S INDEL or a 2014 S INDEL PEDV isolate were evaluated for cross-neutralization against the 2024 PEDV variant.

Results and Discussion

Fifty-four of 69 samples tested positive for PEDV and negative for PDCoV, TGEV, and SADS-CoV. S1 sequences from the 15 samples (7 from Illinois and 8 from Iowa) all phylogenetically clustered with non-S INDEL PEDV but contained a previously unreported 6-nucleotide deletion compared to the U.S. non-S INDEL PEDV identified in 2013. Virus isolation was successful for four samples. Illinois and Iowa isolates shared 99.9% whole-genome nucleotide identity and 99.8% S1 nucleotide identity and consistently exhibited the 6-nt deletion in the S1 gene, with no insertions or deletions observed in other genomic regions. Sera from pigs inoculated with a 2013 non-S INDEL PEDV isolate showed low cross-neutralization against the 6-nucleotide deletion variant. Sera from pigs inoculated with a 2014 S INDEL PEDV isolate showed minimal cross-neutralization.

Conclusion

The 2024 PEDV outbreaks involved a novel non-S INDEL variant containing a unique 6-nucleotide deletion in the S1 gene. This PEDV variant was successfully isolated in cell culture. Limited cross-neutralization by antibodies induced by earlier PEDV strains suggests challenges for effective control of this novel PEDV variant. Future studies will evaluate the virulence, shedding dynamics, and cross-protective immunity of this variant in pigs.

Keywords: 6-nucleotide deletion variant, Cross-neutralization, PEDV, Spike gene, Virus isolation,

Acknowledgements: This project was partially funded by Swine Health Information Center.

ONE WAY OR ANOTHER: HOW COMBINATIONS OF COMMERCIAL INFLUENZA A VIRUS VACCINES IN PIGS AFFECT THE IMMUNE RESPONSE

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Introduction and Objectives

Whole virus inactivated adjuvanted vaccines are widely used and are in some countries the only option for swine influenza A virus (swIAV) control, however, the broadness of protection of these vaccines has been questioned. A recent study showed that the order of different swIAV strains in a three dose-vaccination scheme affected the level of cross-protection. The objective of this study was to evaluate the immune responses and efficacy of five different three-dose vaccination schemes using two commercial vaccines in heterologous, homologous or double-shot combinations. The double-shot included both vaccines at each vaccination.

Materials and Methods

In total, 38 five-weeks-old pigs were divided into five vaccination groups (n = 6/group) and one control groups (n = 8). All groups were vaccinated three times spanned by three weeks. Two weeks after each vaccination blood was obtained to evaluate the level of NP and neutralizing -antibody levels. After the last vaccination, the two heterologous vaccination groups were exposed to two different swIAV strains by direct contact to infected non-vaccinated pigs.

Results and Discussion

A significantly higher NP antibody titer was observed in one of the heterologous vaccination groups after the second vaccination, whereas the double-shot vaccination group was the only group with higher titers after the third vaccination. The virus neutralization tests against twelve different contemporary swIAV strains including the challenge strains revealing differing but generally high titers with extensive cross-reactions. However, the double-shot vaccination group showed similar titers as the heterologous vaccination groups. Finally, 11/12 vaccinated pigs exposed to swIAV by direct-contact tested swIAV-positive in nasal swabs and tissues from the upper respiratory tract and 8/12 were positive in lungs, illustrating that despite high neutralizing antibody titers there was limited effect on swIAV infection.

Conclusion

Combinations of two currently available commercial swIAV vaccines produced differing antibody responses in pigs with mainly the NP antibody response impacted by the different vaccine schemes contrary to the neutralizing antibody responses. Importantly, after three vaccinations all but one pig was infected with two currently circulating swIAV strains highlighting the limited effect on viral shedding of the currently available swIAV vaccines and the need for novel control strategies.

Keywords: Influenza A virus, Inactivated vaccines, Neutralizing antibodies, Respiratory infections, Vaccinations.

Acknowledgements: We acknowledge the Danish Swine Levy Foundation and the Novo Nordisk Foundation (NNF19OC0056326) for funding this study.

EVALUATION OF HUMORAL IMMUNE RESPONSE AND SAFETY FOLLOWING LIVE JAPANESE ENCEPHALITIS VACCINATION IN SOWS

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Introduction and Objectives

Japanese encephalitis virus (JEV) is endemic in Asia and Vietnam, where pigs act as major amplifying hosts and suffer reproductive losses (Li et al., 2025; Mulvey et al., 2021). Vaccination is essential for control, yet field data on humoral immune response and vaccine safety in sows remain limited in Vietnam. This study evaluated the humoral immune response and safety of a live attenuated JEV vaccine in sows under commercial farm conditions.

Materials and Methods

A total of 120 clinical healthy sows already artificially inseminated were intramuscularly vaccinated one time with SuiShot® JE vaccine (CAVAC, Korea) and monitored for post-vaccination abnormalities including reproductive disorder and performance to evaluate the safety and efficacy of vaccine. Among them, 30 sows were blood-sampled on Day 0 and Day 21 post-vaccination to assess the humoral immune response with commercial indirect ELISA kit for IgG detection (MEDIAN Diagnostics, Korea). Pre- and post-vaccination S/P ratios were comparatively analyzed. The data were managed and analyzed using Microsoft Excel.

Results and Discussion

All 120 vaccinated sows exhibited clinically tolerance, with rectal temperatures within physiological limits, mild self-limiting vomiting in 2.5% of animals, and no viral shedding detected by real-time RT-PCR (30/30 oral swabs negative). All 30 vaccinated sows were seropositive at 21 days after vaccination compared to 22 seropositive sows before vaccination, and the mean ELISA S/P ratios increased from 0.99 (SD 0.64; CV 65%) at Day 0 to 1.06 (SD 0.44; CV 41%) at Day 21. In comparison with non-vaccinated sows, the vaccinated sows showed numerically higher total born (14.17 ± 1.95 vs. 13.34 ± 2.72) and live-born piglets (12.00 ± 2.17 vs. 11.05 ± 2.82), with stillbirths, early piglet mortality, birth weight, and reproductive disorders (1/12 vs. 13/93), but not differed significantly ($P > 0.05$).

Conclusion

The live JEV vaccine demonstrated good safety and effective antibody responses without evidence of viral shedding or adverse reproductive effects. A higher reproductive performance in vaccinated sows vs. non-vaccinated sows, although not statistically significant, suggests that vaccination is compatible with and may support reproductive performance under field conditions

Keywords: Japanese encephalitis virus vaccine, Sow, ELISA, Reproductive performance.

Acknowledgements: The authors thank the Sistar Company Vietnam for the financial support and P&Y Livestock Services Company Limited, Vietnam for providing testing facilities.

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INTRANASAL VACCINATION AGAINST PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS

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Introduction and Objectives

Achieving consistent protection against porcine reproductive and respiratory syndrome virus (PRRSV) remains challenging due to viral heterogeneity and limited respiratory mucosal immunity elicited by intramuscular vaccination. In this study, intranasal (IN) versus intramuscular (IM) vaccination routes for an experimental PRRSV modified-live virus vaccine strain A2P90 (Ma et al. 2016) were investigated in a PRRSV challenge model using the virulent MN184 strain.

Materials and Methods

Thirty-four 3-week-old pigs naïve to PRRSV were randomly assigned to four groups with 7-9 pigs each. Vaccination or sham-vaccination was done at 3 weeks of age followed by challenge or sham-challenge at day post-vaccination (dpv) 35. All pigs were euthanized and necropsied 10 days post-challenge (dpc). Serum (dpc 3, 7, and 9) and nasal swabs (dpc -1, 3, 5, and 9) were collected. Groups A2P90-IN and A290-IM received the A2P90 attenuated PRRSV vaccine adjuvanted with Montanide gel and Montanide IMS intramuscularly or intranasally, respectively. Pigs in the POS-CONTROL and NEG-CONTROL groups were sham-vaccinated with saline intramuscularly and intranasally. At dpv 35, pigs in the POS-CONTROL, A2P90-IM and A2P90-IN groups were challenged intranasally with 2 ml of PRRSV MN184 strain at a dose of 2×105 TCID50. The NEG-CONTROL group was sham-challenged.

Results and Discussion

Before challenge, 4/9 IN and 6/9 IM pigs had seroconverted against PRRSV. After the challenge on dpv 35, all inoculated pigs, regardless of vaccination status, significantly lower group mean average daily weight gain than NEG-CONTROL pigs. On dpc 7 and 9, mean PRRSV RNA load in the A2P90-IN group was reduced by more than 1 log compared to the POS-CONTROL group. Seroconverted pigs in the A2P90-IN and A2P90-IM groups had high levels of MN184-specific interferon gamma secreting peripheral blood leukocytes, indicating robust cellular immunity. The seroconverted A2P90-IN pigs had lower nasal shedding and lower serum PRRSV RNA levels than the seroconverted A2P90-IM pigs and the unvaccinated, challenged group.

Conclusion

The experimental A2P90 candidate vaccine elicited better protection when administered intranasally than intramuscularly. Pig-to-pig spread of the A2P90 was not observed in vaccinated pigs. The intranasal route for A2P90 vaccination is promising and warrants further exploration, though improvements in administration are needed.

Keywords: Challenge, PRRSV, Vaccination.

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A META-ANALYSIS OF THE EFFECT OF SUIGEN PCV2 AGAINST OTHER VACCINES ON PIGS' WEIGHT AT FINISHING PHASE AND THE WEAN TO FINISH MORTALITY

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Introduction and Objectives

PCV2 is a ubiquitous virus in the swine industry, affecting economical sustainability and animal welfare. Many vaccines are available in the market (Karuppannan et al., 2017) effectively preventing clinical disease and decreasing the disease burden when compared with no vaccination status (Kirstensen et al., 2011). Here we aim to assess the effect of Suigen PCV2® vs other vaccines on the finishing weight and wean to finish mortality in commercial piglets.

Materials and Methods

We analyzed posters published between 2019 and 2025 comparing Suigen PCV2® performance against other commercial vaccines. Six trials assessed finishing weight via mean difference (MD) (i.e., Suigen PCV2® - other vaccines) while nine trials evaluated relative risk (RR) of mortality (i.e., mortality risk of Suigen PCV2®/mortality risk of other vaccines) from weaning to finish period. Random-effects meta-analysis weighting by inverse variance. Both models used a restricted maximum likelihood (REML) estimator via the "metafor" library in R (Viechtbauer, 2010, R Core Team, 2024).

Results and Discussion

The analysis revealed no significant effect in the MD in finishing weight between the Suigen PCV2® and other vaccines: -0.227 kg (-0.88; 0.43; 95% CI), $P = 0.49$. In an interesting manner, the RR of mortality in the wean to finish period was significantly smaller in the Suigen PCV2® compared with other vaccines: 0.52 (0.37; 0.71 95% CI), $P < 0.001$. We can hypothesize that the lower mortality in the Suigen PCV2® group can also be responsible for keeping smaller piglets, resulting in the observed slightly lower (and non-significant) weight in the Suigen PCV2® vaccinated animals.

Conclusion

This pooled evidence indicates that Suigen PCV2® achieves equivalent growth performance to leading commercial vaccines. More importantly, Suigen PCV2® was associated with a reduction of the wean-to-finish mortality risk by 48% relative to other treatments.

Keywords: Mortality, Meta-analysis, Porcine circovirus type 2, Vaccination.

Acknowledgements: We thank to Eric Bousquet, who was involved in all these trials and posters and have made this meta-analysis feasible.

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FOOT-AND-MOUTH DISEASE VIRUS VP4 INTERFERES WITH HOST INTERFERON RESPONSE BY TARGETING THE NUCLEAR TRANSLOCATION OF INTERFERON REGULATORY FACTOR 3

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Introduction and Objectives

Foot-and-mouth disease (FMD) is a highly infectious virus that causes acute vesicular disease in hoofed mammals. In this study, we evaluated the specific mechanism by which FMDV VP4, a known capsid protein of FMD virus, contributes to immune evasion.

Materials and Methods

The VP4 gene was cloned into Flag, Strep, and GST-tagged vectors. Mass spectrometric analysis identified potential binding partners, consistent with the luciferase assay results. Immunoprecipitation and immunofluorescence assays confirmed the interactions. Competition assays evaluated VP4 binding affinity for its partners. Confocal microscopy assessed IRF3 nuclear localization in the presence of VP4, followed by a fractionation assay. To assess functional impact, replication of the RNA viruses Influenza-PR-8-GFP and Vesicular stomatitis virus (VSV-GFP) and the DNA virus Herpes Simplex virus (HSV-GFP) was evaluated in VP4-expressing porcine and human cells. ELISA quantified cytokine secretion.

Results and Discussion

Overexpression of VP4 markedly enhanced replication of both RNA and DNA viruses while suppressing cytokine secretion and interferon (IFN)-stimulated gene transcription in PK15, and 3D4/21 cells. Luciferase reporter assays indicated that VP4 targets a host factor downstream of IRF3 in the type I IFN system, and mass spectrometry identified karyopherin alpha (KPNA) family members as candidate interactors. Immunoprecipitation and immunofluorescence assays confirmed interactions between VP4 and KPNA2 and KPNA4, and competition assays revealed that VP4 binds these proteins with higher affinity than IRF3. Collectively, these results indicate that VP4 disrupts the IRF3–KPNA interaction required for IRF3 nuclear translocation, as evidenced by confocal microscopy in PK15 cells and subcellular fractionation analyses in 3D4/21 cells, thereby impairing downstream activation of the IFN response.

Conclusion

Collectively, these results suggest that FMDV-VP4 negatively regulates the type I IFN pathway, thereby promoting severe FMDV infection by inhibiting IRF3 nuclear translocation. IRF3 is a common molecule in both DNA and RNA virus-mediated IFN pathways. The results also showed that DNA virus replication was elevated and that the examined cytokine levels were diminished in the presence of VP4.

Keywords: Foot-and-mouth disease, IRF3, KPNA, Type-1 interferon, VP4.

Acknowledgements: This work was supported by the National Research Foundation (RS-2021-NR060136)

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THE CD46 RECEPTOR – DOES THIS "PATHOGENS' MAGNET" RESTRICT THE RISK FOR A PESTIVIRAL HOST SWITCH?

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Introduction and Objectives

The complement regulatory protein CD46 is exploited as receptor by different pathogens including pestiviruses. Previous own work provided strong evidence that some pestivirus species, including classical swine fever virus (CSFV), can enter host cells independently on CD46 (Cagatay et al., 2021; Leveringhaus et al., 2022). Pestiviruses isolated from ovine hosts affiliated with three different viral species show high genetic similarity to CSFV. The most closely related virus, designated ovine Italy pestivirus (ovIt PeV), was discovered only recently and can infect pigs under experimental conditions. It was aim of the study to investigate whether these ovine pestiviruses can efficiently replicate in porcine cells and whether their mechanism of host cell entry relies on CD46.

Materials and Methods

Different porcine cell lines were used to study the replication of pestiviruses isolated from ovine host comprising border disease virus (BDV) as well as the CSFV-related virus species ovIt PeV, Aydin pestivirus (Aydin PeV), and Tunisian sheep virus (TSV). CD46 knockout and trans-complemented knockout cells were generated to study the dependency on ovine CD46. We further investigated how CD46 contributes to host cell specificity and studied its possible role in a host cell switch. For this purpose, permissivity of cross-complemented cells was tested using porcine cells expressing ovine CD46 and ovine cells expressing porcine CD46.

Results and Discussion

All ovine pestiviruses proved to be highly adapted to ovine cells but showed no or limited replication in porcine cells. Replication of ovine pestiviruses was revealed to be strictly dependent on ovine CD46. Although the viruses showed flexibility to use different CD46 isoforms as well as genetically modified CD46 variants, they were not able to utilize the porcine orthologue. Porcine cells expressing ovine CD46 showed increased permissivity to these viruses with the strongest effects observed for ovIt PeV.

Conclusion

Although CD46 is used by different pathogens as receptor, it is at the same time a molecular determinant contributing to host cell specificity of pestiviruses. Overcoming this bottleneck at the cell entry level could result in efficient infection of porcine hosts with severe consequences for pig production, established CSF diagnosis and control.

Keywords: Classical swine fever, Pestivirus, Entry, Host cell specificity, Complement regulatory protein CD46

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BRIDGING CONTINENTS: A COMPARATIVE GENOMIC EVOLUTION OF THE AFRICAN SWINE FEVER VIRUS GENOTYPE II BETWEEN EUROPE AND VIETNAM

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Introduction and Objectives

The African swine fever virus (ASFV) genotype II remains a major transboundary threat to global swine production. Following its introduction into the Caucasus region in 2007, the virus has spread extensively across Europe and Asia. Bulgaria and Vietnam represent epidemiologically distinct regions within this spread. This study aims to characterize the micro-evolutionary patterns of genotype II isolates from both regions and evaluate the implications for diagnostics and surveillance.

Materials and Methods

A curated dataset of 28 complete ASFV genome sequences was retrieved from NCBI GenBank, including 10 Bulgarian isolates (2019 - 2024), 15 Vietnamese isolates (2020 - 2025), and 3 global reference strains, including Georgia 2007/1. The genomic regions analyzed consisted of B646L (p72), E183L (p54), EP402R (CD2v), and the hypervariable intergenic region (IGR) between I73R and I329L. Complete genome sequences were aligned, and phylogenetic relationships were defined using Maximum Likelihood methods with 1,000 bootstrap replicates in MEGA X (v10.2.6).

Results and Discussion

All isolates clustered within genotype II and showed high nucleotide similarity compared to the Georgia 2007/1 reference strain. The Bulgarian isolates demonstrated a marked genomic stability consistent with the European lineage. The Vietnamese isolates showed increased micro-evolutionary variability, particularly in the IGR I73R/I329L region characterized by tandem repeat expansions corresponding to the IGR II and III variants. An 18 bp deletion in the EP402R (CD2v) gene was identified in selected Vietnamese isolates, potentially influencing the serotype-associated characteristics. These findings indicate region-specific evolutionary trends and a greater diversification in the Asian isolates.

Conclusion

A comparative genomic analysis reveals divergent evolutionary dynamics of genotype II isolates between Bulgaria and Vietnam. Continuous genomic surveillance and international data sharing are essential for the early detection of emerging variants and the optimization of control strategies.

Keywords: African swine fever virus, Comparative genomics, Genotype II, Phylogenetics, Surveillance

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SEROLOGICAL SURVEILLANCE OF PRRSV IN COLOMBIA: A RETROSPECTIVE ANALYSIS OF PORKCOLOMBIA LABORATORY DATA (2022–2025)

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Introduction and Objectives

PRRSV represents a major economic burden on the global swine industry (Holtkamp et al., 2013) and is endemic in several regions of Colombia, where national control and monitoring programs have been implemented (ACP, 2013). Since the establishment of the Porkcolombia laboratory, ELISA has served as the primary tool for large-scale surveillance to assess herd immune status (Zimmerman et al., 2012). This study aimed to describe the temporal evolution of PRRSV seroprevalence in Colombian swine herds.

Materials and Methods

A retrospective descriptive study was conducted using the Porkcolombia laboratory database. A total of 37,483 serum samples collected between 2022 and 2025 from commercial farms in 24 Colombian departments were analyzed. All samples were tested using ELISA kits (IDEXX and IDvet), and those with S/P ratios ≥ 0.4 were considered positive. Annual positivity rates were calculated, and serological patterns across regions were evaluated.

Results and Discussion

Seropositivity ranged from 39.4 to 40.4% (95% CI) during the study period. Positivity increased from 28.3% in 2022 to 45.7% in 2025, parallel with a rise in the number of samples tested. Across departments, prevalence varied from 4.9 to 71.3%, with the highest rates in Valle (71.3%), Atlántico (67.4%), Nariño (60.0%), and Antioquia (32.3%). This variability is consistent with the complex immune response to PRRSV, as antibody titers may persist for several months (Murtaugh et al., 2002), potentially influencing seroprevalence estimates. The progressive increase in laboratory submissions likely reflects greater producer awareness and adoption of diagnostic and sanitary programs. Furthermore, the incorporation of alternative sampling matrices such as oral fluids, family oral fluids, tongue tips, and processing fluids has strengthened surveillance and stabilization strategies due to their high sensitivity and broader population coverage. Complementary molecular testing through qRT-PCR and genome sequencing has further enhanced national epidemiological monitoring capacity.

Conclusion

PRRSV remains widely distributed in Colombian swine herds, with increasing seropositivity observed between 2022 and 2025. Continuous serological surveillance through ELISA provides essential epidemiological information to support evidence-based disease control strategies in Colombia.

Keywords: Epidemiology, PRRSV, Seroprevalence, Surveillance, Swine.

Acknowledgements: The authors thank the Porkcolombia technical team and swine producers from Colombia for their collaboration in sample submission and data collection.

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ASSESSING THE ROLE OF GILT-RELATED RISK FACTORS FOR PRRSV TIME-TO-LOW-PREVALENCE

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Introduction and Objectives
Elimination of porcine reproductive and respiratory syndrome (PRRS) has become increasingly challenging. Age at PRRSV exposure may influence infection duration and transmission, as younger pigs experience longer viremia and higher viral loads in pulmonary macrophages compared to older pigs. Therefore, questions regarding the impact of gilt age on exposure on elimination success arise. The objectives of this study were to evaluate the post-LVI infection dynamics across gilt age groups and to evaluate the effect of gilt age on the probability of producing PRRSV-negative litters.

Materials and Methods
A study was conducted on a 2,500-head category 1A PRRS-infected sow farm that allowed entry of gilts of varying ages at closure. Two-to six-month-old gilt cohorts were longitudinally sampled following the initial LVI event. Oral fluids were collected at approximately 1, 3, 7, 11, and 16 weeks post-LVI. Tonsil-oral scrubbing (TOSc) samples were collected from 15 gilts at various gestational stages and prior to farrowing. Aggregated processing fluids were collected weekly from gilt and P2+ litters. Samples were tested by PRRSV RT-PCR. Time-to-PRRSV-negative post-LVI by gilt age was evaluated using Kaplan-Meier survival analysis and Cox proportional hazard models, with descriptive analyses used to assess litter PRRSV status.

Results and Discussion
The time-to-PRRSV negative status varied by gilt age ($P = 0.035$). Notably, 4-month-old gilts were more likely to clear the virus sooner than 2-month-old gilts ($P = 0.022$; HR = 7.03). There was no difference in the positivity rate of PRRSV-negative litters from gilts and periparturient sows. These findings suggest that younger gilts may require a longer cooling-off period post-exposure, without negatively impacting litter status

Conclusion
Results from this study indicate that gilt age at the time of PRRSV exposure influences the rate of viral clearance, though it may not impact litter status at farrowing. Further research across multiple farms and PRRSV strains is warranted to expand upon these findings.

Keywords: Control, Elimination, Gilts, Porcine reproductive and respiratory syndrome, Risk factors.

PHYLOGENETIC CHARACTERIZATION OF PCV2D FIELD STRAINS FROM SOUTHERN BRAZIL AND COMPARISON WITH VACCINE-RELATED REFERENCE SEQUENCES

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is the etiological agent of porcine circovirus-associated diseases (PCVD) and remains a major concern for swine production worldwide (Zanella et al., 2017). A genotype shift from PCV2a to PCV2b and, more recently, to PCV2d has been widely reported (Dupont et al., 2018; Kwon et al., 2017). In Brazil, PCV2d has been frequently detected in commercial herds, particularly in high-density production areas (Zanella et al., 2017; Miotto et al., 2024; Nascimento et al., 2025). This study aimed to molecularly characterize PCV2d field strains obtained from routine diagnostic submissions in southern Brazil and to compare their genetic relationship with reference sequences corresponding to commercial vaccine genotypes.

Materials and Methods

Thirteen PCV2-positive samples classified as PCV2d were selected from routine diagnostic submissions originating from commercial swine herds from 2022 to 2026 located in the southern Brazilian states of Paraná (PR), Santa Catarina (SC), and Rio Grande do Sul (RS), which represent the main swine-producing region of the country (Miotto et al., 2024). Although a larger number of samples had previously tested positive and were genotyped as PCV2d, only thirteen presented adequate DNA quality for successful ORF2 sequencing. Viral DNA was sequenced using the Sanger method (Dupont et al., 2018). Sequences were aligned with each other and with reference sequences retrieved from GenBank, including GU799576.1, AF264042.1, and GU049340.1 (Nascimento et al., 2025). Phylogenetic reconstruction was performed using the Maximum Likelihood method with 1,000 bootstrap replicates, and pairwise genetic distances were estimated using the p-distance model.

Results and Discussion

All analyzed samples clustered within the PCV2d genotype (Miotto et al., 2024). Field strains grouped into distinct subclusters, indicating intra-genotype genetic variability among sequences obtained from southern Brazil. The vaccine-related reference sequences formed a separate, well-supported cluster (Nascimento et al., 2025). Most field sequences showed measurable genetic distance from these references, reflecting genetic divergence within circulating PCV2d lineages.

Conclusion

PCV2d field strains exhibit substantial genetic diversity, highlighting dynamic viral evolution in Brazilian swine herds. Continuous molecular surveillance integrating sequencing and phylogenetic analyses is essential to support effective PCV2d control strategies.

Keywords: Genetic variability; ORF2 sequencing; PCV2d; Phylogenetic analysis; Southern Brazil.

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COMPARATIVE EFFICACY OF A HOMOLOGOUS PCV2D VACCINE VERSUS A BIVALENT PCV2A+B VACCINE IN MEXICAN FIELD CONDITIONS

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Introduction and Objectives

Porcine Circovirus Type 2d (PCV2d) has emerged as the predominant global genotype and is frequently associated with field vaccination failures (Kim K et al. 2021). This study compares the clinical and zootechnical efficacy of a homologous PCV2d vaccine versus a bivalent PCV2a+b combination under natural challenge conditions in Mexico.

Materials and Methods

The study was conducted on a 1,500-sow farrow-to-finish farm (PRRSV, SIV, and PCV2d positive). 466 weaned piglets (3 weeks old; WOA) were allocated by litter to either a Test (T) or Control (C) group and were vaccinated via the intramuscular route: Group T with a whole inactivated PCV2d vaccine (Suigen® PCV2, Virbac) and a monovalent *M. hyopneumoniae* (Mh) vaccine (1ml), Group C with a combined inactivated recombinant chimeric PCV1-2a/b and Mh vaccine (2 ml). Individual weights were recorded at 3, and 22 WOA (subgroup, n = 60/group) and at 10WOA (all animals). Respiratory-related mortality and the mean age of first departure to slaughterhouse were monitored. Statistical analyses were performed using t-tests for weights and Fisher's exact test for mortality rates.

Results and Discussion

Initial weights at 3 WOA on the subgroups were uniform (6.8 ± 1.2 kg for T; 6.7 ± 1.0 kg for C). At 10 WOA, taking into account all animals, Group T presented a significantly higher mean weight than Group C (28.3 ± 5.0 vs 26.7± 5.2 kg; $P = 0.001$). At 22 WOA, the bodyweight measure done on the T subgroup still showed a numerical advantage (90.0 ± 13.5 vs 89. ± 12.7 kg). Notably, respiratory mortality was significantly lower in Group T (5.1%) than in Group C (12.1%; $P < 0.01$). Furthermore, the mean age of first departure for Group T (all animals) was about 13.2 days earlier than for Group C (141.5 vs 154.7 days).

Conclusion

Homologous PCV2d vaccination provides clinical benefits by reducing mortality and enhancing growth performance in PCV2d-challenged environments. The observed 13-day reduction in time-to-market represents a substantial economic gain, with estimated feed cost savings of € 21 per pig. These findings underscore the critical importance of genotype matching as a cornerstone of modern PCV2 vaccination strategies.

Keywords: Field efficacy, Homologous protection, PCV2d genotype, Swine vaccination, Zootechnical performance.

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DETECTION OF NOVEL PORCINE PARVOVIRUSES (NPPVS) AND COINFECTIONS WITH PORCINE REPRODUCTIVE FAILURE VIRUSES IN GILT DEVELOPMENT UNITS IN COLOMBIA

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Introduction and Objectives

Novel PPVs (nPPVs, PPV2 - PPV8) have been identified, but their pathogenesis and clinical implications remain unknown. Their behavior within gilt development units (GDUs) is also uncharacterized. This study aimed to determine the presence of PPV1 - PPV8 in pigs from GDUs at three commercial pig farms in Colombia. It also examined PCV2, PCV3, PCV4, PRRSV, and the frequency of viral coinfections within GDUs.

Materials and Methods

A total of 380 samples - 299 serum, 36 oral fluids, and 75 stool - were collected from three GDUs on commercial Colombian farms, covering piglets, weaners, rearing gilts, and pre-insemination gilts. Detection of PPV1–PPV8 used independent endpoint PCR with validated group-specific primers to prevent cross-reactivity. In addition, primary swine viruses (PRRSV, PCV2, and PCV3) were identified by real-time PCR using TaqMan probes.

Results and Discussion

Six of eight PPVs (PPV1 to PPV5 and PPV7), along with PCV2, PCV3, and PRRSV, were detected. Table 1 shows detection frequencies for each sample group. Coinfections occurred in 27% of serum samples, mainly involving PPV1/PCV2, while triple and quadruple coinfections appeared in all sample types.

Table 1. Percentage prevalence of viruses

Virus	Piglets			Weaners			Rearing gilts			Pre-insemination		
	SE	OF	ST	SE	OF	ST	SE	OF	ST	SE	OF	ST
PPV1	32	nc	45	28	45	52	34	50	40	21	nc	52
PPV2	0	nc	0	0	0	0	0	0	0	1	nc	0
PPV3	1	nc	0	4	0	8	15	16	0	0	nc	0
PPV4	8	nc	0	6	0	0	15	11	0	2	nc	0
PPV5	8	nc	0	1	0	6	14	11	12	5	nc	6
PPV7	0	nc	0	0	0	20	1	5	2	0	nc	6
PCV2	48	nc	28	55	32	40	48	28	32	31	nc	22
PCV3	4	nc	20	6	28	20	9	16	8	11	nc	8
PRRSV	11	nc	0	6	5	0	1	0	0	0	nc	0

SE: Serum samples, OF: Oral fluids, ST: Stool samples, nc: Non collected.

Conclusion

nPPVs were detected in the GDUs as infected gilts entered the reproductive cycle. While it is not known whether nPPVs affect PRF, their concurrent presence with primary PRF viruses suggests possible involvement in this syndrome.

Keywords: Coinfections, nPPVs, PCV2, PCV3, PRRSV.

CLASSIFICATION SCHEME AND PHYLOEVOLUTIONARY ANALYSIS FOR PORCINE PARVOVIRUSES (PPV1 TO PPV7)

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Introduction and Objectives

Eight porcine parvovirus (PPV) species, designated PPV1 to PPV8, are known to infect swine. Despite their genetic similarities, limited information exists regarding their global distribution and genetic diversity, resulting in uncertainties in their classification. In this study, we analyzed genome sequences of PPV1 to PPV7 from Colombia and compared them with sequences available in GenBank from other geographic regions to propose a refined classification scheme and conduct a comprehensive phyloevolutionary analysis.

Materials and Methods

Sera from 234 gilts aged 180 to 200 days were collected from 40 herds in Colombia. Each PPV (PPV1-PPV7) was detected individually using endpoint PCR. For PPV1, complete nucleotide sequencing of the viral protein (VP) was performed, whereas for novel porcine parvoviruses (PPV2-PPV7), near-complete genome (NCG) sequencing was performed. Phylogenetic analyses compared PPV1-VP sequences with 94 available references and nPPVs with 565 NCG, 846 nPPV-VP, and 667 nPPV-nonstructural protein (NS) sequences. Bayesian phylogenetic analysis estimated substitution rates and the time to the most recent common ancestor for each PPV.

Results and Discussion

The highest prevalence was detected for PPV3 (40.1%), followed by PPV5 (20.5%), PPV6 (17%), PPV1 (14.5%), PPV2 (9.8%), PPV4 (4.2%), and PPV7 (1.3%). Notably, all samples were negative for PPV8 genomes. An analysis of the PPV1-VP sequences revealed two main clades, similar to those of PPV2, PPV3, PPV6, and PPV7, while PPV4 and PPV5 showed three clades. Within each subclade, they were grouped by PPV type. Genetic distances for PPV2-PPV7 were significant in NCG (> 6.5%), NS (> 6.3%), and VP (> 7.5%) regions compared to global strains. Phyloevolutionary studies indicated that nPPVs have been circulating for decades, with some strains dating back up to 50 years, despite their recent emergence in various regions worldwide.

Conclusion

This study highlights the endemic circulation of nPPVs in Colombian pig herds, specifically among gilts. Additionally, it contributes to the phylogenetic classification and evolutionary studies of these viruses by describing how proposed clades and subtypes are delineated. The proposed method aims to categorize and divide subtypes according to established clade definitions, based on current knowledge and the genomes available in databases.

Keywords: Emerging pathogens, Novel PPVs (nPPVs), Phylogenetic classification, Porcine parvoviruses (PPVs).

FIRST DETECTION, DISTRIBUTION, AND DYNAMICS OF SWINE PARAINFLUENZA VIRUS TYPE 1 (PPIV-1) IN COLOMBIAN PIG FARMS

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Introduction and Objectives

Swine parainfluenza virus type 1 (PPIV-1) was first identified in Hong Kong in 2013 and has since been reported in the USA, Chile, and several European countries. The virus has been detected in a variety of respiratory samples, including nasal swabs, oral fluids, turbinates, trachea, and lung tissue—from both clinically affected and asymptomatic pigs. This study aimed to determine the prevalence and tissue distribution of PPIV-1 in pig farms across Colombia.

Materials and Methods

A study was conducted on 24 pig farms in the five largest pig-producing regions of Colombia. Serum, turbinate, tracheal, and lung samples were obtained from 131 pigs exhibiting respiratory disease, representing three age groups (3 - 5, 6 - 8, and 9 - 12 weeks), for a total of 524 samples. PPIV-1 detection was performed using RT-qPCR, with samples exhibiting a Ct < 35 considered positive. Samples with a Ct < 30 were selected for partial sequencing of the L gene (555 nucleotides).

Results and Discussion

PPIV-1 was detected in all regions and in 50% of the farms. The overall individual prevalence was 29.7%, with similar rates observed across the age groups: 30.9% (3 - 5 weeks), 27.0% (6 - 8 weeks), and 31.1% (9 - 12 weeks), showing no statistically significant differences. Detection was observed in all sample types, with prevalence ranging from 19.8 to 27.0%. The highest prevalence was found in turbinate samples, followed by lung tissue. Although no significant differences in viral loads were observed between tissues, higher viral loads tended to occur in the turbinate. Of the 39 PPIV-1–positive individuals, partial sequencing of the L gene was accomplished in 6 cases. Phylogenetic analysis revealed a high nucleotide identity (97.5 - 99.8%) among these sequences, indicating the circulation of genetically related viruses. These sequences also showed 96.5% identity with those reported in Chile in 2018.

Conclusion

This is the first report of PPIV-1 in Colombia and demonstrates its widespread circulation in the country's main pig-producing regions. Detection in all age groups evaluated and in 50% of the farms suggests the virus is endemic. These findings suggest that PPIV-1 may be contributing to porcine respiratory disease complex as an emerging virus in the Colombian swine industry.

Keywords: Emerging viruses, PPIV-1, Porcine respiratory disease, Turbinate.

MONITORING OF PRIMARY (PCV2, PPV1, PRRSV) AND EMERGING (PCV3, PCV4, NPPVS) PORCINE REPRODUCTIVE VIRUSES IN PRIMIPAROUS AND MULTIPAROUS SOWS AND THEIR LITTERS

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Introduction and Objectives

Several viruses, mainly PCV2, PPV1, and PRRSV, cause porcine reproductive failure (PRF). Emerging viruses such as PCV3, PCV4, and novel parvoviruses (nPPVs; PPV2 - PPV8) may also contribute. In this study, we examined both primary and emerging viruses associated with PRF by comparing their associations with primiparous (gilts) and multiparous sows.

Materials and Methods

A longitudinal study involved 40 healthy sows (20 gilts and 20 multiparous sows) across four herds in Colombia. The study covered three phases: pregnancy (PP), farrowing (FP), and lactation period (LP), including their litters. During PP, serum samples were collected on the day of insemination and at 40-day intervals until delivery. During FP, colostrum, placenta, and umbilical cord samples were obtained. In LP, after piglet birth, samples were collected at pre-suckling and at weeks 1 and 3 of age. Both primary and emerging viruses were detected by PCR, and viral mono and coinfections were subsequently assessed.

Results and Discussion

Primary viruses were present during all three phases, with PCV2 being the most frequently detected. PCV3 positivity was highest at the time of insemination, and PPV1 was found in all. Additionally, PPV1-positive fetuses and pre-suckling piglets were identified, indicating vertical transmission. PRRSV was also present in an unstable herd, with the PRRSV2 lineage A detected and evidence of vertical transmission. The majority of coinfections were either dual or triple. The most common coinfections in the PP and LP were PCV2/PPV1 and PCV2/PCV3, while in the FF, PCV2/PPV1 and PCV2/PRRSV were most common. Notably, coinfection with PCV2/PPV1 altered PCV2 replication. In contrast, the likelihood of detecting PRRSV decreased in fetuses coinfected with PRRSV and either PCV2, PCV3, or PPV1. The detected viruses exhibited low viral loads, indicating subclinical infections. Therefore, we propose recognizing a subclinical presentation of PRF and establishing criteria to differentiate it from symptomatic PRF.

Conclusion

This study offers new findings into the complex dynamics of porcine viral infections during PP, FP, and LP. Despite vaccination strategies, we observed a high frequency of subclinical infections. We also identified different patterns of vertical transmission and characterized viral coinfections, exploring their potential synergistic effects.

Keywords: Coinfections, nPPVs, PCV2, PPV1, PRRSV.

DETECTION OF PORCINE PARVOVIRUS 8 (PPV8) IN COLOMBIA IN PIGS EXHIBITING RESPIRATORY DISEASE AND COINFECTED WITH PCV2 AND PRRSV

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Introduction and Objectives

Porcine respiratory disease complex (PRDC) is a significant contributor to economic losses in the swine industry, mainly attributed to PRRSV, PCV2, SIV, and ADV. Over the past two decades, seven novel porcine parvoviruses (PPV2–PPV8) have been identified, some of which are associated with clinical syndromes. The most recent, PPV8, was first reported in China in 2022 and proposed as a member of the Protoparvovirus genus. This study aims to report, for the first time, the detection of PPV8 in Colombia.

Materials and Methods

Lung tissue samples were collected from 76 pig farms across Colombia's five largest pig-producing regions. Of the 146 samples collected, 122 were from nursery pigs (3 - 8 weeks old) and 24 from grow-finisher pigs (8 - 23 weeks old), all showing signs of PRDC. Samples were tested for PCV2, PCV3, and PRRSV by real-time PCR, and for PPV8 by conventional nested PCR.

Results and Discussion

Among the primary PRDC viruses, PRRSV was the most prevalent (65%; 96/146), followed by PCV2 (63%; 93/146) and PCV3 (24%; 36/146). PPV8 was identified in 4.1% (6/146) of lung samples overall. At the farm level, PPV8 was present in 3.1% (3/76) of pigs; by age group, it was detected in 3.3% (4/122) of nursery pigs and 8.3% (2/24) of grow-finisher pigs. Geographically, PPV8 was found in 2/5 regions evaluated (Cundinamarca and the Eje Cefetero). Sequencing and phylogenetic analysis of two Colombian PPV8 isolates (GenBank PP335559 and PP335560) confirmed their classification within the genus Protoparvovirus. Notably, PPV8 was also detected in coinfections involving PCV2/PPV8 and PRRSV/PPV8. The detection of PPV8 in pigs with PRDC, particularly in combination with primary viruses, suggests that PPV8 may play a role in the development of PRDC.

Conclusion

This study represents the first detection of PPV8 outside China. It is the first report on the Americas. PPV8 in pigs affected by PRDC, especially in cases of coinfection with PRRSV and PCV2, raises the possibility that PPV8 may play a role in PRDC. As with other nPPVs, it is unclear whether PPV8 is a component of the normal porcine virome or contributes to disease during coinfections.

Keywords: Coinfections, nPPVs, PPV8, PPVs, PRDC.

PATHOGENS ASSOCIATED WITH PORCINE RESPIRATORY DISEASE COMPLEX (PRDC) DURING NURSERY AND EARLY FINISHING PHASE IN FARMS IN COLOMBIA

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Introduction and Objectives

Key pathogens of PRDC are PRRSV, PCV2, IAV-S and *Mycoplasma hyopneumoniae* (MHP). PCV2 and PRRSV are widespread in Colombia. This study determined the frequency of these pathogens in the lungs of pigs with respiratory signs.

Materials and Methods

This study included 24 full-cycle pig farms, each with an average of over 100 sows across five provinces in Colombia. On these farms, pigs are routinely vaccinated against PCV2 and MHP, but not against PRRSV or IAV-S. A total of 130 clinical cases consistent with PRDC were collected: 40 post-weaning piglets (PW; 3 - 5 weeks-old), 45 from the mid- to late nursery stage (MLN; 6 - 9 weeks-old), and 45 from early-finishing piglets (EF; 10 - 12 weeks-old). Lung samples were analyzed by qPCR and histopathology to detect PRRSV, PCV2, PCV3, IAV-S, and MHP, and to evaluate their associations with the production stage.

Results and Discussion

PCV2 was detected in 86% (112/130) of the cases, followed by IAV-S at 45% (59/130), PRRSV at 43% (56/130), and MHP at 18.4% (24/130). PRRSV was significantly associated with the production stage (P = 0.039). Specifically, PW had a 68% lower probability of PRRSV detection than MLN (OR = 0.32, 95% CI: 0.13–0.82) and EF (OR = 0.32, 95% CI: 0.13–0.82). The prevalence of PRRSV was 25% in PW compared with 51.1% in both MLN and EF. In contrast, PCV2 and PCV3 showed no association with production stage (P = 0.187 and P = 0.970, respectively); likewise, for IAV-S (P = 0.583), although a higher prevalence was noted in PW (52.5%) compared to MLN and EF (42.2%). Similarly, MHP showed no association (P = 0.400), although there was a trend toward higher frequency in EF (24.4%) than in PW (17.5%) and EF (13.3%). Exudative bronchopneumonia and interstitial pneumonia were the most frequently observed microscopic lesions. Additionally, some pigs had concurrent bronchiolitis associated with broncho-interstitial pneumonia.

Conclusion

PRRSV affects all age groups and is more common in the MLN and EF phases. PCV2 is highly prevalent on all farms, showing ongoing viral circulation. IAV-S and MHP tend to rise in EF, supporting age-specific monitoring. Therefore, it is important to develop surveillance programs tailored to these pathogen patterns, especially PRRSV in MLN and EF.

Keywords: Colombia, Infection dynamics, PCV2, PRDC, PRRSV.

DISTRIBUTION AND DYNAMICS OF PRRSV IN THE NURSERIES OF TECHNIFIED COLOMBIAN FARMS

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Introduction and Objectives

PRRSV affects global swine production (Valdes-Donoso et al., 2018). The virus circulates in swine clinically or subclinically, and its impact on productivity depends on immune status and viral strain. Due to these variable effects, understanding PRRSV dynamics is crucial for effective control. In this study, we evaluated PRRSV distribution and dynamics across tissues and ages and identified circulating strains in unvaccinated Colombian swine nurseries.

Materials and Methods

A longitudinal study was conducted on 23 pig farms in Colombia. We collected serum, tonsil, and lung samples from 130 pigs under the selection criterion of respiratory disease. Pigs were divided into three age groups: 3 - 5, 6 - 8, and 9 - 12 weeks. These groups spanned the nursery stage to the start of the fattening period. In total, we collected 390 samples, each evaluated individually. PRRSV was detected by RT-qPCR ($Ct < 40$). Samples with higher viral loads ($Ct < 30$) were selected for ORF5 sequencing. Statistical analyses included chi-square tests, linear trend analysis, and ANOVA.

Results and Discussion

Results showed PRRSV circulation in all regions and on 78.2% of farms. The individual prevalence was 44.6%. Prevalence increased by age group: 33.3% in 3 - 5-week-old pigs and 53.3% in 9 - 12-week-old pigs. This trend was not statistically significant. Lung, tonsil, and serum samples showed similar prevalence rates. Ct values indicated moderate to high viral loads. The highest loads appeared in the lungs of 6–8-week-old pigs. Of 58 PRRSV-positive animals, 25 ORF5 sequences had high nucleotide identity (96.5% - 99.8%), suggesting related strains. Phylogenetic analysis identified 19 sequences as lineage 1A, 4 as 1B, and 2 as 1C. Lineage 1B sequences were detected in only one region, suggesting limited circulation.

Conclusion

The results indicate that PRRSV circulates endemically in Colombia's main dairy-producing regions. The high prevalence and increased infection rates with age suggest ongoing farm transmission. Moderate to high viral loads were detected. Lineage analysis points to multiple regional introductions and sustained viral circulation. These findings are essential for developing targeted PRRSV control strategies in Colombia, where no licensed vaccines are available.

Keywords: Colombia, Infection dynamics, Lineage 1, PRRSV.

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ISOLATION AND EXPERIMENTAL CHARACTERIZATION OF CONTEMPORARY PORCINE SAPOVIRUS GENOGROUP III STRAINS IN WEANED PIGS

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Introduction and Objectives

Porcine sapovirus (PSaV) is a genetically diverse enteric virus frequently detected in swine diagnostic submissions, especially genogroup III (GIII), yet its pathogenicity and characteristics in pigs remain poorly understood due to difficulties in culturing and lack of isolates. This study aimed to isolate contemporary PSaV GIII strains from diagnostic submissions and characterize their pathogenicity, viral shedding, and protective immunity in weaned pigs under experimental conditions.

Materials and Methods

Fifty-eight intestinal and fecal samples that tested PSaV-positive by PCR were used for virus isolation in LLC-PK1 cells. Four selected PSaV isolates were further characterized in cell culture. Two contemporary PSaV GIII isolates (IL25663/2022 and IA79982/2022) that share 89.5% nucleotide identity were selected for characterization in wean pigs. Forty-five 3 - 4-week-old pigs negative for PSaV, PEDV, PDCoV, and TGEV were randomly assigned to three groups (n = 15/group): Group 1 (Neg/IL25663), Group 2 (IA79982/IL25663), and Group 3 (IL25663/IL25663). Pigs were inoculated at 0 days post-inoculation (DPI) and challenged with IL25663 at 35 DPI (10^5 TCID50/pig). Clinical signs and rectal temperatures were monitored through 42 DPI. Rectal swabs, serum, and oral fluids were collected for testing. Five pigs per group were euthanized at 4 DPI for histopathology and immunohistochemistry (IHC).

Results and Discussion

Among 58 PSaV PCR-positive samples, 10 contemporary isolates were obtained. Four selected PSaV isolates demonstrated efficient growth through 10 serial culture passages, reaching 10^5 TCID50/ml. The four isolates had 89.5 - 95.5% nucleotide identity at the whole genome level. Two isolates were further characterized in wean pigs and both established productive infection, with viral shedding detected for approximately 14 - 21 days post-inoculation. PSaV IHC staining was observed within the intestinal epithelium, with differences in lesion severity and staining intensity between strains, indicating strain-dependent pathogenicity. Homologous challenge (IL25663/IL25663) resulted in the greatest reduction in viral shedding, while heterologous challenge (IA79882/IL25663) provided partial protection. Although concurrent rotavirus A infections in all pigs and rotavirus C infections in some pigs were detected, PSaV-specific effects on shedding dynamics and tissue pathology were evident.

Conclusion

Contemporary PSaV GIII strains can be successfully isolated and propagated, exhibiting genetic and pathogenic diversity and inducing partial cross-protective immunity in weaned pigs.

Keywords: Cross-protection, Experimental infection, Pig, Porcine sapovirus, Virus isolation.

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PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME TYPE 2 VIRUS (BETAARTERIVIRUS AMERICENSE) WHOLE GENOME CLASSIFICATION SYSTEM COMBINING ORF5, NSP3-4-5 AND INDELS

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome disease was first observed in 1987 in the United States of America. This disease is responsible for the loss of billions of dollars worldwide in the pig industry and since the discovery of its etiological agent, the virus denomination and classification method has often changed. The current PRRS type 2 virus classification system is based on the ORF5 viral gene phylogeny which represents only 4% of the viral genome. However, veterinarian practitioners are confronted with cases of unexpected severity while viral isolates are classified as vaccinal strains. As this virus evolves at high speed by combining an error prone RNA polymerase and a high recombination rate, an improved classification system is hereby proposed to better discriminate vaccinal strains from viral recombinants while remaining simple to use.

Materials and Methods

This system was made using a dataset of 1809 publicly available complete genome sequences from 14 countries, including 130 newly deposited sequences. This system combines the current ORF5 classification with a phylogeny of the nsp3, nsp4 and nsp5 segments of ORF1a viral gene as well as groups based on insertions and deletions (indels) at the whole genome scale. Clades of nsp3-4-5 were determined using sequence identities, while indel groups were made using hierarchical clustering based on the presence of events.

Results and Discussion

For example, the reference strain ATCC VR-2332 would be classified as 5A-n67-IDVR-2332 in this proposed system. Lineages of ORF5 and nsp3-4-5 groups are shown to be more frequently associated than others, allowing the quick identification of unusual strains. For example, of 50 Canadian PRRS virus strains sharing the same ORF5 lineage as the MLV vaccinal strain, 22 were identified as different using the full classification.

Conclusion

Bioinformatic tools will be presented and made available for anyone who would like to analyze their own sequences in the form of a Nextstrain community dataset and the IDindel suite of python scripts.

Keywords: Classification, Indel, ORF5, Porcine Reproductive and Respiratory Syndrome virus type 2.

SEROPREVALENCE OF INFLUENZA VIRUSES IN SWINE POPULATIONS

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Introduction and Objectives

This report aims to detect antibodies in pig sera collected from active farm visits in 2024 that are specific to several representative influenza (flu) viral antigens obtained from swine and avian populations, as part of an active surveillance program to monitor flu activity swine herds.

Materials and Methods

A total of 930 pig sera were collected from 62 actively visited swine herds (15 pigs per herd) during 2024. These sera were tested using hemagglutination-inhibition assays to detect antibodies specific to various influenza viral antigens, including seven flu A viruses (two A/H1, two A/H3, A/H5, A/H6, and A/H7) (Tsai et al., 2003) and the swine flu B virus (Tsai et al., 2019).

Results and Discussion

A total of 251 sera from 45 farms tested positive for specific antibodies against at least one of the flu viral antigens. The true prevalence rate of positive sera for at least one of the five swine flu viruses [SIV: (1) A15-29-8(H1), (2) A24-48-17(H1), (3) A10-28-9(H3), (4) A11-158-2(H3), and (5) sFluB was approximately 29.3% (95% CI: 26.3 - 36.5%). The true prevalence rate (29.1%; 95% CI: 26.1 - 32.2%) of positive sera (249) from 44 positive farms for the sA/H1 subtype [at least one of the two swine flu A/H1 viruses: (1) A15-29-8(H1) and (2) A24-48-17(H1)] was significantly higher than that (0.8%; 95% CI: 0.3%–1.6%) for the sA/H3 subtype [at least one of the two swine flu A/H3 viruses: (1) A10-28-9(H3) and (2) A11-158-2(H3)]. The true prevalence rates of positive sera for A15-29-8(H1), A24-48-17(H1), A10-28-9(H3), and A11-158-2(H3) were approximately 17.5% (95% CI: 15.1 - 20.2%), 24.5% (95% CI: 21.7 - 27.5%), 0.2% (95% CI: 0.2 - 0.8%), and 0.6% (95% CI: 0.2 - 1.3%), respectively. No antibodies against three avian flu viruses (H5, H6, and H7) or the swine flu B virus were observed.

Conclusion

The group 3-2 (new reassorted H1N2-1) flu virus is predominant!

Keywords: Serology, Epidemiology, Surveillance.

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OTUB1 STABILIZES PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS MATRIX PROTEIN THROUGH A NON-CANONICAL DEUBIQUITINATION MECHANISM TO PROMOTE VIRAL REPLICATION

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) inflicts a profound economic burden on the global swine industry. The viral matrix (M) protein is indispensable for virion assembly. However, the host-directed post-translational mechanisms governing M protein stability remain largely undefined. This study aimed to elucidate the degradation kinetics of the M protein and to identify specific host deubiquitinases subverted by PRRSV to sustain viral replication.

Materials and Methods

Host factors interacting with the viral M protein were identified using immunoprecipitation coupled with liquid chromatography-mass spectrometry in HEK-293T cells and validated through endogenous co-immunoprecipitation in PRRSV-infected MARC-145 cells. The regulatory functions of the deubiquitinase OTUB1 and the specific E2 enzyme target UBE2D2 were investigated using RNA interference, lentivirus-mediated knockdown, and site-directed mutagenesis targeting the C91A and D88A domains. Viral replication kinetics were quantified in MARC-145 cells and primary porcine alveolar macrophages using a recombinant reporter virus and diverse wild-type PRRSV strains.

Results and Discussion

We demonstrated that the M protein undergoes rapid degradation via the ubiquitin-proteasome system (UPS). Biochemical analyses identified OTUB1 as an interacting partner that physically associates with the C-terminal ectodomain of the M protein. OTUB1 overexpression significantly prolonged M protein half-life by specifically removing K48-linked polyubiquitin chains responsible for proteasomal targeting. Crucially, stabilization was independent of the catalytic activity of OTUB1 and depended entirely on a non-canonical mechanism. Through a targeted siRNA screen, we identified UBE2D2 as the specific host E2 ubiquitin-conjugating enzyme sequestered by OTUB1. The D88A mutation in OTUB1 resulted in a complete loss of M protein stabilization. Depletion of either OTUB1 or UBE2D2 severely attenuated viral replication. This stabilization mechanism was highly specific to the M protein and broadly conserved across genetically diverse PRRSV lineages, including PRRSV-1, PRRSV-2, and emerging NADC30-like and NADC34-like variants.

Conclusion

This study elucidates a novel strategy in PRRSV pathogenesis where the virus exploits the non-canonical E2-binding function of host OTUB1 to sequester UBE2D2, consequently protecting the essential M protein from UPS-mediated degradation. Targeting this highly conserved host-pathogen interaction provides a strong foundation for developing broad-spectrum antiviral therapeutics against diverse PRRSV variants.

Keywords: Matrix protein, OTUB1, PRRSV, UBE2D2, UPS.

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GENETIC CHACTERIZATION OF THE AFRICAN SWINE FEVER VIRUS STRAIN ISOLATED IN WILD BOAR IN CATALONIA, SPAIN

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Introduction and Objectives

An African swine fever (ASF) outbreak in wild boars is currently affecting Spain after 30 years of ASF-free status. To date, over 150 infected wild boars have been identified. Here, we describe the whole-genome sequence of the first ASF virus (ASFV) from an infected wild boar and compare it against more than 800 publicly available ASFV sequences.

Materials and Methods

Viral DNA was obtained from a blood sample collected from the index wild boar case in Spain. Sequencing was performed at the IRB laboratories (Barcelona) by high throughput MGI technology. Comparative genomic analyses were conducted by mapping sequencing reads of more than 800 publicly available genomic datasets from the Sequence Read Archive and the National Center for Biotechnology Information databases, including the Georgia 2007 reference genome.

Results and Discussion

The new ASFV isolate belongs to genotype II, showing a ~10 kb deletion at the left end of the genome affecting several genes associated with host interaction and immune modulation. Additionally, the genome has multiple single-nucleotide polymorphisms (SNPs) compared to the Georgia 2007 strain, including one in the MGF505 gene (MGF1-V1) that is absent from all other genotype II strains characterized to date. The European Reference Laboratory for ASF obtained the same results and classified the current isolate as a new genetic group within genotype II (genetic group 29) using the harmonized scheme based on the six variable regions used for intra-genotypic classification (CVR, IGRI73R/I329L, O174L, K145R, MGF5059R/10R, and ECO2).

Conclusions

The ongoing ASF outbreak in wild boars in Spain is caused by a genotype II ASFV strain showing unique genetic features not previously reported in other ASF outbreaks. The identified genetic markers indicate that this new variant represents a novel lineage derived from Georgia 2007, evolving independently from the main ASFV genetic groups circulating in Europe. Notably, the outbreak strain shows higher similarity to isolates from Eastern Europe and Asia than to those recently detected in Central and Western Europe. Given the low mutation rate of ASFV, the number of SNPs identified may correspond to several years of evolutionary divergence from the Georgia 2007 strain.

Keywords: African swine fever virus, Spain, wild boar, whole-genome sequencing.

Acknowledgements: The authors thank all personnel of IRTA-CReSA for their invaluable work in the monitoring and surveillance studies related to the ASF outbreak in Spain.

VACCINATION WITH A PRRS MODIFIED LIVE VACCINE TO PIGLETS LESS THAN ONE WEEK OF AGE PROVIDES PROTECTION TO A ROSALIA PRRSV CHALLENGE

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Introduction and Objectives

Suvaxyn® PRRS MLV (Suvaxyn PRRS) can be administered IM from 1 day of age onwards and nasal (IN) from 3 days onwards, which is ideal for antibody production prior to weaning. Our objective was to determine if Suvaxyn PRRS administered at processing would be protective in piglets challenged with PRRSV-1 Rosalia strain (Rosalia) at weaning.

Materials and Methods

Naïve-PRRSV piglets were randomly assigned to treatment prior to vaccination (< 7 days of age, Day 28) with a 0.5 mL dose (full antigen content, micro volume): T01:Saline (IM; n = 14); T02:Suvaxyn PRRS (IM; n = 14), and T03:Suvaxyn PRRS (IN; n = 14). At weaning (Day 0), pigs were weighed, co-mingled, and challenged with Rosalia. Blood and oronasal swabs taken at 0 (pre-challenge), 2, 4, 7, 9, 11 and 15 days were assayed for Rosalia via RT-qPCR. Weights were recorded on Day 0 and 15 (study end). Variables were analyzed with the fixed effects of treatment, and when appropriate, day, and treatment-by-day as well as all random effects.

Results and Discussion

PRRSV antibodies were not detected prior to vaccination (Day -28) in any piglet; on Day 0 (just before challenge), T01 animals remained seronegative whereas all vaccinated pigs (T02, T03) seroconverted and had greater antibody S:P compared to saline (0.016 ± 0.001, 1.996 ± 0.068, 2.289 ± 0.076 for T01, T02, T03 respectively). Weight and ADG (Day 0 to 15) did not differ across treatment groups. On Day 15, percentage of lung lesions were greatest (P = 0.0042) in T01 (5.09 ± 1.58%) compared to T02 (0.70 ± 0.60%) and T03 (0.35 ± 0.42%), which did not differ. Treatment affected viremia (P = 0.0016) with T01 > T02 = T03 [Area under the curve (P = 0.0403): T01: 9.03 x 10^9 ± 3.6 x 10^9; T02: 2.7 x 10^9 ± 1.1 x 10^9; T03: 2.3 x 10^9 ± 0.9 x 10^9 genome copies/mL)]. There were no differences (P = 0.0890) for shedding from oronasal swabs among treatments, most likely due to the commingling of pigs at the time of challenge where vaccinated pigs would have been exposed to additional virus from the shedding of non-vaccinated pigs.

Conclusion

Suvaxyn PRRS MLV administered by IN or IM route at < 7 days of age is protective against a PRRSV-1 Rosalia strain challenge.

Keywords: Porcine Reproductive and Respiratory Syndrome, PRRS MLV, Rosalia, Viremia.

A MODIFIED LIVE PRRS VACCINE ADMINISTERED AT PROCESSING IN MATERNALLY DERIVED ANTIBODY POSITIVE PIGLETS AND CHALLENGED WITH A HIGH PATHOGEN PRRSV STRAIN

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Introduction and Objectives

Fostera PRRS® is labeled for healthy piglets as early as one day of age, which is ideal for antibody production prior to weaning. Our objective was to determine if Fostera PRRS administered at processing in piglets with maternally derived antibodies (MDA) would have less lung lesions than non-vaccinated pigs.

Materials and Methods

Gilts, vaccinated with Fostera PRRS 60 days prior to breeding, had serum neutralizing antibodies (SNA) specific for Fostera PRRS quantified prior to farrowing (study day 0) to randomize to a room designated for piglets to receive saline (n = 46) or Fostera PRRS (2 mL IM; experimental serial K1224AM01; n = 48) at 3 days of age. Before vaccination, blood samples were collected to determine piglet MDAs which were used as a covariate in the analysis (Fostera PRRS: Range: 2 to 32; Median: 8; Mean ± standard deviation: 8.42 ± 7.97; Saline: Range: 2 to 256; Median: 32; Mean ± standard deviation: 66.42 ± 76.46). On day 70, pigs were weighed, co-mingled, and challenged with PRRSV 1-7-4 (L1C). Clinical observations were performed daily for respiratory distress, behavior, and cough. On day 82, weights and lung lesions were recorded. Variables were analyzed with fixed effects of transformed MDA level (covariate), treatment, day and treatment-by-day and all random effects. If MDA was not significant, it was removed from the model.

Results and Discussion

No adverse reactions were observed. Weight was affected by MDA ($P = 0.001$); other variables were not ($P > 0.64$). There was a treatment×day interaction ($P = 0.0025$) for weight; day 70 weights were similar (31.1 vs 29.6 ± 0.8kg), but vaccinated pigs were heavier than saline on day 82 (32.9 vs 29.8 ± 0.8 kg). Average daily gain was greater ($P = 0.0001$) in the vaccinated vs saline pigs (0.144 vs 0.017 ± 0.038 kg/day). There were greater ($P = 0.0001$) clinical observations in saline vs vaccinated pigs (5.15 vs 1.76 ± 0.60). Lung lesions were reduced ($P = 0.0001$) in vaccinated vs saline (16.51 ± 2.66 vs 38.53 ± 3.87%) pigs.

Conclusion

Fostera PRRS vaccination at processing in MDA positive pigs resulted in greater gain, fewer clinical signs, and fewer lung lesions than in non-vaccinated pigs after a PRRSV challenge.

Keywords: Lung lesions, Maternally derived antibodies, Porcine Reproductive and Respiratory Virus.

EVALUATION OF WELFARE-FRIENDLY SAMPLING METHODS FOR PRSSV DETECTION IN ADULT PIGS: FILTER PAPER AND TONSIL ORAL SCRUBBING

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Introduction and Objectives

Effective surveillance is essential for controlling and eliminating porcine reproductive and respiratory syndrome (PRRS), and the industry continues to seek cost-effective and reliable sampling alternatives to evaluate viral presence in a herd. Studies have shown that blood-soaked filter papers dry blood spots (DBS) and tonsil oral scrubbing (TOSC) can detect pathogens in experimentally infected swine, but their application on real outbreak has not been evaluated.

Materials and Methods

The study was conducted on a sow farm with an ongoing PRRS outbreak, prior to live virus inoculation (LVI). Ear-prickling DBS, TOSC, and blood (jugular venipuncture) were collected from 213 animals, those in gestation stalls were selected using systematic spatial sampling and those in farrowing stalls were randomly selected. Serum and DBS samples were submitted for ELISA testing, and all samples were submitted for PRRSV RT-PCR. Sampling methods for detecting PRRSV were compared to the gold standard of jugular venipuncture.

Results and Discussion

A total of 38 serum samples (17.8%), 184 TOSC samples (86.4%) and 12 DBS (5.6%) samples were RT-PCR positive. TOSC and DBS samples had a sensitivity of 89.5% and 13.2%; and a specificity of 14.3% and 96.0%, respectively, when contrasted with serum. All serum samples and three (1.43%) DBS samples were ELISA positive. No clear spatial patterns of diagnostic clustering were observed. DBS showed a low sensitivity, which may be associated with higher Ct values in blood (lower viremia) when compared to the previous study. TOSC samples had higher sensitivity but low specificity when compared to serum. However, this might be justified by prolonged oral shedding compared to viremia.

Conclusion

This study demonstrates that TOSC is a sensitive sample for PRRSV detection while DBS shows low sensitivity for both RT-PCR and ELISA in the conditions of this study. This highlights that PRRSV diagnosis in adult pigs is complex and timing of infection might affect diagnostic performance of certain tests.

Keywords: Dried blood spots, PRRS, Sows, Surveillance, Tonsil-oral scrubbing.

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DETECTION OF ANTIBODIES AGAINST VESICULAR STOMATITIS VIRUS IN PIGS FROM PERU

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Introduction and Objectives

Vesicular stomatitis is a vesicular disease that primarily affects cattle, pigs, and horses. The causative agent is an arbovirus, called vesicular stomatitis virus (VSV), which has two main serotypes: Indiana (IND) and New Jersey (NJ) (Pelzel-McCluskey et al., 2020). In swine, the clinical signs and lesions are indistinguishable from foot-and-mouth disease virus, from which Peru has been free since 2018 (WOAH, 2025). For this reason, the objective of this study was to detect neutralizing antibodies against VSV, serotypes IND and NJ, in serum samples from swine with clinical signs suggestive of VSV.

Materials and Methods

We worked with 331 porcine serum samples collected from 2022 to 2025 from Lima, Ica, and San Martin regions. The samples were taken between 7 and 10 days after the clinical signs appeared. All samples were processed using the virus neutralization test for each viral serotype (IND and NJ), as described by the Manual of diagnostics Tests and vaccines for terrestrial animals of World Organisation for Animal Health, which considers an animal positive for antibodies against VSV when it presents a neutralizing index greater than 1.5.

Results and Discussion

A total of 18.4% (61/331) were positive for antibodies against VSV of which 93.4% (57/61) were positive for serotype NJ. These animals showed clinical signs characterized mainly by vesicles in the oral cavity and hooves. Peru is free of foot-and-mouth disease, however it is necessary to evaluate the presence of other vesiculoviruses in Peru, such as the Seneca Valley virus, porcine vesicular exanthem, and swine vesicular disease. Thus, Peruvian health authorities should take preventive measures against these vesicular diseases, which have a significant productive and economic impact on the country's swine production.

Conclusion

This is the first study on the presence of neutralizing antibodies against vesicular stomatitis virus in pigs from farms in Peru, where the NJ serotype is the most frequent.

Keywords: Neutralization test, New Jersey, Peru, Pig, Vesicular stomatitis virus.

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PCR-DETECTION AND GENOTYPING OF PORCINE CIRCOVIRUS TYPE 2 (PCV2) IN THE PHILIPPINES FROM 2020 TO 2024

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Introduction and Objectives

The Philippine swine industry is ranked among the top eight pork producing countries globally and characterized by mixed production systems with persistent disease pressures that significantly affectproductivity. A major disease of concern, Porcine circovirus type 2 is a key viral pathogen and the causative agent of Porcine Circovirus-Associated Diseases (PCVAD) (AASV, 2006). At present, at least eight PCV2 genotypes (PCV2a-2h) have been proposed based on the phylogenetic analysis of the ORF2 capsid gene (Xiao et al., 2016; Foss et al., 2023). Despite its economic importance, information on the epidemiologic profile of PCV2 in the Philippines remains limited. Knowledge on genotypic classification of field PCV2 is essential as it will aid in the formulation of more effective prevention and control strategies, including optimized vaccination programs.

Materials and Methods

A total of 39 commercial swine farms from different regions of the Philippines with clinical signs suggestive of PCVAD were investigated. Management and farm history records of each herd were obtained. Pooled tissue samples, serum, processing fluids and mummified fetuses were collected. Multiplex PCR was performed to determine PCV2 positivity rates and genotypic classification.

Results and Discussion

All 39 field samples (87% Luzon; 13% Visayas region) collected were positive for PCV2. The predominant clinical signs observed were wasting, rough hair coat, respiratory distress, thumping, elevated mortalities and reduced body weight in finisher farms as well as reproductive problems in breeder farms. Cycle threshold (Ct) values were generally low, ranging from 5 to 33.51, although all samples were from herds vaccinated with PCV2a-based vaccines. Around 2.56% of the analyzed samples were PCV2a, 2.56% were PCV2b and 94.87% were PCV2d. The yearly genotypic distribution was 2020 (n = 2): 50% PCV2a and 50% PCV2b; 2021 (n = 3): 100% PCV2d; 2022 (n = 3): 100% PCV2d; 2023 (n = 15): 100% PCV2d; 2024 (n = 16): 94% PCV2d and 6%PCV2b.

Conclusion

This study demonstrates the clinical profile and genotypic distribution of the different PCV2 genotypes in the Philippines. The study highlights that PCV2d is the predominant genotype in the country. These findings will serve as a useful guide in the development of more effective swine management and prevention strategies against PCVAD.

Keywords: genotype, multiplex pcr, Philippines, porcine circovirus associated-diseases, PCV2.

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ISOLATION AND CHARACTERIZATION OF A CHINESE-LIKE EMERGING VIRULENT PEDV STRAIN IDENTIFIED IN KOREA

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) continues to cause substantial economic losses in the swine industry despite the use of commercial vaccines (Lei et al., 2024; Park, 2024). This study reports the first isolation and comprehensive characterization of a PEDV strain (KPED2021-1) identified in Korea, genetically distinct from previously circulating domestic G2b strains and closely related to recently emerged Chinese PEDV variants. The objectives were to isolate and assess genetically characteristics, its pathogenicity, and its immunogenic properties following inactivation.

Materials and Methods

KPED2021-1 was isolated from clinical field samples and propagated in Vero-CCL81 cells. Viral identity was confirmed by PEDV N protein-specific immunofluorescence assay and RT-qPCR. Genetic characterization was conducted using whole-genome and spike (S) gene sequencing followed by phylogenetic analysis. Pathogenicity was evaluated in suckling piglets after oral inoculation by monitoring clinical signs, viral shedding, and intestinal lesions. For immunological assessment, the virus was BEI-inactivated, formulated with six different adjuvants, and administered twice to guinea pigs, and neutralizing antibody responses were measured by the virus neutralization assay.

Results and Discussion

Phylogenetic analysis showed that KPED2021-1 formed a distinct clade closely related to recently emerged Chinese PEDV variants but clearly segregated from previously reported Korean strains. The isolate shared more than 99% whole-genome nucleotide identity with recent Chinese variants, compared with 96.6 - 98.7% identity with PEDV strains from Korea and other regions, supporting its classification as a putative novel clade (tentatively designated G2c). In experimental infection of 5-day-old suckling piglets, the isolate caused severe diarrhea with marked villous atrophy and intestinal lesions. All infected piglets died, resulting in 100% mortality under the experimental conditions. An inactivated KPED2021-1 induced adjuvant-dependent neutralizing antibody responses in guinea pigs, and selected formulations generated neutralizing antibody titers exceeding 1:64.

Conclusion

This study provides a molecular and biological characterization of a newly identified Chinese-like PEDV strain detected in Korea, demonstrating its genetic divergence and pathogenicity in neonatal piglets. These findings contribute to understanding PEDV evolution and emphasize the importance of continuous surveillance of emerging variants.

Keywords: Chinese-like strain, Inactived vaccine, Neutralizing antibody, Genetic characterization, PEDV.

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EFFICIENT PROPAGATION OF GENETICALLY DIVERSE KOREAN FIELD AND VACCINE PRRSV STRAINS USING A CD163-OVEREXPRESSING CELL LINE

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a major swine pathogen characterized by extensive genetic diversity (Fiers et al., 2024). In Korea, many circulating PRRSV field strains, particularly genetically divergent PRRSV-2 variants and PRRSV-1 Sub1A strains, exhibit poor or inconsistent growth in the commonly used MARC-145 cell line, limiting virus isolation and downstream characterization (Kim et al., 2025; Jeong et al., 2024). The objective was to establish a PRRSV-susceptible receptor-expressing cell line and to evaluate its ability to support efficient propagation of genetically diverse PRRSV-1 and PRRSV-2 field and vaccine strains, including under scalable culture conditions.

Materials and Methods

CD163 expression in the receptor-expressing cell line was confirmed using a CD163-specific antibody, and receptor localization was assessed by immunofluorescence staining. The stability of receptor expression was monitored during continuous passaging for up to 100 passages. A panel of PRRSV strains, including field-derived isolates and commercial vaccine strains representing both PRRSV-1 and PRRSV-2 species, was inoculated onto the receptor-expressing cell line, with MARC-145 cells used as a reference. Viral propagation was evaluated by cytopathic effect observation, real-time RT-PCR, and virus titration in 96-well plates. Selected strains were further assessed using a roller bottle culture system to evaluate scalability.

Results and Discussion

The receptor-expressing cell line supported efficient and sustained propagation of genetically diverse PRRSV strains, including PRRSV-2 sublineages L1C (NADC30-like) and L1A (NADC34-like), Korean lineages LKA, LKB, and LKC, as well as lineages 5 and 8, together with PRRSV-1 Sub1A isolates. Several strains that showed limited or no productive growth in MARC-145 cells exhibited stable replication and consistent propagation in the receptor-expressing cell line over serial passages. These findings demonstrate enhanced permissiveness of the developed cell line to PRRSV strains poorly adapted to conventional cell culture systems.

Conclusion

This study demonstrates that a receptor-expressing cell line enables efficient and stable propagation of genetically diverse PRRSV strains from both PRRSV-1 and PRRSV-2 species. Its stability during extended passaging and performance under scalable culture conditions highlight its utility for PRRSV isolation, biological characterization, and downstream research applications.

Keywords: Genetic diversity, Field strains, PRRSV, Receptor-expressing cell line, Virus propagation.

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EVALUATION OF AN INTRANASAL VACCINATION STRATEGY FOLLOWED BY A CHALLENGE WITH THE THAILAND PRRSV-2 STRAIN DURING THE NURSERY PHASE

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) remains a devastating global disease (Holtkamp et al., 2013). The increased detection of Lineage 1 (L1) of PRRSV-2 has been associated with increased clinical severities (Yim-im et al., 2023). While intramuscular (IM) vaccination is standard, intranasal (IN) administration enhances mucosal immunity (Opriessnig et al., 2021). This study evaluated the efficacy and immune responses of intramuscular (IM) and intranasal (IN) MLV against a Thailand PRRSV-2 L1 challenge in nursery pigs.

Materials and Methods

Forty-five 4-week-old PRRS-seronegative piglets were randomly assigned to five groups (n = 9/group): Group A (negative control), Group B (positive control), Group C (PRRS Vaccine-Z IM), Group D (PRRS Vaccine-Z IN), and Group E (PRRS Vaccine-B IM). At 35 days post-vaccination (DPV), all groups except Group A were intranasally challenged with Thai PRRSV-2 Lineage 1 (10^6 $TCID_{50}$/mL). Pigs were necropsied at 9 days post-challenge (DPC). Serum and blood samples were collected at 14 and 35 DPV, and 3, 6, 9 DPC. PAMs were harvested from bronchoalveolar lavage fluid (BALF) at necropsy. Lung and tracheobronchial lymph nodes were analyzed by PCR and immune responses assessed by ELISA and ELISPOT. Rectal temperature and post-challenge average daily gain (ADG) were recorded. Data were analyzed using one-way ANOVA, Kruskal–Wallis, and repeated measures ANOVA ($P < 0.05$).

Results and Discussion

Vaccinated groups (C, D and E) showed significantly reduced fever compared with the positive control (B) from 4 days post-challenge (DPC) onward, higher average daily gain (ADG), and lower lung lesion scores ($P < 0.05$). PRRSV viremia and nasal shedding were significantly reduced from 6 DPC. Viral loads in lung and lymph nodes were significantly lower in Groups C and D, but not Group E. IM vaccination (C and E) induced higher systemic IL-10 and IFN-γ, whereas IN vaccination (D) elicited stronger local IFN-γ in pulmonary alveolar macrophages, suggesting increased local immune activation in the respiratory tract.

Conclusion

Modified live PRRS vaccination reduced clinical severity, improved growth, and lowered viremia and viral loads. IM vaccination provided systemic protection, while IN vaccination enhanced local immunity, fever control, and reduced viral shedding in nursery pigs.

Keywords: Intranasal vaccination, Modified live vaccine, Nursery pigs, PRRSV-2.

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EARLY IMMUNITY INDUCED BY A MODIFIED LIVE VACCINE AND COMPETITIVE DYNAMICS BETWEEN CLASSICAL SWINE FEVER VIRUS GENOTYPES 2.1 AND 3.4 IN DUAL INFECTION

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Introduction and Objectives

Classical swine fever (CSF), caused by the CSF virus (CSFV), is highly contagious in pigs. In the field, CSFV genotype 2.1 (G2.1) replaced the previously dominant genotype 3.4 (G3.4) during extensive vaccination with the modified live vaccine (MLV) LPC strain, prior to Taiwan's official recognition by WOAH as "CSF-free without vaccination." This study aimed to evaluate the early immune responses induced by MLV LPC vaccination and to characterize competitive interactions between CSFV G2.1 and G3.4 during dual infection in pigs.

Materials and Methods

Eighteen 4-week-old SPF pigs were randomly assigned to five groups and housed in three separate rooms. Groups 1 and 2 were vaccinated with the LPC modified live vaccine and challenged at 2 or 4 days post-vaccination (dpv), respectively. Group 3 served as an unvaccinated positive control and was housed separately. Pigs in Groups 1–3 were intranasally dual-infected with CSFV G2.1 and G3.4 strains. The day of challenge was defined as 0 days post-infection (dpi). Groups 4 and 5 were designated as cohabitation groups corresponding to Groups 1 and 2, respectively, to assess viral shedding and transmissibility. All pigs were monitored for rectal temperature and clinical scores, and blood, serum, oral swabs, and fecal swabs were collected for downstream analyses.

Results and Discussion

Early immune responses provided partial protection against both genotypes. Clinical signs first appeared at 6 dpi in the unvaccinated group, whereas both vaccinated groups showed reduced disease severity. Complete blood count analysis revealed lower white blood cell and platelet counts in the unvaccinated group. CSFV E2-specific antibodies and cross-neutralizing activity against three CSFV genotypes were detected in the vaccinated groups and in the co-habitation group paired with the 2 dpv group. A stronger CSFV-specific IFN-γ response to G3.4 than to G2.1 was also observed. qPCR further showed that G3.4 was undetectable in both cohabitation groups, suggesting that the higher fitness of G2.1 enables more efficient persistence and transmission, whereas vaccine-induced immune responses suppress G3.4 more effectively.

Conclusion

These results indicate that vaccine-induced immunity and within-host immune dynamics shape CSFV epidemiology and likely contribute to the genotype shifts observed in the field.

Keywords: Classical swine fever virus, Dual infection, Early immunity, Modified live vaccine.

DYNAMIC MODEL OF PRRS TRANSMISSION THROUGH SWINE MOBILIZATION IN COLOMBIA

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Introduction and Objectives

PRRS is a disease with a substantial economic impact on swine production. This study aims to quantify the directional probability of PRRS transmission across Colombian municipalities based on swine mobilization networks, identifying likely origins and destinations of infection from a selected municipality and estimating the potential number of infected farms through an interactive web platform.

Materials and Methods

The directional transmission model used national registry of 5.181 georeferenced commercial swine farms, PRRS seroprevalence data based on 750 positive cases of 3.868 samples collected in 301 farms located in 16 departments, municipal PRRS Sanitary Risk Model, and official 2.024 dataset of swine mobilization with 208.770 flows of 11.570.395 animals to slaughterhouses, farms and swine trading hubs. Municipalities were modeled as nodes in a directed weighted network, with weekly pig movements as edges. For a selected municipality, two probabilities were estimated: likely sources of infection (incoming flows) and likely destinations of spread (outgoing flows). Transmission probability depended on movement intensity and destination risk score. Infection scenarios where there is a potential outbreak were defined from high-mobilization municipal clusters and simulated using Monte Carlo methods. Directional probabilities were computed as the proportion of simulations with transmission and visualized in an interactive web viewer for 12 months.

Results and Discussion

The model and developed tool allow visualization, starting from a municipality of interest where a potential outbreak originates, of the municipalities and departments that would likely be affected, their probabilities, and the number of infected farms. In Colombia for 834 municipalities, for both scenarios it was found 59,80% (seroprevalence 0,3 - 0,7) and 75,50% (seroprevalence > 0,7) of farms become infected by the end of the study period. In both cases, Antioquia acts as a major axis for virus dissemination. For example, for outgoing flow, if the outbreak begins in Medellín (Antioquia), and the focus is on analyzing transmission from Bello (Antioquia), 38 municipalities in six departments could potentially be affected, with an 11,29% probability and 100% of farms affected.

Conclusion

PRRS dynamics highlight the need for quantitative epidemiological tools to inform intervention strategies based on connectivity within animal movement networks.

Keywords: Dynamic epidemiological surveillance model, PRRS, Swine mobilization, Transmission.

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SPATIAL-TEMPORAL DISTRIBUTION OF SWINE INFLUENZA IN MEXICO (2014 TO 2024)

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Introduction and Objective

Swine Influenza (SI) is a globally distributed disease associated with Porcine Respiratory Disease Complex, causing significant economic losses in production. Due to its capacity for genetic reassortment, it also represents a public health risk, as demonstrated during the 2009 H1N1 pandemic. In Mexico, subtypes H1N1, H3N2 and H1N2 have been reported. However, nationwide analyses describing long-term epidemiological trends remain limited. This study evaluated the spatial and temporal distribution of Si in Mexico from 2014 to 2024 through a retrospective study.

Materials and Methods

A retrospective case-control study was conducted using data from the National Epidemiological Surveillance System in Mexico from 2014 to 2024. Records included state, municipality, sampling date, and test result. A case was defined as any record with at least one positive test, while controls were defined as records with exclusively negative results. Municipalities were georeferenced using official coordinates from the National Institute of Statistics and Geography. Spatial and temporal analyses were performed in QGIS to generate point distribution maps and Kernel density heatmaps. Descriptive analysis was conducted.

Results and Discussion

The analysis demonstrated a wide geographic distribution of SI in Mexico, with 3520 of 9095 records (38.7%) classified as cases. The central-western region registered the highest proportion of cases (2 230/3 520), followed by the northwestern region (501/3 520). Spatial clustering identified through Kernel density analysis revealed persistent hotspots, particularly in areas corresponding to regions with high swine and poultry density. Quarterly analysis showed consistent seasonal patterns, with increased case frequency during April - June across multiple regions.

Conclusion

SI showed wide geographic distribution and sustained presence in Mexico during the 2014 - 2024 period. The central-western region accounted for the highest proportion of cases. Recurrent seasonal patterns were identified, with increased case frequency during the April-June quarter. These findings contribute to a better epidemiological understanding of the disease and may support the development of targeted surveillance and control strategies.

Keywords: Epidemiology, Public health, Swine influenza, Virus.

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AIRBORNE DISTRIBUTION OF SWINE INFLUENZA VIRUS IN PIG FARMS AND THE NEED FOR EARLY MONITORING TO MITIGATE INFECTION RISK

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Introduction and Objectives

Airborne spread of respiratory pathogens can accelerate within-farm transmission, and influenza A virus in swine can be shed into aerosols, supporting air-based surveillance as an early-warning approach (Torremorell et al., 2012; Corzo et al., 2013). Because SIV may circulate sub-clinically, timely detection from barn air could reduce infection risk by prompting earlier biosecurity actions. This study evaluated the airborne distribution of SIV in Korean pig farms and applied air-sampling-based NGS to characterize barn-air virus composition (virome).

Materials and Methods

Air samples were collected from five pig farms in Korea across production-stage barns (e.g., gestation, farrowing, nursery, growing/finishing). Nucleic acids from air samples were analyzed by NGS on an Illumina MiSeq platform for virome profiling, with bioinformatics used to identify viral reads and summarize composition by farm and barn type. In parallel, PRRSV, PCV-2, SIV-A, and PEDV were tested by qRT-PCR/qPCR (Ct < 35 positive). For each PCR-confirmed virus, virus isolation was attempted using appropriate cell culture systems; live virus was verified by virus-specific molecular confirmation from culture supernatants.

Results and Discussion

All farms and barn types yielded detectable viral nucleic acids for four major swine viruses. Ct ranges were PRRSV 25.55 - 33.42, PCV-2 26.17 - 34.76, SIV-A 30.52 - 34.31, and PEDV 32.41 - 34.96. Notably, SIV-A was detected across all production stages, including groups without observable clinical signs, suggesting subclinical circulation with an airborne footprint and potential for within-farm airborne dissemination. Virus isolation supported the presence of viable virus among PCR-positive air samples, and successful isolation showed a positive correlation with PCR signal strength (lower Ct values were more likely to yield live virus).

Conclusion

Barn-air monitoring combined with NGS virome analysis detected SIV-A and other key swine viruses across multiple production stages, including clinically normal groups. Confirmation of viable virus and the Ct–culture correlation reinforce airborne surveillance as a practical early-warning tool to mitigate infection risk and guide timely farm-level control measures.

Keywords: Air sampling, Early warning surveillance, Pig farm biosecurity, Swine influenza virus, Virome.

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DETECTION, ISOLATION AND DETERMINATION OF GENETIC CHARACTERISTICS OF PIG CIRCOVIRUS TYPE 2 FROM PIGS ASSOCIATED WITH DEBILITATING SYNDROME IN VIETNAM

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is a major pathogen associated with post-weaning multisystem debilitation syndrome (PMWS), causing growth retardation, respiratory failure, and economic loss. Although several studies on PCV2 detection and genetic characteristics have been reported in Vietnam, reports of viral isolation still need to be further documented. This study aims to detect, isolate and genetically characterize PCV2 from a depleted pig herd in southern Vietnam.

Materials and Methods

Swine tissue samples (spleen, lungs, and lymph nodes) were collected from debilitating symptomatic pigs in Southern Vietnam and screened for swine circovirus types 1, 2 and 3 using conventional PCR methods. Positive samples were cultured into PK-15 cells to isolate the virus for serial segments, with cultures monitored daily after innocence. The PCR-confirmed isolates underwent full genomic Sanger sequencing. The resulting sequences were processed using ATGC software, then compared via BLAST with the reference circovirus sequence in Genbank, followed by phylogenetic analysis of ClustalW/MEGA species.

Results and Discussion

PCV2 is detected in pig tissue samples by PCR. The virus successfully replicated in PK-15 cells up to two consecutive segments (P2), with cellular changes observed and PCV2 confirmed by PCR in cell culture. Full genome sequencing shows 99 –100% identification with PCV2 reference strains (top BLAST hits). Whole-genome sequencing showed that the resulting isolation had a genome length of 1,767 bp. Phylogenic analysis is based on complete genomic sequences isolated in the PCV2d genotype, which is clearly separate from other PCV2 lineages. These results confirm that the isolate belongs to PCV2d and provide molecular evidence of its presence in the case under investigation. This highlights the value of combining molecular detection, viral isolation, and genomic analysis to accurately identify PCV2 in field samples.

Conclusion

This study reports the detection, isolation, and whole-genome characterization of PCV2d from a herd of pigs with debilitating syndrome in Southern Vietnam. The findings expand Vietnam's PCV2 molecular database and underscore the value of combining PCR genome detection, isolation and surveillance for PCV2 surveillance and effective vaccine development.

Keywords: Debilitating syndrome in pigs, PCV2, Virus isolation.

RISK FACTORS AND GENETIC DIVERSITY OF PCV2 IN SWINE FARMS OF JALISCO, MEXICO

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is the causal agent of Porcine Circovirus Diseases, which significantly affect farm productivity. Its control relies on timely diagnosis, vaccination, and biosecurity, which also shape viral genetic diversity. The ORF2 gene, encoding the capsid protein, is highly variable and has driven genotype shifts worldwide. This study aimed to identify risk factors associated with PCV2 detection and characterize the genetic variability of circulating strains in swine farms from Jalisco, Mexico.

Materials and Methods

Between 2022 and 2023, 80 farms enrolled in the "Sanidad-Jalisco" program were evaluated across four animal-density regions. A total of 4,207 serum samples were grouped into 844 pools and tested by qPCR targeting ORF2 (Ct < 35 as positive). Management information was collected and analyzed using 2 × 2 contingency tables, Chi-square tests, and Odds Ratios (95% CI). Samples with Ct < 30 were selected for full ORF2 (765 bp) amplification and Sanger sequencing. Genetic analyses were performed with MEGA v11.

Results and Discussion

PCV2 molecular detection was higher in high-density regions, particularly in B2 (39.9%). Incomplete vaccination programs and inadequate biosecurity practices were the main risk factors associated with viral DNA detection. In region B2, lack of access control and entry of non-disinfected vehicles were strongly associated with PCV2 detection (OR = 21.5 and 19.3, respectively). Pigs without circovirus vaccination had higher odds of PCV2 molecular detection (OR = 6) compared with vaccinated animals. ORF2 sequencing identified 51/70 (73%) sequences as PCV2d and 19/70 (27%) as PCV2a. Nucleotide divergence analysis showed low intra-genotype variability in PCV2d (0.0 - 3.9%) and broader divergence in PCV2a (0.3–15.0%), associated with two subclades and detection of a recombinant strain classified as genotype A with parental A and D lineages. Inter-genotype divergence ranged from 13% to 31%. All PCV2d sequences exhibited lysine at position 234 of the capsid protein (N234K), a molecular signature previously linked to increased viral load and PCVAD-compatible lesions in experimental models.

Conclusion

In high-density areas, PCV2 occurrence is mainly linked to inadequate vaccination and weak biosecurity. The predominance of PCV2d and the presence of potentially pathogenic variants reinforce the need for continuous molecular surveillance and region-specific control strategies.

Keywords: Biosecurity, Molecular epidemiology, ORF2 divergence, Porcine circovirus type 2, PCV2d.

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MOLECULAR DIVERSITY AND FARM-LEVEL RISK FACTORS ASSOCIATED WITH PRRSV CIRCULATION IN SWINE REGIONS OF JALISCO, MEXICO

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Introduction and Objectives

PRRS virus remains one of the main health challenges for swine production, particularly in high-density systems. ORF5 sequencing is essential to assess viral variability and evolutionary patterns, while identifying risk factors supports the design of effective control strategies. This study aimed to identify the main risk factors associated with PRRSV detection and characterize the genetic diversity of circulating strains in swine farms of Jalisco, Mexico.

Materials and Methods

From 2022 to 2023, 80 farms were sampled across four density-based regions (A, B1, B2, B3). A total of 4,207 serum samples were collected by production stage and grouped into 844 pools for ORF7 qRT-PCR. Farm-level information on management, biosecurity, vaccination, facilities, pest control, and waste handling was analyzed using 2 × 2 contingency tables, Chi-square tests, and Odds Ratios (95% CI). Pools with Ct < 30 were used to amplify ORF5 by endpoint RT-PCR, followed by Sanger sequencing and analysis in MEGA 11.

Results and Discussion

Positive pools were more frequent in weaning (61.1%), growing (40.4%), and lactation (38.2%). Region B2, the area with the highest pig density, showed the greatest positivity (44.6%). Thirty-nine ORF5 sequences were obtained and classified into lineages L1A, L1C, L1I, L2, L5A, L8C, and L8D. Lineage L1A represented 53.8% of sequences and showed low within-group diversity (3.6%), although multiple co-circulating lineages indicate heterogeneous viral movement. Lack of control over farm access was the strongest risk factor associated with PRRSV detection, particularly in region B3 and semi-intensive systems. The absence of vaccination against key bacterial pathogens and PCV2 also increased the likelihood of viral detection, consistent with evidence that co-infections can enhance PRRSV replication and clinical impact.

Conclusion

High pig density, deficient biosecurity, and inconsistent vaccination practices favor PRRSV circulation in Jalisco. The predominance of L1A, alongside additional lineages, highlights the need to strengthen biosecurity and optimize vaccination programs to mitigate the epidemiological impact of the virus.

Keywords: Lineages, Jalisco, Mexico, PRRSV, Risk Factors.

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SEROLOGICAL SURVEY FOR SWINE INFLUENZA VIRUS (SIV) IN FARMS IN JALISCO, MEXICO

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Introduction and Objectives

In Mexico, the seroprevalence of SIV has been identified using reference strains or strains obtained from the field, with a general approach. The objective of this research was to conduct a serological survey using IPV strains isolated in the central-western region of Mexico.

Materials and Methods

As part of the epidemiological surveillance program in the State of Jalisco (with support from the state epidemiological surveillance group), blood samples were taken from farms without active respiratory illnesses (years 2022 - 2024). A total of 2,209 serum samples were collected from 101 farms in the state. The serum samples were analyzed by hemagglutination inhibition (HI) using a standardized protocol for the H1N1 (Jalisco/2013), H1N2 (Guanajuato/2014), H3N2 (Jalisco/2013), and H3N2 JAL (Jalisco/2022) subtypes.

Results and Discussion

A total of 8,836 tests were performed, detecting 100% seropositivity in the farms analyzed. The frequency for the H1N1 subtype was 39.5%, for H1N2 84.1%, for H3N2/2013 42%, and for H3N2/2022 63.7%. Different presentation values were identified according to the antibody titer. In 2014, in Jalisco, 35.2% seropositivity was identified in 12 municipalities, indicating an increase of more than 100% over a 10-year period for the H1N2 subtype. Different presentation values were identified according to antibody titer. Serological analyses allowed for the identification of antibody titer distribution, highlighting the variation in presentation using a recently isolated strain (H3N2) compared to an older strain.

Conclusion

The information generated will support ongoing projects aimed at developing diagnostic tests and biologics adapted to regional needs, in this case, the state of Jalisco.

Keywords: Prevalence, SIV, Serologic.

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SUREVEILLANCE AND UPDATE RFLP PATTERN OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS IN VIETNAM FROM 2021 TO 2025

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) is a significant infectious disease that contributes to massive economic losses in the swine industry. Due to high frequency of viral mutation and recombination, exhibits complex genetic diversity. Surveillance of circulating strains is essential for effective intervention, comprehensive analyses of strains, and update RFLP distribution remain limited in Vietnam. Ongoing surveillance of PRRSV types to identify the current virus strain in circulation is necessary to design a vaccine and control measures.

Materials and Methods

A total of 7736 clinical samples, including blood samples, tissue samples and nasal swabs were collected from three regionsl of Vietnam during 2021-2025. The RNA samples were analyzed by real-time PCR guideline TCVN 8400-21:2014. Seventy-eight positive samples were full-length ORF5 amplification and sequencing. RFLP classification of PRRSV-2 isolates was performed following the methodology described by Yim-im et al (2023).

Results and Discussion

A sum of 7736 samples analyzed, 802 (10.37%) were positive for PRRSV. Among positive, PRRSV-1 (1.62%), PRRSV-2 (6.29%), and HP-PRRSV (2.46%) genotypes prevailed. The PRRSV genotype predominated at 60.72% followed by HP-PRRSV (3.69%) and PRRSV-1 (12%). Temporally, HP-PRRSV (37.5%) is highest in 2021, PRRSV-1 in 2023 (17.5%), and PRRSV-2 (66.56%) in 2024, with PRRSV-2 maintaining dominance throughout. Geographically, HP-PRRSV (25.15%) concentrated highest northern, PRRSV-2 (64.91%), in the Central and PRRSV-1 (46.43%) Southern, reflecting distinct regional epidemiological divergence. A total of 16 RFLP patterns were identified, of which 1-4-3 (30%),1-1-1 (22%) were predominant, followed by 1-3-2 (7.66%), 1-4-4 (5.52%), and 1-39-4 (4.43%). Vaccine related (2-5-2; 1-3-2; 1-4-4) and field strains, including 1-7-4 (NADC34), were detected at moderate frequencies (3.08-6.35%), whereas other RFLP patterns (1-1-1; 1-1-4; 1-2-1; 1-3-1; 1-31-3; 2-5-1; 2-5-2) were observed at low prevalence (1.08 - 4.35%). Collectively, these concordant findings others (Shin et al., 2022; Lee et al., 2023; Giovani et al., 2023; Yim-im et al., 2023; Ruwini et al., 2024).

Conclusion

This study provides a comprehensive overview of the circulation of PRRSV in Vietnam. PRRSV-2 has become the dominant lineage, replacing HP-PRRSV with clear regional differentiation. Sixteen RFLP patterns were identified, predominantly 1-4-3 and 1-1-1, alongside the emergence of the concerning NADC34-like strain. Therefore, continuous monitoring and strengthening of PRRSV prevention and control are necessary.

Keywords: ORF5, PRRSV, RFLP, Surveillance.

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GLOBAL SPATIOTEMPORAL AND GENETIC DISTRIBUTION OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS TYPE 2

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus type 2 (PRRSV-2) remains a major pathogen of global importance. Previous studies characterized PRRSV-2 genetic diversity using curated ORF5 datasets (e.g., Yim-Im et al., 2023); however, heterogeneous fragmentary and whole-genome sequences in NCBI remain analytically challenging. This study investigated the spatiotemporal distribution and genetic diversity of PRRSV-2 using an ORF5 dataset compiled from NCBI, integrating ORF5 fragments and ORF5 regions extracted from whole-genome sequences.

Materials and Methods

A total of 51,976 Betaarterivirus sequences (taxid: 2499674) and associated metadata were retrieved from the NCBI Virus database on 16 October 2025. Data curation was performed by screening for PRRSV-2 ORF5-containing sequences using a reference dataset of 1,100 ORF5 sequences (Yim-Im et al., 2023), followed by length-based stratification, multiple sequence alignment, and reference-guided trimming to ensure accurate delineation of ORF5 and removal of anomalous sequences. Redundancy reduction and phylogeny-based lineage classification were subsequently performed. Only high-confidence lineage assignments were retained for downstream analyses, yielding a final dataset of 33,730 sequences.

Results and Discussion

Analysis of 33,730 PRRSV-2 ORF5 sequences revealed pronounced geographic and temporal structuring. Most sequences originated from the Americas (62.7%) and Asia (29.6%). Lineage 1 dominated the Americas, whereas Asia exhibited greater diversity, led by L8E and L1C-unclade. Europe and Oceania were nearly exclusively L5A. Country-level patterns showed clear regional specificity, including L1 predominance in the USA and L8E dominance in Vietnam. Temporal trends indicated rising sequence reports after 2000, peaking in 2014 - 2015, alongside lineage turnover characterized by L9A decline and post-2020 expansion of variants such as L1C.5. Several lineages remained geographically restricted, underscoring regional evolutionary dynamics.

Conclusion

Large-scale analysis of 33,730 PRRSV-2 ORF5 sequences revealed clear geographic distribution, lineage-specific dominance, and dynamic temporal trends, including the expansion of emerging variants and decline of older lineages. These findings highlight the importance of comprehensive ORF5 surveillance for understanding PRRSV-2 evolution and guiding global epidemiological monitoring.

Keywords: Global spatiotemporal distribution, ORF5 genetic diversity, PRRS-2.

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MOLECULAR CHARACTERIZATION OF PORCINE PARVOVIRUS TYPE 5 NS1 HELICASE PROTEIN FROM A MEXICAN FIELD SEQUENCE

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Introduction and Objectives

NS1 protein is highly conserved, performing helicase, ATPase, nuclease and DNA binding activities as well as having cytotoxic actions (Niskanen at al., 2013). Helicases are relevant for viral replication, belonging to superfamily 3 (SF3) in porcine parvovirus 5 (PPV5). SF3 helicases contain conserved motifs named Walker A, Walker B, B' motif, C motif, and Box VII in which an arginine finger is located. In the current work, the electrostatic potential and SASA of the PPV5 helicase are analyzed and compared to pathogenic PPV1 and canine parvovirus (CVP) since the pathogenic effect for PPV5 is unknown.

Materials and Methods

The whole NS1 was amplified and sequenced from a lymph node sample ADN obtained with a commercial kit (QIAamp DNA FFPE Tissue kit, Qiagen, Germany) to complete a molecular modeling using the Swiss model program. The visualization, edition and electrostatic potential calculation of the model were achieved with the PyMOL software to proceed with the SASA assessment using the GETAREA program. Then, available PPV1 and CPV SASA values were used to compare with the PPV5 results.

Results and Discussion

In the SASA and the electrostatic potential assessments, the main finding was observed within Box VII, revealing that PPV5 NS1 displayed more negative charge than pathogenic viruses which are largely positive. In the whole model, the PPV5 frontal side periphery showed intercalated negative charges, while in PPV1 and CPV that charge is displayed in a continual fashion. Conversely, the PPV5 back surface is mainly negative in charge, but only the central area shows that charge in the pathogenic viruses. These findings are relevant since deviations in electrostatic potential might drive to functional differences.

Conclusion

In the current work, the observed differences between PPV5 and pathogenic parvoviruses are most likely structural, but the Box VII changes might be important since the arginine finger is located within this motif in which ATP hydrolysis occurs. Furthermore, punctual mutations in the positively charged area close to the arginine finger have proved to alter CPV virion assembly (Niskanen et al, 2013). However, that must be ascertained in PPV5 with functional tests.

Keywords: Helicase, Modeling, Electrostatic potential, PPV5, SASA.

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DETECTION, DISTRIBUTION AND OCCURRENCY OF PORCINE CIRCOVIRUS TYPE 2, 3, AND 4 IN BACKYARD SWINE HERDS ON MINAS GERAIS, BRASIL – RETROSPECTIVE ANALYSES 2016-2017

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Introduction and Objectives

Backyard pig farms in Brazil represent a traditional and subsistence-based form of pig production. These farms often lack regular veterinary assistance and typically operate with limited or nonexistent biosecurity practices, including vaccination programs and biocontainment measures. Porcine circoviruses are associated with significant economic losses in the swine industry, yet their circulation in non-commercial backyard herds in Brazil remains poorly understood. This study aimed to characterize the occurrence and spatial distribution of PCV2, PCV3, and PCV4 in backyard pigs in the state of Minas Gerais, representing the first investigation of circoviruses in backyard pig populations in the country.

Materials and Methods

A total of 1010 blood samples were collected between 2016 - 2017 by the official state veterinary service. Samples originated from 170 municipalities across the state, representing 285 backyard pig farms distributed across 12 mesoregions. All samples were tested by qPCR for PCV2, PCV3, and PCV4. Serum samples were initially pooled in groups of five, and positive pools were subsequently tested individually.

Results and Discussion

At the state level, 18.88% (81/429) of the pigs tested positive for PCV2, with a mean Ct value of 35.9; PCV2d was the only genotype identified. For PCV3, 20.72% (46/222) of the pigs tested positive, with a mean Ct value of 34.73. Among samples tested for both viruses, 29.90% (23/77) were co-infected with PCV2 and PCV3. At the regional level, PCV2 occurrence ranged from 30.0% (3/10) to 72.7% (8/11) across 11 of the 12 mesoregions. For PCV3, occurrence ranged from 25.0% (1/4) to 100.0% (5/5) across 10 of the 12 mesoregions. No samples tested positive for PCV4

Conclusion

These findings demonstrate that PCV2 and PCV3 were circulating in backyard pig farms during 2016 - 2017, representing a biosecurity risk to nearby commercial operations. The presence of these viruses also suggests that backyard pig populations probably harbor other pathogens, potentially acting as reservoirs for disease transmission. This includes the risk of maintaining or spreading foreign animal diseases in the event of an outbreak. Therefore, backyard pigs could play an important role in surveillance programs aimed at improving swine health at both regional and national levels.

Keywords: Backyard herds, Pathogen reservoir, Porcine Circovirus, Spatial distribution.

Acknowledgements: The authors thank the Minas Gerais Institute of Agriculture (IMA) for providing the samples to our lab.

T CELL EPITOPE COMPARISON SCORE (EPICC) FOR PORCINE CIRCOVIRUS TYPE 2 SEQUENCES FROM CHINA, 2016 TO 2025

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Introduction and Objectives

T-cell-mediated immunity plays an important role in the protective efficacy for Porcine Circovirus Type-2 (PCV2) vaccines. The degree of matching between vaccines and circulating field strain T-cell-epitopes may influence the breadth of vaccine coverage and can be predicted by in silico algorithms. CircoMatch® is a web-based tool developed by EpiVax and Zoetis to facilitate comparative epitope coverage analysis. Previous studies have shown correlations between predicted T-cell-epitope coverage with vaccine efficacy for IAV-S and PCV2 vaccines3. The objective of this study was to compare predicted T-cell-epitope coverage of a bivalent PCV2a/PCV2b vaccine and monovalent PCV2a vaccines against Chinese PCV2 field strains reported from 2016 to 2025.

Materials and Methods

575-Chinese PCV2-capsid protein sequences collected from 2016-to-2025 were analyzed using CircoMatch®. Sequences were obtained from GenBank or via direct submission. Among sequences with defined geographic origin (453-of-575), most common provinces of origin included Henan-Hubei-Jiangsu-Heilongjiang, and Shandong. Genotypes were confirmed by phylogenetic alignment with reference PCV2a, PCV2b, and PCV2d capsid amino acid sequences (DNASTAR-Lasergene-Ver-18). Genotype assignment was based on sequence distance to the nearest reference strain. The EpiCC-score is a relative measure of predicted T-cell-epitopes in a sequence and is determined for both the field isolates (baseline EpiCC-score) or the vaccine sequences (vaccine-EpiCC-score). The T-cell-epitope coverage of a vaccine is calculated as (vaccine-EpiCC-score/baseline EpiCC-score) x 100%. EpiCC-scores and predicted percent T-cell-epitope coverage were calculated/summarized across genotypes and years.

Results and Discussion

Genotype distribution among analyzed sequences was PCV2a-(13%), PCV2b-(23%) and PCV2d-(65%). The percentage of PCV2d was the highest in 2025-(89.1%), increasing from an average of 59% during 2016 - 2024. Considerable sequence variability was observed within genotypes, including intermediate sequences between PCV2b and PCV2d, consistent with their phylogenetic relatedness. This diversity suggests ongoing viral evolution under vaccine-and-immunity-driven selection pressures4. Average baseline EpiCC-score for all sequences was 10.58. The average EpiCC-score for the bivalent PCV2a/PCV2b vaccine was 8.68, corresponding to 82.0% predicted T-cell-epitope coverage, compared with 63.6 to 67.5% for monovalent PCV2a vaccines.

Conclusion

For this set of Chinese PCV2-sequences, the bivalent PCV2a/PCV2b vaccine demonstrated the highest predicted T-cell epitope coverage compared with monovalent PCV2a vaccines, supporting broader immunologic coverage against circulating genotypes.

Keywords: CircoMatch, Epitope coverage, Porcine Circovirus Type 2; PCV2-genotypes, T cell immunity.

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PHYLOGENETIC STUDY OF PORCINE PARVOVIRUS 5 ORF1 IN MEXICAN SEQUENCES FROM FIELD CASES

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Introduction and Objectives

At present, the Parvovirinae family comprises 8 genera, whose taxonomic classification is based on amino acid (aa) identity of the highly conserved NS1 protein. To be classified within the same genus, 35 - 40% aa identity is required while 85% is needed to be in the same species (Pénzes et al., 2020). The present work objective is to perform the phylogenetic analysis of PPV5 Mexican sequences in order to contribute in PPV5 ICTV classification given that it is still unclassified.

Materials and Methods

ADN from four formalin fixed-paraffin embedded lymph node samples from archival cases in Mexico was obtained using a commercial kit (QIAamp DNA FFPE Tissue Kit, Qiagen, Germany) to perform overlapping PCR series for amplifying and sequencing PPV5 NS1 protein. The sequences were aligned and edited to determine identity matrices, and aa prediction using Bioedit software. The phylogenetic trees were constructed with MEGA7.

Results and Discussion

The highest nucleotide (nt) identity of Mexican PPV5 sequences was with PPV4 (78%) followed by PPV6 (55%). Concerning aa identity, the Mexican sequences OQ702212 and OQ792213 showed 100% identity, whereas 14A and OQ792211 exhibited 100% homology. The latter two displayed 100% identity with Chinese PPV5 sequences (MN326219, MK378337 and MW853953). The Mexican sequences were close to PPV4 (85–85.8%), and PPV6 (54.1 - 54.4%) in aa identity. The phylogenetic trees showed that PPV4 and PPV5 emerge from the same branch (boostrap100). Also, the OQ792212 and OQ792213 grouped together (100%) in a separate branch. OQ792211 clustered with the Chinese sequences.

Conclusion

Because the Mexican sequences OQ792212 and OQ792213 are grouped in a distinct branch with respect to the other PPV5 sequences, they might represent an endemic strain. Furthermore, the Mexican OQ792211 and 14A sequences are identical to Chinese sequences, suggesting that commercial bonds with that country might be involved as live animal movements among countries in global trade contribute-to viral diversity (Cortey et al., 2011). However, that statement must be further assessed in a more comprehensive retrospective phylogenetic analysis. Given that the closest nt and aa identities were found with Copiparvovirus (PPV4 and PPV6), it could be plausible to consider PPV5 within this genus.

Keywords: Copiparvovirus, Identity, Parvovirinae, PPV5, Taxonomy.

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GENETIC DIVERSITY OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS IN THE PORKCOLOMBIA PRRS CONTROL PROGRAM

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Introduction and Objectives

Understanding the genetic diversity of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is essential for assessing viral evolution, recombination, and transmission risks associated with pig movement (Murtaugh et al., 2012) Characterizing viral lineages, together with movement analysis, supports the identification of high-risk farms and enables targeted biosecurity interventions. This study aimed to characterize the genetic diversity of PRRSV in eight Colombian departments participating in the Pork Colombia PRRS Control Program to strengthen external biosecurity measures.

Materials and Methods

Between 2021 and 2025, 38 swine farms enrolled in the Pork Colombia–FNP PRRS Control Program were sampled. PRRSV detection was performed in pigs aged 6 to 8 weeks. Thirty-three PCR-positive samples were submitted to the University of Minnesota Diagnostic Laboratory for ORF5 sequencing and phylogenetic analysis.

Results and Discussion

Thirty PRRSV strains (90%) were classified into established lineages and sub-lineages, predominantly 1A.2, while three strains (10%) were identified as unclassified within lineage 1A.2. Lineage 1A.2 was the dominant lineage, consistent with its known prevalence in Colombia. Genetic similarity among analyzed strains was ≤ 96%. No vaccine-derived strains were detected, in accordance with the prohibition of PRRSV vaccination in Colombia.

Conclusion

Lineage identification enabled monitoring of PRRSV across 30 farms located in eight departments, facilitating the tracking of outbreaks and viral movement between production regions. These findings supported the identification of potential superspreader farms and high-risk movement areas, contributing to real-time biosecurity improvements through the External Biorisk Program® and the establishment of Colombia's first supervised and controlled washing and disinfection center.

Keywords: Genetic diversity, Porcine Reproductive and Respiratory Syndrome.

Acknowledgements: The authors thank Porkcolombia-FNP directors, its Swine Board, associates, and farm staff for their support and contributions to this project.

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RELATIVE VIRAL LOAD OF PORCINE PARVOVIRUS 5 IN CASES OF PORCINE CIRCOVIRUS ASSOCIATED DISEASE

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Introduction and Objectives

Among porcine parvoviruses (PPVs), only PPV1 is acknowledged as pathogenic which in coinfection with PCV2 increases the severity of porcine circovirus associated disease (PCVAD) (Hu et al.,2017). However, in Mexico, PPV5 prevalence was found related to PMWS as well as farms affected with PCV2-associated reproductive failure (PCV2+–RF) (García et al., 2020). To further establish PPV5 relationship with PCVAD, the relative viral load of PPV5 was recorded in selected cases.

Materials and Methods

Cases from archive that fulfill the PCVAD diagnostic criteria (Chae, 2005) were selected comprising 24 lymph nodes PMWS-affected and 31 fetal hearts from PCV2+–RF. In addition, 18 age-matched PCV2-unaffected tissues from healthy piglets, 30 fetal hearts from RF unrelated to PCV2 (PCV2- –RF), and 18 PCV2- abattoir fetal hearts (AFH) were used. Each case DNA was used to determine the relative viral load of PPV5 and PCV2 by qPCR. Values from relative load were converted to log10. ANOVA, Tukey's test and Spearman correlation were used to establish statistical significance.

Results and Discussion

The PPV5 relative viral load was higher in PMWS-affected cases (0.63) than in healthy animals (0.52). Concerning [lg1] RF, the PPV5 viral load in the PCV2- –RF group was higher (0.79) than in the PCV2+–RF and the AFH groups (0.51 and 0.63, respectively). In both instances, these findings were not significant. However, in the PMWS group, the PPV5+ cases had significantly higher PCV2 viral load than the PPV5- (2.36 and 1.43, respectively), and the PCV2 viral load showed a direct correlation with PPV5 observance as well. Similarly, the presence of PPV5 showed a positive correlation with the PCV2 viral load in the PCV2+–RF.

Conclusion

In both, PMWS and PCV2+–RF, it is plausible that the PPV5 presence direct towards a higher PCV2 viral load which is in agreement with previously reported PPV5 relationship in PCVAD (García et al., 2020). Further analysis assessing for absolute viral load might be useful to evaluate the PPV5 relationship with PCVAD.

Keywords: PPV5, PCV2, PCVAD, Relationship, Viral load.

Acknowledgements: This work was funded by PIAPI CI2465 FESC-UNAM, and SECIHTI 829352 scholarship.

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COMPARATIVE FIELD EVALUATION OF A NEXT-GENERATION CPD MLV PRRS VACCINE VERSUS A TRADITIONAL MLV IN A FARM WITH CONCURRENT PRRSV1 AND PRRSV2 CIRCULATION

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Introduction and Objectives
Porcine reproductive and respiratory syndrome (PRRS) remains a major cause of economic loss in swine production. In Thailand, co-circulation of PRRSV1 and PRRSV2 has been reported, complicating disease control. A next generation modified live vaccine (MLV) developed using Codon Pair Deoptimization (CPD) technology (Persoporc®) has been introduced to improve field performance. This study aimed to compare the efficacy of a CPD MLV vaccine with a traditional lineage 1 MLV PRRS vaccine under field conditions with concurrent PRRSV1 and PRRSV2 circulation.

Materials and Methods
The study was conducted on a 1,500 sows farm with a PRRS stable sow herd. The wean to finish unit had a history of both PRRSV1 and PRRSV2 circulation. At weaning, piglets were allocated into two groups: (1) traditional lineage 1 MLV PRRS vaccine (n = 304) and (2) next-generation CPD MLV vaccine (Persoporc®) (n = 394). Groups were housed in separate barns under the same management conditions. Growth performance, mortality, and culling rates were recorded throughout the production cycle. Blood samples were periodically collected for PRRSV PCR testing and strain differentiation.

Results and Discussion
Losses and culling rates were 4.28% in the traditional MLV group and 3.55% in the CPD MLV group. ADG was 666 g and 658 g, respectively. FCR was 2.72 in the traditional group compared with 2.57 in the CPD group. Feed cost per kg gain was 1.02 € versus 1.01 €. PCR monitoring indicated that the traditional MLV group became PCR-positive from 6 WOA, whereas the CPD group became PCR-positive from 8 WOA. Both groups were confirmed PCR-positive for PRRSV1 and PRRSV2, demonstrating exposure to co-circulating field strains.

Conclusion
Under field conditions with concurrent PRRSV1 and PRRSV2 circulation, the next-generation CPD MLV vaccine was associated with improved feed efficiency compared with a traditional lineage 1 MLV vaccine. These findings suggest that CPD based vaccine technology may be a useful tool for PRRS control in complex epidemiological scenarios.

Keywords: Next-generation, Profitability, PRRSV1+2, Return-on-investment, Vaccine.

DEVELOPING STRIP TEST USING SIMPLE PCR LATERAL FLOW FOR AFRICAN SWINE FEVER VIRUS P72 GENE

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Introduction and Objectives

African Swine Fever Virus (ASFV) causes major economic losses in the pork industry. Rapid detection is essential to control its spread using a DNA lateral flow strip test. The P72 gene on the ASFV capsid is targeted because it is specific and conserved across ASFV variants (Hwang et al., 2023). Therefore, this study aims to develop an ATK lateral flow strip test for reliable ASFV detection.

Materials and Methods

The strip test was developed at the Faculty of Veterinary Science, Chulalongkorn University, and subsequently field-validated at the Faculty of Applied Science and Technology, Nguyen Tat Thanh University. To ensure coverage of all ASFV genotypes, both forward and reverse primers targeting the P72 gene were employed. Positive inactivated clinical sera served as reference material with plasmid PCR2.1@TA insertion of the P72 gene used as a control. DNA extraction was performed using a Qiagen kit (Germany). Amplified P72 sequences were detected using a modified ATK lateral flow strip consisting of: (1) an extraction buffer with mobilized anti-FAM conjugated to colloidal gold (Miao et al., 2019; Zhu et al., 2022), and (2) a test strip with streptavidin on the T line to capture biotin-labeled P72 amplicons and IgG on the C line as an internal control. Detection involved mixing amplified DNA with the buffer, applying it to the strip, and observing red signals at the T line (target present) and C line (procedural control).

Results and Discussion

DNA from five ASFV-positive pig sera was successfully amplified and detected by the ATK lateral flow strip. The P72 gene produced clear gold signals on both T and C lines, while the IPC plasmid confirmed assay reliability. These results show effective ASFV DNA detection with diagnostic confirmation and procedural control.

Conclusion

A PCR-based DNA lateral flow strip targeting the ASFV P72 gene shows promise for rapid ASF diagnostics, though field use may be limited by the need for electrical equipment.

Keywords: African swine fever virus, DNA, P72 gene, simple PCR.

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GENERATION AND CHARACTERIZATION OF CD163-EDITED PRRSV-RESISTANT PIGS UNDER COMMERCIAL PRODUCTION CONDITIONS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a major disease affecting global swine production. The CD163 receptor, specifically its scavenger receptor cysteine-rich domain 5 (SRCR5), is required for PRRSV infection. Deletion of this domain prevents viral genome release, conferring resistance to PRRSV (Calvert et al. 2007; Burkard et al. 2018). The objective of this study was to generate a commercial-scale population of pigs carrying a targeted deletion of CD163 exon 7 (CD163ΔE7), to evaluate resistance under controlled disease challenge, and to evaluate performance characteristics under commercial production conditions as an innovative therapeutic strategy.

Materials and Methods

A targeted deletion of exon 7 of the CD163 gene, encoding the SRCR5 domain, was introduced via CRISPR-Cas9-mediated genome editing in porcine embryos to generate CD163ΔE7 founder animals. Edited founders were molecularly characterized and introgressed into elite nucleus breeding lines, with propagation through conventional multiplication systems to establish commercial-scale populations. CD163ΔE7 and wild-type pigs were evaluated under controlled PRRSV challenge using type 1 and type 2 isolates, with infection status and clinical outcomes assessed following exposure. In parallel, animals were evaluated under commercial production conditions for reproductive performance, growth, carcass characteristics, and meat quality. Phenotypic characterization analyses were conducted between genotypes for key production traits.

Results and Discussion

A commercial-scale population carrying the CD163ΔE7 allele was established and propagated through conventional breeding systems. The edited allele segregated according to Mendelian expectations across generations. Across evaluated populations, CD163ΔE7 pigs showed no detectable differences in reproductive performance, growth, carcass characteristics, or meat quality relative to wild-type comparators.[5] Controlled PRRSV challenge studies have demonstrated that CD163ΔE7 pigs are resistant to infection with both type 1 and type 2 PRRSV isolates, confirming the functional impact of the edit.[1–3] These results indicate that CD163 modification can be integrated into commercial breeding programs to confer resistance to PRRSV without adverse effects on production performance.

Conclusion

The generation and characterization of CD163ΔE7 pigs demonstrate the feasibility of deploying gene-edited disease resistance within commercial swine breeding systems. This approach represents a potential innovative therapeutic strategy for PRRSV control while maintaining production performance relevant to the pork industry.

Keywords: Disease Challenge, Disease Resistance, Gene Editing, PRRSV Swine Production.

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RAPID AND EXTRACTION-FREE DETECTION OF AFRICAN SWINE FEVER VIRUS USING A LAMP ASSAY

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Introduction and Objectives

African swine fever (ASF) is caused by the African swine fever virus, the only member of the family Asfarviridae, and can result in up to 100% mortality, characterized by high fever and multi-organ hemorrhage (Sánchez-Vizcaíno et al., 2015). Rapid detection of ASFV has been achieved using isothermal amplification methods such as LAMP and RPA (James et al., 2010; Miao et al., 2019). The objective of this study was to develop a LAMP-based protocol for the rapid detection of ASFV directly from blood samples without the need for total DNA extraction.

Materials and Methods

A total of 43 ASFV-positive and 20 ASFV-negative whole blood samples were collected from the Veterinary Hospital of Nong Lam University, Ho Chi Minh City. The closed-tube LAMP assay was performed using a commercial master mix with three primer sets (F3–B3, FIP–BIP, LF–LB) following Wang et al. (2021), with fluorescence-based detection. DNA extracted from all samples was first used to establish and validate the assay's sensitivity and specificity. The protocol was then optimized for direct detection without DNA extraction. For this, diluted samples (1:2) underwent heat-shock treatment (95°C for 5 min, 100°C for 5 min), centrifugation (10,000 rpm, 1 min), and 1 - 3 µL supernatant was used as the LAMP template.

Results and Discussion

All 43 ASFV-positive and 20 ASFV-negative DNA samples showed complete agreement with real-time PCR, confirming high assay accuracy. Direct detection from heat-treated whole blood also achieved 100% concordance, demonstrating reliability without DNA extraction. Sensitivity testing revealed strong amplification at low concentrations, with a limit of detection of ~1.734×10^{-6} ng/µL (10^{-7} dilution), equivalent to 1.734×10^{-6} - 5.202×10^{-6} ng per reaction. The assay produced results within 14 - 15 minutes, and specificity was confirmed by a melting peak at ~ 85°C.

Conclusion

These findings are consistent with previous studies (Wang et al., 2021) and demonstrate that the developed LAMP method is a rapid, sensitive, and practical tool for ASFV detection under field conditions.

Keywords: African swine fever virus (ASFV), Molecular diagnostics, LAMP assay, Rapid detection, Whole blood samples.

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POSTERS

TOPIC 2: BACTERIAL AND PARASITIC DISEASES (BPD)

PREVALENCE OF INTESTINAL PARASITIC PROTOZOA IN PIG FARMS IN RUSSIA

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Introduction and Objectives

Pig breeding is one of the main branches of animal husbandry in Russia. According to literature sources, coccidiosis is known to be common in many countries of the world: China, USA, Russia, Vietnam, Japan, Canada, European countries and others. There are large numbers of pigs in these countries. This study examines the prevalence of intestinal parasitic protozoa in industrial pig farms in Russia.

Materials and Methods

An analysis of intestinal protozoan parasites of pigs in commercial pig farms in Russia was carried out during 2021 - 2025. Original parasitological studies of faeces of 3, 5, 7, 10, 15, 20 and 30-day-old piglets for Isospora suis infection were performed by analyzing 30 faecal samples collected directly from the rectum using the McMaster method. The study was carried out in two large-scale industrial pig farms (each with an annual stock of 54,000 pigs) located in the Moscow Region and the Republic of Mordovia. Parasitological examination of faeces of 20, 30, 60, 90 and 120-day-old piglets for the presence of Eimeria spp. and Balantidium coli was done by the combined Darling method.

Results and Discussion

According to data of veterinary laboratories in Russia, it is known that the average prevalence of Eimeria spp. infection over the noted period was 23% and of Balantidium coli infection was 29%. The results of our research showed that the prevalence of cystoisosporosis in piglets was from 20 to 29%, eimeriosis from 10 to 36%, balantidiosis from 10 to 50% in pig farms of the Moscow region. The 0 - 2-month-old piglets were infected with Isospora by 18% in the «Mordovian Bacon» pig complex. No other parasites were detected. The 2 - 4-month-old piglets were infected with Eimeria by 21%, Balantidium by 29%, Ascaris by 18% and Trichuris by 7%. Piglets up to the age of 30 days had mono-infection with Isospora suis.

Conclusion

Analysis of coccidial infections in pigs has shown that these are widespread in industrial pig farms in Russia, piglets under the age of 30 days were infected with Isospora suis by 10 - 40%.

Keywords: Parasitic protozoa, Prevalence, Pig farms.

EFFECT OF PAROMOMYCIN AND ENROFLOXACIN ADMINISTRATION ON INTESTINAL MICROBIOTA DEVELOPMENT OF PIGS DURING THE FIRST 6 WEEKS POST-WEANING

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Introduction and Objectives

Prevotellaceae, Ruminococcaceae, Lachnospiraceae, Veillonellaceae and Acidaminococcaceae are part of the core gut microbiota of healthy piglets post-weaning (Guevarra et al., 2019). In this study, the effect of paromomycin (Parofor) and enrofloxacin administration in post-weaning pigs on gut microbial composition and abundance was investigated.

Materials and Methods

Fifteen clinically healthy weaned pigs were assigned to a control (unmedicated) and two treatment groups (5 pigs per group). One week after weaning paromomycin (25 mg/kg bw) was administered orally for 3 days (D0 - D3) via drinking water and enrofloxacin (5 mg/kg bw) was administered parenterally for 3 days (D0 - D3). Rectum faecal samples were collected prior to antibiotic treatment (D0) and after initiation of treatment (D3, D7, D10, D14, D21, D28, D35, D42). Faecal samples were processed for DNA isolation and full-length 16S rRNA gene amplicon sequencing (Oxford Nanopore Technologies) to identify the bacterial composition and diversity.

Results and Discussion

Changes in bacterial abundance of the core bacterial families under the antibiotic treatments were found. Higher abundances of Lachnospiraceae and Veillonellaceae were determined in paromomycin-treated pigs compared to enrofloxacin and the control group. On the other hand, abundances of Clostridiaceae and Peptostreptococcaceae were lower at nearly all time points (D0 - D42) in the paromomycin group compared to the enrofloxacin and control group.

Conclusions

Abundances of the core bacterial families in paromomycin-treated pigs differed from enrofloxacin and non-medicated pigs. Higher abundances of Lachnospiraceae and Veillonellaceae are in line with the shift of the microbial composition observed post-weaning and linked to a carbohydrate-fermenting microbiota. The decrease in Clostridiaceae and Peptostreptococcaceae abundances further contributes to this microbiota shift post-weaning. Reduced abundance of Clostridiaceae may lead to a reduction of opportunistic outbreaks of diarrhoeal disease. These results verify that the physiological microbiota transition and maturation post-weaning can be supported by the use of paromomycin (Parofor). Paromomycin can contribute to gut microbiota homeostasis and stabilization of the intestinal microbial community.

Keywords: Enrofloxacin, Microbiome, Paromomycin, Post-weaning pigs.

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PK/PD AND CLINICAL RELATIONSHIPS OF TULATHROMYCIN FOR SWINE RESPIRATORY DISEASE (SRD) TREATMENT

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Introduction and Objectives

The pharmacokinetics (PK) of tulathromycin (Huvexxin - Huvepharma NV) in lung and macrophages based on parenteral administration was related to tulathromycin MICs for *M.hyopneumoniae* (Mh), *G.parasuis* (Gp), *P.multocida* (Pm), *B.bronchiseptica* (Bb) and *A.pleuropneumoniae* (App) strains from Europe (pharmacodynamics - PD).

Materials and Methods

The tulathromycin lung concentration was determined in a PK study with 36 healthy non-infected pigs (bodyweight 20 - 25.5 kg), which were medicated by single-dose i.m. injection (dose 2.5 mg/kg bw). Pigs were euthanized on days 1, 3, 6, 10, 15 after treatment cessation to determine the tulathromycin concentration in blood and lungs. Cellular uptake of tulathromycin in porcine phagocytic cells was determined in an in-vitro study. Tulathromycin MIC data were generated based on susceptibility testing of pig respiratory pathogens from SRD cases in a pan-European (BE, CH, DK, DE, FR, HU, IR, NL, ES, PL, UK) project between 2015 and 2016. 611 EU isolates were MIC tested (MIC dilutions: 0.001 - 128 µg/ml) according CLSI guidelines (3). MIC_{90} and MIC ranges were determined.

Results and Discussion

The tulathromycin lung concentration was recorded at 3.47 µg/g 24 h post-dose and at 1.24 µg/g 10 days post-dose. The tulathromycin macrophage concentration was recorded at 16.5µg/ml. Tulathromycin concentrations in lung and alveolar macrophages exceed the MIC_{90} value for Mh (0.5), for Gp (2.0), for Pm (8.0) and for Bb (8.0). A lung elimination half-life $t_{1/2}$ of 142 hours (appr. 6 days) was found. The long half-life results in tulathromycin lung concentrations which remained at levels above 1.2µg/g for 10 days. Tulathromycin accumulates intracellularly in porcine macrophages (Intracellular:Extracellular ratio 8:1). Macrophage tulathromycin concentrations are substantially higher than in the lung and play an important role for definition of CLSI breakpoints (sensitive Pm, Bb ≤ 16.0 µg/ml; App ≤ 64.0 µg/ml - resistant ≥ 64.0 µg/ml) to provide therapeutic effects against App and other respiratory pathogens.

Conclusions

An excellent therapeutic effect of Huvexxin (Huvepharma) in the case of treatment of swine respiratory disease infections caused by *M.hyopneumoniae*, *G.parasuis*, *P.multocida*, *B.bronchiseptica* and *A.pleuropneumoniae* is predicted, based on the available tulathromycin PK/PD data.

Keywords: PK/PD, Swine Respiratory Disease, Tulathromycin.

IMPACT OF NANONISATION ON FLORFENICOL RECOVERY WHEN USED IN A PROPORTIONER

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Introduction and Objectives
Florfenicol demonstrates poor solubility, resulting in precipitation and crystallisation when used at therapeutic dose in highly concentrated stock solutions. The suitability for use in proportioners was investigated in an ethically responsible study for two liquid florfenicol-containing products: a standard florfenicol formulation and Amphen® 200 mg/ml nanonised florfenicol. Nanonisation is an advanced formulation technique based on particle size reduction (d90 < 1.7µm).

Materials and Methods
Pigs (25.5 kg), housed in the same compartments under the same conditions in an independent institute, were assigned to two groups and treated with 10 mg florfenicol/kg bodyweight/day: Group 1 (n = 462): nanonised florfenicol - Group 2 (n = 465): standard florfenicol formulation. Medicated water was consumed within 12 hours after start of administration using a proportioner set at a 1% injection rate. At start of the trial, both stock mixtures were stirred for 20 seconds and showed equal florfenicol concentrations and volumes. The visual appearance in the proportioners and the florfenicol recovery at nipple level and in plasma were investigated. Water samples from 10 nipples and blood samples (LOQ-LOD: 2.5-0.01 and 100-17.7 ng/ml, respectively) from 10 pigs were taken at different time points after administration started to determine florfenicol concentrations (validated UHPLC-MS/MS analysis).

Results and Discussion
Substantial sedimentation of insoluble florfenicol crystals starting immediately after mixing was observed in the proportioner when using the standard florfenicol formulation. On the other hand, the nanonised formulation demonstrated excellent homogeneity throughout the administration period. Mean florfenicol recovery in the final drinking water was 3.6, 2.9 and 4.0 times higher than the standard formulation after 3, 6 and 10 hours, respectively (all $P < 0.001$). Coefficient of variation in drinking water after 10 hours was 2.8 and 24.6%, respectively. Mean plasma concentrations were 2.2 ($P = 0.002$), 2.8 ($P < 0.001$), 2.4 ($P = 0.002$) and 3.4 ($P < 0.001$) times higher after 6, 9, 12 and 24 hours, respectively.

Conclusion
Product formulation largely determined the convenience to use and expected efficacy. Nanonisation (Amphen® 200 mg/ml florfenicol) resulted in superior homogeneity in highly concentrated stock solutions and subsequently, in superior florfenicol recovery in drinking water and in plasma. The standard florfenicol formulation was not suitable for use via proportioners.

Keywords: Florfenicol, Nanonisation, Proportioner, Recovery.

PK/PD AND CLINICAL RELATIONSHIPS OF PHARMASIN WATER SOLUBLE GRANULES (TYLOSIN TARTRATE) AND TYLOVET PREMIX (TYLOSIN PHOSPHATE) FOR THE TREATMENT OF NECROTIC ENTERITIS (NE)

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Introduction and Objectives

The objective of the work was to compare the pharmacokinetics (PK) of tylosin (Pharmasin/Tylovet - Huvepharma NV) colon contents concentration (CCC) after oral administration and to relate this to MICs against *C.perfringens* Type A (Cp) strains derived in a Thailand susceptibility study (pharmacodynamics - PD).

Materials and Methods

Pharmacokinetics: Tylosin CCC was determined in two different pig PK studies. Eleven animals (equally male and female); bodyweight 20–25kg) in the individual studies were medicated with tylosin phosphate (Tylovet 250 mg/g Premix) or with tylosin tartrate (Pharmasin 100% WSG) at 10 mg/kg bw/24h via feed or water for 5 consecutive days. Medicated feed or water were offered at libitum.

Pharmacodynamics: Tylosin MICs were generated in a susceptibility study conducted in Thailand. Fifteen Cp strains (isolates from 2023–2025) isolated from NE clinical cases were used for MIC testing according to CLSI guideline. The Cp strains originated from 4 different Thai provinces, which represent the major pig-producing areas in Thailand. MIC_{50}, MIC_{90} and MIC ranges were determined.

Results and Discussion

Pharmacokinetics: The tylosin CCC was recorded at 76.3 µg/g after feed and 68.1 µg/g after water medication (medication for five consecutive days) at a dose of 10 mg/kg bw.

Pharmacodynamics: For the fifteen Cp strains from Thailand < 1.0 - 32 µg/ml MIC ranges were determined. MIC_{50} was 1.0 µg/ml, the MIC_{90} was 16.0 µg/ml. The determined MIC values indicate that tylosin was capable of inhibiting the growth of Cp strains in the in vitro microdilution test system.

PK/PD relationships: The MIC values determined for tylosin are below the tylosin concentration achieved in the colon after feed (76.3 µg/g) and water (68.1 µg/g) medication at registered treatment dosage. The PK/PD relationship data show that the tylosin CCC`s exceed the MIC values of all tested Thai Cp strains.

Conclusions

In the susceptibility study low tylosin MIC values were determined with an MIC_{90} of 16.0 µg/ml and MIC range of < 1.0 – 32 µg/ml which indicate susceptibility to tylosin. An excellent therapeutic effect of Tylovet by feed and Pharmasin by water medication in the case of *C.perfringens* infection treatment can be expected based on the available PK/PD data.

Keywords: *Clostridium perfringens*, MIC data, Pharmacokinetic, Tylosin.

PK/PD AND CLINICAL RELATIONSHIPS OF APRAMYCIN PREMIX ADMINISTERED TO PIGS FOR THE TREATMENT OF ENTERIC INFECTIONS CAUSED BY *ESCHERICHIA COLI*

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Introduction and Objectives

The pharmacokinetics (PK) of apramycin sulfate (Apravet - Huvepharma NV) small intestine concentration (SIC) based on feed medication was related to apramycin MICs against *Escherichia coli (*EC) strains from Japan (pharmacodynamics - PD).

Materials and Methods

The apramycin SIC was determined in a PK study with twenty healthy 4 - 5-week-old pigs (bodyweight 8.8-10.5kg), which were medicated at a dose of 8mg/kg bw. Medicated feed was offered 21 consecutive days. On day 21 pigs were euthanized at 12, 24, 36 and 48 hours after treatment stop to determine the apramycin concentration (HPLC) in the small intestine. Apramycin MIC data were generated based on susceptibility testing of *EC* strains in an in vitro study in Japan (Kusumoto et al., 2023). In total 1708 *EC* strains (mostly serotypes O139, O149, O116, OSB9) were generated from EC diseased pigs 1991 to 2019 for susceptibility monitoring. The Japan strains were MIC tested according to agar dilution method (CLSI 2018). MIC_{50}, MIC_{90} and MIC ranges were determined.

Results and Discussion

Pharmacokinetics: The apramycin SIC was recorded at 45.0 µg/g at 8 mg/kg bw dose. 12 and 24 hours after treatment stop the apramycin SIC remained high, respectively at 33.2 and 10 µg/g. *Pharmacodynamics*: For the 1708 EC strains MIC_{50} value of 4.0 µg/ml and MIC_{90} value of 8.0 µg/ml were determined with MIC range of 1.0 to > 512 µg/ml and bimodal MIC distribution. Over time period of 19 years no changes in susceptibility patterns of EC on apramycin were determined. PK/PD relationships*:* The MIC values determined for apramycin are below the apramycin intestine concentration achieved after medication directly after euthanasia (45.0 µg/g) and 12 hours after medication stop (33.2 µg/g). The PK/PD relationship data show that apramycin SIC`s exceed the MIC values of 93% of the tested Japanese EC strains.

Conclusions

In the susceptibility study low apramycin MIC values were determined with an MIC_{90} value of 8.0 µg/ml and MIC range of 1.0 to > 512 µg/ml. Excellent therapeutic and metaphylactic effects of Apravet by feed medication in the case of *Escherichia coli* infection treatment at registered dosage of 8 mg/kg bw can be expected based on available PK/PD data.

Keywords: Apramycin, *Escherichia coli*, Pharmacokinetic, Pharmacodynamic.

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RETURN ON INVESTMENT (ROI) AND IMPACT ON INTESTINAL SCORE IN PIGS VACCINATED WITH PORCILIS® LAWSONIA ID ON A COMMERCIAL FARM

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Introduction and Objectives

Lawsonia intracellularis infection reduces growth performance and feed efficiency in swine, causing economic losses during the fattening phase. Intradermal vaccination with Porcilis® Lawsonia ID is proposed to mitigate clinical and subclinical ileitis and improve production metrics. This study assessed production, pathological and economic outcomes following implementation of a Porcilis® Lawsonia ID vaccination program on a commercial Colombian farm.

Materials and Methods

On a single commercial fattening farm, pigs were assigned to receive Porcilis® Lawsonia ID according to the farm's standard vaccination schedule while conventional management practices were maintained. Production data (feed conversion ratio [FCR], average daily gain [ADG], final live weight), and health outcomes (frequency and severity of intestinal lesions at slaughter) were compared with historical farm records. Economic analysis estimated vaccine program costs against gains in feed efficiency and marketable weight to calculate return on investment (ROI).

Results and Discussion

Implementation of Porcilis® Lawsonia ID vaccination was associated with improved production performance: enhanced feed efficiency, increased final live weight, and higher ADG compared with historical benchmarks (exact numerical values in source document). Necropsy and slaughter lesion scoring demonstrated reduced prevalence and severity of intestinal lesions consistent with *Lawsonia intracellularis* infection in vaccinated cohorts. Economic modelling reported an ROI of 2.45:1 for the vaccination program under the farm's management and market conditions, indicating that for every unit of currency invested in vaccination, approximately 2.45 units were returned through improved productivity and reduced lesion-associated losses.

Conclusion

In this commercial farm setting, Porcilis® Lawsonia ID vaccination correlated with measurable improvements in growth performance and gut health during the fattening period and yielded a favorable economic return. While farm-specific factors and use of historical controls limit causal inference, the combined production, pathology and economic indicators support Porcilis® Lawsonia ID as an effective intervention to mitigate impacts of *Lawsonia intracellularis*. Prospective randomized field trials across diverse production systems would strengthen evidence for generalizability and refine economic projections under varying market scenarios.

Keywords: Economic impact, Feed conversion ratio (FCR), Intradermal vaccination, *Lawsonia intracellularis*, Porcilis® Lawsonia ID.

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PREVALENCE OF *ACTINOBACILLUS PLEUROPNEUMONIAE* SEROTYPES IN CLINICAL PIGS FROM SOUTHEASTERN, VIETNAM

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Introduction and Objectives

Actinobacillus pleuropneumoniae (APP) is a major bacterial pathogen causing porcine pleuropneumonia, leading to significant global economic losses (Frey, 1995). In Vietnam, information on circulating serotypes remains limited, fragmented, and lacking systematic surveillance, impeding the development of effective serotype-specific control strategies. This study aimed to determine the prevalence of APP serotypes in swine populations in southeastern Vietnam.

Materials & Methods

Between June and December 2025, a total of 85 samples (79 lung and 7 tonsil samples) were collected from pigs exhibiting clinical signs of respiratory disease or showing suggestive lesions at slaughterhouses across five provinces in Southeastern, Vietnam. Serotyping was performed using a multiplex PCR assay capable of differentiating 19 serotypes (Stringer et al., 2021), followed by 1.5% agarose gel electrophoresis for product visualization.

Results and Discussion

A total of 85 samples were collected from pigs, including 17 from farms and 68 from slaughterhouses, to investigate the prevalence and distribution of APP serotypes in Southeastern Vietnam. Thirteen out of 85 samples tested positive, all of which were lung samples. Three serotypes were identified, including serotype 1 (10/13, 76.9%), serotype 5 (2/13, 15.4%), and serotype 2 (1/13, 7.7%). On farms, only serotypes 5 were detected. Serotypes 5 are considered highly virulent and are commonly associated with acute pleuropneumonia, leading to rapid clinical deterioration and mortality. In contrast, serotype 1 was predominated in clinical pigs from slaughterhouse, exclusively in lung tissues. The detection of the highly virulent serotype 1 despite prior vaccination suggests persistent circulation within the swine population. Survival to market age likely reflects the effectiveness of herd management and therapeutic interventions in mitigating mortality. These findings underscore the necessity for continuous surveillance, optimized vaccination protocols, and robust herd management practices to achieve effective control of APP infections in swine herds.

Conclusion

Serotype 1 was predominant in pigs sampled at slaughterhouses, whereas serotypes 2 and 5 were mainly detected on farms. These observations emphasize the need for sustained surveillance and the implementation of effective monitoring and control strategies.

Keywords: *Actinobacillus pleuropneumoniae*, farm prevalence, serotype, slaughter.

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NEW IGM PROTEASE SCREENING PCR FOR *STREPTOCOCCUS SUIS* STRAINS REVEALS TYPE A AS DOMINANT TYPE IN DUTCH PIG FARMS

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Introduction and Objectives

Streptococcus suis is a leading bacterial pathogen in swine causing meningitis, septicemia and reproductive losses. Recently described IgM proteases may influence host immunity and vaccine responsiveness. We evaluated a novel PCR assay targeting IgM protease types to classify *S. suis* isolates from Dutch pig farms and to assess serotype diversity relevant to vaccine design.

Materials and Methods

A total of 101 *S. suis* isolates recovered (between March 2024 and November 2024) from clinical and farm surveillance samples across affected Dutch herds were screened using a newly developed PCR assay differentiating IgM protease type A and type B genes. The metadata of each isolate including the farm of origin and the available serotype was recorded. Farms submitting multiple isolates were examined for within-farm serotype diversity and protease type distribution. Results were summarized to inform potential benefits of serotype-independent vaccine approaches.

Results and Discussion

IgM protease type A was detected in 84% (85/101) of isolates, while type B was present in 15% (15/101); one isolate was negative for both targets. Type A isolates were widespread, occurring on the majority of farms. Multiple serotypes were identified within 65% of farms that provided more than one isolate, indicating high local serotype diversity. Several farms harbored both IgM protease types among different isolates, although type A predominated. The PCR assay demonstrated robust differentiation between protease types and provided rapid screening capacity suitable for epidemiologic surveillance. The predominance of type A and frequent co-existence of multiple serotypes on individual farms underscore challenges for serotype-specific vaccine strategies and support exploration of serotype-independent or protease-targeted vaccine designs.

Conclusion

Application of an IgM protease–targeted PCR across Dutch *S. suis* isolates revealed a dominant type A protease distribution and widespread within-farm serotype diversity. These findings highlight the limitations of serotype-focused vaccination and suggest that vaccines targeting conserved virulence determinants, such as IgM proteases, or approaches conferring cross-serotype protection may offer improved control. Further work will be warranted to validate the PCR across larger datasets, to correlate protease type with clinical outcomes and immune evasion, and to assess the protective potential of protease-based vaccine candidates.

Keywords: Classification, PCR testing, Screening; *Streptococcus suis*.

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TREATMENT OF ACUTE SWINE ILEITIS WITH TIAMULIN IN FATTENING PIGS

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Introduction and Objectives

There is a high positive rate of ileitis in pig farms in China. It has been reported that a farm-level positive rate could reach 96.4%. In 2023, fattening pigs on a farm in Gansu Province had a high incidence of diarrhea. Over half of the pigs had diarrhea, some even with bloody stools. More than 25% of the pigs in the batch exhibited uneven and stunted growth, with a mortality rate of approximately 3% over nearly 10 days. The pigs dying from bloody stools were necropsied. The ileal mucosa bled extensively, and thickened mucosa in the ileum was observed while the cecum was normal. Based on clinical observation and lesions of the ileum during necropsy, *Lawsonia intracellularis* infection was suspected.

Materials and Methods

In two fattening pig houses (total 1,345 pigs) showing clear clinical signs, bloody and loose fecal samples were collected and sent to Huazhong Agricultural University for PCR testing. *Lawsonia intracellularis* was detected in 9 of 15 samples; all were negative for PCV2 and *Brachyspira hyodysenteriae*, confirming porcine proliferative enteropathy (PPE). Five *L. intracellularis* strains were isolated, all tiamulin-sensitive (MIC: 0.006 - 0.25 µg/mL). Pigs were grouped by house: the experimental group (667 pigs) received tiamulin (125 g of 80% Denagard®/ton feed = 100 mg active/kg feed) for 10 days via feed; the control group (678 pigs) received no treatment.

Results and Discussion

In the experimental group, bloody stools decreased by day 3, and loose stools dropped markedly by day 5. From days 3 - 10, mortality remained below 0.3%, far lower than the 3% during the outbreak. By day 10, fewer pigs showed pale skin, and the herd gradually recovered. Meanwhile, the control group showed no significant changes in morbidity or mortality.

Conclusion

Pig farms must take corresponding measures to address swine ileitis. This case shows that treating acute outbreaks of swine ileitis with tiamulin is effective, practical, and economically important for farms.

Keywords: Diarrhea, *Lawsonia intracellularis*, Swine ileitis, Tiamulin.

PREVALENCE OF ANTIBODIES TO *LAWSONIA INTRACELLULARIS* IN PIG FARMS IN AUSTRALIA

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Introduction and Objectives

Lawsonia intracellularis is the causative agent of proliferative enteropathy (PE) commonly known as ileitis. The disease is characterised by poor growth, diarrhoea and in acute cases sudden death and dysentery in grower and finisher pigs (Lawson and Gebhart 2000). A study by Holyoake et al (2010) in Australia reported a seroprevalence of 100% in 63 herds sampled with a within-herd mean prevalence of 84.2% (range, 31.3 - 100%) in finisher pigs. The objective of this study is to present an update on the current prevalence in Australian pig farms.

Materials and Methods

A total of 1183 serum samples from unvaccinated pigs against *L. intracellularis* ranging from 2 - 22 weeks from 12 farms across Australia were collected and tested for antibodies to *L. intracellularis* using a commercial ELISA test (BioScreen ELISA, Svanova, Sweden). The size of the farms sampled ranged from 300 - 10,000 sows and included indoor and outdoor production systems.

Results and Discussion

All the farms tested positive for *L. intracellularis*-specific antibodies. The mean percentage of positive samples within each herd was 34.9% (range 13.3 - 74.1%). Overall, 35.5% of the samples tested positive, while 11.3% and 53.2% were classified as suspect and negative respectively. The distribution of positive samples per age group revealed a higher seroprevalence in the pigs from 16-18 weeks-old (75.6%) and 20-22 weeks-old (79.6%) subsets compared to the pigs from 2–6 weeks-old (24.3%), 8 - 10 weeks-old (6.2%), and 12-14 weeks-old (21.0%). The differences in the within-farm results with previous studies (Holyoake, Emery et al. 2010) can be explained by the differences in the ages of the pigs sampled in each study. The presence of antibodies in all farms and age groups demonstrate that despite the use of prophylactic antibiotics in these farms, pigs are still exposed to *L. intracellularis* levels sufficient to elicit an immune response.

Conclusion

Lawsonia intracellularis remains an important pathogen in pig production in Australia and these results confirm the endemic status of the disease. Furthermore, current control strategies are inadequate to prevent infection as demonstrated by the results of this study. Vaccination, cleaning and disinfection protocols are effective strategies to control ileitis.

Keywords: ELISA, *Lawsonia intracellularis*, Seroconversion.

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PREVENTIVE VACCINATION FOR PWD DUE TO *E. COLI* F4 REDUCES ANTIMICROBIAL USE AND PERCENTAGE OF RUNT PIGLETS AT THE END OF NURSERY

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Introduction and Objectives

During the post-weaning period piglets might undergo infectious challenges such as enterotoxigenic *Escherichia coli* (ETEC) resulting in post-weaning diarrhea (PWD) and increased variation of piglets at the end of the nursery period. To prevent the negative effects of PWD due to E. coli, a preventive vaccination with live avirulent oral *E. coli* F4F18 vaccine (Coliprotec F4 F18; Elanco AH) was implemented. The objective was to evaluate the effect of *E. coli* vaccination on PWD-related clinical disease, mortality and number of runt piglets at the end of the nursery period.

Materials and Methods

A 800-sow farm with Topigs 70 sows operating in a 1-week BMS suffered from PWD due to *E. coli* F4 during the post-weaning period. Following confirmation of the *E. coli* pathotype (F4-ETEC), a vaccination with a live avirulent oral *E. coli* F4F18 vaccine (Coliprotec F4F18; Elanco AH) was implemented at 18 days of age. Data capture included number of piglets (d0-40), mortality, number of runt piglets and antimicrobial use (TI100). Statistical analysis was performed using JMP 17.1.

Results and Discussion

Mortality following E. coli vaccination significantly reduced both in number (7 vs. 19; $P = 0.001$) and percentage (3.1 vs. 0.9%; $P = 0.003$). Following E. coli vaccination, there was a significant improvement in the number (6 vs. 55; $P = 0.001$) and percentage (0.9% vs. 8.6%; $P = 0.006$) of runt piglets at the end of the nursery period. The number of days on antimicrobial treatment, given as TI100, reduced from 12.5 days to 0 days following E. coli vaccination ($P < 0.001$). Based on our return-on-investment calculator, we could generate a positive ROI of + 2.06 with the vaccine cost already included into the calculation. For the 800-sow farm, this resulted in an increased income of € 57,771.55.

Conclusions

In conclusion, implementation of a preventive vaccination of a live avirulent oral *E. coli* F4F18 vaccine (Coliprotec F4F18) could reduce mortality post-weaning and number of runt piglets at the end of the nursery period, while reducing the TI100. Overall, a positive return on investment of 2.06 could be obtained per piglet produced.

Keywords: Coliprotec F4F18, *E. coli* vaccination, Post-weaning diarrhea, Runt piglets.

SUCCESSFUL *BRACHYSPIRA HYODYSENTERIAE* ERADICATION THROUGH A COMBINED APPROACH OF A ZINC CHELATE TREATMENT AND ADAPTED MANAGEMENT MEASURES

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Introduction

Brachyspira hyodysenteriae (*B. hyodysenteriae*) is the primary cause of swine dysentery, characterized by bloody to mucoid diarrhea due to mucohaemorhagic colitis in pigs. A worldwide re-emergence of the disease has recently been reported with an increasing number of isolates demonstrating decreased susceptibility to several crucially important antimicrobials in the control of swine dysentery. This compromises the possibilities to eradicate *B. hyodysenteriae* from infected pig farms. A novel non-antibiotic zinc chelate has been reported to demonstrate positive effects on fecal quality and consistency, general clinical signs, average daily weight gain and *B. hyodysenteriae* excretion during and after a 6-day oral treatment. Until now, no resistance has been reported to the product. The objective was to evaluate the zinc chelate (IntraDysovinol® 499 mg/ml; IntraCare) within an eradication schedule with naturally occurring swine dysentery due to *B. hyodysenteriae* resistant to pleuromutilins under field conditions in Belgium.

Materials and Methods

We evaluated a 14-day treatment schedule (0.023 ml of zinc chelate per kg bodyweight per 24 h) combined with alternative management measures (including partial depopulation of post-weaning facilities and improved external and internal biosecurity measures) and thorough cleaning and disinfection (including 2% NaOH) of the buildings and the sows from day 7 of treatment onwards. This alternative approach for *B. hyodysenteriae* eradication was evaluated on 18 swine farms over a 5-year period. All enrolled eradication programs were evaluated as successful at least 6–9 months after the finalization of the protocol.

Results

All enrolled farms in the field study tested *B. hyodysenteriae* negative at 6-9 months after the finalization of the eradication procedure. No clinical signs of *B. hyodysenteriae* were observed and no positive culture or PCR result was obtained following eradication.

Discussion & Conclusion

In conclusion, the zinc chelate product has an excellent potential for application within an eradication protocol of *B. hyodysenteriae* that were diagnosed resistant to pleuromutilins. The combined approach of zinc chelate treatment and alternative management measures demonstrated to be successful in the eradication of farrow-to-wean, farrow-to-finish and finishing swine farms under field conditions in Belgium.

Keywords: *Brachyspira hyodysenteriae*, Eradication, Management measures, Zn-chelate.

META-REGRESSION ON FACTORS AFFECTING VARIATION OF *MYCOPLASMA HYOPNEUMONIAE* VACCINATION

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Introduction and Objectives

Mycoplasma hyopneumoniae (M. hyopneumoniae) is the etiologic agent of enzootic pneumonia, leading to pneumonia of the cranial lung lobes, reduced performance, reduction in average daily weight gain (ADWG), and decreased feed efficiency. The control of *M. hyopneumoniae* primarily relies on commercially available inactivated bacterins or live attenuated vaccines. However, recent studies examining the impact of *M. hyopneumoniae* vaccination have produced conflicting results, possibly due to variations in experimental set-up, group size, co-infections, infection duration, and different types of vaccines administered. Therefore, this study aimed to conduct a meta-analysis to evaluate the effects of *M. hyopneumoniae* vaccination on ADWG and macroscopic lung lesion scores (LLS) in placebo-controlled studies involving fattening pigs affected by enzootic pneumonia.

Materials and Methods

For the identification of relevant studies, two text-based search strategies were employed: "vaccine AND *Mycoplasma hyopneumoniae* AND pig" and "vaccine AND *Mycoplasma hyopneumoniae* AND swine". After screening and eligibility evaluation, 24 and 25 studies remained to evaluate the vaccination effect respectively on ADGW and LLS. No other parameters were retained due to lack of sufficient number of studies.

Results and Discussion

The meta-analysis results revealed a statistically significant intervention effect, showing a difference of 17.43 grams in ADWG (95% CI [9.88; 24.98], $P < 0.001$) among animals vaccinated against *M. hyopneumoniae* compared to control animals. The effect was observed to be smaller after a single vaccination (one shot strategy), with a difference of 11.66 grams (95% CI [4.55; 18.77]), compared to 28.97 grams (95% CI [10.30; 47.65]) following multiple vaccinations. This study characteristic also explained part of the variation of the treatment effect variation on ADWG. Vaccination against *M. hyopneumoniae* also led to a statistically significant difference in LLS equal to 7.78% (95% CI [3.67; 11.90], $P < 0.001$).

Conclusions

In summary, this meta-analysis quantified the effectiveness of vaccination against *Mycoplasma hyopneumonia*e on ADWG and LLS in pigs and determined factors that are associated with the large effectiveness variation. Despite the significant positive effect of vaccination, it is rather small and the economic benefits of *M. hyopneumoniae* vaccination may depend on current market value of slaughter pigs.

Keywords: ADWG, LLS, Meta-regression, *Mycoplasma hyopneumoniae*, Vaccination.

CASE REPORT: FOCUS ON CLEANING AND DISINFECTION TO TACKLE SEVERE POST-WEANING DIARRHEA

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Case description

A 1000-sow farm operating in a standard 1-week management system, weaning piglets at 24 days of age, had a history of post-weaning diarrhea due to F4-ETEC. The piglets were vaccinated against PWD with a commercial *E. coli* F4F18 vaccine. However, following 9 months of piglet vaccination, a new episode of severe watery diarrhea occurred resulting in increased mortality, reduced performance and increased number of runt piglets. A vaccination audit revealed no critical issues regarding vaccine preparation, administration and uptake by the piglets.

Diagnostic approach

To identify the cause of severe watery PWD, 5 fecal samples of severely affected piglets were collected at day 2 post-weaning for diagnostic examination using 3rd generation sequencing (Oxford Nanopore Technology; PathoSense, Merelbeke, Belgium). Analysis of the fecal samples revealed a total of 19 different bacterial and viral pathogens, of which several pathogens with impact on the intestinal integrity were Enterovirus sp., Rotavirus A-B-C-H, Picobirnavirus and Astrovirus. Several of these pathogens are known to be resistant in the environment. Therefore, cleaning and disinfection (C&D) of the premises prior to the start of a new batch of post-weaned piglets was extensively checked. Hygiene evaluation using Rodac plates was performed comparing different C&D scenario's (1 - 4). Only glutaraldehyde (3) and the extended NaOH + glutaraldehyde (4) following thorough cleaning resulted in a significantly lower ($P < 0.05$) hygiene score as compared to the uncleaned positive control (1) and the standard disinfection with peroxide (2). Subsequently, all post-weaning compartments were subjected to the extended C&D protocol. Evaluation of post-weaned piglets placed into the optimally cleaned compartments revealed major improvement in clinical condition.

Discussion & Conclusions

Occurrence of clinical episodes of PWD in a previously stable situation should be examined more broadly to identify potential pathogens. Besides preventive therapeutic and immunological measures, basic management practices should also be considered in the overall approach of a case resolution. Macroscopic evaluation of C&D practices does not allow to identify potential gaps in hygiene management and more specific quantitative hygiene scores using Rodac plates can help in identifying the C&D issue.

Keywords: Cleaning and disinfection, *E. coli* F4, PathoSense, Post-weaning diarrhea.

SEROCONVERSION IN GILTS VACCINATED WITH A TWO-SHOT *M. HYOPNEUMONIAE* VACCINE AT THE END OF REARING PERIOD - CASE REPORT

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Introduction and Objectives

The present case describes a study in a gilt rearing farm vaccinating the newborn gilts with a one-shot *M. hyopneumoniae* vaccine at day 3 of age followed by booster vaccination with a two-shot *M. hyopneumoniae* vaccine at 18 and 22 weeks of age. Therefore, a comparative trial was conducted in a gilt-rearing system to determine if the serological response to *M. hyopneumoniae* was due to the booster vaccination on itself or the potential *M. hyopneumoniae* infection circulating within the gilts.

Materials and Methods

Gilts from the same farm of origin were placed in two different rearing compartments for the comparative trial. The gilts were followed throughout the entire rearing period through blood serum sampling and trachea-bronchial swab (TBS) samples combined with mPCR at 18-22-26 and 29 weeks of age. The gilts in the Control group remained exceptionally unvaccinated at 18 and 22 weeks of age, whereas the gilts in the Vaccine group received their standard booster vaccination at 18 and 22 weeks of age and were treated orally with tiamulin for 7 days after their second vaccination to omit potential spread of *M. hyopneumoniae* that might interfere with seroconversion to *M. hyopneumoniae*. Statistical analysis was performed using JMP 15.0.

Results and Discussion

The S/P ratio of the gilts in the Control group was 0.39 ± 0.07 (18 wks) and significantly increased ($P < 0.05$) to 0.54 ± 0.08 (22 wks) and a maximum of 0.68 ± 0.09 (26 wks). In the Vaccine group, the S/P ratio of the gilts was 0.20 ± 0.05 (18 wks) and significantly increased ($P < 0.001$) to 1.34 (22 wks) and a maximum of 1.41 (26 wks). The TBS swabs were all negative for *M. hyopneumoniae* at 18-22-26 and 29 weeks of age in both study groups, indicating that no circulating *M. hyopneumoniae* infection was present.

Conclusions

Administration of a booster vaccination for *M. hyopneumoniae* to rearing gilts, already vaccinated in early life with a one-shot *M. hyopneumoniae* vaccine, induced an increase in serological titers and the percentage of *M. hyopneumoniae* serologically positive animals at the end of the rearing period.

Keywords: Gilts, *Mycoplasma hyopneumoniae*, Seroconversion, TBS, Vaccination.

VACCINATION WITH A LIVE AVIRULENT *E. COLI* VACCINE RESULTED IN IMPROVED PRODUCTION PERFORMANCE COMBINED WITH A SIGNIFICANT REDUCTION IN ANTIMICROBIAL USE

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Introduction and Objectives

During the post-weaning period, piglets might undergo infectious challenges with enterotoxigenic *Escherichia coli* (ETEC) resulting in post-weaning diarrhea (PWD), and meningitis due to *Streptococcus suis*. Therefore, metaphylactic and curative antimicrobial therapy is frequently applied, leading to increased treatment incidence per 100 days at risk (TI100). This study reports the results of an antimicrobial coaching trajectory in a 1000-sow farm with high antimicrobial use during the post-weaning period.

Materials and Methods

For a period of 21 weeks, we evaluated the effect of an oral live avirulent E. coli F4F18 vaccine (Coliprotec® F4F18; Elanco AH) for active immunization of piglets against PWD caused by F4- and F18-ETEC on production parameters, clinical signs of PWD and S. suis, and reduction of antimicrobial use during the post-weaning period. A 1000-sow farm with PIC sows operating in a 1-week BMS was rated as an 'attention farm'. A farm visit including a biosecurity check was carried out together with all associated stakeholders. Subsequently, an antimicrobial coaching trajectory was enrolled to follow-up on the improvement of the reduction of antimicrobial use after implementation of the advice.

Results and Discussion

We compared the results obtained in period 1 (P1; vaccination week 1 - 6; 5,106 piglets) to period 2 (P2; vaccination week 7 - 21; 11,280 piglets), since practical field experience has demonstrated that a 'stabilization period' of about 6 weeks is necessary to obtain maximal effect of vaccination. There was a significant improvement in mortality (5.7% to 2.0%) and average daily weight gain (366 to 392 g/d) following vaccination with a simultaneous reduction in number of days in nursery (45 to 38 days). Meanwhile, the weight at the end of nursery remained at a similar level. No clinical signs were observed. There was a clinically relevant though non-significant decrease in the TI100 (32.8 to 20.6 days).

Conclusions

Implementation of biosecurity measures combined with the use of an oral live avirulent *E. coli* F4F18 vaccine (Coliprotec F4F18) could improve performance and mortality, while reducing the number of days in nursery and the TI100. Overall, a positive return on investment of 2.72 could be obtained per piglet.

Keywords: Antimicrobial coaching trajectory, Antimicrobial reduction, Live oral *E. coli* vaccination, Post-weaning diarrhea.

EFFECT OF YEAST BETA-GLUCANS IN MITIGATING THE NEGATIVE IMPACT OF *LAWSONIA INTERACELLULARIS* IN EXPERIMENTALLY CHALLENGED PIGS OR PIGS EXPOSED TO NATURAL INFECTION

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Introduction and Objectives

Ileitis is economically important disease of pigs caused by *Lawsonia intracellularis*. Beta-glucans (BG) are known to stimulate the innate immune response against pathogens. This study evaluated the effect of a yeast-derived beta-glucan (Safglucan) in reducing the negative impact of *L. intracellularis* infection in pigs.

Materials and Methods

Two independent experiments were conducted. In the first experiment, 96 pigs from Lawsonia-free sows were randomly assigned to either control diet or a diet supplemented with 250 g/ton of BG and feed from D0 to D49. All pigs were orally challenged with 10^7 *L. intracellularis* after 4 weeks of supplementation on D28 and necropsied on D49 to collect intestinal tissue-samples. The second experiment was a field study involving 270 grower pigs randomly assigned to one of three treatment groups: control, BG supplementation for 50 days (T1), or for 110 days (T2). In both trial performance, blood, and fecal samples were collected at different time points.

Results and Discussion

In the challenge study, BG supplementation significantly ($P < 0.05$) increased average daily gain, and improved feed efficiency during the post-challenge period. BG-fed pigs had reduced ileum lesion scores compared to controls. There was no significant difference in seroconversion, but anti-lawsonia antibody titer was lower in the treated group. In the field trial, BG-supplemented pigs demonstrated greater body weight on days 100 and 130 ($P < 0.001$) compared to controls. Average daily gain was higher in both treated groups during Phase I ($P < 0.001$), with T2 showing further improvement over control and T1 during Phase II ($P = 0.012$). Fecal shedding of *L. intracellularis* was significantly reduced in treated groups compared to control by day 134 ($P < 0.05$), and more pigs in the treated groups seroconverted to negative status by day 155.

Conclusion

These findings suggest that dietary supplementation with yeast-derived beta-glucans (Safglucan) effectively mitigates the negative impacts of *L. intracellularis* infection in both experimentally challenged and naturally infected pigs by improving growth performance and reducing intestinal pathology. The beneficial effects observed may be attributed to the positive impact of beta-glucans on gut health and immune function, offering a promising nutritional strategy for controlling ileitis in swine production.

Keywords: Beta-glucans, Ileitis, *Lawsonia*, Pigs, Yeast.

EFFECT OF INJECTABLE TOLTRAZURIL AND GLEPTOFERRON ADMINISTRATION ON WEANING WEIGHT OF PIGLETS COMPARED TO IRON DEXTRAN AND ORAL TOLTRAZURIL

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Introduction and Objectives

Iron deficiency anemia and neonatal coccidiosis are two of the most frequent and economically relevant diseases of piglets. (Calveyra et al., 2020, Vallejo et al., 2022). The objective of this study was to compare the effect of treatment with a combination of injectable toltrazuril and gleptoferron (T1) and oral toltrazuril and iron dextran injectable (T2) on the pre-weaning weight gain of piglets under commercial conditions.

Material and Methods

The study was conducted on a 1,000-sow commercial farm in Neuquén, Argentina, between July and September 2025. The trial was carried out in seven consecutive farrowing houses, 3,368 piglets from 264 litters included. In each house, half of the litters received T1 (45 mg of toltrazuril and 200 mg of iron as gleptoferron - Forceris - Ceva Animal Health) on day three of age, and the rest of the piglets (T2) received standard treatment applied on the farm (200 mg of iron dextran injectable and 5% oral toltrazuril (20 mg/kg) on day three of age). The litters were assigned randomly. The piglets were weighed at birth and at weaning (21 DOA), and the average weight per litter was recorded. The data were analyzed using ANOVA.

Results and Discussion

The average birth weight did not show significant differences between treatments ($P = 0.7733$), with a mean value of 1.35 ± 0.02 kg for both T1 and T2 groups respectively. The final weaning weight showed a significant difference between two treatments: T1 = 7.09 ± 0.97 kg and T2 = 6.68 ± 1.10 kg ($P = 0.0028$). The results of the study demonstrated that injectable administration of toltrazuril combined with gleptoferron resulted in better weight gain at weaning compared to conventional treatment with 5% oral toltrazuril and injectable iron dextran. This is the first study conducted in Argentina using an injectable combination of toltrazuril and gleptoferron recently registered in the country.

Conclusion

The results are consistent with previous studies conducted in various Latin American countries, which describe an improvement of between 0.3 and 0.6 kg at weaning with this treatment.

Keywords: Gleptoferron, Injectable toltrazuril, Weaning weight.

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PREVALENCE OF *CYSTOISOSPORA SUIS* IN PIG FARMS IN ARGENTINA

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Introduction and Objectives

Porcine neonatal coccidiosis is a parasitic enteropathy caused by *Cystoisospora suis*, considered the most common intestinal protozoan in intensive pig production systems worldwide. The objective of this study was to determine the prevalence of *Cystoisospora suis* in suckling piglets on farms in Argentina.

Material and Methods

The study was conducted between December 2024 and September 2025. A total of 196 litters from 19 farms located in different provinces of Argentina were analyzed: Buenos Aires (9), Córdoba (5), Santa Fe (1), Río Negro (1), La Rioja (1), and Neuquén (1), representing more than 10% of the sows housed in intensive production systems in Argentina. The size of the farms ranged from 250 to 7,000 sows, and all operated under intensive production systems with total confinement. Ten percent of piglet litters were sampled at 9 and 12 days of age (first sampling) and repeated the same piglets at 16 and 21 days of age, according to the protocol of Joachim et al., 2018.

Results and Discussion

57.9% of the farms (11/19) and 44.9% of the litters (88/196) were positive for *Cystoisospora suis*. Almost half of the sampled litters presented oocysts in the feces, regardless of the presence of clinical signs. This finding demonstrates a high subclinical circulation of the parasite in the intensive systems studied. The results of this study confirm that *Cystoisospora suis* is widely distributed in confined pig production systems in Argentina. The prevalence of 57.9% of positive farms and 44.9% of positive litters demonstrates endemic circulation of the parasite in the evaluated farrowing facilities, with values like those reported in international studies conducted in intensive systems (Joachim et al., 2018, Calveyra et al., 2023, Sperling et al., 2022).

Conclusion

The results obtained in this study constitute the first national survey of *Cystoisospora suis* prevalence in confined systems in Argentina, providing updated evidence on the magnitude of the infection in technologically advanced establishments.

Keywords: *Cystoispospora suis*, Prevalence.

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PREVALENCE AND SEVERITY OF ENZOOTIC PNEUMONIA AND PLEUROPNEUMONIAE IN MEXICO

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Introduction and Objectives

Respiratory diseases such as enzootic pneumonia and pleuropneumonia continue to be present in swine herds (Maes et al., 2008). Monitoring these diseases is necessary to identify and correct control programs. One of the tools used is examination in slaughterhouses through macroscopic identification of lung lesions (Garcia-Morante et al., 2016). This study aimed to determine the prevalence and severity of respiratory lesions in slaughterhouses in Mexico.

Material and Methods

From January to October 2025, 2,830 lung audits were conducted in 11 slaughterhouses for bronchopneumonia lesions, covering 180 farms distributed throughout the country and totaling 168,000 lungs evaluated. And for pleuropneumonia lesions, 2,229 audits were carried out on 176 farms, totaling 136,000 lungs assessed. The Ceva Lung Program (CLP - Ceva Animal Health, France), a system for scoring lung lesions, was used. The Mhyo-like lesions and App-like lesions indicators were considered as parameters of prevalence and severity of lung injuries: bronchopneumonic lungs (%), affected surface area of bronchopneumonic lungs (%), and dorsocaudal pleuritis (%). The evaluation for each farm was calculated as the average.

Results and Discussion

The average percentage of affected lungs in the examined population was 34.79%, and the affected surface area was 6.4%. Additionally, 33.6% of lungs presented scarring, and 27.57% presented cranioventral pleuritis. For bronchopneumonia lesions, 16.17% presented dorsocaudal pleuritis, with an APP index of 0.45.

Conclusion

These results, compiled from data from various farms across the country, provide an overview of the prevalence of lung lesions. Knowing the incidence of these diseases allows us to determine their economic impact and evaluate vaccination programs, therapeutic treatments, and management practices on pig farms.

Keywords: Enzootic pneumonia, Pleuropneumoniae.

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REDUCTION OF OOCYST EXCRETION IN LITTERS THROUGH EARLY ADMINISTRATION OF THE TOLTRAZURIL AND INJECTABLE GLEPTOFERRON COMBINATION

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Introduction and Objectives

Coccidiosis in piglets is caused by the protozoan *Cystoisospora suis*, which is one of the most prevalent enteric parasites found on pig farms (Sperling et al., 2022; Lindsay et al., 2019). The practice on pig farms is to administer one shot of Gleptoferron and Toltrazuril between 24 and 96 hours of the piglet's life. The objective of this study was to compare two protocols with different application times, through oocyst counting.

Material and Methods

The study was conducted on a Brazilian farm housing 7,500 breeding sows. 36 sows were selected based on parity and body condition score and divided into two groups of 18 each. Each litter was identified using numbered ear tags. Feces were collected twice when the piglets were 10 and 18 days of age (DOA). Feces samples (minimum 5 piglets per litter) were pooled and examined by flotation. Group 1 received treatment between 48 - 72 hours (n = 90), and Group 2 was treated with an average of 27 hours (n = 90). The average oocyst count (OPG) was determined using a T-test.

Results and Discussion

Group G1 showed a prevalence of 66%, with an average oocyst count of 16,347, and Group G2 showed a prevalence of 6%, with only 1 positive litter, with an oocyst count of 6,000, $P < 0.05$.

Conclusion

We understand that early administration of the product brings benefits, in this case a significant reduction in oocyst count when the molecule is applied earlier. In addition to the reduction in oocysts.

Keywords: *Cystoisospora suis*, Oocysts, Toltrazuril.

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FIELD EXPERIENCE OF THE PREVENTION AND CONTROL EFFECT OF ONE NEW EDEMA VACCINE ON CLINICAL EDEMA DISEASE IN CHINA

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Introduction and Objectives

Edema disease (ED) is an acute toxaemia in nursery and fattening pigs caused by verotoxin 2e-producing Escherichia coli (VTEC) (Mallorquí et al., 2018). In Europe, restrictions on antimicrobial use have made vaccination the preferred and most cost-effective strategy for ED control. In China, most farms still rely heavily on antimicrobials for prophylaxis and treatment, and the availability of commercial vaccines remains limited. This study aimed to evaluate the clinical and economic impact of VEPURED® on ED control by comparing performance data before and after vaccination under field conditions.

Materials and Methods

The study was conducted in a 6000 sows industrial farm. In February 2025, it was reported that clinical ED accompanied by a sharp increase in post-weaning mortality, the presence of ED was confirmed by autopsy and by PCR using the VEROCHECK diagnostic kit (HIPRA) (Poucke et al., 2019). Despite pharmacological interventions and strengthened management practices, outcomes remained unsatisfactory. From September, VEPURED® was administered by intramuscular injection to piglets at two days, but management condition remained the same as before. A comparative analysis was performed using eight pre-vaccination batches (10,900 piglets) and eight post-vaccination batches (12,662 piglets). Mortality was recorded weekly. An economic assessment was also conducted to quantify financial differences between vaccinated and non-vaccinated groups, considering direct losses due to mortality only. The analysis of mortality data was performed using a Test of Proportions.

Results and Discussion

Each batch contained approximately 1,500 piglets. Cumulative mortality from 4 to 10 WOA was significantly higher ($P < 0.05$) in the non-immunized group than in the immunized group (5.23% ± 1.68 vs 0.9% ± 0.75). Weekly analysis showed consistently lower mortality in vaccinated pigs, particularly between 8 and 10 WOA.

Conclusion

Farms affected by ED typically have experienced higher mortality, ranging from 50 to 100%, consistent with reports from Europe. Conventional management and antimicrobial strategies have limited impact for ED control; however, vaccination will allow for better control of this disease and minimize the impact on production.

Keywords: China, Edema, Pig, Vaccine.

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BORDETELLA BRONCHISEPTICA PREVALENCE IN CHINESE PIG FARMS DURING 2022–2024

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Introduction and Objectives

Bordetella bronchiseptica (Bb) is one of the main pathogens causing Porcine Atrophic Rhinitis (PAR), may lead to significant economic losses in swine production due to its pathogenic effect and its role as a predisposing factor in the porcine respiratory disease complex (Huan et al., 2019). Porcine oral fluid (POF) sampling offers a non-invasive alternative for Bb pathogen detection (Maldonado et al., 2017). This study assessed Bb prevalence on Chinese farms and analyzed the prevalence of Bb from 2022 to 2024.

Materials and Methods

A total of 143 farms (≥ 500 sows) were sampled across China from 2022 to 2024. 10 pens per farm (n = 1,430 samples) from nursery to fattening pigs. POF samples were collected and transferred to FTA Elute cards, then sent to HIPRA DIAGNOS China. A Previously validated qPCR assay was used to confirm the presence of Bb genes in the samples.

Results

From the total number of farms, 89% (127/143) were Bb PCR positive. There was no significant difference between different years, the positive rates of 2022 - 2024 were 88, 100 and 88%, respectively. However, there were significant differences in the positive rates at different stages from nursery to fattening. The positive rates for the age groups of 4 - 6, 7 - 9, 10 - 13, 14 - 16, 17 - 21 and over 21 weeks were 29, 38, 48, 35, 19, and 14%, respectively.

Discussion and Conclusion

Based on these results, Bb is widely present in Chinese farms despite recent changes in production practices. The highest positive rate occurred at the age of 10-13 weeks. This is consistent with the medication patterns in Chinese pig farms. Most Chinese pig farms use drugs from weaning to the early stage of nursery stage and/or after 13 weeks of age, while medication is relatively less during the period from the end of the nursery stage to the early fattening stage. This might imply that when antibiotic use is reduced, PAR infection may become more severe. In this scenario, pig farms should pay more attention to other prevention and control measures for PAR, among which vaccination should be considered one of the most effective methods.

Keywords: *Bordetella bronchiseptica*, China, Pig.

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SURVEY OF ILEITIS INFECTION IN MAJOR SWINE FARMING REGIONS OF CHINA

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Introduction and Objectives

Proliferative enteropathy (PE), also known as ileitis, is caused by *Lawsonia intracellularis* (LI) and is widely distributed in swine populations worldwide. The disease has a high infection rate and causes significant economic losses in pig production. This study aimed to assess the prevalence of LI infection across major swine-producing regions of China, by herd type and production system. Additionally, it examined the association between clinical fecal characteristics (normal, watery/pasty, bloody) and bacterial shedding across production stages, providing a scientific basis for effective prevention and control strategies.

Materials and Methods

From September 2022 to August 2025, 5,646 fecal samples were collected from 518 pig farms (1,000–10,000+ pigs) across 28 provinces, municipalities, and autonomous regions in China. Samples included 3,101 watery/pasty feces, 1,970 normal feces, and some bloody feces. All samples were tested for LI using PCR with the Thermo VetMax™ L.intracellularis kit.

Results and Discussion

Of the 5,646 samples, 4,362 tested positive for LI (77.15%). The infection rates did not show a significant correlation to farm size. At the farm level, 474 of 518 farms (91.51%) were infected. Provincial detection rates ranged from 51.06% to 93.35%, with the highest rates in Guangdong, Fujian, Shandong, Chongqing, and Guangxi. Quarterly detection remained above 50% (Q1: 62.72%, Q2: 82.97%, Q3: 84.98%, Q4: 55.92%). During the nursery phase, multi-site systems had a numerically lower detection rate (71.76%) compared to single-site systems (79.71%). In comparison, rates were numerically similar and high after the nursery phase (single-site: 76.88% vs. multi-site: 77.55%) and in sow herds (single-site: 79.29% vs. multi-site: 80.21%). Bloody stools were detected positive in 58 of 61 farms with a sample detection rate of 92.47% (221/239). It should be noted that bloody stools can also be caused by other pathogens such as *Brachyspira hyodysenteriae*, which should be considered in differential diagnosis.

Conclusion

LI infection is widespread in Chinese pig farms, with high positivity rates across production stages, herd types, and seasons. These findings suggest that comprehensive control programs targeting the entire herd throughout the year are necessary to reduce the impact of ileitis.

Keywords: *Lawsonia intracellularis*, Positive rate, Proliferative enteropathy.

IMPACT OF VACCINATION AGAINST *GLÄSSERELLA PARASUIS* IN A 3 500-SOW FARROW-TO-FINISH FARM: A PROSPECTIVE LONGITUDINAL FIELD TRIAL

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Introduction and Objectives
In a 3,500-sow farrow-to-finish farm in the Russian Federation, increased mortality during the finishing phase was observed from 80 days of age onwards. Polyserositis was detected in approximately 70% of the dead pigs, and lameness and neurological signs were also reported. *Glässerella parasuis* (GPS) infection was confirmed by PCR analysis of serosal swabs; however, the circulating serotypes were unknown.
Previous studies (De Souza & Baraldi, 2023; Bruguera et al., 2007) have demonstrated that vaccination against GPS can reduce mortality and improve performance, and some vaccines have shown efficacy regardless of the GPS serotypes present on the farm (Zhao et al., 2017). The objective of this field trial was to evaluate the impact of piglet vaccination against GPS on mortality and productive performance under the routine rearing conditions of this farm.
Materials and Methods
A prospective longitudinal field trial was conducted using six consecutive weekly batches of non-vaccinated piglets as controls (C) and six subsequent batches vaccinated twice with 2 ml of HIPRASUIS® GLASSER at 30 and 55 days of age (V). Mortality, culling rate, average daily weight gain (ADWG), and slaughter weight were recorded during fattening. Data were analyzed using the Kruskal–Wallis test and logistic regression models.
Results and Discussion
Vaccinated pigs showed significantly lower mortality (6.24 vs. 11.69%; $P < 0.01$) and culling rates (8.57 vs. 11.26%; $P < 0.01$) compared to controls. Additionally, vaccination significantly improved ADWG (0.756 vs. 0.684 kg; $P < 0.01$) and slaughter weight (129.21 vs. 123.75 kg; $P = 0.03$).
Conclusion
In this farm experiencing severe production losses associated with GPS infection during the finishing phase, piglet vaccination with two doses of HIPRASUIS® GLASSER was associated with a significant reduction in mortality and culling rates, as well as a significant improvement in growth performance and final slaughter weight.
Keywords: *Glässerella parasuis*, Polyserositis, Piglet vaccination.

NATIONWIDE PREVALENCE AND SEASONAL DYNAMICS OF *CYSTOISOSPORA SUIS* INFECTION IN CHINESE PIG FARMS: INSIGHTS FROM A 2024 SURVEY USING SATURATED UREA FLOTATION

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Introduction and Objectives

Porcine neonatal coccidiosis is a protozoal infection caused by the intestinal parasite *Cystoisospora suis* (formerly *Isospora suis*). This disease is a major cause of diarrhea and poor growth performance in piglets, resulting in significant economic losses in the pig breeding industry (Aliaga-Leyton et al., 2011). However, nationwide data on its prevalence in China remains limited. To address this gap, the technical department of Elanco Animal Health employed the saturated urea flotation method to investigate the nationwide prevalence of coccidiosis, aiming to provide foundational data for the development of effective prevention and control strategies for Chinese pig farms.

Materials and Methods

In 2024, we surveyed 202 pig farms across China and collected a total of 2,164 fecal samples. These farms cover a scale of 500 to 5,000 sows, with ages ranging from 1 to 7 years. The samples are all from farms where piglets have diarrhea in the farrowing house. 10 samples of piglet feces were collected from each farm on a per-litter basis. Detection was performed using the saturated urea flotation method, which removes interfering fats and proteins from piglet feces to enhance microscopic clarity and detection sensitivity. A positive determination is made when oocysts are observed under the microscope.

Results and Discussion

In 2024, 85.6% of the farms detected positive, while 44% of all samples were positive, indicating widespread infection. The positive rate on pig farms remained above 80% throughout the year. Notably, the sample detection rate was highest during the hot and humid summer months (47% in June to August), compared to 12.4% in the cooler months of March to May. Regional differences were observed where farms in southern China had a higher detection rate (89.7%) than those in the north (67%). Pig farms with a stock of more than 5,000 sows have the highest detection rate (94%). Coccidiosis prevalence increases with farm age: 94% of farms older than five years tested positive, compared to 55% of one-year-old farms.

Conclusion

Coccidiosis infection is widespread in pig farms across the country, and related to climates, regional distributions.

Keywords: China, *Cystoisosporosis*, Positive rate, Regional distribution, Seasons.

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VEROTOXIN 2E POSITIVE RATE IN THAILAND DURING 2019–2024 BY QPCR DETECTION TARGETING THE GENE CODING FOR THE VEROTOXIN 2E

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Introduction and Objectives

Edema disease (ED) is caused by verotoxigenic *E. coli* (VTEC) that colonizes the small intestine and produces verotoxin 2e (VT2e), which enters the bloodstream and damages vessel walls, resulting in edema in targeted tissues (1). The aim of this study was to describe the positive rate of the Vt2e gene in samples collected from pigs in Thailand from 2019 to 2024, categorized by region, province and age at sampling.

Materials and Methods

Retrospective data of VEROCHECK results in Thailand from 2019 to 2024 by HIPRA DIAGNOS (Thailand) were gathered. A total of 634 samples were collected: 633 samples were oral fluid samples and 1 intestinal content sample, which were transferred to FTA Elute cards and sent for analysis. Then qPCR analysis targeting the gene coding for the Vt2e was performed.

Results and Discussion

Overall sample positivity was 38.0% (241/634). The results by region in Thailand, showed that the northeastern region had the highest positive rate followed by southern, western, eastern, central and northern regions. These results indicate the presence of Vt2e gene in all regions of Thailand. Amongst the 40 provinces, 80% (32/40) had at least 1 positive sample. By age group, samples ranged from 1 to 16 weeks of age, the only age group found to be negative is 2-week-old piglets (0/6). Causes that can trigger a clinical outbreak of ED in a herd are multifactorial; however, a necessary condition is the overgrowth of VTEC. Previously reviewed risk factors included crude protein level, poor protein quality, stress factors, and water quality amongst others (2). Commercial vaccines for ED prevention are available. Previous studies have shown results of VEPURED® usage. One study that was conducted in a herd without clinical signs or mortality related to ED and Vt2e gene positivity, showed significantly higher individual growth performance at the end of the fattening period in the vaccinated animals (3).

Conclusion

This study shows that the Vt2e gene was present in all 6 regions of Thailand and across a wide range of ages. A commercial vaccine such as VEPURED® is available and supported by positive study results.

Keywords: Oedema disease.

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DYNAMICS OF *MYCOPLASMA HYOPNEUMONIAE* SEROCONVERSION IN CHINESE WEAN-TO-FINISH PIG HERDS

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Introduction and Objectives

Mycoplasma hyopneumoniae (Mhp) is the principal pathogen responsible for enzootic pneumonia, leading to substantial economic losses in the pig industry. Understanding the infection dynamics within pig herds is essential for the effective control of *Mhp*, as seroconversion is closely related to clinical manifestations[1,2]. This study aimed to elucidate the infection dynamics of *Mhp* in Chinese wean-to-finish pig herds using cross-sectional serological assays.

Materials and Methods

A total of 1891 blood samples were collected from 49 wean-to-finish pig herds, with approximately 40 blood samples per herd at five age intervals: 6 - 8, 10 - 12, 14 - 16, 18 - 20, and over 20 weeks of age, between April 2024 and May 2025.Antibodies against *Mhp* were detected using a commercial ELISA kit (IDEXX) at the Zoetis Swine Disease Diagnosis Laboratory, Beijing .Among these herds, 47 were vaccinated with *Mhp* vaccines at 7 - 28 days of age, while 2 herds remained unvaccinated. The proportion of *Mhp* antibody-positive animals in each age group was analyzed using box-and-whisker plots to assess seroconversion dynamics.

Results and Discussion

In the 6 - 8, 10 - 12, and 14 - 16-week age groups, both the median and lower quartile of seropositive percentages were zero, while the upper quartile increased from 8% to 27%. From 18 - 20 weeks onward, all quartiles increased markedly: the lower quartile rose from 10% to 40%, the median from 40 to 71%, and the upper quartile from 64 to 88%. The maximum seropositive rate remained at 100% from the 14 - 16-week group onward, while the minimum value persisted at zero across all age groups. These findings indicate that only a minority of herds did not experience seroconversion during the wean-to-finish phase. Despite widespread vaccination, a small proportion of herds began seroconversion as early as mid-to-late nursery, but the majority seroconverted during the mid-to-late finishing phase. Seroconversion confirms the timing of *Mhp* infection, but lung lesion scoring at slaughter remains crucial for assessing economic impact.

Conclusion

The results showed that most wean-to-finish pig herds in China experience *Mhp* seroconversion during the finish phase, even with routine *Mhp* vaccination, Enhanced and targeted *Mhp* control measures are necessary to further mitigate *Mhp* infection in these herds.

Keywords : Dynamics, ELISA, *Mycoplasma hyopneumoniae*, Seroconversion.

Acknowledgements: The authors thank all participating farms and laboratory staff for their invaluable contributions.

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EFFECTS OF MATERNAL AND POST-WEANING SUPPLEMENTATION OF A *BACILLUS* MULTI-STRAIN PROBIOTIC ON *STREPTOCOCCUS SUIS* SEROTYPE 9 COLONIZATION IN A CHALLENGE STUDY WITH WEANED PIGLETS

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Introduction and Objectives

Streptococcus suis is a major pathogen driving antibiotic use in pig production. This study explored the effects of dietary supplementation with a *Bacillus* dual-strain probiotic in weaned piglets with or without maternal supplementation, on *S. suis* colonization in a *S. suis* serotype 9 (SS9) challenge trial.

Materials and Methods

Sixty piglets were enrolled at weaning (30 days of age), with 3 pens of 5 piglets per treatment. Piglets assigned to T1, T2 and T4 were from sows fed control diets, whereas piglets in T3 were from lactating sows fed a diet with *B. amyloliquefaciens*-516 and *B. subtilis*-541 (1.1E + 09 CFU/kg feed). Piglets from T1 and T2 received a control nursery diet, whereas T3 and T4 piglets were fed a diet supplemented with the same probiotic at 2.2E + 09 CFU/kg. Piglets from T1 were housed in a lab facility from weaning until study end, whereas T2, T3 and T4 piglets were housed in a commercial facility until D18, then moved to the lab facility and regrouped by treatment. Subsequently, T2, T3 and T4 piglets were inoculated nasally and orally with SS9 (1.25E + 09 CFU). Tonsil swabs were collected from all piglets on days 0, 8, 15 (pre-challenge), and days 19, 20, 22, 25 (post-challenge). DNA from swabs was analysed by qPCR for total *S. suis* and SS9. Relative abundance (RA) of SS9 was $\log_{10}$-transformed and analysed pre- and post-challenge.

Results and Discussion

No clinical signs were observed. Post-challenge daily gain was higher in T1 than T2 (608 vs. 516 g/day, P = 0.05), with T3 and T4 intermediate (571, 587 g/day). Pre-challenge, T3 showed the greatest SS9 RA (1.78), T4 the lowest (1.06) and T1 and T2 intermediate (1.39, 1.34, P = 0.01). Post-challenge, RA was lower in T3 (2.04) compared to T2 (2.98), with T1 and T4 intermediate (2.33, 2.35, P = 0.03). RA increased post-challenge (2.17 on D19 vs. 2.65 on D22).

Conclusion

This study examined maternal and post-weaning *Bacillus* dual-strain probiotic supplementation on SS9 tonsillar colonization in challenged piglets. Findings suggest possible modulation of SS9 relative abundance, warranting further investigation as part of strategies to manage *S. suis*.

Keywords: *Bacillus, Streptococcus suis*, tonsil, maternal supplementation, post-weaning.

COMPARISON OF INJECTABLE TOLTRAZURIL-GLEPTOFERRON AND ORAL TOLTRAZURIL+ IRON DEXTRAN FOR THE PREVENTION OF ANAEMIA AND COCCIDIOSIS UNDER THE FIELD CONDITIONS ON LARGE SCALE FARM IN VIETNAM

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Introduction and Objectives

Coccidiosis is a widespread protozoal disease of the piglets, which is characterized by watery or creamy diarrhoea, and causes negative impact on the zootechnical performance. Iron deficiency anemia (IDA) is a frequent problem occurred on farms, which negatively impacts body condition, immune response, and animal welfare of affected piglets. The objective of the presented study was to evaluate the effect of an injectable toltrazuril (TLZ)/ gleptoferron based product on performance and hematological status of piglets at weaning.

Materials and Methods

Comparative randomized study was performed on large scale farm (13500 sows inventory) located in Vietnam. Two treatment groups were compared in the parallel design, group A (fixed injection 45 mg TLZ + 200 iron gleptoferron, 1.5 ml fixed dose, Forceris, Ceva Sante Animale) injected 2nd day of life (DOL) vs. group B (1 mL oral TLZ, 50 mg + 200 mg of iron dextran) applied according to farm practice 3rd DOL. Total 241 piglets were randomly selected and included. Bodyweight gain was analyzed using a linear model with the daily bodyweight gain as response variable, the group and the bodyweight at D0 as fixed effects. Hemoglobin (Hb) change from D0 was analyzed using a linear model with the hemoglobin change as response variable, the group and the hemoglobin at D0 as fixed effects.

Results and Discussion

No records on the local safety or adverse reactions were recorded during the study in both groups. The average daily weight gain (expressed as mean and min/ max value) was significantly better in group A: 260 g; 170 - 360 vs. group B: 250 g; 150 - 380 ($P = 0.047$). Despite the difference in Hb status on the beginning of the study in favor of group B, the average value of Hb was higher in group A (111.85 vs. 77.39 g/l), with the significant difference in the distribution of Hb change from D0 in favor the group A ($P < 0.001$).

Conclusion

The injectable combo product, which was recently introduced–in Vietnam improved the zootechnical performance as well as hematological status of the piglets at weaning, under the conditions of large, commercial farm.

Keywords: Coccidiosis, IDA, Iron, Hemoglobin, Toltrazuril.

EFFECT OF PARENTERAL IRON IN DIFFERENT DOSES ON THE COURSE OF *CYSTOISOSPORA SUIS* INFECTION IN PIGLETS

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Introduction and Objectives

Iron deficiency Anaemia (IDA) and porcine cystoisosporosis are important pathologies in piglets and iron supplementation during the first days of life is a compulsory procedure. The purpose of this study was to compare the effects of a standard (100 mg/kg of body weight; BW) vs. a low (40 mg/kg of BW) dose of iron on hematological parameters and parasitological course of experimental *Cystoisospora suis* infection.

Materials and Methods

Piglets from three litters were randomized according to BW on birthday; 13 received a standard iron dose (group S) corresponding to an average dose of 184.62 ± 24.36 mg per piglet and 14 piglets a low dose (group L), corresponding to 75.00 ± 9.41 mg per piglet, on 3rd day post-natum (dpn 3). On the dpn 10, all piglets were infected orally with 1000 sporulated oocysts of *C. suis*. Oocyst excretion (dpn 15 - 27) and clinical (faecal consistency, body weight development) parameters were evaluated based on previously published method (Joachim et al., 2019). Blood sampling for hematologic examination was done on dpn 2, 10, 21 and 29.

Results and Discussion

Group S gained on average 241 g/day, group L 262 g/day ($P > 0.05$). Oocyst excretion was detected by autofluorescence (L: 29.1%, S: 39.1% of samples), when all piglets except one in group L excreted oocysts at least once. McMaster analysis determined oocysts per gram of faeces (OpG) in all piglets in group S and 11/14 piglets in group L. The number of days with countable excretion (S: 39.1%, L: 29.1% of the samples) was significantly different ($P = 0.0037$). No significant differences in the parameters for faecal consistency or diarrhoea were observed. Group L showed significantly altered haematological values indicative of IDA and leukopenia.

Conclusion

A lower dose of iron was not sufficient to prevent IDA and other hematologic parameters. Duration of oocysts excretion was significantly reduced in group L, suggesting a possible positive effect of iron on parasite development. Practical implications for swine producers include the importance of diagnosing and management of *C. suis* on farms, since standard iron management which is necessary to avoid IDA may influence the progression of parasite infection.

Keywords: *Cystoisospora suis*, Coccidiosis, IDA, Iron

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EFFICACY OF INJECTABLE TOLTRAZURIL AGAINST EXPERIMENTALLY INDUCED CYSTOISOSPOROSIS IN PIGLETS: EFFECTS ON PERFORMANCE, INTESTINAL INTEGRITY AND IMMUNE STIMULATION

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Introduction and Objectives

The purpose of this study was to compare the efficacy Forceris® against *Cystoisospora suis* after experimental infection in neonatal piglets, and its effect on immune stimulation and intestinal integrity, in comparison with an untreated control.

Materials and Methods

The study was performed in a parallel, randomised, blinded experimental design comparing the Treatment (F, 14 piglets) (45 mg of toltrazuril plus 200 mg gleptoferron/piglet) and the Control (C, 14 piglets; 200 mg gleptoferron/piglet) administered on SD2 (3rd day of life: DOL). Experimental infection (1,000 sporulated oocysts/piglet) was performed on the 4th DOL (SD3). Parasitological and clinical parameters were evaluated based on previously published methods (Joachim et al., 2019). Tissue samples (jejunum, ileum and colon) were collected from eight randomly selected piglets in each group at the end of the study (SD 28) in RNA later and gene expression for selected cytokines (IL6, IL10, IL12p35, TGFβ) and Calprotectin in jejunum, ileum and colon, was determined using a previously published method (Ramis et al., 2022).

Results and Discussion

Oocyst excretion ($P < 0.0005$) and weight gain ($P = 0.0099$) were significantly improved in the treated group. Mean daily body weight gain (MDBWG) (g, SD) was 230 (59.8) in treated group vs. 174 (68.7) in control pigs. The control animals shed oocysts for 2.2 days on average and showed diarrhea for an average of 5.5 days (treated animals 0.3 and 0.6 days respectively). Treatment completely suppressed oocyst excretion except in one piglet, with low shedding. Significant increases were observed for calprotectin ($P = 0.036$), zonulin ($P = 0.037$) and IL6 ($P = 0.037$) in the control group, with a trend towards a difference in the other biomarkers. A significant increase ($P = 0.016$) of IL12p35 level was observed in colon samples of the control group.

Conclusion

Toltrazuril treatment significantly improved zootechnical performance and eliminated parasite shedding almost completely. Differences observed for biomarkers indicated an increased Th1 activation in the control group. Upregulation of zonulin was associated with patent C. suis infection, and its upregulation may correlate with increased intestinal permeability. This indicates a lasting negative effect of C. suis on intestinal integrity which was reverted by toltrazuril treatment in the pre-patent period.

Keywords: Cystoisosporosis, *Cystoisospora suis*, Toltrazuril.

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CYSTOISOSPORA SUIS IN JAPAN: A PILOT STUDY ON FARM POSITIVITY, MANAGEMENT, AND RISK FACTORS

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Introduction and Objectives

Coccidiosis caused by *Cystoisospora suis* is the most important parasitic disease of piglets and is characterized by diarrhea, causing negative impact on zootechnical performance. Prevalence rates appear to be high worldwide, although no recent data are available for Japan. The present study evaluated *C. suis* farm positivity in Japanese farms and assessed selected risk factors associated with facilities and farm rearing practices.

Materials and Methods

In 10 Japanese industrial swine farms with average size of 560 sows (95 - 1200) selected by convenience according to the farmer's willingness to participate, a total of 323 pooled samples of piglet feces were collected during 2025. In each farm, the farm manager filled out a written survey to collect data related to control and management of disease and informed consent to participate in the study. Sampling strategy (repeated litter samples) and adopted flotation method with evaluation of number of oocysts per gram (OPG) were used according to previously described methodology (Joachim et al., 2018). Statistical analysis was performed using R version 4.5.1 and Fisher exact test was performed.

Results and Discussion

The farm positivity rate was 60% (6/10 farms), with relatively low frequency of positive samples 7.7% (25/323 samples) with an average of 23.7% of positive litters per positive farm. Feces with higher fecal score (2.3) had a higher probability of containing oocysts than solid samples ($P = 0.006$). Four farms were using oral toltrazuril for metaphylaxis and these were significantly less positive for oocysts ($P = 0.010$).

Conclusion

The *C. suis* farm positivity in Japanese swine farms appears to be similar to the prevalence found in European countries. Frequency of positive litters and individual litter samples seems to be lower compared to previously published results. Possible explanation might be less sensitive diagnostic method used in the present study. Finally, the *C. suis* control programs appear to be effective in reduction of parasite presence.

Keywords: Coccidiosis, Toltrazuril.

Acknowledgements: Authors would like to recognize Shokukanken Inc. for the expertise and laboratory diagnostics service.

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TRANSSECTIONAL DETECTION OF *BRACHYSPIRA HYODYSENTERIAE* AND *BRACHYSPIRA PILOSICOLI* IN 74 SWINE FARMS ACROSS GERMANY, FRANCE, AND SPAIN (OCTOBER-DECEMBER 2025)

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Introduction and Objectives

Brachyspira (B.) hyodysenteriae, the agent of swine dysentery (SD), and *B. pilosicoli,* causing porcine intestinal spirochaetosis (PIS), are relevant enteric pathogens. While swine dysentery induces severe mucohaemorrhagic diarrhea, PIS often presents as mild or subclinical infection (Hampson et al., 2019). Reported prevalence in European countries ranges from < 3% to > 40% (Reiner et al., 2019, Arnold et al., 2023). Detection and clinical expression vary with age, co-infections, diagnostic methods, sampling approaches, and management factors (Hampson et al., 2019, Arnold et al., 2023, Herbst et al., 2004). This study investigated which age groups test positive and whether detected groups consistently show diarrhea.

Materials and Methods

A total of 74 farms in Germany (n = 22), Spain (n = 28), and France (n = 24) with known or suspected SD were sampled using standardized sock sampling across nursery (early, mid, late) and fattening (early, mid, late) stages. Diarrhea status was recorded per sampled age group. All samples were tested by PCR for *B. hyodysenteriae* and *B. pilosicoli.*

Results and Discussion

Sample-level positivity for *B. hyodysenteriae* was France 25/117 (21.4%), Germany 8/122 (6.6%), Spain 27/162 (16.7%); for *B. pilosicoli*: France 23/117 (19.7%), Germany 31/122 (25.4%), Spain 6/162 (3.7%). Herd level positivity for *B. hyodysenteriae/B. pilosicoli* was in France 41.7%/41.7%, Germany 22.7%/40.9%, and Spain 57.1%/7.1%. *B. hyodysenteriae* positivity increased with age when diarrhea was present. Co-detection occurred in France (6 farms), Germany (2 farms), and Spain (1 farm). In France (1 farm) and Spain (2 farms), *B. hyodysenteriae* appeared first in non-diarrheic groups and later in diarrheic groups. Seven farms (France 5, Germany 1, Spain 1) showed *B. hyodysenteriae* exclusively in non-diarrheic groups, aligning with intermittent shedding and subclinical infection (1, 3). Country differences reflect known geographic heterogeneity.

Conclusion

These findings highlight the need for age-aware, multi-stage surveillance using sock samples and show that routine testing in clinically quiet groups is essential in farms facing diarrhea. Including co-pathogen diagnostics, monitoring transition points, and strengthening biosecurity enable earlier interventions such as vaccination, improving herd stability and reducing disease impact.

Keywords: *Brachyspira hyodysenteriae*, Swine dysentery, *Brachyspira pilosicoli*, Diarrhea, Co-infection.

Acknowledgements: We sincerely thank the veterinarians, farmers, and colleagues whose dedicated support of on-farm sampling and metadata collection was essential to this work.

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EPIDEMIOLOGICAL ANALYSIS OF GLÄSSER'S DISEASE IN CHINESE FARMS

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Introduction and Objectives

Glässer's disease (GD), caused by *Glaesserella parasuis*, remains a major health and economic challenge in swine production. In China, the world's largest pig-producing country, the disease leads to significant losses due to mortality, impaired growth, and frequent therapeutic interventions. The rise of antimicrobial-resistant *G. parasuis* strains has further complicated disease control, as the misuse of antibiotics accelerates resistance and reduces treatment effectiveness. These factors highlight the need for accurate diagnostics, prudent antimicrobial use, and vaccination. The objective of this study was to assess the prevalence of *G. parasuis* in Chinese farms showing clinical signs of GD.

Materials and Methods

In 2025, a total of 446 samples from pigs exhibiting clinical signs suspected with GD, including wasting and fibrinous polyserositis, were collected from 45 farms were analyzed by PCR at HIPRA Diagnos China. All the samples were collected from swabbing surfaces of affected organs (pericardium, fibrous exudates on the surface of the liver or intestine, pleura and peritoneum). Positivity was evaluated at both the farm and the individual sample levels.

Results and Discussion

Out of the 45 farms, 43 (96%) had at least one PCR-positive animal, confirming the widespread presence of *G. parasuis* in the evaluated production systems. At the individual level, a total of 446 samples were analyzed, of which 391 tested positive and 55 tested negative, resulting in a positivity rate of 88%. These findings indicate high infection pressure and a strong likelihood of recurrent clinical outbreaks within affected farms.

Conclusion

The results demonstrate that *G. parasuis* was highly prevalent in Chinese pig farms. The high proportion of positive farms and animals highlights the urgent need to strengthen diagnostic protocols, optimize antimicrobial use, and reinforce vaccination strategies. Appropriate antimicrobial selection, together with targeted vaccination programs in sows and piglets, is essential to reduce disease impact and improve long-term productivity.

Keywords: Antibiotics resistance, China, *Glaesserella parasuis*, Glässer's disease.

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EFFECT OF ORAL LIVE VACCINATION AGAINST *LAWSONIA INTRACELLULARIS* ON PRODUCTION PERFORMANCE IN A GILT DEVELOPMENT UNIT IN THAILAND

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Introduction and Objectives

Porcine Enteropathy (PE) caused by *Lawsonia intracellularis* is a prevalent bacterial gastrointestinal infection in pig production globally. In Thailand, the prevalence among gilts and sows reaches 88.8% (1). PE manifests in various clinical forms, including subclinical, porcine intestinal adenomatosis (PIA), and proliferative hemorrhagic enteropathy (PHE). The latter associated with bloody diarrhea and sudden death in high-value populations such as gilts, and sows. This study aims to evaluate the efficacy of an oral live *Lawsonia intracellularis* vaccine in a gilt developing unit (GDU) in central Thailand, where ileitis was previously managed solely through in-feed medication.

Materials and Methods

The GDU farm receives 4-week-old weaned female piglets from a grandparent farm and raises them under good management until 17 weeks of age, when selection for replacement gilt begins. Although no clinical signs of ileitis were observed, IPMA serological responses at 12 weeks and poor herd uniformity suggested subclinical infection. The treatment group (n = 936) received an oral live *Lawsonia intracellularis* vaccine (Enterisol® Ileitis via drinking water at 6 weeks of age) while the control group (n = 935) was not vaccinated and followed the existing in-feed medication program (4-5 weeks: Amoxicillin and colistin, 7 weeks: Tiamulin). Production performance data, including weight in, weight out, average daily weight gain (ADG), days in house, and selection rate, were collected and analyzed using Student's T-test and chi-square.

Results and Discussion

Vaccinated animals showed a 5% higher selection rate, which is important for a GDU farm. Also, vaccinated animals demonstrated a significantly higher ADG to 513 g, 20 g higher than control group ($P < 0.05$) and reduced days in GDU to 106.12 days, 7 days shorter ($P < 0.05$). These improvements yielded a 1:5 return on investment (ROI), driven by higher selection rates and increased sales of replacement gilts. Additionally, vaccination was associated with lower antibiotics used in GDU.

Conclusion

Vaccination with an oral live *Lawsonia intracellularis* vaccine improved production performance in a GDU setting, even under field condition. Compared to in-feed medication alone, vaccination offers a valuable return on investment and aligns with responsible antibiotic use practices in livestock. These findings may support the further promotion of vaccination in fattening pig.

Keywords: *Lawsonia intracellularis*, Gilt development unit, Oral live vaccine, Production performance, ROI.

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FIELD EFFICACY OF VACCINATION AGAINST OEDEMA DISEASE ON A CHINESE SWINE FARM

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Introduction and Objectives

Shiga toxin-producing *Escherichia coli* (STEC) causes oedema disease in pigs, resulting in significant losses for farmers. The aim of the study is to test the efficacy of a recombinant Shigatoxin 2e (Stx2e) based vaccine against clinical signs and mortality of Stx2e-induced toxaemia on STEC positive farm.

Materials and Methods

The randomized study with parallel design was conducted on a breeding farm with suspected STEC *E. coli* infection history in southern China with 4,800 sows and its associated finishing facility. From June to September 2025, 11,030 piglets from randomly selected sows were included and allocated based on the litter to the study groups at 4 days of age. In Group A, 4,507 piglets were vaccinated with Ecoporc SHIGA® (Ceva, Sante Animale). In Group B, 6,523 piglets were non-vaccinated. Evaluation criteria included mortality: number of piglet deaths due to oedema disease during the study period (4 - 13 weeks of age)/ total number of the animals and death rate: total number of piglet deaths during the study period/ total number of the animals. PCR testing (Stx2e toxin and F18 genes): 20 pooled fecal samples were collected from the nursery pens (20 pens, 5 fecal samples per pen) 2 - 3-week post-weaning (without the use of zinc oxide/colistin) in order to confirm circulation of STEC E. coli. During the trial, pigs showing edema disease symptoms were treated with apramycin and colistin, while asymptomatic pigs received no antibiotics.

Results and Discussion

By the end of 13 weeks of age, the total death in the vaccination group (Group A) was 39, resulting in a death rate of 0.87%. No deaths were due to edema disease which was confirmed by clinical symptoms observation (neurological signs and sudden death) and necropsy (edema at various tissues). In the non-vaccinated group (Group B), the total death piglets was 189, corresponding to a death rate of 2.90%. Among these, 133 deaths were caused by oedema disease, resulting in an OD mortality of 2.04%. Circulation of Stx2e STEC *E. coli* was confirmed by PCR during the trial.

Conclusion

The benefit of vaccination in reduction of mortality and total treatment was confirmed on the farm.

Keywords: Mortality, Oedema disease, Stx2e, Vaccination.

DOES A BOOSTER VACCINATION AT THE START OF THE FATTENING PERIOD IMPROVE CONTROL OF *MYCOPLASMA HYOPNEUMONIAE* INFECTION IN PIGS?

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Introduction and Objectives

Mycoplasma hyopneumoniae remains a major health challenge in pigs despite widespread vaccination. Most vaccines are administered between one and three weeks of age to protect during the wean-to-finish period (Maes et al., 2020). However, the persistence of immunity and its effect on infection dynamics and performance are poorly understood. This study assessed whether a booster vaccination at the start of fattening reduces infection and improves growth under field conditions.

Materials and Methods

A commercial farm with confirmed *M. hyopneumoniae* circulation was selected. Three hundred pigs from the same batch were randomly assigned to two groups: (1) booster group (n = 150), vaccinated with Ingelvac MycoFLEX® at weaning and again at fattening start; and (2) one-dose group (n = 150), vaccinated only at weaning. Tracheal catheter samples (PCR) and serum (ELISA) were collected at entry, and at 60 and 90 days of fattening. Body weights were recorded at the same time points, and carcass weights at slaughter.

Results and Discussion

At entry, both groups showed low infection prevalence and similar body weights. At 60 days, infection slightly increased in both groups, while weights remained comparable. By 90 days, infection rose sharply, especially in the one-dose group (56.2% booster vs. 97.2% one-dose; $P < 0.0001$). Despite infection pressure, booster pigs had significantly higher body weight (89.22 vs. 85.16 kg; $P = 0.018$). Carcass weights reflected this improvement, with least square means of 93.35 vs. 88.64 kg, an average difference of ~5 kg ($P < 0.0001$). These findings indicate that while booster vaccination did not fully prevent infection, it positively influenced growth performance. It should be noted that, in the EU, Ingelvac MycoFLEX® is approved for a single administration. Therefore, the booster strategy evaluated here does not comply with the current marketing authorisation and should be considered off-label use.

Conclusion

A booster vaccination at fattening start improved final body and carcass weights despite high infection pressure. These results support booster strategies as a practical tool to enhance productivity in herds under natural *M. hyopneumoniae* infection conditions.

Keywords: Booster vaccination, Carcass weight, Field trial, Growth performance, *Mycoplasma hyopneumoniae*.

Acknowledgements: The authors thank Vall Companys S.A. for their support and collaboration in providing facilities and resources for this study.

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PREVENTIVE VACCINATION FOR PWD DUE TO *E. COLI* F4 OPTIMIZES PRODUCTION WITH A REDUCTION OF MORTALITY AND ANTIMICROBIAL USE DURING THE POST-WEANING PERIOD

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Introduction and Objectives

During the post-weaning period piglets might undergo infectious challenges such as enterotoxigenic *Escherichia coli* (ETEC), resulting in post-weaning diarrhea (PWD) and increased variation of piglets at the end of the nursery period. To prevent the negative effects of PWD due to *E. coli*, a preventive vaccination with live avirulent oral *E. coli* F4F18 vaccine (Coliprotec F4F18; Elanco AH) was implemented. The objective was to evaluate the effect of *E. coli* vaccination on PWD-related production data, mortality and antimicrobial use compared to a prior period using ZnO under UK conditions.

Materials and Methods

Data from 10 different nursery barns were collected both in Q1 2024 using the standard preventive approach with inclusion of ZnO 2,500 ppm into the feed and in Q1 2025 using the preventive vaccination with a live avirulent oral E. coli F4F18 vaccine (Coliprotec F4F18; Elanco AH) at 4 weeks of age. Data capture included number of piglets in the nursery, weight at entry and exit of the nursery period, average daily weight gain (ADWG), mortality, and antimicrobial use (mg/kg). Statistical analysis was performed using JMP 17.1.

Results and Discussion

Weight at the end of nursery significantly improved following *E. coli* vaccination (39.42 ± 1.56 kg vs. 45.69 ± 1.49 kg; $P = 0.000006$). The ADWG significantly increased by + 52 g/d from 566.9 to 608.4 g/d ($P = 0.0012$). Following *E. coli* vaccination, there was a trend for improvement in percentage of mortality (3.7% vs. 2.3%; $P = 0.057$). The antimicrobial use (expressed in mg/kg) significantly decreased (142.6 ± 23.8 vs. 34.5 ± 18.4; $P = 0.0076$).

Conclusions

In conclusion, implementation of a preventive vaccination of a live avirulent oral *E. coli* F4F18 vaccine (Coliprotec F4F18) could improve weight at the end of nursery and ADWG with a trend to reduce mortality during the post-weaning phase. Moreover, there was a significant reduction in antimicrobial use following *E. coli* vaccination.

Keywords: Coliprotec F4F18, *E. coli* vaccination, Post-weaning diarrhea, Optimized performance.

SUCCESSFUL *MYCOPLASMA HYOPNEUMONIAE* ERADICATION IN A MULTIPLIER HERD USING TRACHEO-BRONCHIAL SWAB MONITORING COMBINED WITH VACCINATION AND TREATMENT PROTOCOL

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Introduction and Objectives

Mycoplasma hyopneumoniae (M. hyo), the pathogen of Enzootic Pneumonia, occurs worldwide and causes major economic losses to the pig industry. Affected pigs show chronic coughing, are more susceptible to other respiratory infections and have a reduced performance. Piglets become infected with *M. hyo* during the suckling period and have been shown positive from weaning onwards. Moreover, once infected with *M. hyo*, animals can excrete the pathogen over a long period of time (254 days post-infection). Therefore, dedicated programs to monitor for freedom of *M. hyo* have been developed consisting of serological screening and further confirmation tests using PCR. The objective of the current case report was to describe a successful *M. hyo* eradication in a multiplier sow herd, using a combined program of vaccination and treatment while monitoring progress and freedom of disease with tracheo-bronchial swab (TBS).

Materials and Methods

A high health breeding farm (400-sow herd with internal breeding gilt facility) had been negative for *M. hyo* for 40 years using a standard serological monitoring schedule. After a suspected outbreak, *M. hyo*-positivity was confirmed with TBS, an eradication program was established combining an additional triple *M. hyo* one-shot vaccination (4-weeks interval) with a double individual injection of all pigs present on-farm with tulathromycin (2-weeks interval). Furthermore, a 2-weeks stop was introduced for breeding gilt replacement. Monitoring was carried out using TBS at 12 and 24 weeks after the second antimicrobial treatment to confirm *M. hyo* eradication in the herd.

Results & Discussion

TBS sampling revealed several pools as *M. hyo*-positive in breeding sows in Q1 2025. Following the completion of the eradication protocol, including vaccination and treatment, no *M. hyo*-positive TBS samples could be detected at 10 weeks post-treatment in post-weaned piglets.

Conclusions

The current case report demonstrated that *M. hyo* eradication is possible in a multiplier sow herd. Monitoring of *M. hyo* infection using TBS sampling in sows and piglets is a reliable diagnostic technique to confirm infection and follow-up the evolution towards freedom of disease.

Keywords: Eradication, *Mycoplasma hyopneumoniae*, PCR, Tracheo-bronchial swab sampling, Vaccination.

COMPARATIVE ANALYSIS OF DIAGNOSTIC METHODS (QPCR VS. CULTURE + PCR) AND HIGH PREVALENCE OF *CLOSTRIDIUM PERFRINGENS* TYPE A AND *CLOSTRIDIUM DIFFICILE* IN KOREAN NEONATAL PIGLET DIARRHOEA

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Introduction and Objectives

Neonatal diarrhoea causes substantial economic losses through reduced growth and mortality. While pathogens like PEDV are common, *Clostridium perfringens* type A (CpA) and *Clostridioides difficile* (CD) are emerging contributors to recurrent diarrhoea (1,2). Since prevalence data in Korean herds remains limited, this study aimed to assess CpA and CD occurrence and compare diagnostic concordance between two approaches: qPCR and bacterial culture followed by PCR.

Materials and Methods

This study included 11 commercial Korean farms reporting neonatal diarrhoea. Twenty pooled faecal samples (each derived from ≥ 3 diarrhoeic piglets) were collected and divided into paired subsamples. Lab A (HIPRA) utilized FTA Elute cards for real-time PCR (qPCR) detection of the α -toxin (cpa) and CD A, B toxins gene. Lab B (Local Laboratory) processed fresh refrigerated samples for bacterial isolation and culture, followed by PCR confirmation of cpa, β2 -toxin (cpb2) and CD A and B toxins gene. This design primarily compared DNA-based detection (Lab A) against viable pathogen recovery (Lab B).

Results and Discussion

CpA and CD were confirmed prevalent, though detection rates varied. Lab A detected CpA in 100% (20/20) and CD in 60% (12/20), whereas Lab B identified CpA in 65% (13/20) and CD in 80% (16/20). Method-based discrepancies occurred in 35% of samples for CpA and 40% for CD. The markedly higher CpA detection by qPCR (Lab A) suggests that antibiotic treatment history in these herds renders bacteria non-viable for culture, while genetic material remains detectable. Conversely, higher CD detection by culture (Lab B) aligns with CD's antibiotic tolerance and enrichment benefits. Notably, variations in PCR targets (e.g., specific toxin genes) also contribute to discrepancies. Despite technical variations, both approaches highlight the high pathogen burden.

Conclusion

Regardless of method, this study confirms high CpA and CD prevalence in Korean neonatal diarrhoea cases, necessitating their inclusion in differential diagnoses. Diagnostic methods are complementary; thus, clinical interpretation must account for antibiotic usage and methodological characteristics. Given this prevalence, implementing control strategies, including accurate diagnosis and vaccination, is strongly recommended.

Keywords: *Clostridium perfringens* type A, *Clostridioides difficile*, Neonatal diarrhoea, Prevalence.

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CHARACTERIZATION OF *ESCHERICHIA COLI* VIROTYPES IN DIARRHEIC PIGS IN TAIWAN: PREDOMINANCE OF ETEC AND EMERGENCE OF HYBRID STEC/ETEC

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Introduction and Objectives

Escherichia coli (E. coli) is one of the major causes leading to lethal neonatal and post-weaning diarrhea worldwide. The major pathogenic types include enterotoxigenic *E. coli* (ETEC), Shiga toxin-producing *E. coli* (STEC) and enteropathogenic *E. coli* (EPEC). It has been reported that hybrid STEC/ETEC strains had increased prevalence in the United States in recent years and has been isolated in Taiwan as well (Nammuang et al., 2024; Paiva et al., 2025). This project aims to investigate the virotypes of *E. coli* in diarrheic pigs in Taiwan.

Materials and Methods

A total of 35 fecal samples or intestinal contents collected from diarrheic neonatal or post-weaning pigs from the Animal Disease Diagnosis Center of National Taiwan University during 2020-2025 were studied. After bacterial isolation, bacterial DNA was extracted and multiplex and conventional PCRs for detecting virulence genes, such as *STX2e, EAE, ELTA, F18*, were conducted.

Results and Discussion

Escherichia coli strains were isolated from 23 of 35 samples (65.71%). ETEC was the predominant pathotype, accounting for 69.57% of the isolates, followed by hybrid STEC/ETEC strains (21.74%). The most common fimbrial adhesins and enterotoxins were F18 (30.43%) and EAST1 (52.17%), respectively, and the most common virotype was F18:LT:Sta:STb:Stx2e:EAST1 among the collected samples.

Conclusion

In summary, ETEC remained the predominant pathotype; however, hybrid STEC/ETEC strains were increasingly prevalent in recent years, warranting further study of their characteristics and antimicrobial resistance genes as well as the potential risk for the emergence and dissemination of multidrug resistance.

Keywords: *Escherichia coli*, Taiwan, Hybrid STEC/ETEC, Swine diarrhea, Virotype.

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OPTIMIZATION OF THE GENERATION OF PORCINE *ESCHERICHIA COLI* FIMBRIAL ADHESINS

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Introduction and Objectives

Enterotoxigenic *Escherichia coli* (ETEC) is a major cause of neonatal and post-weaning diarrhea in pigs, with fimbrial adhesins playing a critical role in intestinal colonization and disease development. The objective of this study was to generate subunit vaccine candidates and antigens for serological assays by constructing and expressing the major ETEC fimbrial adhesins F4 and F18 using *Escherichia coli* (*E. coli*) expression systems.

Materials and Methods

Genes encoding fimbrial adhesins F18 (*FedF*; GenBank: KM260188.1) and F4 (*FaeG*; GenBank: ACB72721.1) were synthesized, while the *FedF* gene was subcloned into the pET101 vector to generate a His-tagged recombinant protein. The *FaeG* gene was subcloned into the pMAL-C4X vector to produce the maltose binding protein (MBP)-*FaeG* fusion protein for enhancing the solubility. All constructs were transformed into *E. coli* BL21(DE3) for protein expression.

Results and Discussion

Recombinant F18 was successfully expressed in *E. coli* BL21(DE3) and purified by Ni-NTA affinity chromatography, producing a distinct protein band at the expected molecular weight, 33-kDa, on SDS-PAGE, and further confirmed by western blot analysis. The expression of the MBP-F4 protein and F4 protein is detected, producing a distinct protein band at the expected molecular weight, 30-kDa and 73-kDa, respectively.

Conclusion

This study establishes an *E. coli*-based platform for the production of recombinant F18 and F4 fimbrial antigens. These adhesins represent valuable antigenic tools for serological evaluation and provide a basis for the development of subunit vaccines targeting fimbriae-mediated ETEC infections in neonatal and post-weaning pigs.

Keywords: Enterotoxigenic *Escherichia coli*, F4 fimbriae, F18 fimbriae, Post-weaning diarrhea.

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ELISA-BASED DETECTION OF ANTIBODIES AGAINST STX2E TOXIN IN PIGLETS FROM KOREAN PIG FARMS

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Introduction and Objectives

Porcine edema disease (ED) is an infection with a worldwide distribution, primarily affecting piglets within the first two weeks post-weaning. Characterized by a high mortality rate, the clinical presentation of this disease includes symptoms such as eyelid edema, altered vocalizations, and neurological alterations, indicative of its systemic impact in affected swine. ED can also occur in young fattening pigs and has been documented in wild boars, suggesting a broad ecological and epidemiological significance. The economic impacts of ED are considerable, encompassing direct losses from mortality and morbidity, as well as indirect costs related to prevention, control measures, and potential trade restrictions due to public health concerns. This study was conducted to evaluate the proportion of pigs with antibodies against Stx2e toxin on Korean pig farms.

Materials and Methods

In this study, a modified Stx2e (mStx2e) antigen was expressed and purified using commercial *E. coli* expression system. Monoclonal antibody was serviced by Ynto Ab Inc. using Phage Display Technique. Anti-Stx2e antibodies in piglets were measured by indirect ELISA using mStx2e antigens. Naive Stx2e in piglets were detected by Sandwich ELISA using Stx2e-monoclonal antibodies and commercial Stx2e-polyclonal antibodies.

Results and Discussion

Among 3,480 piglets, anti-Stx2e antibodies were observed in 2,573 piglets. Of the 830 piglet serum samples, 49.4% contained 0.625 µg/mL or more of Stx2e proteins, while 18.3% showed a level of 0.313 µg/mL. The remaining 32.3% had 0.156 µg/mL or less. These findings are thought to be attributed to the increased application of recombinant modified Stx2e toxoid-based vaccines in Korean pig farms. This widespread vaccination has reduced sudden deaths and clinical symptoms associated with edema disease, leading to an increased number of piglets maintaining high antibody titers and antigen levels without manifesting clinical signs.

Conclusion

These results show that indirect ELISA using mStx2e antigen and Sandwich ELISA using Stx2e-monoclonal and polyclonal antibodies can be useful to detect ED in piglets.

Keywords: ELISA, Monoclonal antibody, Porcine edema disease, Recombinant modified Stx2e proteins.
Acknowledgements: This research was supported by the budget of the Glocal University 30 Regional Coexistence Project of Jeonbuk State.

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PREVALENCE AND QUANTIFICATION OF EARLY *LAWSONIA INTRACELLULARIS* INFECTION IN BRAZILIAN NURSERY PIGS

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Introduction and objectives:
Lawsonia intracellularis (Li) is a pathogen that typically infects pigs during the finishing phase, causing subclinical or clinical ileitis, which can result in significant zootechnical and economic losses. This study aimed to investigate the potential early excretion of Li in pigs aged 50 to 65 days.

Material and methods:
Pooled fecal samples (three piglets per pool) were collected from piglets aged between 50 to 65 days of life across ten farms in Brazil: A total of 67 pools were distribute in 2 different provinces: seven farms (55 samples) in Goiás state (GO) and three farms (12 samples) in Rio Grande do Sul state (RS). All samples were analyzed by qPCR to detect and quantify Li.

Results and discussion:
In GO farms, 58% of samples tested positive for Li, with bacterial loads ranging from 10^4 to 10^{10} DNA copies/g. Four farms showed positivity rates of 80% or higher. In RS, all farms were positive, and 25% of samples tested positive with bacterial loads ranging from 10^5 to10^6 DNA copies/g. Previous studies have shown that subclinical ileitis can significantly reduce performance, particularly when bacterial loads reach $\geq 10^4$ DNA copies/g (Paradis et al., 2005), leading to decreased average daily gain (Pedersen et al., 2012; Paradis et al., 2005) and increased feed efficiency (2). Therefore, in the cases studied, performance losses may already be occurring during the nursery phase. These findings highlight the importance of reviewing the correct timing of LI vaccination.

Conclusion:
This study demonstrated that Li infection can occur at an early age in Brazilian pig farms, underscoring the importance of conducting lab exams (serology and qPCR) to define a more effective vaccination protocol and ensure timely, effective immunization.

Keywords: Ileitis, Piglets, Vaccine.

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STUDY ON THE EFFECTS OF TOLTRAZURIL ON PRODUCTION PERFORMANCE IN SUCKLING AND NURSERY PIGLETS

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Introduction and Objectives

Cystoisospora suis (C. suis) causes porcine neonatal coccidiosis, primarily characterized by yellowish-grey diarrhea that progresses from pasty to fluid, affecting production performance. This study evaluated the effect of oral toltrazuril (TZL) on mortality and culling rates in suckling and nursery pigs on *C. suis* positive farms.

Materials and Methods

On a 100,000-sow operation in South China, 9 farms reported persistent, antibiotic-unresponsive yellowish-grey diarrhea in 10 - 15 days of age (DAO) piglets. Fecal samples (10 litters from each farm) from 7 - 11 DAO piglets confirmed *C. suis* via qPCR. From September 2024, 3 - 5 DOA piglets were treated with a single oral dose of Cevazuril® (5% toltrazuril, 1 mL). Piglets from January - August 2024 served as controls (1,526,000 pigs), and those treated from September-December 2024 formed the experimental group (762,300 pigs). All other management was consistent. Monthly mortality and culling rates were analyzed via t-test.

Results and Discussion

The qPCR test results showed that all 9 farms were positive for *C. suis*, among which the sample positive rate of 8 farms exceeded 80%. After oral administration of toltrazuril, the piglet mortality and culling rates decreased obviously. There were 4 farms showing statistically significant differences (P <0.05). The average piglet mortality and culling rates of the 9 farms from January to August were 8.2%, while those from September to December were 5.8%, (P = 0.04). Based on the market price of 400 RMB per weaned piglet during the period, the profit was 9.6 RMB/pig. The return on investment (ROI) was 1:7.4. The 7 - 11 DOA piglets from all farms tested positive for *C. suis*. *C. suis* could damage the intestinal mucosa, compromising the mucosal barrier and increasing susceptibility to secondary infections (e.g., *E. coli, C. perfringens* type A, rotavirus), which could elevate mortality and culling rates (Matsubayashi *et al*., 2016; Mengel *et al*., 2012; Pettersson *et al*., 2019).

Conclusion

Oral toltrazuril administered at 3 - 5 DOA in farms with early *C. suis* infection, could reduce piglet mortality and culling rates. To further study the effects, it is necessary to track the changes in *C. suis* qPCR detection after toltrazuril treatment.

Keywords: *Cystoisospora suis*, Toltrazuril, Mortality and culling rate, qPCR

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EVALUATION AND APPLICATION OF TIAMULIN FOR THE CONTROL OF *MYCOPLASMA HYOPNEUMONIAE*

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Introduction and Objectives

Mycoplasma hyopneumoniae is a major pathogen responsible for porcine respiratory disease complex (PRDC), leading to significant economic losses due to reduced average daily gain (ADG), increased feed conversion ratio (FCR), uneven growth, and elevated mortality and culling rates. Effective control strategies are essential to mitigate its impact. This study aimed to evaluate the susceptibility of *M. hyopneumoniae* to tiamulin through minimum inhibitory concentration (MIC) testing.

Materials and Methods

A total of 21 *M. hyopneumoniae* strains (including ATCC 25934 and 20 clinical isolates collected from 2023 to 2025) were tested using the broth microdilution method to determine MIC values. The procedures followed established guidelines.

Results and Discussion

Tiamulin exhibited high efficacy against all tested strains, with an MIC range of 0.004 - 0.063 µg/mL, MIC_{50} of 0.016 µg/mL, and MIC_{90} of 0.032 µg/mL. No resistance development was observed compared to historical data (range of 0.03–0.06 µg/mL in 1991, 0.015 - 0.25 µg/mL in 2020). Lung tissue concentrations exceeded the MIC_{90} at feed dosage levels above 150 ppm.

Conclusions

The results of this study indicate that *Mycoplasma hyopneumoniae* isolates collected in China from 2023 to 2025 remain highly susceptible to tiamulin, with no evidence of emerging resistance. A dosage of 6.6 mg/kg bw administered via feed for 7 - 14 days is recommended to achieve effective lung concentrations. Combination therapy with tetracyclines is advised for enhanced efficacy under high disease pressure.

Keywords: Antimicrobial susceptibility, MIC, *Mycoplasma hyopneumoniae*, Swine respiratory disease, Tiamulin.

PROFILING ENTEROTOXIGENIC *ESCHERICHIA COLI* (ETEC) ADHESIN AND ENTEROTOXIN CAUSING POST WEANING DIARRHEA (PWD) IN COMMERCIAL SWINE FARMS IN THE PHILIPPINES

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Introduction and Objectives

Enterotoxigenic *Escherichia coli* (ETEC) infection causing post-weaning diarrhea (PWD) causes morbidity and mortality in newly weaned piglets which leads to significant losses in the swine industry due to production losses and higher medication costs during the early nursery phase (Kim et al., 2022). Commensal *E. coli* is part of the beneficial gut microbiota, potentially pathogenic strains may cause disease under specific conditions. Enterotoxigenic *E. coli* (ETEC) has virulence factors as fimbrial adhesins F4 and F18 and heat labile (LT) and heat stable (ST) enteroxins significantly influence the pathogenesis of PWD. Development of vaccines have focused on anti-adhesin strategies, as the first step in ETEC pathogenesis. Newer vaccines are being developed which include both adhesin and enterotoxins (Dubreuil, 2021). Identifying the predominant strains of ETEC in the Philippines could be a step in developing more effective vaccines.

Materials and Methods

100 samples (n = 100) were collected from 10 farms with reports of PWD. Each farm submitted 10 fecal samples from 10 piglets with clinical diarrhea. Five samples were pooled and tested by Polymerase Chain Reaction (PCR) assays. The PCR primers are targeted to detect the presence of both fimbriae (F4, F18) and the different toxins (LTa, STb, STa, EAST1, ST x 2e).

Results and Discussion

90% fecal samples have detections of *E. coli* F4 and/or F18 fimbriae and enterotoxins. Fimbriae F18 was most detected among the samples, followed by the virulent F4. The most common enterotoxins detected were EAST1 (90%), Sta (70%), and STb (70%). From these results, 80% of collected samples from piglets with clinical diarrhea had ETEC virotypes, majority had the combination of fimbriae F4 and F18 with enterotoxins LT, STa, STb and EAST1 (40%). A combination of only F18 with different toxins was detected (30%) and nonpathogenic combination made up 10% of the samples.

Conclusion

These data underscore the importance of further investigation into the epidemiology of ETEC-associated PWD in the Philippines. A comprehensive understanding of circulating ETEC strains and their virulence factors will inform the development of targeted interventions, such as oral vaccination strategies, aimed at mitigating PWD and reducing reliance on antibiotics in swine production.

Keywords: Adhesin, ETEC, Enterotoxin, Post weaning diarrhea.

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REVIEW OF FARM MITIGATION STRATEGIES IN THE PHILIPPINES FOR POST WEANING DIARRHEA CASES DUE TO ENTEROTOXIGENIC *ESCHERICHIA COLI* (ETEC)

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Introduction and Objectives

Post-weaning diarrhea (PWD) is a significant disease in pigs, primarily caused by enterotoxigenic *Escherichia coli* (ETEC). Stressors such as abrupt dietary changes, separation from the sow, relocation, and social mixing during weaning compromise the piglet's immune competence, thereby increasing susceptibility to enteric infection by pathogenic *Escherichia coli* (He et al., 2022.). To mitigate PWD, antibiotics have traditionally been incorporated into piglet diets. However, this approach poses a significant risk of promoting antimicrobial resistance in bacterial populations, with implications for both animal and human health (Laine et al., 2008). This study aims to evaluate and review alternative strategies for mitigating PWD associated with ETEC infection in piglets.

Materials and Methods

Ten commercial pig farms across the Philippines were surveyed for the presence of ETEC. Fecal samples were collected from 100 piglets with ages ranging from days 35 to 42 and exhibiting clinical signs of diarrhea (n = 10). ETEC detection was done using polymerase chain reaction (PCR) targeting fimbriae F4 and F18, and enterotoxins (LTa, STb, STa, EAST1, ST x 2e). Farm-level data on medication protocols and other PWD mitigation strategies were recorded through structured interviews.

Results and Discussion

90% (90/100) fecal samples have detections of E. coli F4 and/or F18 fimbriae and enterotoxins, with 7 out of 10 farms positive for ETEC. Reported interventions for PWD included antibiotic therapy, vaccination, and management-based strategies such as nutritional optimization and improved husbandry. Among ETEC-positive farms, 5 out of 7 used antibiotics, such as amoxicillin, norfloxacin, colistin and doxycycline, with only 1 out of 7 farms implementing vaccination and the remaining farm (1/7) reported other modes of treatment used. The emergence of antimicrobial-resistant bacterial strains underscores the need to reduce antibiotic use for sustainable pig production.

Conclusion

Antibiotic therapy remains the predominant approach for managing PWD in Philippine pig farms. However, sustainable alternatives, such as vaccination and targeted nutritional strategies are available and should be prioritized. Implementing an integrated control program that minimizes reliance on antibiotics is essential to mitigate the growing threat of antimicrobial resistance.

Keywords: Enterotoxigenic *Escherichia coli*, Post-weaning diarrhea.

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APPLICATION OF A VERTEBRAL OSTEOMYELITIS CLASSIFICATION SCHEME TO REDUCE UNNECESSARY CARCASS CONDEMNATION IN SWINE

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Introduction and Objectives

Vertebral osteomyelitis (VO) is a major cause of total carcass condemnation in swine slaughterhouses, resulting in significant economic losses. Although VO is closely associated with pyemia, not all VO-affected carcasses are in an active pyemic state at the time of slaughter. This study aimed to investigate the characteristics of swine VO cases in South Korea and to evaluate the application of a VO classification scheme to reduce unnecessary total condemnation while ensuring food safety.

Materials and Methods

Post-mortem inspection data from a South Korean slaughterhouse between 2021 and 2023 were retrospectively analyzed to assess VO occurrence trends. In addition, 20 VO cases collected from February 2023 to April 2024 were macroscopically examined and classified according to the Vieira-Pinto et al. (2020) classification scheme based on lesion chronicity and the number of purulent lesions. Bacterial cultures were performed on VO lesions and corresponding muscular tissues. True pyemia was defined when identical bacteria were isolated from both sites. Statistical analyses were conducted to assess associations between VO classification and pyemia status.

Results and Discussion

The incidence of VO increased significantly from 2021 to 2023. Among the 20 VO cases examined, 75% were classified as acute VO and 25% as chronic VO. Most lesions were located in the posterior vertebrae, and 65% of cases showed evidence of tail-biting injuries, indicating tail biting as a major risk factor. *Trueperella pyogenes* was the most frequently isolated pathogen. Only 10% (2/20) of VO cases were confirmed as true pyemia, and all true pyemia cases were classified as acute VO. The VO classification scheme demonstrated 100% sensitivity, effectively preventing false-negative judgments, and allowed 22.2% of carcasses to be excluded from unnecessary total condemnation.

Conclusion

True pyemia at the time of slaughter was rare among swine VO cases, suggesting that routine total condemnation of all VO-affected carcasses leads to avoidable economic losses. The application of a VO classification scheme can serve as a practical tool to reduce unnecessary carcass condemnation while maintaining food safety.

Keywords: Carcass condemnation, Pyemia, Slaughterhouse, Vertebral osteomyelitis.

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EFFICACY OF WHOLE-HERD ORAL VACCINATION IN CONTROLLING *LAWSONIA INTRACELLULARIS* IN A PREVIOUSLY INFECTED SOW HERD: A THAI FIELD STUDY

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Introduction and Objective

Ileitis caused by *Lawsonia intracellularis* is a major enteric disease that reduces production efficiency in swine farms. Serological data from Thailand indicate that pigs of all ages are widely exposed to this pathogen (Nguyen et al., 2023). This study evaluated the effectiveness of an oral live vaccine in controlling ileitis-associated problems in a previously infected sow herd.

Materials and Methods

A commercial breeding farm with approximately 800 sows operating under an evaporative cooling system was included in this observational study. In May 2025, all replacement gilts and sows of all parities were orally vaccinated with Enterisol® Ileitis. Blood samples were collected from replacement gilts (n = 5) and sows (n = 15) before vaccination and six weeks later for indirect Immunoperoxidase Monolayer Assay (IPMA). Reproductive and health performance parameters from the pre-vaccination period (2023 - 2024) were descriptively compared with those from the post-vaccination period (2025).

Results and Discussion

During 2023 - 2024, ileitis-related deaths represented 4.99% of sow mortality, while overall sow mortality averaged 6.29%. Before vaccination, seropositivity for *L. intracellularis* was 33.3% in replacement gilts and 93.5% in sows. Six weeks post-vaccination, seropositivity reached 100% in both groups, suggesting a uniform serological response, although this finding does not directly indicate protective immunity. Herd performance improved substantially following vaccination: ileitis-associated sow mortality declined from 4.99% to 0.5%, and the farrowing rate increased from 84.70 to 89.10%. Other performance indicators showed similar improvements, reflecting enhanced herd stability and gut-health status after vaccine implementation. However, these findings are presented as descriptive observations due to the limited sample size and absence of statistical analysis.

Conclusion

The implementation of an oral live *L. intracellularis* vaccination program in replacement gilts and sows was associated with improved herd stability and reproductive performance in a previously infected breeding herd. Further controlled studies are needed to confirm these observations.

Keywords: Farm performances, Ileitis, Oral vaccine, Sow herd

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PHYLOGENETIC ANALYSIS OF THE TRANSFERRIN BINDING PROTEIN B OF *GLAESSERELLA PARASUIS* IN TAIWAN

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Introduction and Objectives

Glässer's disease (GD) caused by *Glaesserella parasuis* leads to high morbidity and mortality in pigs. In general, *G. parasuis* comprises strains with heterogeneous virulence, and the virulence-associated trimeric autotransporter gene (*vtaA*) has been widely used as a molecular marker to predict pathogenic potential (Galofré-Milà *et al*., 2017). The transferrin-binding protein B (TbpB), a surface-exposed component of the iron acquisition system, has been demonstrated to be conserved among *G. parasuis, Actinobacillus pleuropneumoniae*, and Pasteurella spp. (Curran et al*.,* 2015; Ramos Prigol et al*.,* 2022). This study aims to characterize the sequences of TbpB of *vtaA*-positive Taiwan *G. parasuis* field isolates collected between 2019 and 2025 and analyze their phylogenetic relationships with global strains to guide the selection of representative antigens for subunit vaccine development.

Materials and Methods

From 2019 to 2025, a total of nineteen *G. parasuis* isolates were collected from pigs exhibiting GD. Swabs from lung tissue, adjacent pleura, pericardial fluid, or joint cavity were obtained and cultured on chocolate agar. After bacterial isolation, genomic DNA was extracted. The *vtaA* gene was amplified by PCR using primers AV1-F and V1-R to identify potentially virulent strains. The amplified *TbpB* gene was cloned into the pCR™2.1 TA cloning vector using the TA Cloning Kit (Thermo Fisher Scientific) for sequencing.

Results and Discussion

All *G. parasuis* isolates were positive for the virulence-associated *vtaA* gene. The genes of *TbpB* of *G. parasuis* were successfully amplified, sharing nucleotide and amino acid sequence identity from 62.10 - 99.90% and 55.00 - 99.90%, respectively. Among these Taiwan *G. parasuis* isolates, nine isolates were clustered in cluster I (47.4%), sharing nucleotide sequence identity from 98.10 - 99.90%, whereas ten isolates were clustered in cluster III (52.6%), sharing nucleotide sequence identity from 96.70 - 100.00%.

Conclusion

This study provides updated information on potentially virulent *G. parasuis* strains circulating pig farms between 2019 and 2025 in Taiwan. The co-circulation of TbpB clusters I and III *vtaA*-positive isolates highlight their relevance in the epidemiology of Glässer's disease in Taiwan. These findings would be important for facilitating the development of broadly protective subunit vaccines.

Keywords: *Glaesserella parasuis*, Glässer's disease, Phylogenetic clustering, TbpB, vtaA.
Acknowledgements: The authors thank the National Taiwan University GIMCP, Taiwan for the support with providing testing facilities.

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SEASONAL COMPARISON AND ANALYSIS OF LUNG LESION SCORING IN SLAUGHTERED PIGS FROM A CHINESE COMPANY

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Introduction and Objectives

Mycoplasma hyopneumoniae (*M. hyo*), the causative agent of enzootic pneumonia (EP) is a major health concern for pig farms around the world. This study was to analyze the seasonal variation of the lung lesion scores in a Chinese pig company.

Materials and Methods

A northern Chinese pig company conducted continuous lung scoring (via Ceva Lung Program, CLP) on slaughter pigs from the same breeding farm in the past 12 months. Seasons were categorized as 4 clusters for risk assessment: Q1 (Jan 1 - Mar 31, 2025; 130 batches), Q2 (Apr 1 - Jun 30, 2025; 43 batches), Q3 (Jul 1 - Sept 30, 2025; 51 batches), Q4 (Dec 1 - 31, 2024 & Oct 1 - Nov 30, 2025; 71 batches). Lung lesion indicators included: % of lungs with EP-like broncho-pneumonic lesions (BP), % average affected area of all lungs (AAA-lungs), Scarring (prevalence of fissures from older EP-like lesions), and Enzootic Pneumonia Index (EP index). Welch's ANOVA and Games-Howell test were used for statistical significance analysis. Corresponding city meteorological data was retrieved from https://m.tianqi.com.

Results and Discussion

The average temperatures of Q1 - Q4 were 4, 20, 24 and 7°C, respectively. In terms of average, minimum and maximum temperature, Q1 resembled Q4, and Q2 resembled Q3. BP, AAA-lungs and EP index peaked in Q1 and reached the lowest in Q2, with all four indicators higher in Q1/Q4 than in Q2/Q3. Pairwise seasonal comparisons revealed: No significant differences were observed in the indicators between Q1 and Q4, as well as between Q2 and Q3 (except for an extremely significant difference in scarring between Q2 and Q3); Extremely significant differences in the four indicators between Q1/Q4 and Q2/Q3.

Conclusion

This study indicated that EP-like lesions were more severe in Q1 and Q4 (quarters with low ambient temperatures), suggesting temperature is a critical risk factor for *M. hyo* infection, consistent with previous research (Joaquim et al., 2012). This may be attributed to cold-season management in farms, where increased stocking density and reduced ventilation exacerbated EP like lesions. Meanwhile, M. hyo-containing bio-aerosols facilitate airborne pathogen transmission between herds, and Q1/Q4 conditions (low temperature, insufficient sunlight, low wind speed) further elevate this aerosol-mediated risk.

Keywords: Enzootic Pneumonia (EP), Extremely Significant Difference, *Mycoplasma hyopneumoniae (M. hyo)*, Season, Temperature.

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CASE STUDY ON PRODUCTIVITY IMPROVEMENT BY ENTERISOL® ILEITIS VACCINATION AND COST-EFFECTIVENESS EVALUATION USING ROI NAVI

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Introduction and Objectives

Porcine proliferative enteropathy (PPE), caused by *Lawsonia intracellularis* (LI), commonly results in subclinical infections that impair growth performance during the finishing period and cause significant economic losses. In recent years, vaccination has become a widely adopted disease control strategy; however, its implementation requires strategic decision making based on economic indicators rather than disease prevention alone. This study evaluated the impact of Enterisol® Ileitis (EI) vaccination on productivity and profitability at a multiplication farm using ROI Navi, an economic analysis tool developed by ASCO.

Materials and Methods

The study was conducted at a multiplication farm in the Tokai region housing approximately 1,400 sows. Two production periods were compared: a non-vaccinated control group consisting of 6,172 pigs shipped between May and October 2024, and a vaccinated group consisting of 5,879 pigs shipped between May and October 2025. The vaccinated group received oral EI at 18 days of age. Key performance indicators, including days to market, carcass weight, and carcass feed conversion ratio (FCR), were analyzed. Economic impact was calculated using ROI Navi based on these performance data.

Results

To increase carcass weight, days to market were intentionally extended from 2024 to 2025. Days to market increased by 18.3 days, from 168.2 to 186.5 days, and average carcass weight increased by 10.6 kg, from 70.5 to 81.1 kg. Carcass yield improved from 65.9% to 66.5%, and carcass FCR slightly improved from 3.85 to 3.81. Based on annual production data from 2024, ROI Navi estimated an additional annual profit of ¥30.52 million, with a return on investment of 480%, indicating strong economic benefits.

Discussion

Despite unfavorable conditions, including extended days to market and reduced pen space, oral Li vaccination was associated with improved feed efficiency and weight gain, resulting in productivity. Although causality cannot be confirmed due to the before and after design, ROI Navi estimated ¥30 million in additional annual profit and an ROI of 480%. Under typical conditions, higher stocking density and heavier slaughter weights worsen feed conversion, yet vaccination appeared to support performance and profitability. A more controlled side by side study is needed to confirm these findings.

Keywords: *Lawsonia intracellularis*, PPE, FCR, ROI.

SSU_RS09155, A VIRULENCE-ASSOCIATED GENE ENCODING A PROTEIN OF UNKNOWN FUNCTION, IS ESSENTIAL FOR *STREPTOCOCCUS SUIS* SEROTYPE 2 VIRULENCE

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Introduction and Objectives

Streptococcus suis is an important swine pathogen and zoonotic agent, with the capsular polysaccharide recognized as its major virulence factor. Recent genomic studies have identified several virulence-associated genes (VAGs), including *SSU_RS09155, SSU_RS09525*, and *SSU_RS03100*, as potential markers of pathogenicity. The current study evaluated the direct contribution of these genes to *S. suis* virulence using isogenic deletion mutants of the serotype 2 reference strain P1/7.

Materials and Methods

VAGs-defective mutants were constructed using precise in-frame deletion of *SSU_RS09525, SSU_RS09155,* and *SSU_RS03100* genes. Mutants were tested in vitro for resistance to phagocytosis and blood bacterial killing, adhesion and invasion of swine epithelial cells and virulence in a mouse and pig model of infection.

Results and Discussion

In a murine infection model, *ΔSSU_RS09525* and *ΔSSU_RS03100* mutants displayed virulence comparable to the parental strain, whereas the *ΔSSU_RS09155* mutant was significantly attenuated. In vitro, the *ΔSSU_RS09155* mutant demonstrated increased susceptibility to killing in whole blood and enhanced phagocytosis by murine macrophages. Complementation restored the wild-type phenotype, confirming the specific role of *SSU_RS09155*. Adhesion to and invasion of porcine tracheal epithelial cells were unaffected. In pigs, the natural host, the ΔSSU_RS09155 mutant was almost completely avirulent, with minimal bacteremia. *SSU_RS09155* encodes a hydrophobic, membrane-associated protein potentially involved in resistance to innate immune mechanisms, although the real function remains unknown.

Conclusion

This study underscores the importance of experimentally validating genomic associations to distinguish true virulence factors from lineage- or context-dependent markers in *S. suis*. Deletion of *VAG SSU_RS09155* results in clear attenuation of *S. suis* serotype 2 in both mouse and swine models. In contrast, deletion of *SSU_RS09525* or *SSU_RS03100*, despite their previously reported statistical association with pathogenic strains, had no detectable impact on virulence, indicating that these loci serve as virulence markers but are not factors. The increased susceptibility of the *SSU_RS09155* mutant to blood killing and phagocytosis indicates that this locus contributes, directly or indirectly, to innate-immune resistance. Extending this approach to other VAGs identified in large-scale genomic surveys could refine our understanding of the virulence of *S. suis* and help distinguish core virulence factors from lineage-specific markers.

Keywords: Innate-immune resistance, *Streptococcus suis*, virulence, Virulence-markers.

EFFICACY OF A WATER-SOLUBLE PHYTOGENIC FEED ADDITIVE ON THE CONTROL OF *LAWSONIA INTRACELLULARIS* IN FATTENING PIGS

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Introduction and Objectives

Porcine proliferative enteropathy (PPE), caused by *Lawsonia intracellularis* (LI), is characterized by reduced growth, diarrhea and increased mortality in pigs. Recently, phytogenic feed additives with bioactive compounds such as thymol, or carvacrol have gained interest in LI control programmes (Gómez-Osorio et al., 2025). The study aimed to assess the efficacy of water-soluble phytogenic preparation (PWP) with thymol, carvacrol, linalool, lysozyme and niacinamide on the control of LI-associated enteropathy.

Materials and Methods

Two trials were conducted in two farms in the Russian Federation with confirmed PPE diagnosis based on clinical and necropsy findings, and quantitative PCR (*LI* qPCR Ct values range: 13.09 - 17.8 in farm A; 9.46 - 30.38 in farm B). Treatment group consisted of 4,347 animals and control group of 4,310 in farm A (mean age: 151 days), whereas in farm B respective groups consisted of 1,700 animals each (mean age: 149 days, mean weight: 110 kg). Sectors received PWP via medicators at 0.5 kg per ton of drinking water for 7 days in farm A and 10 days in farm B. Clinical monitoring and fecal scoring were performed, whereas fecal samples on FTA cards from the same 8 diarrheic animals/group were collected pre- and post- PWP treatment for LI qPCR (same commercial PCR kit for both farms).

Results and Discussion

A consistent reduction in diarrhea severity, from scores of 3 - 4 (loose to profuse diarrhea) to 1 - 2 (formed to soft feces), was observed within 3 - 5 days of PWP application in both farms. Comparison of Ct values pre- and post-PWP administration revealed improved Ct values in 7 out of 8 samples / farm. Moreover, 4 samples / farm exhibited strong Ct increases, with alterations ranging from +4.23 to +8.44 in Farm A, and +3.9 to +20.68 in Farm B. Overall, qPCR results post-PWP administration indicated a reduction in LI fecal shedding intensity in both farms.

Conclusion

The PWP administration in drinking water effectively reduced clinical signs of PPE in fattening pigs. The PWP can be considered an effective complementary mitigating tool within integrated LI control programs.

Keywords: Antimicrobial alternative, Enteropathy, *Lawsonia intracellularis*, Phytogenic feed additive.

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IMPROVED LIVE BORN AND WEANING WEIGHT OF PIGLET BY SUING SUISENG® VACCINATION

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Introduction and Objectives

Neonatal diarrhoea negatively affects piglet performance. The loss of absorptive apical enterocytes impairs nutrient absorption, leading to reduced weaning weight and a decrease in average daily weight gain of 9 - 14 g/day (Kongsted et al., 2014). The major causative agents include enterotoxigenic *Escherichia coli* (ETEC) (Melkebeek et al., 2013), *Clostridium perfringens* type A/C, and *Clostridioides difficile* (Songer and Uzal, 2005). SUISENG® is a multivalent vaccine indicated for the prevention of neonatal colibacillosis and necrotic enteritis in piglets, as well as sudden death in sows. The objective of this study was to evaluate the effect of SUISENG® vaccination in sows on piglet weaning performance, particularly weaning weight.

Materials and Methods

Data was collected from a total of 69 routing operation batches of weaned piglets. Among these, 36 batches (8766 piglets) originated from sows vaccinated with SUISENG® vaccine in 4 weeks before farrowing, while 33 batches (7124 piglets) originated from unvaccinated sows (before the farm adopted the vaccination program). The piglets weaned at 35 day-olds, the average number of weaned piglets, weaning weight, and pre-weaning mortality were statistically analysed by HIPRASTATS.

Results and Discussion

The application of SUISENG® vaccination in sows resulted in improvements neonatal diarrhoea in farm and statistically significant improvements in weaning performance. The average number of weaned piglets per sow increased from 9.30 ± 0.71 to 10.06 ± 0.98 ($P < 0.001$). In addition, weaning weight showed a significant increase from 8.09 ± 0.79 kg to 8.42 ± 0.50 kg ($P < 0.05$). Pre-weaning mortality in piglets born to SUISENG®-vaccinated sows decreased by 2%; however, this reduction was not statistically significant ($P = 0.2544$).

Conclusion

The results of this study demonstrate that vaccination of sows with SUISENG® pre-farrowing can significantly improve piglet weaning performance, particularly by increasing weaning weight and the number of weaned piglets.

Keywords: SUISENG®, Sow, Weaning weight.

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THE STUDY OF ANTIMICROBIAL SUSCEPTIBILITY IN *ACTINOBACILLUS PLEUROPNEUMONIAE* AND *STREPTOCOCCUS SUIS* ISOLATED FROM DISEASED PIGS IN THAILAND

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Introduction and Objectives

Actinobacillus pleuropneumoniae (APP) and *Streptococcus suis* (*S. suis*) are the most common bacteria which cause economic loss in Thai swine industry. Overuse and misuse of antibiotics is one of the factors that cause antimicrobial resistance in bacteria. This study aims to evaluate the susceptibility of antimicrobial drugs for APP and *S. suis* in Thailand.

Materials and Methods

Isolates of APP (n = 22) and *S. suis* (n = 68) were collected from diseased pigs by necropsy at Kamphaeng Saen Veterinary Diagnostic Center (KVDC) in 2025. The susceptibility test was done by using agar disc diffusion method, using CLSI breakpoints. Antibiotics in this study include amoxicillin-clavulanic acid (AMC), amoxicillin (AMX), ceftriaxone (CEF), cephalexin (CEP), doxycycline (DOX), enrofloxacin (ENR), florfenicol (FLO), and tilmicosin (TIL). The susceptibility data were categorized to high susceptible (≥ 90%), intermediate susceptible (60 to 89%), and high resistance (< 60%) (Vilaró et al., 2020).

Results and Discussion

The results showed that no antibiotics had high susceptibility for both bacteria. APP showed intermediate susceptibility to AMC (73%). ENR (59%), FLO (50%), and DOX (45%) were high resistance for APP. Unfortunately, AMX, CEF, CEP, and TIL were not effective against APP. *S. suis* showed intermediate susceptibility to AMC (87%), AMX (66%), DOX (84%), and FLO (66%). Meanwhile, *S. suis* showed high resistance to ENR (41%), and TIL (1%). The susceptibility levels observed in this study were lower than in the previous study (Siteavu et al., 2023), this may be due to samples often coming from farms where treatment was failed.

Conclusion

Most antibiotics were low susceptible to APP and *S. suis*. Therefore, appropriate antimicrobial use and surveillance of farm-level antimicrobial resistance are important.

Keywords: *Actinobacillus pleuropneumoniae*, Antimicrobial susceptibility, *Streptococcus suis*.

Acknowledgements: The authors would like to thank the Kampaeng Saen Veterinary Diagnostic Center (KVDC), Thailand, for assistance in managing clinical samples and providing testing facilities.

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TEMPORAL EVALUATION OF HALQUINOL SUSCEPTIBILITY IN SWINE ENTERIC PATHOGENS IN THAILAND, 2019–2024

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Introduction and Objectives

Porcine diarrhea causes significant economic losses and is commonly associated with enteric pathogens such as *E. coli* and *Salmonella* spp. Halquinol is a broad-spectrum antimicrobial widely used to control digestive disorders in swine. This study aimed to evaluate antimicrobial susceptibility patterns of major swine enteric pathogens to halquinol.

Materials and Methods

Clinical isolates of *E. coli* (n = 931), hemolytic *E. coli* (n = 146), and Salmonella spp. (n = 81) were obtained from diagnostic submissions of pigs with diarrhea between 2019 and 2024. Susceptibility to halquinol (Quixalud®) was determined by the Kamphaeng Saen Veterinary Diagnostic Center, Kasetsart University, using the agar disc diffusion method. Annual susceptibility data were summarized to evaluate trends over the six-year period.

Results and Discussion

Halquinol showed high activity against major swine enteric pathogens. *E. coli* maintained high susceptibility throughout the six-year period (93.55 - 100%), indicating sustained field effectiveness. Hemolytic *E. coli* showed predominantly high susceptibility (93 - 100%), with a reduction observed in 2021 (5.26%). Similarly, for Salmonella spp., susceptibility remained at 100% until a decline to 80% in 2024, which might reflect localized strain variation. Overall, these findings are consistent with the low resistance potential of halquinol, possibly related to metal-ion chelation and enzyme interference (Prachayasittikul et al., 2013), and supported by sustained field efficacy (Kongpanna et al., 2025).

Conclusion

This multi-year surveillance demonstrated that halquinol maintains high antimicrobial effectiveness against major swine enteric pathogens, with consistently high susceptibility observed across most years. These findings support its use as a valuable option for controlling enteric disorders in swine, while continued monitoring remains important.

Keywords: Antimicrobial susceptibility, Diarrhea, *E. coli*, Halquinol, *Salmonella* spp.

Acknowledgements: The authors acknowledge Elanco (Thailand) for financial support and the Kamphaeng Saen Veterinary Diagnostic Center, Kasetsart University, for providing facilities.

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BIOLOGICAL FEATURES AND ANTIBIOTIC RESISTANCE OF *E. COLI* STRAINS: A ONE HEALTH CONCERN

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Introduction and Objectives

Pathogenic *E. coli* is one of the most prevalent infectious agents in swine industry that causes neonatal, postweaning diarrhea, edema disease and could be harmful for humans. Despite the variety of commercial vaccination programs that pathogen evolves and acquires new virulence factors (Castro et al., 2022; Barros et al., 2023). There is no data about distribution, biochemical characteristics, virulence, and antibiotic resistance of *E. coli* isolated from pigs with colibacillosis in Ukraine. That is why the aim of this study was to investigate biological features of these isolates.

Materials and Methods

Routine autopsy of dead animals (n = 506) was performed for lesion evaluation and bacterial isolation in 2015 - 2022 years. Identification was made by APi20 E test-system. Virulence of *E. coli* strains was detected based on mouse model bioassay, serotyping and presence of hemolysis. Susceptibility to antibiotics was determined by Kirby-Bauer disk diffusion method.

Results and Discussion

It was isolated 502 strains of *E. coli* among which 475 were pathogenic. Animals with pathogenic *E. coli* were characterized by catarrhal inflammation of small intestine, petechial hemorrhages in kidneys and hyperemia of stomach in 97.6, 51.4 and 38.7% of cases, respectively. Moreover in 4.8% of infected animals were detected the signs of Edema disease. It should be noted that pathogenic *E. coli* strains were characterized by α (89.1%), β (6,1%) and γ (4.8%) hemolysis. The largest number of resistant strains were detected to amoxicillin (97,5%), amoxiclav (86.3%), spectinomycin (76.2%), trimethoprim (76.4%), doxycycline (79.6 %) and oxytetracycline (91.4%). The lowest resistance rate was observed to colistin (12.6%), gentamicin (30.5%), ceftiofur (40.2%), florfenicol (45.5%), enrofloxacin (42.7%), norfloxacin (29.1%), and ciprofloxacin (37.7%).

Conclusion

E. coli was identified as one of the leading causative agents of swine infectious diseases in Ukraine and characterized by high level of resistance development to applied antimicrobials. Therefore, the strategy for controlling *E. coli* infection should be based not only on rational antibiotic treatment and conventional immunoprophylaxis, but also on complex diagnostic and vaccination based on local strains.

Keywords: Antibiotic resistance, Colibacillosis, Pathogenic *E. coli*.

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USING GASTROINTESTINAL FLUIDS FROM WEANED PIGLETS TO ASSESS THE ANTIBACTERIAL ACTIVITY OF GLYCERIDES OF LAURIC ACID AGAINST *STREPTOCOCCUS SUIS*

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Introduction and Objectives

Feed additives have emerged as promising alternative strategies to control bacterial challenges, such as *Streptococcus suis*. Previous minimum inhibitory concentration (MIC) assays demonstrated antibacterial activity of lauric acid glycerides (GC12) against *S. suis* (Neath et al., 2021). However, translating *in vitro* MIC values into practical inclusion rates for feed is challenging due to complex *in vivo* factors like digestion, absorption, and microbiota interactions. Therefore, this study aimed to develop an *ex vivo* model to assess the antimicrobial potential of digestive fluids from GC12-supplemented piglets against *S. suis*, providing evidence of GC12 efficacy under physiological conditions.

Materials and Methods

Weaned piglets of 24 days of age with an average body weight of 8.7 kg were allocated to two groups. The control group (n = 6) received a commercial diet for 50 days, and the treatment group (n = 6) was fed the same diet supplemented with GC12 (FRA® C12 Dry) at the recommended dose level of 4kg/ton for the first 11 days, followed by 3kg/ton. Fifty days after weaning digestive fluids were extracted from digesta from the ileum, distal colon and rectum by centrifugation and filtration with 0.22µm filters and tested for antibacterial activity against *S. suis* CRBG BB-3 serotype 7 using a MIC assay at a 1:1 dilution with the bacterial culture. Binary outcomes (0 = growth, 1 = inhibition) were analyzed by Fisher's Exact Test (one-sided).

Results and Discussion

In the control group, 17% of the ileum and distal colon samples and 40% of the rectal samples showed antibacterial activity against *S. suis*. In GC12-supplemented piglets, *S. suis* inhibition reached 83% in ileum samples ($P = 0.040$), 67% in distal colon samples ($P = 0.121$), and 60% in rectal samples ($P = 0.500$). These results indicate that intestinal fluids from GC12-supplemented pigs exhibit an increased antibacterial activity against *S. suis*, which was most potent in the upper intestinal tract (ileum).

Conclusion

This *ex vivo* method validated that the recommended *in vivo* dose level of GC12 provided antibacterial activity against *S. suis* in the ileum of weaned piglets. These findings support the potential of GC12 as a feed additive to help mitigate bacterial challenges.

Keywords: Antibiotic resistance, Gastrointestinal fluids, Glycerides of C12, MIC, *S. suis*.

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RAPID IDENTIFICATION OF PIG VETERINARY BACTERIAL PATHOGENS USING AN ARTIFICIAL INTELLIGENT RAMAN MICROBIAL ANALYZER FOR BIOLOGY

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Introduction and Objectives

Rapid and accurate identification of bacterial pathogens is critical for effective disease control in pig farms. Conventional culture-based and molecular diagnostic methods are time-consuming and often impractical for decision-making. Raman spectroscopy, combined with artificial intelligence, offers a label-free alternative and provides isolate-level identification within approximately 2 minutes. This study aimed to evaluate the performance of the commercial Artificial Intelligent Raman Microbial Analyzer for Biology (AIRMAB) for the rapid identification of clinically relevant pig bacterial pathogens.

Materials and Methods

Clinical bacterial isolates were collected from various tissues of diseased pigs at pig farms in Taiwan between March and November 2025 at the Animal Disease Diagnostic Center, National Pingtung University of Science and Technology. Species identity of all isolates was confirmed using species-specific PCR assays prior to Raman spectral acquisition, ensuring the accuracy of reference labels. For each PCR-confirmed isolate, multiple Raman spectra were collected under controlled measurement conditions and subsequently analyzed using the AIRMAB platform. Classification probabilities derived from multiple spectra per isolate were aggregated to generate isolate-level identification results. Model performance was evaluated using recall for each bacterial species.

Results and Discussion

Overall, the AIRMAB system demonstrated high identification performance across all 14 clinically relevant pig bacterial pathogens. Notably, perfect recall (1.00) was achieved for several clinically common species with higher numbers of isolates, including *Pasteurella multocida* (n = 30) and *Salmonella Choleraesuis* (n = 20). In addition, high recall values (> 0.90) were observed for other clinically relevant species, including *Escherichia coli* (0.97) (n = 33), *Streptococcus suis* (0.94) (n = 35) and Glaesserella parasuis (0.93) (n = 30). The high recall observed for clinically prevalent pathogens with larger isolate numbers indicates stable model performance with sufficient data. To further improve model generalization, continued collection of isolates remains necessary for rare species.

Conclusions

This study demonstrates that AIRMAB system provides rapid, accurate, and label-free identification of pig bacterial pathogens, delivering results within 2 minutes per isolate, demonstrating practical value for timely decision-making in routine veterinary diagnostics, especially for common and clinically relevant species. Continued data collection for rare species will further enhance model generalization.

Keywords: Artificial intelligence, Pig bacterial pathogens, Raman spectroscopy, Veterinary diagnostics

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IMPACT OF SUISENG® VACCINATION ON SOW SUDDEN-DEATH REDUCTION IN A CHINESE FARM

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Introduction and Objectives

Sow sudden death causes significant economic losses on farms, and Clostridium novyi is considered an important pathogen associated with sow sudden death (Uzal et al., 2012). SUISENG® (HIPRA) is formulated to protect piglets against enterotoxigenic *E. coli* and *C. perfringens* type C, and to reduce sudden death associated with *C. novyi* in sows. This study aimed to control sow sudden death (SD) under commercial production conditions through SUISENG® vaccination.

Materials and Methods

A 3,500-sow farrow-to-finish farm with increased sow SD was investigated. *C. novyi* was identified using NovyiCheck, a quantitative PCR (qPCR) assay. Infection was supported by qPCR detection in liver samples collected within 12 hours of death from sows with SD, with 6 of 8 samples testing positive prior to vaccination. Based on these findings, a mass vaccination program was implemented. SUISENG® was administered once to the entire sow herd at week 30 and again at week 33. Weekly sow SD counts were recorded from week 24 to week 43. Weekly mortality rates were calculated as the number of SD cases divided by the total sow inventory. Mean weekly values were derived from aggregated weekly data, and annualized mortality rates were estimated based on mean weekly mortality rates extrapolated to a 52-week period. This field study was conducted under routine production conditions. Due to stable management and relatively consistent climate in southern China, no concurrent control group was included. A before–after observational design was applied, and potential confounding factors cannot be completely excluded. Data were analyzed using a linear regression model with group as a factor.

Results and Discussion

Before vaccination, weekly sow SD cases ranged from 6 to 9. After vaccination, cases decreased to 0 - 3 per week. Mean weekly SD cases declined from 7.17 cases (0.21% ± 0.03) before vaccination to 1.67 cases (0.05% ± 0.03) after vaccination, representing a 76.2% reduction (linear regression model, $P < 0.001$). On an annualized basis, sow mortality decreased from 10.92% before vaccination to 2.60% after vaccination. The SUISENG® vaccination regimen was associated with a rapid and sustained reduction in sow SD.

Conclusion

Whole-herd SUISENG® vaccination was associated with a marked reduction in sow sudden death in a commercial farm.

Keywords: *Clostridium novyi*, SUISENG®, Sow sudden death, Vaccination.

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COMPARATIVE PREVALENCE OF *GLAESSERELLA PARASUIS* AND *MESOMYCOPLASMA HYORHINIS* IN SEROSITIS OF PIGS: A PCR-BASED EVALUATION

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Introduction and Objectives

Mesomycoplasma hyorhinis (M. hyorhinis) and *Glaesserella parasuis (G. parasuis)* are important pathogens in pigs. They can cause considerable economic losses through serositis (Yang et al., 2025; Mugabi et al., 2023). Despite their clinical relevance, comparative investigations on the anatomical distribution are limited. To address this gap, the present PCR-based evaluation compares results for both pathogens, providing insights into their occurrence across different localisations (Silva et al., 2023). Additionally, other bacterial agents were considered as differential diagnoses.

Materials and Methods

For this analysis, 106 samples from various European countries sent to SAN Group Biotech over a one-year period (December 2024 - 2025) were retrospectively selected based on the availability of PCR results for *G. parasuis* and *M. hyorhinis*. Samples originated from pleura, pericardium, central nervous system (CNS), and joints (Bonilla et al., 2022). As a diagnostic laboratory, we assumed that the majority of samples submitted originate from clinical cases. Testing for *G. parasuis* (Kylt® HPS) and *M. hyorhinis* (Kylt® *Mycoplasma hyorhinis/hyosynoviae*) was performed according to the manufacturers' instructions. In 29 PCR-negative cases, alternative pathogens were identified via aerobic bacterial culture.

Results and Discussion

PCR testing was positive for *M. hyorhinis* in 41 samples (36.79%) and for *G. parasuis* in 41 samples (36.79%). Both pathogens were detected in 23.58% of samples. PCR results were negative for both agents in 50.00% of samples. Additional pathogens identified through aerobic bacterial culture in these negative cases were primarily classified as *Streptococcus* spp. and *Escherichia coli*. The distribution of positive findings varied across anatomical locations; for example, no CNS samples tested positive for *M. hyorhinis*, whereas 3.45% were positive for *G. parasuis*. Detailed results are presented in the contribution.

Conclusion

The results indicate that *M. hyorhinis* and *G. parasuis* are implicated in serositis in pigs, occurring at equivalent frequencies. Remarkably, in almost half of the cases, neither of the two pathogens was detected by molecular methods, highlighting the need for further clarification. Potential factors such as inappropriate sampling time or the involvement of additional pathogens should be considered. Further investigations are warranted to assess potential viral involvement and its influence on disease complexity.

Keywords: Arthritis, *Glaesserella parasuis*, Meningitis, *Mesomycoplasma hyorhinis*, Serositis.

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ETIOLOGICAL CAUSES OF PIGLET NEONATAL DIARRHOEA IN CHINA DURING 2025

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Introduction and Objectives

Neonatal diarrhoea (ND) remains one of the most common and economically damaging diseases in Chinese pig farms. Multiple pathogens, including enterotoxigenic *Escherichia coli* (ETEC), clostridial toxins, and viral agents, contribute to its complexity. This study aimed to characterize the current aetiology of ND in China by analysing pathogen detection profiles to identify dominant agents and co-infection patterns supporting prevention strategies.

Materials and Methods

From Jan - Nov 2025, 829 diarrhoeic samples from 128 farms across China were analysed at HIPRA China DIAGNOS using ENTEROCHECK PLUS. Each pooled sample consisted of diarrhoeic faeces from three piglets within the same litter (1 - 15 days old) and was tested by qPCR. ETEC fimbriae (F4, F5, F6) and LT toxin were tested in all samples. Clostridium difficile toxins (TcdA, TcdB) and Clostridium perfringens toxins (α, β, ε) were analysed in 627 samples from 103 farms. Viral pathogens, including Rotavirus A (RVA), Rotavirus C (RVC), and PEDV, were tested in 308 samples from 50 farms. A farm was considered positive if at least one sample tested positive.

Results and Discussion

ETEC F4 (24.73%) and LT (26.18%) were the dominant ETEC factors. For C. difficile, TcdA (46.89%) and TcdB (34.13%) were frequently detected. Positivity for C. perfringens α toxin (Ct < 26), β toxin, and ε toxin were 52.31, 0.00, and 0.84%, respectively. RVA showed the highest viral positivity (35.71%， RVC 21.43%), while PEDV was low (3.90%). At farm level, positivity was 60.94% for ETEC, 70.87% for C. difficile, and 83.50% for *C. perfringens*. Rotavirus-positive farms accounted for 74.00% (RVA 64.00%, RVC 40.00%). Mixed infections were common, with 48.00% virus-ETEC and 46.00% RVA-ETEC co-infections.

Conclusion

ETEC, rotavirus, *C. difficile*, and *C. perfringens* toxins were widely detected on Chinese farms. The low PEDV detection compared with previous years may reflect improved awareness, vaccination, and batch production systems. Frequent mixed infections highlight the need for integrated prevention and routine pathogen monitoring to improve piglet survival and farm productivity.

Keywords: ETEC, Epidemiology, Mixed infection, Neonatal diarrhoea.

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EVALUATION OF THE THERAPEUTIC EFFICACY OF TILDIPIROSIN ON AN ESTABLISHED *ACTINOBACILLUS PLEUROPNEUMONIAE* PERSISTENT INFECTION MODEL IN SWINE

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Introduction and Objectives

Actinobacillus pleuropneumoniae persistent infection arises from environmental contamination or incomplete bacterial clearance after acute infection (Sassu et al., 2017). The tonsils are key sites for persistent *A. pleuropneumoniae* colonization (Zhang et al., 2023). In this study, a porcine persistent infection model of *A. pleuropneumoniae* was established and the therapeutic efficacy of tildipirosin was evaluated on this model.

Materials and Methods

A prevalent serovar 15 strain was used to establish the persistent infection model, with swine intranasally inoculated at a non-lethal dose. Clinical symptoms were observed for 35 days, during which nasopharyngeal swabs were collected for bacterial identification. After sacrifice, lungs and tonsils were harvested to detect bacterial loads and observe bacterial distribution by FISH. Tildipirosin therapeutic efficacy was evaluated on this model.

Results and Discussion

Following inoculation of *A. pleuropneumoniae*, body temperature in the cohort exhibited a rapid elevation, returned to baseline levels by 12 - 14 dpi, and coincided with invisibility of clinical manifestations. The detection rate of bacteria reached lowest at 7 - 11 dpi before increasing again, a trend suggestive of incomplete pathogen clearance after acute infection signs. qPCR quantification and FISH localization confirmed a higher *A. pleuropneumoniae* burdens in tonsils compared with that in lungs. Using an independent cohort, tildipirosin was administered at 13 dpi (post symptoms disappear), pharyngeal swabs were tested to be negative for *A. pleuropneumoniae* by PCR at 23 dpi. qPCR further revealed significantly lower *A. pleuropneumoniae* loads in lungs and tonsils of treated swine compared with untreated controls from the same cohort.

Conclusion

This study successfully established a persistent *A. pleuropneumoniae* infection model using a serovar 15 isolate, with tonsils confirmed as persistent colonization sites. On this model, tildipirosin treatment effectively reduced *A. pleuropneumoniae* excretion rates and significantly decreased *A. pleuropneumoniae* loads in both lungs and tonsils.

Keywords: *Actinobacillus pleuropneumoniae*, Persistent infection, Tonsils, Tildipirosin.

Acknowledgements: This research was supported by the National Natural Science Foundation of China (NO.32473032).

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FIELD EVALUATION OF SUISENG® ON REDUCING PRE-WEANING MORTALITY IN A 2000-SOW FARM IN CHINA

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Introduction and Objectives

Enterotoxigenic *Escherichia coli* (ETEC) is a major cause of neonatal diarrhoea (ND), leading to dehydration, impaired growth, and increased pre-weaning mortality (PWM), resulting in significant economic losses in swine production. SUISENG® (HIPRA) is formulated to protect piglets through sow vaccination against ETEC and Clostridium perfringens type C. This study aimed to evaluate the field impact of SUISENG® vaccination on PWM, production performance, and economic outcomes under field conditions.

Materials and Methods

A commercial 2,000-sow farrow-to-weaning farm experienced recurrent ND throughout 2023, resulting in elevated and unstable PWM. PCR testing of diarrhoeic piglet samples detected ETEC. Therefore, the farm implemented the SUISENG® vaccination programme starting in November 2023. SUISENG® vaccination was applied according to the manufacturer's instructions, with two doses administered at 6 and 3 weeks before farrowing, followed by a booster dose at 3 weeks before farrowing. The sow population remained comparable between 2023 (pre-vaccination) and 2024 (post-vaccination) in terms of breed, parity, litter size, health status, management, and non-vaccine preventive measures. To address a practical production problem under unchanged farm management, facilities, personnel, and environmental conditions, a year-to-year before-after observational design without a concurrent control group was applied. Monthly PWM data from 2023 and 2024 were collected at the farm level. No immunological measurements were performed due to the lack of commercially available diagnostic kits. Mortality percentages were analyzed using a linear regression model with group as a fixed effect ($P < 0.001$). Economic outcomes were calculated based on changes in pigs weaned per sow per year (PSY) and weaning cost per pig.

Results and Discussion

Across 2024, PWM consistently decreased compared with 2023. Annual mean PWM declined from 13.57% to 8.95%, representing a reduction of 4.62 percentage points (37.2%). Following the reduction in PWM, PSY increased by 1.8 pigs, corresponding to an additional 3,422 weaned pigs annually. The weaning cost decreased from 280 RMB to 266.28 RMB per pig (-13.72 RMB). These improvements were temporally associated with SUISENG® vaccination.

Conclusion

Implementation of the SUISENG® vaccination programme was associated with a marked reduction in pre-weaning mortality and improved production stability in a 2,000-sow commercial herd.

Keywords: Enterotoxigenic *E. coli*, Neonatal diarrheoa, Pre-weaning mortality, Sow vaccination.

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PATHOLOGICAL AND BACTERIOLOGICAL FINDINGS IN SOWS, FINISHER PIGS, AND PIGLETS, BEING CULLED FOR LAMENESS

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Introduction and Objectives

Lameness is a common pig disorder. The aetiology may be difficult to establish since primary pathogenesis is obscured by delayed diagnosis, chronic changes and sequelae, and thorough investigation usually requires culling and transport to a pathological laboratory for necropsy. Thus, treatments are mostly based on a tentative diagnosis, commonly including antibiotics to eliminate infectious agents. The study aimed to investigate the aetiology of lameness in various age-categories of pigs, compare the tentative clinical diagnosis with post-mortem findings, and discuss the findings in relation to the adequacy of antibiotic treatment.

Materials and Methods

By the aid of veterinarians from the advisory company Farm & Animal Health, 29 sows, 45 finisher pigs, and 130 suckling piglets diagnosed with lameness were euthanised at the farm and submitted for necropsy. Susceptibility testing was performed on isolates from suckling piglets.

Results and Discussion

Eight sows, two finisher pigs and one suckling piglet suffered from fractures. Arthritis was demonstrated in 13 sows, 30 finisher pigs, and 126 piglets. Of these, 99% were interpreted as being chronic. 86% of all sows and 71% of all finisher pigs had been treated with antibiotics. In six finisher pigs, beta-haemolytic streptococci were found. In the suckling pigs, the most common bacteria were *S. hyicus* (n = 73 isolates) and *S. dysgalactiae* ssp. equisimilis (n = 58). 46 of 64 *S. hyicus*-isolates tested were resistant to penicillin, whereas all 44 isolates of *S. dysgalactiae* ssp. equisimilis tested were sensitive to penicillin.

Conclusion

Necropsy mostly presented pathological findings, explaining the clinical signs of lameness. However, the rationale for antibiotic treatment must be questioned since 37% of the sows and finisher pigs treated with antibiotics suffered from lameness inflicted by non-infectious causes. Further, most cases of arthritis were interpreted as being chronic. In piglets, *S. equisimilis* or *S. hyicus* was isolated in 64% of the samples and a majority of these isolates were susceptible to penicillin, still rendering this a valid drug for treatment.

Keywords: Arthritis, Antimicrobial susceptibility, Post-mortem examination.

Acknowledgements: The authors thank all members of the SVARMp at pig group, financed by the Swedish Board of Agriculture, and the veterinarians within the Farm & Animal Health for helpful and skilled assistance.

DIETARY BUTYRATE GLYCERIDES IMPROVE PIGLET RESILIENCE TO ETEC-INDUCED POST-WEANING SYNDROME

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Introduction and Objectives

Post-weaning syndrome (PWS) triggered by enterotoxigenic *Escherichia coli* (ETEC) remains a major constraint in pig production, leading to growth impairment, mortality, and economic losses. Butyrate glycerides (BG) are known for their gut health benefits and antimicrobial properties. This study evaluated BG supplementation as a strategy to improve piglet resilience against ETEC-induced PWS.

Materials and Methods

Fifty-four weaned male piglets (6.3 kg average BW), genotyped as ETEC-F18-sensitive, were assigned to three groups: Control (CTRL), Challenged (Chall), and Challenged + BG (Chall BG, 2 kg/MT). Challenged groups received an oral inoculation of 10^8 CFU/piglet of ETEC F18 (O141:K94) on day 28 of age. Over four weeks, growth performance, survival, fecal scores, and salivary biomarkers of inflammation, stress, and immunity were monitored. Data were analyzed using one-way ANOVA and Tukey's honestly significant difference (HSD).

Results and Discussion

ETEC challenge reduced survival (88.9%) and daily gain (ADG, 68 vs. 209 g/day; -67.4%, $P = 0.008$) during the first post-challenge week. BG supplementation significantly mitigated these effects, recovering 70% of the growth loss caused by the challenge (168 g/day ADG, $P = 0.054$) and 88.9% of feed efficiency (0.53 vs. 0.21 gain/feed ratio, $P = 0.050$). Mortality decreased to 5.6%, and diarrhea severity dropped by 46% ($P = 0.013$). While ETEC challenge did not significantly alter salivary CRP, adenosine deaminase and cortisol concentrations ($P = 0.220$, 0.219 and 0.989, respectively), it significantly increased inflammatory markers S100A12 and haptoglobin ($P = 0.032$ and 0.024), sympathetic stress (α-amylase, $P = 0.012$), and oxidative stress index (OSI, $P = 0.030$). BG-fed piglets showed reduced levels of all these biomarkers, comparable to non-challenged control group ($P = 0.285$, 0.602, 0.286 and 0.726, respectively), indicating improved health and welfare. Additionally, BG supplementation significantly increased serum IgG levels ($P = 0.008$), indicating enhanced humoral immunity.

Conclusion

Butyrate glycerides supplementation improved piglet resilience to ETEC-induced PWS by reducing mortality, diarrhea severity, and stress while restoring growth and strengthening immune response. These findings support BG as a nutritional strategy to improve health and productivity during the critical post-weaning phase.

Keywords: Glycerides of butyric acid, Enterotoxigenic *Escherichia coli*, Post-weaning diarrhea, Stress.

PCR-BASED SURVEILLANCE OF *GLAESSERELLA PARASUIS* IN PIG FARMS IN VIETNAM

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Introduction and Objectives

Glässer's disease (GD), caused by *Glaesserella parasuis*, is an important bacterial disease affecting swine production, particularly in high-density pig-producing countries such as Vietnam. The disease is associated with increased mortality, reduced growth performance, and economic losses related to treatment and control measures. The objective of this study was to describe the detection of *G. parasuis* by PCR in Vietnamese pig farms presenting clinical signs compatible with GD and to provide updated data on the occurrence of the pathogen at farm and individual animal levels.

Materials and Methods

Between January 2024 and December 2025, a total of 99 samples were collected from 37 pig farms located in Vietnam. Samples were obtained from necropsied pigs showing clinical lesions compatible with Glässer's disease, including polyserositis. Molecular detection of *G. parasuis* was performed by PCR at the HIPRA DIAGNOS laboratory in Vietnam. Results were analyzed descriptively at both the farm and individual sample levels.

Results and Discussion

At the farm level, 27 out of 37 farms (73%) had at least one PCR-positive result for *G. parasuis*. At the individual level, 54 of the 99 samples (55%) tested positive. These results indicate a frequent detection of *G. parasuis* in pigs with clinical suspicion of GD in Vietnamese farms. Similar detection rates have been reported in other swine-producing regions, supporting the relevance of this pathogen worldwide. Antimicrobial treatment and vaccination are commonly applied approaches for the control of Glässer's disease. However, increasing concerns regarding antimicrobial resistance (1) emphasize the importance of prudent and controlled use of antibiotics. Vaccination is therefore widely considered as a preventive tool in herds with recurrent GD problems (2), although these aspects were not evaluated in the present study.

Conclusion

This study demonstrates a high frequency of PCR detection of *G. parasuis* in Vietnamese pig farms with clinical suspicion of Glässer's disease. The results provide updated descriptive data on the occurrence of the pathogen and emphasize the importance of laboratory diagnostics for confirming GD in clinically affected herds.

Keywords: Antibiotics resistance, *Glaesserella parasuis*, Glässer's disease, Vietnam.

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PREVALENCE OF *LAWSONIA INTRACELLULARIS* IN VIETNAMESE SWINE FARMS AND A COUNTERACTIVE DIETARY INTERVENTION WITH ESSENTIAL OILS

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Introduction and Objectives

Lawsonia intracellularis (LI) - attributed clinical disorders are a major constraint to intensive pig production (Jinanan et al., 2025), whereas epidemiological data on LI prevalence in Vietnamese farms remain scarce. The objectives of this study were to (i) assess LI prevalence across intensive Vietnamese pig farms, and (ii) evaluate the mitigating effects of an essential oils blend (Thymus vulgaris, Origanum vulgare, Coriandrum sp., extract of Castanea sativa, and lysozyme, nicotinamide) feed additive in growing pigs under LI challenge.

Materials and Methods

A cross-sectional survey involved 18 farms across North, Central, and South Vietnam, with 324 pooled fecal samples (18 sampling sites per farm) analyzed by qPCR for LI. Additionally, a 60-day field trial was conducted on an LI-positive farm using growing pigs (initial body weight (BW): 30 - 40 kg, ~11 weeks old). The control group (n = 40) received a basal diet supplemented with tiamulin hydrogen fumarate at 240 g/tone of feed continuously for the trial period. The treatment group (n = 40) received the same diet and tiamulin level plus an essential oils blend feed additive (DYSGUARD-S) at 2 kg/tone of feed. Performance parameters [BW, average daily gain (ADG), feed conversion ratio (FCR)] were recorded. Independent samples t-tests were performed in SPSS Ver. 29.

Results and Discussion

All 18 surveyed farms tested PCR-positive for LI, confirming its widespread prevalence in Vietnamese intensive swine production. In the field trial, pigs receiving the essential oils blend outperformed the tiamulin-only control group: ADG increased to 769 ± 29 g/day (vs. 749 ± 35 g/day; $P = 0.115$), FCR improved to 2.86 (vs. 3.05), and final mean BW was also improved (79.03 ± 1.34 vs. 77.25 ± 1.53 kg; $P = 0.002$). Findings indicate that the test product can induce a beneficial effect on productive parameters, which could be associated with properties of essential oils such as improved intestinal enzyme activity and eubiosis.

Conclusion

The investigation confirmed that LI is widespread in Vietnamese intensive pig farms. Dietary supplementation with essential oils enhanced growth performance and feed efficiency, supporting their role as a complementary strategy in control programs against LI.

Keywords: Essential oils, Feed additive, *Lawsonia intracellularis*, Swine, Vietnam.

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PARASITE BURDEN IN PERI-URBAN FREE-ROAMING PIGS IN GERT SIBANDE DISTRICT MUNICIPALITY, MPUMALANGA PROVINCE, SOUTH AFRICA

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Introduction and Objectives

Parasite infections, unlike regulated animal diseases, often receive limited attention despite causing substantial financial losses in pig production, particularly among smallholder and subsistence farmers. The present study aimed to identify and quantify the prevalence of ecto- and endo-parasites among peri-urban free-roaming pigs (FRP) in Gert Sibande District Municipality (GSDM), Mpumalanga Province.

Materials and Methods

In the lack of a complete sampling frame, pig owners were discovered using snowball sampling. Pigs for parasite testing were selected using stratified sampling. Pigs on each farm were categorized by age and gender: boars (≥ 12 months, n = 33), sows (≥ 12 months, n = 78), finishers (8 - 11 months, n = 33), growers (5 - 7 months, n = 64), and piglets/weaners (1 - 4 months, n = 75). Each stratum had one pig randomly selected, providing 283 samples from 124 pig producers. Faecal egg counts (FECs) were measured using the McMaster approach of Roepstroff and Nansen (1998) and Kaufmann (1996) on fresh feces samples (5 g) obtained with gentle rectal massage. Following American Mini Pig Association visual standards, body condition scores (BCS) were calculated. Pairwise correlation, chi-square tests, multi-response crosstabs, and MANOVA were used to determine marginal mean parasite burdens by municipality. Statistical significance was set at $\alpha < 0.05$.

Results and Discussion

A high prevalence of parasitism was observed, with 91.2% of pigs infected with at least one parasite. Detected species included *Haematopinus suis, Sarcoptes scabiei, Ascaris suum, Fasciola hepatica, Trichuris suis, strongylids* (Oesophagostomum dentatum), Eimeria *spp., Moniezia expansa*, and Siphonaptera *spp* (pule irritans). The prevalence varied among age groups, and pairwise correlation analysis showed a weak but statistically significant relationship between *Ascaris suum* infection and body condition ($r = 0.24$; $P < 0.05$). Multivariate analysis highlighted differences in parasite burdens among municipalities.

Conclusion

The findings demonstrate that ecto- and endo-parasites are widespread among peri-urban free-roaming pigs in GSDM, with potential impacts on pig health and productivity. Policy makers, animal health researchers, and veterinary services should prioritize the development of targeted policies, risk communication strategies, and community engagement initiatives aimed at improving parasite control and management in peri-urban pig production systems.

Keywords: Gastro-intestinal parasites, Ecto-parasites, Free-roaming pigs, Disease, Zoonosis.

Acknowledgements: Thank you to the M&D bursary at the University of South Africa (UNISA) and the Department of Agriculture, Rural Development, and Land and Environmental Affairs (DARDLEA) for funding this research. All peri-urban pig participants for allowing us to collect samples from their pigs and and the Journal of the South African Veterinary Association for publishing this work.

ORGANOTYPIC 3D TRACHEAL MODEL RESEMBLES NON-PATHOGENIC RESPONSES TO *MYCOPLASMA FLOCCULARE* AND *MYCOPLASMA HYOPNEUMONIAE* STRAIN J

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Introduction and Objectives

Aggravation of pneumonia lesions by *Mycoplasma hyopneumoniae* (*Mhp*) has been linked with both commensal *M. flocculare* (*Mfloc*) and *Mhp* strain diversity. Previously, we demonstrated that porcine-derived airway epithelial cells cultured at the air-liquid interface (ALI-PRECs) support *Mhp* strain 232 infection. Here, we evaluated ALI-PREC susceptibility to *Mfloc* and non-pathogenic *Mhp* J.

Materials and Methods

Tracheal-derived PRECs from three-weeks-old high-health pigs (n=3) were cultured under ALI conditions for 4 weeks. Epithelial integrity was assessed by Transepithelial Electrical Resistance prior to inoculation. Differentiated ALI-PRECs were inoculated with *Mfloc* 27399 (10^5 CCU/mL) or *Mhp* J (5 x 10^9 CCU/mL). Positive control included viable *Mhp* 232 (*Mhp* 232v), while negative controls included heat-inactivated *Mhp* 232 and medium alone. Cells were monitored every 24 h up to 96 h post-inoculation (hpi) for cytopathic effect (CPE), cytotoxicity (LDH-Glo Cytotoxicity Assay), viability (bacterial culture), and bacterial DNA (qPCR). Cytotoxicity was evaluated in apical washes and subnatants, *Mhp* viability in cell fractions, and qPCR on cells and subnatants to assess epithelial disruption.

Results and Discussion

Ciliary motility was preserved in *Mfloc*-, *Mhp* J-, and negative control treatments. Overt CPE was absent in *Mhp* J cultures, while *Mfloc* induced localized cell lifting without evident epithelial discontinuity. In contrast, *Mhp* 232v caused marked CPE, absent in its inactivated counterpart. Viable mycoplasmas were recovered up to 96 hpi in all inoculated ALI-PRECs, with earlier detection in *Mhp* J treatments. *Mycoplasma* DNA was detected by 24 hpi in all inoculated cultures, and epithelial disruption was evidenced by *Mhp* 232v and *Mfloc* DNA detection in subnatants at 24 and 48 hpi, respectively. Consistent with these findings, *Mhp* 232v exceeded 50% of cytotoxicity by 24 hpi, while *Mfloc* peaked near 45% at 48 hpi. Importantly, cytotoxicity in subnatants was only detected in *Mhp* 232v treatments.

Conclusion

ALI-PRECs reliably mirror epithelial responses to swine mycoplasmas, capturing species- and strain-specific divergences. Our findings suggest that commensal *Mfloc* can induce mild but sustained epithelial disruption, potentially increasing susceptibility to secondary infections with pathogenic mycoplasmas. Future co-infection studies are needed to further investigate these interactions.

Keywords: ALI-PRECs, Bacterial culture, *Mycoplasma flocculare, Mycoplasma hyopneumoniae.*

Acknowledgements: The authors thank Dr. Nubia Macedo for the support with these experiments.

DEVELOPMENT AND APPLICATION OF A BLOCKING ELISA KIT FOR DETECTING ANTIBODIES AGAINST *LAWSONIA INTRACELLULARIS*

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Introduction and Objectives

Lawsonia intracellularis (LI) is the key pathogen causing Porcine Proliferative Enteropathy (PPE), which severely endangers the development of the swine industry (Arnold et al., 2019; Jensen et al., 2006). There is a lack of commercial blocking ELISA kits in China. This study aimed to develop an efficient and accurate blocking ELISA kit for detecting LI antibodies.

Materials and Methods

The LI-OmpA recombinant antigen peptide was used as the coating antigen, which was prepared and purified by a prokaryotic expression system to obtain high-purity antigen. Balb/C mice were immunized with this antigen, and positive hybridoma cell line 5F2 was established through cell fusion, screening, and subcloning. The horseradish peroxidase (HRP)-labeled specific monoclonal antibody was prepared by the periodate oxidation method. The kit includes complete components such as antigen-coated plates, enzyme-labeled antibodies, positive and negative controls, and sample diluent, with key parameters such as coating concentration, reaction temperature, and time optimized.

Results and Discussion

The kit could detect positive serum diluted 1:8, demonstrating good sensitivity; it had no cross-reactivity with positive sera of various common pathogens such as Classical Swine Fever Virus (CSFV) and Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), indicating strong specificity; the intra-batch coefficients of variation (CV) were all less than 10% (0.8 ~ 9.8%) and the inter-batch CV were all less than 15% (1.0 ~ 13.56%), showing excellent repeatability; the coincidence rate with a commercial indirect ELISA kit for detecting 150 clinical serum samples was good (128/150). Application of this kit for dynamic monitoring of serum antibody levels in LI-challenged SPF pigs could effectively evaluate the immune antibody response effect.

Conclusion

The blocking ELISA kit developed in this study fills the gap in related fields in China, featuring simple operation and rapid detection, and provides a reliable tool for the serological diagnosis and immune prevention and control of LI infection.

Keywords: Blocking ELISA, *Lawsonia intracellularis*, Monoclonal Antibody, OmpA, Serological Diagnosis.

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DEVELOPMENT AND CLINICAL APPLICATION OF A BIVALENT QUADRIVALENT INACTIVATED VACCINE AGAINST SWINE STREPTOCOCCOSIS (SEROTYPE 2+7) AND INFECTIOUS PLEUROPNEUMONIA (SEROTYPE 1+5)

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Introduction and Objectives

Swine Streptococcosis (SS) and *Actinobacillus pleuropneumoniae* (APP) are highly prevalent bacterial diseases in large-scale pig farms, with no clinical vaccines covering their major epidemic serotypes. This study developed a bivalent quadrivalent inactivated vaccine against SS (serotypes 2 + 7) and APP (serotypes 1+5) using clinically isolated epidemic strains, to achieve one-shot multi-protection and provide efficient disease prevention for pig farms.

Materials and Methods

Candidate vaccine strains of SS2, SS7, APP1 and APP5 were screened from Hainan, Guangxi, Xinjiang and Guangdong, China. A bivalent quadrivalent nano-aluminum gel inactivated vaccine was prepared for safety tests and challenge-based immunogenicity evaluation, combined with clinical trial in a large-scale Guangdong pig farm to assess its practical application effect.

Results and Discussion

The vaccine exhibited good safety, with immunized piglets showing stable normal body temperatures (38.5 - 39.5°C) with no clinical abnormalities. Challenge trials showed 100% protection (5/5) vs. 100% mortality (5/5) in the control group after SS2-HN challenge; 80% protection (4/5) in the immunized group vs. 100% mortality (5/5) in the control group after APP1-TK challenge. Clinical trials revealed the immunized finishing pigs achieved a marketing rate of 98.52% (0.89% higher than the 97.63% of the control group), with over 7% reduction in animal health costs.

Conclusion

The developed vaccine exhibits excellent safety and >80% protection against mixed infections of SS2, SS7, APP1, and APP5. In clinical application, it increases finishing pig marketing rates by 0.89%, reduces health costs by > 7%, and improves breeding economic benefits. It elevates the marketing rate and cuts breeding costs significantly, simplifies immunization protocols, and provides an effective one-shot dual-disease prevention strategy for pig farms.

Keywords: *Actinobacillus pleuropneumoniae, Streptococcus suis,* Vaccine.

STREPTOCOCCUS SUIS STK1 SENSITIZES EPITHELIAL CELLS TO FERROPTOSIS AND EXACERBATES DISRUPTION OF THE RESPIRATORY EPITHELIAL BARRIER

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Introduction and Objectives

Streptococcus suis serotype 2(SS2) is a major zoonotic pathogen causing invasive disease in pigs and humans (Weinert et al., 2015). Disruption of the respiratory epithelial barrier is a critical step for SS2 dissemination, yet the underlying mechanisms remain unclear. Ferroptosis, an iron-dependent form of regulated cell death, has recently been implicated in host–pathogen interactions (Cao et al., 2023.). This study investigated whether SS2 induces ferroptosis and how this process contributes to epithelial barrier disruption and bacterial dissemination.

Materials and Methods

Respiratory infection models in mice and piglets were established by intranasal inoculation of *Streptococcus suis* serotype 2 to evaluate epithelial damage and bacterial dissemination. Polarized porcine respiratory epithelial cells were used as an in vitro barrier model, with epithelial integrity assessed by transepithelial electrical resistance and permeability assays. Ferroptosis was analyzed using lipid peroxidation, iron accumulation, mitochondrial morphology, and cell viability assays. Genetic (Δstk1, host gene knockout) and pharmacological approaches were applied to dissect underlying mechanisms, together with biochemical and protein interaction analyses.

Results and Discussion

SS2 infection disrupted respiratory epithelial integrity in mice, piglets, and in vitro models. SS2 induced ferroptosis marked by iron accumulation and lipid peroxidation, while ferroptosis inhibition partially rescued barrier function. Mechanistically, SS2 induces ferroptosis by promoting ubiquitin-proteasome-ediated degradation of Nrf2, while lipid peroxidation subsequently activates Snail1 to disrupt epithelial junctions. The bacterial kinase Stk1 hijacks the Keap1 - Nrf2 axis to drive ferroptosis, epithelial barrier disruption, and bacterial dissemination in vivo.

Conclusion

SS2 exploits ferroptosis to disrupt the respiratory epithelial barrier. The effector Stk1 hijacks the Keap1–Nrf2 axis, driving lipid peroxidation–induced ferroptosis and Snail1-mediated junctional loss. Targeting ferroptosis or restoring Nrf2 activity may limit SS2 infection and dissemination.

Keywords: Ferroptosis, Nrf2, Respiratory epithelial barrier, Stk1, *Streptococcus suis*.

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IN SILICO DESIGN OF A UNIVERSAL MULTI-EPITOPE VACCINE CANDIDATE TARGETING CONSERVED ANTIGENS OF *STREPTOCOCCUS SUIS*

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Introduction and Objectives

Streptococcus suis is a significant pathogen in pigs, causing septicemia and meningitis, and presenting a zoonotic risk (Zhang et al., 2023). Antimicrobial therapy continues to be a prevalent control strategy in intensive systems, increasing the selection pressure for antimicrobial resistance (AMR). This research aimed to develop a universal multi-epitope vaccine candidate aimed at conserved S. suis antigens through immunoinformatics to facilitate wide, antibiotic-free protection (Zhang et al., 2009).

Materials and Methods

A distinct *S. suis* protein dataset was obtained and assembled from the NCBI database to cover strain diversity. Candidate antigens were prioritized for universal coverage based on conserved, vaccine-relevant targets, including *eno (enolase), fbpS* (fibronectin-binding protein), *ideSsuis/igd*E (Ig-degrading enzyme), *pilus/srtF*-cluster proteins (associated with colonization), and a proposed universal subunit set (*pdhA, ldh, mal*X). Furthermore, *sly, mrp,* and *epf* were incorporated as targets linked with high-virulence lineages when present. Various techniques were used to forecast linear B-cell epitopes and swine leukocyte antigen (SLA) class I/II T-cell epitopes. Epitopes were selected based on their conservation among strains, anticipated antigenicity, absence of toxicity, non-allergenicity, and minimal resemblance to Sus scrofa proteins (Liu et al., 2024). Selected epitopes were combined into a multi-epitope construct utilizing rational linkers. The resulting construct was assessed in silico for physicochemical parameters (molecular weight, isoelectric point, stability/solubility indices), structural modeling and validation, and docking-based evaluation of interactions with immune receptors (Fang, 2025).

Results and Discussion

The system discovered conserved epitope sets from the chosen antigen panel, expected to trigger both humoral and cellular immune responses and facilitate cross-strain coverage. The resultant construct exhibited advantageous expected safety characteristics (non-toxic/non-allergenic) and satisfactory stability/antigenicity profiles, with modeled structures revealing surface-accessible epitope sites. Integrating conserved targets related to colonization and virulence *(eno, fbpS, ideSsuis/igdE, pilus/srtF, pdhA/ldh/malX*) alongside optional high-virulence markers (*sly/mrp/epf*) establishes a logical framework for candidate selection in universal vaccine development.

Conclusion

A universal multi-epitope vaccine candidate targeting conserved S. suis antigens has been identified in silico, exhibiting promising projected immunogenicity and safety, hence facilitating advancement to in vivo and in vitro expression and piglet immunization/challenge experiments.

Keywords: conserved antigens, immunoinformatics, multi-epitope vaccination, *Streptococcus suis*.

Acknowledgements: Thanks to Professor Ba Xiaoliang for his continued support and providing a platform to do research work in his lab under his supervision.

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PREVALENCE AND SEROTYPE SHIFT OF PORCINE *PASTEURELLA MULTOCIDA* IN CHINA (2024 - 2025): IMPLICATIONS FOR DISEASE PREVENTION AND CONTROL

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Introduction and Objectives

Pasteurella multocida (PM) is a significant zoonotic and primary swine pathogen implicated in major infectious diseases. PM-induced pneumonia is a leading cause of mortality in post-weaning and finishing pigs, while atrophic rhinitis reduces growth efficiency and feed conversion, causing substantial economic losses to the swine industry. Historical data in China (2010 - 2024) show that PM serotypes A and D were predominant, with type A being dominant. However, our 2025 isolation data indicate a significant epidemiological shift, with type D emerging as the predominant serotype. This changing trend underscores the need for corresponding adjustments in Pm prevention and control strategies.

Materials and Methods

A cross-sectional surveillance study was conducted from December 2024 to November 2025 across 21 provinces in China. We collected 5,662 clinical samples (nasal swabs and lung tissues) from 1,708 small- to medium-scale swine farms, with all samples sourced from pigs exhibiting respiratory symptoms. Samples were subjected to bacterial isolation, identification, and subsequent PCR-based serotyping for capsular types A, D, and F of PM.

Results and Discussion

From 5,662 clinical specimens, 124 porcine-origin PM strains were isolated (2.19% isolation rate). Serotyping revealed 47 serotype A strains (37.90%), 69 serotype D strains (55.65%), and 2 serotype F strains (1.61%), with 6 strains (4.84%) untyped. A decade-long analysis of PM isolation data indicates that serotype A was historically dominant. However, the isolation rate of serotype D has shown an increasing trend since 2023, becoming the predominant serotype in 2025.

Conclusion

This report reviews the epidemiological trends of porcine PM in China. A passive surveillance study revealed a high prevalence of antimicrobial usage in small- to medium-sized farms, which correlates with a high Pm detection rate but a low isolation rate. Furthermore, a concerning serotype mismatch exists between commercial vaccines (primarily targeting capsular types B and A) and the circulating field strains. The current limitation of these vaccines in covering serotype D has contributed to its rising prevalence. Consequently, China's disease control strategies and vaccine strains must be updated to align with these evolving epidemiological patterns. The study acknowledges limitations associated with passive sampling and incomplete background data.

Keywords: Isolation rate, Porcine pasteurellosis, Serotype, Vaccine development.

Acknowledgements: The authors would like to thank Huazhong Agricultural University for providing platform support

THE CAMP RECEPTOR PROTEIN GENE CONTRIBUTES TO GROWTH, STRESS RESISTANCE, AND COLONIZATION OF *ACTINOBACILLUS PLEUROPNEUMONIAE*

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Introduction and Objectives

Porcine infectious pleuropneumonia (PCP), caused by *Actinobacillus pleuropneumoniae* (APP), is a severe respiratory disease that causes major economic losses in pig production. The cAMP receptor protein (CRP) is a global transcriptional regulator that enables bacteria to adapt to environmental changes, particularly during infection. However, its role in APP remains unclear. This study aimed to investigate the contribution of CRP to APP pathogenesis, focusing on stress adaptation, biofilm formation, host–pathogen interactions, and in vivo colonization.

Materials and Methods

A crp deletion mutant (Δcrp) was generated from the wild-type (WT) APP strain. The WT and mutant strains were compared in terms of growth, resistance to acidic and osmotic stress, and biofilm formation. Iron utilization was evaluated under iron-limited conditions. Host-pathogen interactions were assessed through phagocytosis, adhesion, and invasion assays using cell lines. In addition, a murine infection model was used to evaluate lung colonization and bacterial load.

Results and Discussion

The Δcrp strain showed impaired growth under stress conditions and increased sensitivity to acidic and osmotic environments compared with the WT strain. Biofilm formation and iron utilization were significantly reduced in the mutant. In host–pathogen interaction assays, the Δcrp strain exhibited decreased resistance to phagocytosis and reduced adhesion to and invasion of host cells. In the murine infection model, mice infected with Δcrp had significantly lower lung bacterial loads than those infected with the WT strain. These results indicate that CRP regulates multiple virulence-related processes in APP.

Conclusion

CRP plays an important role in APP pathogenesis by regulating stress resistance, iron acquisition, biofilm formation, host cell interactions, and lung colonization. These findings provide new insights into the mechanisms of APP infection and suggest potential targets for future control strategies.

Keywords: *Actinobacillus pleuropneumoniae*, cAMP receptor protein, Colonization, Growth, Stress resistance.

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AN INDIRECT RECOMBINANT ANTIGEN ELISA TO DETECT *LAWSONIA INTRACELLULARIS*-SPECIFIC ANTIBODIES

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Introduction and Objectives

Lawsonia intracellularis (LI) causes the disease proliferative enteropathy. The chronic form is characterised by diarrhoea and reduced DWG, leading to substantial economic losses in swine (Holyoake et al., 2010). Currently, the only serological assay being commercially available is based on whole-cell antigen preparations (Jacobson et al., 2011). However, ELISA using recombinant proteins may induce a high-affinity LI antibody binding, thus possibly increasing the specificity. Our aim was to identify potential antigens of LI, produce them as recombinant proteins and evaluate their antigenic potential to be used in an indirect ELISA to selectively detect LI antibodies in porcine serum.

Materials and Methods

The five proteins LatAC, LFlgLD, LFliDD, LhlyAC and LYopN (3) were selected based on literature and bioinformatics methods. Genes encoding the recombinant proteins were synthesised, inserted into a plasmid, expressed by E. coli and purified. An indirect ELISA was developed with recombinant proteins coated on separate wells. 16 serum samples from verified positive and 16 serum samples from verified negative pigs were tested. Based on the results of the assay, a ROC curve of every antigen was plotted using Graphpad Prism 10.

Results and Discussion

The five recombinant proteins were successfully produced and purified. With all five recombinant proteins, a significant difference was found between the positive samples and the negative samples ($P < 0.0001$). The area under the ROC curve was > 0.99 from four of the five proteins, and > 0.96 from the fifth protein. These results indicate the ability of all five proteins to selectively bind LI serum antibodies.

Conclusion

All five recombinant proteins show great potential to be used as diagnostic antigens. Future steps to validate ELISA should be to test more serum samples from verified positive and negative pigs. Further the assay needs to be evaluated on naturally infected as well as vaccinated pigs and animals of different age groups. We will proceed with these recombinant proteins, validating and optimizing the diagnostic ELISA.

Keywords: ELISA, Enzyme linked immunosorbent assay, *Lawsonia intracellularis*, Proliferative enteropathy, Serology.

Acknowledgements: The authors thank the Swedish University of Agricultural Sciences and The Swedish farmer's foundation for agricultural research for their contribution.

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ISOLATION, ANTIMICROBIAL SUSCEPTIBILITY PROFILES AND VACCINE PROTECTION EVALUATION OF *STREPTOCOCCUS SUIS* FROM A COMMERCIAL PIG FARM

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Introduction and Objectives

Streptococcus suis (SS) is a major bacterial pathogen causing systemic infections in pigs and remains difficult to control in intensive production systems due to antimicrobial resistance and variable vaccine protection. This study aimed to isolate and characterize SS strains from a commercial pig farm, assess antimicrobial susceptibility to guide clinical treatment, and evaluate the protective efficacy of a commercial vaccine using a murine model.

Materials and Methods

Clinical samples, including blood, joint fluid and brain tissue, were collected from diseased pigs in a commercial pig farm. *Streptococcus suis* was isolated and identified by species-specific PCR, followed by serotyping using multiplex PCR and genotyping. Antimicrobial susceptibility testing was performed using the broth microdilution method, including antimicrobials routinely used on the farm and a broader laboratory-based panel to evaluate current treatment options and explore potential alternatives. Two predominant SS isolates were used to establish a murine challenge model, and vaccine protective efficacy was evaluated in an immunization–challenge experiment based on survival rates.

Results and Discussion

Four SS strains (SS-2, SS-3, SS-11, SS-12) were isolated and identified. Antimicrobial susceptibility testing showed all strains were fully resistant to aminoglycosides but highly sensitive to cephalosporins and tiamulin, with distinct resistance profiles among strains, indicating potential therapeutic options for clinical treatment. A murine challenge model was successfully established using the SS-2 and SS-3 isolates. In the immunization–challenge experiments, mice vaccinated with the same commercial vaccine exhibited partial protection against both strains. The protective efficacy reached 40.0% following SS-2 challenge and 42.86% following SS-3 challenge. These results suggest strain-dependent variation in vaccine-mediated protection, highlighting the potential impact of strain diversity on vaccine performance under field conditions.

Conclusion

This study clarified the resistance profiles of four SS strains, supporting cephalosporins and tiamulin as preferred clinical treatments. Successful murine models and vaccine efficacy data highlight the need for optimized prevention strategies, contributing to precise SS control in a commercial pig farm.

Keywords: Antimicrobial susceptibility, Challenge model, *Streptococcus suis*, Vaccine protection.

EFFECT OF LACTOCOCCUS LACTIS CELL-FREE SUPERNATANT (NUVIO) ON POST-WEANING DIARRHEA IN PIGLETS AND ENTEROTOXIGENIC *ESCHERICHIA COLI* PATHOGENICITY

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Introduction and Objectives

Post-weaning diarrhea caused by F4 and F18 + enterotoxigenic *E. coli* (ETEC) poses a significant economic threat due to treatment costs, performance losses and mortality. Conventional control strategies such as mineral therapies (ZnO) or antibiotics face regulatory pressures, and a need for new, novel therapeutic approaches. Quorum-sensing is a cell-to-cell communication system used by ETEC to control expression of colonization factors, and toxin expression, which represents a promising therapeutic target. The aim of this work was to demonstrate the inhibition of QS-virulence by NUVIO and show improved disease and performance results.

Materials and Methods

Three randomized controlled trials were conducted using a total of 270 weaned piglets (90 per trial). Piglets received either a placebo or 6 to 24 mg/kg body weight NUVIO via drinking water for 14 days post-weaning. Diarrhea incidence, prevalence, frequency, fecal scores, and performance parameters were recorded. Fecal swabs were collected to assess the presence of hemolytic *E. coli* and F41 ETEC. NUVIO was tested in vitro against ETEC gene expression and QS production. Pathogenicity was evaluated in C. elegans survival assays with F4+ and F18+ ETEC.

Results and Discussion

Across trials, administration of CFSM at 24 mg/kg significantly reduced diarrhea frequency and prevalence compared with placebo, particularly during peak post-weaning challenge periods. No negative effects on growth performance or feed conversion were observed. In vitro treatment with NUVIO resulted in the significant repression of colonization (faeG), QS (luxS) and virulence (estB, eltB) genes in F4+ ETEC; and reduced AI-2 production during growth. NUVIO protected *C. elegans* from F4 and F18 ETEC induced death.

Conclusion

This report demonstrates the effectiveness of NUVIO cell-free fermentation material to reduce post-weaning diarrhea under natural challenge conditions and suppress expression of critical ETEC virulence gene necessary for pathogenesis. Targeting the QS system used by bacteria to cause disease represents a natural and novel therapeutic target to mitigate post-weaning diarrhea in piglets.

Keywords: Enterotoxigenic *Escherichia coli*, *Lactococcus lactis*, Quorum sensing, Virulence gene expression.

VALIDATION OF A NEW GENERATION ELISA TEST FOR ANTIBODY DETECTION FOR *MYCOPLASMA HYOPNEUMONIAE*

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Introduction and Objectives

Mycoplasma hyopneumoniae, the etiologic agent of enzootic pneumonia, is a major economic concern for swine producers worldwide due to its negative effects on growth performance, feed efficiency, and increased susceptibility to secondary respiratory infections. Control strategies, including vaccination, antimicrobial use, and eradication programs, rely on accurate serological monitoring. However, confidence in diagnostic outcomes is often limited by variability in commercial assay performance. To address this need, IDvet developed the ID Screen® *Mycoplasma hyopneumoniae* competitive ELISA, which uses a monoclonal antibody targeting a conserved epitope of the P65 protein, as assessed by absence of cross-reactivity with other porcine Mycoplasma species.

Materials and Methods

Diagnostic specificity was evaluated using serum samples from breeding herds confirmed free of *M. hyopneumoniae* through routine surveillance. Analytical specificity was assessed using sera from pigs experimentally inoculated with *Mycoplasma flocculare, M. hyorhinis,* or *M. hyosynoviae*. Samples were obtained from Iowa State University (ISU) and tested at 0- and 56-days post-inoculation (dpi). Diagnostic sensitivity was assessed using sequential serum samples collected between 0 and 56 dpi from eight pigs experimentally infected with *M. hyopneumoniae*. A comparative evaluation with the IDEXX indirect ELISA was conducted at the ISU Veterinary Diagnostic Laboratory (VDL).

An independent analysis was performed at the University of Minnesota VDL, where 152 field samples classified as false positives by the IDEXX ELISA were tested using the IDScreen®ELISA from IDVet. Samples were collected over 10 months from herds confirmed to be negative for *M. hyopneumoniae*. The UMN VDL also evaluated both ELISAs using sera from a site including vaccinated and acutely infected animals.

Results and Discussion

All sera from *M. hyopneumoniae*-negative herds and pigs inoculated with other Mycoplasma species tested negative with the IDScreen®ELISA, confirming high analytical and diagnostic specificity. The IDScreen®ELISA detected seroconversion earlier (17–49 dpi) than the IDEXX ELISA (24–49 dpi). In the UMN VDL field study, the IDScreen®ELISA demonstrated improved sensitivity (68%) and specificity (95.39%) relative to IDEXX within the evaluated population.

Conclusion

Together with previously presented findings by Dr. Devi Patnayak at AAVLD 2024, these results support the ID Screen® *M. hyopneumoniae* competitive ELISA as a robust tool for serological surveillance in swine production systems.

Keywords: Diagnostic test, ELISA, *Mycoplasma hyopneumoniae*, Serology, Swine.

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FIRST ISOLATION OF *CLOSTRIDIUM DIFFICILE* FROM DIARRHEIC NEONATAL PIGLETS IN VIETNAM AND ANTIMICROBIAL SUSCEPTIBILITY

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Introduction and Objectives

Neonatal piglet diarrhea (NPD) remains one of the major challenges due to its negative impact on animal health and economic losses. High detection and isolation of *C. difficile* in diarrheic piglets in recent years have raised concerns about the potential role of this microorganism in NPD (Kim et al., 2018). Therefore, this study aims to inspect the occurrence of *C. difficile* in diarrheic neonatal piglets in Vietnam and determine the antimicrobial susceptibility of the isolates.

Materials and Methods

A total of eighty-six fecal samples were collected from diarrheic piglets from 6 farms in Southern Vietnam. Identification was based on colony morphology on CCFA, characterized by small, flat, pale-yellow colonies with a ground-glass appearance and filamentous margins, and on blood agar, where colonies were small, grayish, and non-hemolytic, together with Gram staining and biochemical tests. The isolates were confirmed using PCR using 16S rRNA primers. Vancomycin, metronidazole, rifampicin, amoxicillin/clavulanic acid, erythromycin, tylosin, and lincomycin were used for the antimicrobial susceptibility test of C. *difficile*. The testing method was performed according to the EUCAST standard, and the results were interpreted based on previously published studies.

Results and Discussion

Four *C. difficile* isolates (4.7%) were recovered from 86 fecal samples. This prevalence was significantly lower than previous reports in Asia (18–53.6%), which may be attributed to the difference in isolation method, as an enrichment step was not performed before CCFA plating (Kim et al., 2018; Zhang et al., 2019). Susceptibility to vancomycin, metronidazole, rifampicin, and amoxicillin/clavulanic acid was observed in 100% (4/4) of isolates. In contrast, resistance to erythromycin and tylosin was detected in 100% (4/4) of isolates, while resistance to lincomycin was observed in 75% (3/4) of isolates

Conclusion

To our knowledge, this is the first report to isolate *C. difficile* in diarrheic neonatal piglets in Vietnam and characterize their antimicrobial resistance. The result will provide baseline data for future surveillance and epidemiology.

Keywords: Antimicrobial susceptibility, *Clostridium difficile*, Isolation, Neonatal piglet diarrhea.

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ASSESSMENT OF THE ADHESION OF ATYPICAL SHIGA TOXIN-PRODUCING *E. COLI* STRAINS TO THE PORCINE SMALL INTESTINAL EPITHELIUM

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Introduction and Objectives

Edema disease (ED) affects piglets and causes substantial production losses to farmers. It is caused by Shiga toxin-producing *Escherichia coli* (STEC) strains, which are typically characterized by the presence of two key virulence factors: F18 fimbriae and the Shiga toxin Stx2e. However, strains isolated from pigs on farms with ED frequently do not carry the F18 fimbrial operon, while they carry genes encoding Stx2e. Our study aimed to explore whether these atypical STEC strains can bind to the small intestinal epithelium using an in vitro villus adhesion assay as well as an enteroid monolayer binding assay.

Materials and Methods

The F18-fimbriated reference STEC strain F107/86 and three field strains (1717, 1730 and 4056), previously collected from farms with ED, were selected. These field strains lacked the F18 fimbrial operon and secreted Stx2e (Van hoorde et al., 2025). An *in vitro* villus adhesion assay was performed using jejunal villi of three piglets (two were F18R+ and one was F18R- as determined by the FUT1 assay). An enteroid monolayer adhesion assay was conducted as previously described (Vermeire et al., 2021). Stx2e secretion was measured by ELISA.

Results and Discussion

As expected, the F18-fimbriated reference STEC strain F107/86 adhered to the F18R+ villi and weakly to the F18R- villi in the villus adhesion assay. In contrast, strain 4056 and 1730 did not adhere to the villi, while strain 1717 adhered weakly. Next, adhesion of the strains to enteroid monolayers was evaluated to further confirm these findings. Remarkably, two atypical STEC strains (1717 and 1730) adhered to the enteroid monolayers, just like the reference strain, while strain 4056 did not adhere. The reference strain and the two atypical STEC strains with proven adherence also secreted Stx2e upon adhesion to the enteroid monolayers.

Conclusion

Our results show that these atypical STEC strains can adhere to small intestinal epithelial cells independently from F18 fimbriae and that they secrete Stx2e upon adhesion. Further research is, however, needed to identify the factor(s) used by these strains to bind to the small intestinal epithelium in piglets.

Keywords: Adhesion, Edema disease, Gut epithelium, Shiga toxin.

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THE EFFLUX PUMP SUGE2 INVOLVED IN PROTECTION OF *SALMONELLA* 4,[5],12:I:- AGAINST QUATERNARY AMMONIUM SALTS AND INHIBITION OF VIRULENCE

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Introduction and Objectives

The escalating global public health concern posed by multidrug-resistant *Salmonella* 4,[5],12:i:-, a monophasic variant of *S. Typhimurium*, has garnered widespread attention (Frasson et al., 2016). Our previous studies have found that the isolates from pig farms exhibited an increasing trend in resistance to quaternary ammonium compounds (QACs) disinfectants (Tian et al., 2021). The mechanisms underlying the acquisition of QACs tolerance by S. 4,[5],12:i:- remain unclear.

Materials and Methods

We collected S. 4,[5],12:i:- isolates from this pig farm to determine their minimum inhibitory concentration (MIC) values, and then, employed whole genome sequencing and RNA-seq to identify the genes responsible for the high tolerance to disinfectants. The efflux pumps SugE1 and SugE2 as essential for conferring tolerance to disinfectants in S. 4,[5],12:i:- ZC055 were identified. Furthermore, The efflux pump SugE2 is evaluated to influence the virulence of S. 4,[5],12:i:- ZC055 both in vitro and in vivo.

Results and Discussion

The isolates of S. 4,[5],12:i:- resistant to QACs were identified, displaying elevated MIC values (200 μg/mL). The efflux pumps SugE1 and SugE2 could be induced by didecyldimethylammonium bromide (DDAB) and found to be indispensable for S. 4,[5],12:i:- resistance to DDAB. Moreover, the ΔsugE2 and ΔsugE1ΔsugE2 mutant strains exhibited an enhanced ability to disrupt the intestinal barrier, leading to systemic infection. Notably, our results demonstrate that intestinal extract can induce sugE2 expression and inhibit SPI-1 expression, which mediate the adhesion, invasion, and oral infection of S. 4,[5],12:i:- both in IPEC-J2 cell experiment and in murine infection model.

Conclusion

We discovered the co-existence of sugE1 and sugE2 genes within the IncHI1B plasmid, which can efflux of QACs disinfectants, thereby conferring resistance to QACs in S. 4,[5],12:i:-. The results unveiled a previously unnoticed role of the SMR-type efflux pump SugE2 in Salmonella virulence. It will aid in assessing the risks associated with targeting efflux pumps to combat Salmonella dissemination and infection.

Keywords: Disinfectant, Efflux pump, Salmonella, Virulence.

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DIAGNOSIS OF *SALMONELLA CHOLERAESUIS* INFECTION IN PIGS FROM THREE DIFFERENT FARMS

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Introduction and Objective

The Salmonella infection continues to be a cause of disease in pigs as well as a public health problem (Bernard et al., 1983). Swine is one of the most important reservoirs of various serotypes and is susceptible to disease by *Salmonella Cholerasuis*. This work was conducted to compare the agglutination test with other established tests in order to detect seropositive reactors.

Material and methods

A total of 846 pig sera from farms of different sanitary statuses were included in this study. The samples were tested with three serologic tests, namely the slow agglutination test to detect both IgG and IgM (SAL: Slow Agglutination Test) and the slow agglutination test with 2-mercaptoethanol (SAL 2-ME) for IgG, adapted to microplates and the plate agglutination test (PAT), a qualitative test that was also adapted to 96 well microplates. The PAT technique: a drop of serum was placed on the plate and a drop of the antigen (Salmonchtest), any degree of agglutination was observed, this technique only detects Salmonella IgG (1-4)

Results and discussion

The infected pigs are in the convalescent stage of the disease, as IgG antibodies are produced one to two weeks after the onset of infection. The technique detected 506 positive serum samples across the different dilutions, leaving only 340 negative samples in total. This shows that 59.81% of the pigs are infected with Salmonella, while only 40.18% are uninfected. Comparing the techniques that detect only IgG, a 97.99% correlation was observed among the 846 serum samples analyzed. Of the 17 serum samples that tested negative in the 2-mercaptoethanol technique, 14 tested positives in both the plate agglutination test and the tube agglutination test, the latter using different dilutions for each serum sample. Salmonella was isolated in the feces of the animals, and it should be noted that vaccination on these farms is massive.

Conclusion

The SAL and eME techniques utilized serogroup-specific antigens to the Somatic Group C1, allowing for the presumptive identification of *S. choleraesuis* exposure and differentiation from other common serogroup-specific antigens like *S. typhimurium* (Group B)."

Keywords: Diagnosis, Farms, *Salmonella cholerasuis.*
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IMPACT OF APP VACCINATION ON THE APP INDEX (APPI) IN PHILIPPINE SWINE FARMS THROUGH THE CEVA LUNG PROGRAM (CLP)

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Introduction and Objectives

Lung lesion scores vary among individual pigs, farms, and countries. Accurate diagnosis and effective monitoring of the economic impact of respiratory infections in swine require precise identification and quantification of lung lesions during slaughterhouse inspections. This study aims to evaluate the impact of *Actinobacillus pleuropneumoniae* (APP) following the implementation of APP vaccination through the Ceva Lung Program (CLP) App.

Materials and Methods

The trial covers the period from January to December 2025. A total of 778 batches of pigs, comprising 58,272 lungs from various commercial farms across the Philippines, were evaluated using the CLP. APP indices, were systematically scored, recorded, and analyzed through the CLP app.

Results and Discussion

After high incidence and severity of APP-like lesions in Q1 in majority of the participating farms, APP vaccination was initiated starting February 2025. APP Index in Q1 of 2025 was 1.43, .86 at Q2, .39 at Q3, and .44 at Q4, respectively. Among different APP brands used in the same periods in 2025 were Coglapix at 76.3%, Brand M at 4.4%, Brand B at 1.2%, Brand A at .1%, Brand BC at 0.3 and 17.7% were not vaccinated.

Conclusion

A gradual decrease in APPI over time indicates that pigs vaccinated with Coglapix showed fewer APP-like lesions. Among the 778 batches, 76.3% were vaccinated with Coglapix underscoring the continued importance of APP vaccination as a control measure across farms in different regions of the Philippines

Keywords: *Actinobacillus pleuropneumoniae*, APPI, CLP, Coglapix, Lung lesion scores.

ESTIMATED ECONOMIC LOSS DUE TO *MYCOPLASMA HYOPNEUMONIAE*-LIKE LUNG LESIONS IN DENMARK

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Introduction and Objectives

Post-mortem lung scoring is a well-known tool to assess farm respiratory health status. Strong correlation between *Mycoplasma hyopneumoniae* (Mhyo)-like lung lesions and daily gain and/or feed efficiency has been reported historically (e.g. Ferraz 2020, Straw 1989). Ceva Lung Program (CLP) is repeatedly confirmed as a valuable tool to establish the prevalence and severity of Mhyo-like lung lesions at slaughter. The aim of this study was to estimate the impact of Mhyo-like lung lesions on herd productivity, and profitability.

Material and Methods

In the 2024 Danish "Lungvember" best-respiratory-health monitoring campaign, herds, that vaccinated against *M. hyo*, had lungs scored by CLP following slaughter at the Veterinary laboratory, Kjellerup. *M. hyo*-like lung lesions were recorded and scored as volume percent (% MLL). The economic loss was estimated based on daily gain/Feed conversion rate and lung lesions, collected from a meta-analysis of relevant papers. As mortality was not systematically included in such publications it was not included.

Results and Discussion

In 2024, 72 finisher herds participated in Lung vember. Of these 61 had *M. hyo*-like lesions providing 3.13 %MLL in average. The loss per 1 %MLL was estimated to 0.26 €/pig, calculated in the Danish model farm. The average loss in the 61 Danish herds was 0.81 €/pig with a 95 percent confidence interval from 0.46 - 1.24 €/pig. This covers for a loss of 13 grams/day, and an increase of 0.02 kg feed/kg gain. The available data for losses of daily gain due to *M. hyo*-like lesions are from 1989 to 2020. Whereas losses in feed efficiency are data from 1989 and before. The correlation between loss in daily gain and loss in feed efficiency seems realistic.

Conclusion

Postmortem lung scoring is a valuable tool to assess respiratory health status. CLP showed MLL in 85% of the finisher herds, amounting to 3.13 %MLL on average. It was found that Mhyo-like lung lesions of 10 % could be translated to an economic loss of 2.6€ per pig. This emphasizes the importance of reducing pneumonia in finishing pigs, by improving management, all-in all-out batch production and optimizing vaccination, to reduce economic losses, antibiotic use, and improve welfare.

Keywords: Ceva Lung program, CLP, Economic loss, lung lesions, *Mycoplasma hyopneumoniae*.

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EFFECTS OF DRAXXIN ADMINISTRATION AT WEANING ON THE CONTROL OF SWINE RESPIRATORY DISEASE IN PRRS-POSITIVE FARMS IN TAIWAN

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Introduction and Objectives

Swine respiratory disease (SRD) is a persistent challenge in pig production, particularly at weaning period when piglets experience waning maternally derived antibodies and multiple stressors. In Taiwan, the high prevalence of Porcine reproductive and respiratory syndrome (PRRS) further complicates SRD management post-weaning, contributing to increased mortality and nursery losses. This study evaluated whether a single injection DRAXXIN® (tulathromycin) administered at weaning reduces nursery losses in PRRS-positive herds.

Materials and Methods

This study was conducted on a 200-sow, farrow-to-finish, PRRS-positive farm in Taiwan. Piglets were allocated into two groups: a treatment group receiving a single intramuscular dose of DRAXXIN® (2.5 mg/kg body weight) at weaning, while the other group served as an untreated control. Data from 24 production batches (over 5,000 piglets) were analyzed to compare nursery mortality and mortality within the first two weeks post-weaning. Mortality rates were compared between groups, and statistical significance was assessed ($\alpha = 0.05$).

Results and Discussion

Administration of DRAXXIN® at weaning was associated with significantly lower overall nursery mortality compared to the control group (1.61 vs. 3.30%; $P < 0.01$). Mortality within the first two weeks post-weaning was also significantly reduced in the DRAXXIN® group (0.19% vs. 0.74%; $P < 0.05$). These findings indicate that metaphylactic DRAXXIN® administration at weaning can improve early post-weaning survival in PRRS-positive herds, likely by mitigating bacterial components of SRD during a period of elevated susceptibility (King et al., 2014; Sievers et al., 2014). The results are consistent with previous reports on tulathromycin's benefits in PRRS-affected herds, supporting its role in integrated SRD control strategies that complement biosecurity and vaccination programs.

Conclusion

A single dose of DRAXXIN® administered at weaning reduced nursery losses and early post-weaning mortality in a PRRS-positive farm in Taiwan. This intervention may enhance SRD control and contribute to improved piglet health during the nursery phase.

Keywords: DRAXXIN®, Porcine reproductive and respiratory syndrome, Swine respiratory disease, Weaning.

Acknowledgements: We thank the farm staff for data collection and operational support.

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COMPARATIVE GENOMIC ANALYSIS OF *LAWSONIA INTRACELLULARIS* ISOLATES COLLECTED FROM DIFFERENT HOST SPECIES AND COUNTRIES

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Introduction and Objectives

Proliferative enteropathy, also known as ileitis, is caused by *Lawsonia intracellularis* and occurs worldwide in pigs and other animal species. Due to the fastidious growth requirements of *L. intracellularis*, whole-genome sequencing (WGS) data from pure isolates remain scarce, limiting our understanding of the genetic basis of its epidemiology and global transmission patterns. The objective of this study was to characterize the genetic diversity and phylogenetic relationships among *L. intracellularis* isolates from multiple countries and host species, in order to identify genomic regions that could support source attribution and help infer the geographic origin of infection events.

Materials and Methods

WGS was performed on 17 cell-cultured *L. intracellularis* isolates collected from 3 host species in 4 countries: (15 from pigs: USA, Denmark, Brazil, 1 from a hamster: USA, and 1 from a horse: USA). Additionally, WGS was performed using a well-characterized PHE/MN1-00 strain cultured through 18 and 78 passages in vitro to identify potential genomic differences involved in the loss of virulence after several passages in vitro.

Results and Discussion

Through comparative genomic analysis, 4,219 core single nucleotide polymorphisms (SNPs) were identified across all 17 isolates. A single intergenic SNP was identified between the low- and high-passage PHE/MN1-00 strains. Eleven of the identified SNPs were predicted to be high impact (ie, stop codon gained or lost) and 7 of these were found in only the horse and/or hamster isolates. A maximum-likelihood phylogenetic tree demonstrated a single clade for all pig isolates and separate branches for the horse and hamster isolates, in agreement with a recent metagenomic analysis reporting a single clonal lineage in pigs.

Conclusion

Preliminary analyses have identified (SNPs) and distinct phylogenetic clustering according to host species. Further analyses are underway to better characterize the genetic diversity within origin and to clarify the epidemiologic relationship among isolates and different countries.

Keywords: Ileitis, Proliferative Enteropathy, Whole Genome Sequencing.

ACUTE REPRODUCTIVE DISORDERS IN IMPORTED HYPERPROLIFIC SOWS IN VIETNAM: A CASE REPORT WITH SUSPECTED *MYCOPLASMA SUIS* INVOLVEMENT

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Introduction and Objectives

Reproductive disorders are a major cause of economic loss in swine production. Although *Mycoplasma suis (M. suis)* is known to cause anemia and systemic illness, its involvement in acute reproductive failure of hyperprolific sows remains poorly documented (Messick 2004; Bordin et al., 2021). In early 2023, a large commercial farm in Vietnam reported irregular return to estrus, reduced conception rates, mummification, stillbirths, and weak-born piglets.

Materials and Methods

The investigation was conducted on a 5,600-sow farrow-to-finish farm in Vietnam from March to September 2023. Farm production and health records were retrospectively reviewed to assess reproductive performance, including conception rate, farrowing, abortion, stillbirths, and mummified fetuses. Blood samples from affected sows (n = 7) and tissues from mummified (n = 4), and stillbirths (n = 3) were analyzed. PCR/RT-PCR assays targeted *M. suis*, PCV2, PCV3, PPV, PRRSV, CSFV, JEV, and PRV. Hematology and Giemsa-stained smears were examined for anemia and visualization of *M. suis* on erythrocytes. A partial 16S rRNA gene was sequenced for phylogenetic analysis. Supportive treatment included amoxicillin–tiamulin and adjusted management practices.

Results and Discussion

During the study period, 1,693 sows were monitored, of which 442 (26.10%) exhibited reproductive disorders. Irregular return to estrus and repeated insemination occurred in 9–16% of sows, predominantly at 3 - 5 weeks of gestation. Pregnancy failure was observed in 17% of sows, including 3% early losses at week 4, while sow mortality occurred between 13 and 16 weeks of gestation. Farrowing rates ranged from 72.20% to 76.30%, with an average of 8.90 live-born piglets, 4.80 mummified or stillborn fetuses, and 1.10 perinatal deaths per litter. PCV3 was detected in 2/7 (28.57%) blood, M. suis was detected in 100% (7/7) of sow blood samples, 25.00% (1/4) of mummified, and 33.33% (1/3) of stillbirths. All samples were negative for PCV2, PRRSV, PPV, PRV, CSFV, and JEV. Phylogenetic analysis showed 96.42 - 99.34% nucleotide identity with reference strains.

Conclusion

This study documents an acute reproductive disorder associated with *Mycoplasma suis* in a large commercial breeding herd. These findings highlight M. suis as an underrecognized reproductive pathogen and underscore the need for enhanced surveillance and targeted control strategies in high-performing sow herds.

Keywords: Co-infection, *Mycoplasma suis*, Porcine circovirus type 3, Reproductive failure.

Acknowledgements: The authors thank the Nong Lam University HCMC, Vietnam, for the support with providing testing facilities.

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SERODYAMIC PREVALENCE OF *LAWSONIA INTRACELLULARIS* IN TAIWAN

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Introduction and Objectives

Lawsonia intracellularis (LI) causes PE in pigs, manifesting in 3 forms: Acute, (PHE) usually seen at 4–12 weeks old, hemorrhagic diarrhea, sudden death; Chronic, (PIA) affects 6–20 weeks old, gray-green diarrhea, anorexia, growth retardation; and Subclinical, express as pigs with normal feces but reduced growth, persistent shedding (Campillo et al., 2021;). Previous surveys on the prevalence of LI in Taiwan include a 1997 report showing farm-level positivity rate of 30% (12/40) and a sample-level prevalence of 5.5% (31/560) (Chang et al., 1997). LI remains widespread in Taiwan. This study aims to assess current infection status and age-related serodynamics to guide vaccination timing.

Materials and Methods

Pig serum samples submitted to the Animal Disease Diagnostic Center of National Pingtung University in 2022 to 2025 from 11 Taiwanese pig farms located at Yunlin, Chiayi, Kaohsiung, and Pingtung provinces were used in the study. Samples include serum from Sows, 3, 8, 12, 16, 20 and 24 weeks age groups and a total of 70 serum samples per farm. 770 serum samples in total were tested using ELISA (AsurDx™ *Lawsonia intracellularis* Antibody Test Kit) with 99% sensitivity and 98.6% specificity. Data were analyzed and visualized using GraphPad Prism. Positivity rates across age groups and farms were compared using Chi-square test and Fisher's exact test, with $P < 0.05$ considered statistically significant.

Results and Discussion

Results show all 11 farms showed positivity in LI antibody with 36.6% (274/770) of the samples turning out positive. Sows have the highest positivity of 78.2% while piglets show increase positivity while they age. Significant differences in positivity rate at younger age (3-8 weeks) when compared to older (20-24 weeks). Positivity rate was observed in this study to begin at 12 weeks of age. Some of the farms showed early-stage infection, while others showed later stage infection of LI.

Conclusion

LI infection is widespread in Taiwan, with age-dependent prevalence and persistent circulation, indicating the need for targeted control measures especially before finishing stages and in sows. Future studies should include simultaneous fecal swab and serum sampling to identify infection sources and enable targeted interventions at specific production stages.

Keywords: *Lawsonia intracellularis*, Lawsonia vaccination, Prevalence, Seropositivity.

PREVALENCE OF *LAWSONIA INTRACELLULARIS* ON THAI PIG FARMS FROM 2024 TO 2025

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Introduction and Objectives

Lawsonia intracellularis is an obligate intracellular bacterium and the causative agent of porcine proliferative enteropathy (PPE), one of the most prevalent enteric diseases in swine worldwide (Wattanaphansak et al., 2009). PPE occurs in three clinical forms: the hemorrhagic, chronic, and subclinical forms. This study aimed to determine the prevalence of *L. intracellularis* in Thai pig farms by detecting serum antibodies using the immunoperoxidase monolayer assay (IPMA) technique.

Materials and Methods

A total of 439 serum samples were collected from pigs on 14 commercial farms across Thailand between 2024 and 2025. Samples were processed following routine procedures, and serum was stored at -20°C until analysis. Antibodies against *L. intracellularis* were detected using the immunoperoxidase monolayer assay (IPMA), with samples showing specific intracellular staining classified as positive. Statistical analyses were performed using SAS version 9.4. Prevalence at the farm and individual levels was calculated, and differences among farms and pig age groups were evaluated using the Chi-square test.

Results and Discussion

Antibodies against *L. intracellularis* were detected on 12 of the 14 farms, giving a farm-level prevalence of 85.7%. Herd prevalence varied markedly from 0% to 100% ($P < 0.001$). At the individual level, 242 of 439 samples (55.1%) tested positive. Seroprevalence differed significantly among age groups ($P < 0.001$): 74.7% in breeders (56/75), 53.9% in fatteners (132/245), 0% in nursery pigs (0/45), and 100% in pigs of unknown age (49/49). These variations indicate heterogeneous exposure to *L. intracellularis* across farms and age groups. The absence of antibodies in nursery pigs suggests minimal early exposure, while higher prevalence in older pigs reflects increased infection pressure with age. These results emphasize the need for targeted control measures, including strengthened biosecurity and strategic vaccination, to mitigate subclinical infections and associated production losses.

Conclusion

This study confirmed the high prevalence of *L. intracellularis* on pig farms in Thailand. As PPE is an economically important disease, vaccination of sows and piglets against *L. intracellularis* is recommended for improved disease control.

Keywords: Ileitis, IPMA, *Lawsonia intracellularis*, Porcine proliferative enteropathy.

Acknowledgements: The authors thank Boehringer Ingelheim Animal Health (Thailand) Ltd. for their support in providing facilities.

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SAFETY AND EFFICACY OF A BIVALENT VACCINE FOR THE CONTROL OF *MYCOPLASMA HYOPNEUMONIAE* IN SPF PIGS

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Introduction and Objectives

Mycoplasma hyopneumoniae (*M. hyopneumoniae*) is a major pathogen of porcine enzootic pneumonia and a key component of the porcine respiratory disease complex (PRDC) (Maes et al., 2018). Vaccination is the primary strategy for disease control. However, clinical evidence regarding single-dose *M. hyopneumoniae* and porcine circovirus type 2 (PCV2) bivalent vaccines against Taiwanese *M. hyopneumoniae* strain remains limited. Therefore, the aim of this study is to evaluate the safety and efficacy of a *M. hyopneumoniae* and PCV2 bivalent vaccine against *M. hyopneumoniae* using a challenge model.

Materials and Methods

Fourteen 3-week-old specific-pathogen-free (SPF) pigs were randomly assigned to vaccinated (1 mL, Circo/MycoGard® One-Time, *M. hyopneumoniae* + PCV2 bivalent vaccine, n = 6), control (1 mL sterile saline, n = 6), or high-dose vaccinated groups (5 mL, n = 2) for safety and efficacy evaluation. Pigs were intratracheally challenged with 2 × 108 color-changing units of *M. hyopneumoniae* FL04-4 at 28 days post-vaccination (dpv). Body temperature, body weight, serological, and pathological parameters were assessed (Goodwin et al., 1969).

Results and Discussion

No systemic reactions or abnormal fever was observed after vaccination. The seropositive rate reached 100% in vaccinated group at 28 dpv, whereas the control group remained 0%. Following the challenge, vaccinated pigs exhibited significantly higher antibody titers at 28 (1.22 ± 0.47 vs 0 ± 0), 42 (1.87 ± 0.39 vs 0.02 ± 0.05) and 63 dpv (2.45 ± 0.53 vs 0.57 ± 0.54) compared with controls ($P < 0.05$). The gross lung lesion scores of the vaccinated group (3.5 ± 3.62) were significantly lower than the control group (14.83 ± 10.19, $P < 0.05$), demonstrating protective immune responses against *M. hyopneumoniae*.

Conclusion

This bivalent vaccine is safe and effective against *M. hyopneumoniae* challenge, supporting its potential application for the control of porcine enzootic pneumonia and PRDC.

Keywords: Bivalent vaccine, *Mycoplasma hyopneumoniae*, Vaccination.

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SEASONAL INFLUENCE ON THE PREVALENCE OF *LAWSONIA INTRACELLULARIS* IN COMMERCIAL SWINE HERDS IN THAILAND

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Introduction and Objectives

Lawsonia intracellularis is the causative agent of porcine proliferative enteropathy (PPE), an important enteric disease in swine worldwide (Wattanaphansak et al., 2009). In Thailand, seasonal changes, hot, rainy, and cool periods, may influence pathogen survival. Understanding these seasonal patterns is important for improving surveillance, vaccination timing, and farm management. This study aimed to determine the prevalence of *L. intracellularis* in Thai pig farms and assess seasonal influences using the immunoperoxidase monolayer assay (IPMA).

Materials and Methods

A total of 1180 serum samples were collected from pigs on 33 commercial farms across Thailand between 2024 and 2025. All samples were analyzed for antibodies against *L. intracellularis* using the IPMA. To assess seasonal effects, samples were grouped into hot, rainy, or cool seasons based on collection dates. Statistical analyses were performed using SAS 9.4, and differences in prevalence among seasons and pig age groups were evaluated using the Chi-square, with significance at $P < 0.05$.

Results and Discussion

Antibodies against *L. intracellularis* were detected on 31 of the 33 farms, resulting in a farm-level prevalence of 93.9%. Herd-level seroprevalence varied markedly, ranging from 0% to 95.0% ($P < 0.001$), indicating substantial differences in infection pressure among farms. At the individual-animal level, 506 of the 1180 serum samples (42.9%) tested positive. Seroprevalence differed among pig age groups ($P < 0.001$). Antibodies were detected in 43/60 breeders (71.7%), 276/620 fatteners (44.5%), 109/280 nursery pigs (38.9%), and 30/40 pigs of unknown age (75.0%). Seasonal variation was also evident ($P < 0.001$). The prevalence of *L. intracellularis* was 38.0% (213/560) in the cool season, 26.0% (39/150) in the hot season, and highest during the rainy season at 54.0% (254/470). These findings indicated the multifactorial of *L. intracellularis* transmission, age and seasonal factors contributing to exposure risk.

Conclusion

L. intracellularis is highly prevalent in Thai pig farms, with variation among herds, production stages, and seasons. The rainy season showed the highest exposure risk, it needs enhanced biosecurity, hygiene, and vaccination efforts during this period. Control programs tailored to age-specific susceptibility and seasonal trends may improve disease management and reduce production losses from ileitis.

Keywords: Ileitis, IPMA, *Lawsonia intracellularis*, Porcine proliferative enteropathy.

Acknowledgements: We thank MSD Animal Health for their assistance and provision of facilities.

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COMPARATIVE EFFICACY OF FLORFENICOL PREMIX, DOXYCYCLINE, AND TILMICOSIN FOR THE CONTROL OF PORCINE RESPIRATORY DISEASE COMPLEX IN FATTENING PIGS

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Introduction and Objectives

Porcine Respiratory Disease Complex (PRDC) significantly impacts swine production. While the standard therapeutic label dose for Florfenicol is 200 ppm, this study evaluated the efficacy of a low-dose regimen (50 ppm, representing 25% of the standard dose) and a 100-ppm regimen, compared to Doxycycline and Tilmicosin, for the metaphylactic control of PRDC in commercial fattening pigs.

Materials and Methods

The study was conducted on two commercial farms with a history of PRRS-positive status, involving a total of 1,760 fattening pigs (12 weeks old). Metaphylactic treatment was initiated upon the detection of early respiratory signs (Baseline Coughing Index > 2.5). The population was distributed between Farm A (n = 1,200) and Farm B (n = 560). In each farm, pigs were randomized into four treatment groups for a 14-day medication period: Group 1 (Low-dose Florfenicol 50 ppm), Group 2 (Florfenicol 100 ppm), Group 3 (Doxycycline 200 ppm), and Group 4 (Tilmicosin 300 ppm). Respiratory health was assessed using the Coughing Index (CI) protocol adapted from Nathues et al. (2012). Trained observers recorded the frequency of coughing before (baseline) and 14 days after treatment. Mortality rates were recorded throughout the study. Data were analyzed using ANOVA within a Randomized Complete Block Design (RCBD).

Results and Discussion

In Farm A, characterized by a high mortality challenge, Florfenicol groups demonstrated superior survival rates. Mortality was lowest in the Florfenicol 100 ppm (0.3%) and Low-dose 50 ppm (0.7%) groups, significantly lower than Doxycycline (2.3%) and Tilmicosin (3.3%). In Farm B, characterized by a high respiratory morbidity, the Low-dose Florfenicol (50 ppm) group showed the greatest clinical improvement, achieving a 4.5% reduction in Coughing Index compared to baseline, followed by Doxycycline (-3.1%). Conversely, the Tilmicosin group showed an increase in the Coughing Index (+1.0%). These results align with previous findings that Florfenicol, even at a reduced dosage of 50 ppm, effectively mitigates respiratory lesions and clinical signs associated with PRDC pathogens.

Conclusion

In-feed Florfenicol demonstrated superior efficacy over Doxycycline and Tilmicosin. Notably, the low-dose regimen (50 ppm) proved highly effective in reducing mortality and clinical signs, offering a cost-efficient alternative for metaphylactic strategies in high-challenge herds.

Keywords: Florfenicol, Fattening pigs, Metaphylaxis, PRDC.
Acknowledgements: We thank Thaifood group for their assistance and provision of facilities.

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EVALUATION OF MIXED HORSE AND CHICKEN SERA FOR *IN VITRO* CULTIVATION OF SWINE *MYCOPLASMA HYORHINIS* CLINICAL ISOLATES

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Introduction and Objectives

In vitro cultivation of swine *Mycoplasma hyorhinis* remains challenging because growth performance is strongly influenced by serum source, concentration, and isolate-dependent responses. Building on single-serum optimization, this study evaluated whether mixed horse serum (HS) and chicken serum (CS) formulations could improve growth robustness and/or kinetics, particularly for fastidious isolates.

Materials and Methods

Four *M. hyorhinis* clinical isolates (Strains A - D) were cultured in modified Friis medium supplemented with twelve serum formulations, including single-serum (10% - 30% HS or CS) and mixed-sera (HS+CS in varying ratios). Growth performance was assessed by final titers and growth kinetics (time-to-detection to 10^4 CCU/mL) over a 30-day observation period.

Results and Discussion

Overall, 20% horse serum served as the optimal single-serum reference for most isolates; however, mixed-sera formulations provided compensatory benefits for fastidious strains. The most fastidious isolate (Strain D) showed minimal growth in single-serum media, whereas all mixed-sera groups reached the detection threshold and achieved final titers up to 10^8 CCU/mL within 12 days. Notably, adding chicken serum under low HS (10%) conditions consistently increased final yields and/or shortened the time-to-detection (to 10^4 CCU/mL).

Conclusion

Mixed HS and CS supplementation provides a strain-dependent advantage that improves cultivation reliability under suboptimal conditions and can rescue fastidious *M. hyorhinis* isolates. A pragmatic approach is to use 20% HS for routine culture and apply mixed-serum formulations when isolates grow poorly or require faster detection.

Keywords: Chicken serum, Horse serum, *Mycoplasma hyorhinis*, Mixed sera, Modified Friis medium.

EVALUATION OF PRODUCTION PERFORMANCE IN PIGLETS VACCINATED AGAINST SUBCLINICAL EDEMA DISEASE

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Introduction and Objectives

Verotoxins produced by specific strains of *Escherichia coli* (VTEC) are responsible for disease in both humans and animals. In pigs, these toxins trigger extra-intestinal manifestations leading to Edema Disease (ED) (Bertschinger et al., 1992). Beyond clinical cases, subclinical VTEC infections can also impair performance, causing substantial productive losses despite absence of visible edema (Hernandez-Garciaet al., 2025; Gordon et al., 1995). This highlights importance of preventive strategies targeting both clinical and subclinical forms. The study was to assess production performance on piglets vaccinated with a commercial recombinant Verotoxin vaccine.

Materials and Methods

A Taiwanese wean-to-finish farm, total of 39 consecutive batches was included in the study. ED was diagnosed with dead pigshowinged typical lesions in June 2023. Verotoxin 2e (Vt2e) was detected in isolated *Escherichia coli*. Of the 39 batches, 20 batches (Group A [GA]; 8,041 pigs; April 2024 to May 2025) originated from piglets vaccinated at 2 days-old with 1 mL of VEPURED® (HIPRA), whereas 19 batches (Group B [GB]; 7,738 pigs; March 2023 to March 2024) originated from unvaccinated piglets. Following parameters were recorded: body weight at entry (9 weeks-old), slaughter weight, feeding days, mortality rate, average daily gain (ADG), and feed conversion ratio (FCR). All indicators were analyzed using logistic or linear regression models performed in R software (v. 4.5).

Results and Discussion

GA had a higher entry weight (20.57 ± 2.68 kg) than GB (18.52 ± 2.64 kg) ($P = 0.021$). Slaughter weight was also higher in GA (123.33 ± 2.81 kg) than in GB (120.12 ± 5.05 kg) ($P = 0.018$). GA showed increased ADG of 0.78 ± 0.06 kg/day than 0.72 ± 0.06 kg/day in GB ($P = 0.001$). Feeding days were lower in GA (130.33 ± 9.43 days) than in GB (140.59 ± 7.61 days) ($P < 0.001$). Mortality was also lower in GA ($5.22 \pm 1.78\%$) than GB ($6.90 \pm 3.21\%$) ($P < 0.01$). No significant differences in FCR were detected between the two groups. When the observed parameters were translated into economic outcomes, GA achieved an additional net return of 228.7 NTD (6.14 €) per pig compared with GB.

Conclusion

In a farm with a previous history of ED, batches of piglets from a vaccination period showed improved productive and survival parameters compared with batches from a previous non-vaccinated period. These findings are observational and should not be interpreted as evidence of causality.

Keywords: ADG, Edema Disease, FCR, Slaughterhouse, VEPURED®.

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MOLECULAR GENOTYPING AND QUANTIFICATION OF *ESCHERICHIA COLI* VIRULENCE FACTORS IN SWINE FECAL SWABS

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Introduction and Objectives

Enteric colibacillosis, caused by pathogenic *Escherichia coli*, is the most common enteric disease in post-weaning pigs and a major economic burden due to morbidity, mortality, and reduced performance. Because *E. coli* virulence is mediated by multiple fimbrial and toxin genes, rapid detection of these targets is critical for characterizing pathogen diversity and informing mitigation strategies. The objective of this study was to develop and evaluate a quantitative PCR (qPCR) assay for the detection and quantification of *E. coli* and selected virulence genes in swine fecal swab samples.

Materials and Methods

The study included synthetic DNA controls (gBlocks), hemolytic and non-hemolytic *E. coli* cultures (10^9 CFU/mL; n = 14), closely related bacterial species (n = 14), and diagnostic fecal swab samples submitted to the Iowa State University Veterinary Diagnostic Laboratory (n = 575). Nucleic acids were extracted using the MagMAX™ Pathogen RNA/DNA Kit on the KingFisher™ Apex system. Custom primers and probes targeting fimbrial and toxin genes (F18, K88, Stx2e, STa, LTB) and the *E. coli* housekeeping gene *uidA* were used. The 384-well qPCR assays were performed with TaqMan™ Fast Virus 1-Step Master Mix on a QuantStudio™ 7 Pro, and the results were compared with culture, gel-based PCR, and MALDI-TOF analysis with statistical evaluation in GraphPad Prism.

Results and Discussion

No amplification was observed in closely related bacterial species, and non-hemolytic *E. coli* for all targets except *uidA*. Analytical sensitivity ranged from 6.25-25 copies/µL (Cq 35–38). Absolute quantification was based on standard curves generated from gBlocks and cultured *E. coli* (slopes -3.0 to -3.6), with relative quantification normalized to uidA. The *uidA* gene was detected in 545/575 fecal swab samples, with absolute quantification ranging from 79 (K88) to 10^{10} copies/mL (F18), and a greater proportion of F18-positive samples exhibited higher relative quantification values. Findings were concordant with culture and MALDI-TOF, identifying a hemolytic E. coli strain (F18, Stx2e, STa, LTB) with greater sensitivity than conventional methods.

Conclusion

The newly established qPCR assay demonstrates high sensitivity and enables estimation of *E. coli* levels in fecal swabs; however, interpretation of results requires clinical correlation, and studies are underway to establish clinically meaningful Cq thresholds.

Keywords: *E. coli*, Enteric colibacillosis, Edema disease, Post-weaning diarrhea.

Acknowledgements: The authors thank the ISU-VDL molecular and bacteriology section for providing the diagnostic samples.

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PARASITIC INFECTION MANAGEMENT ON KRŠKOPOLJE PIG FARMS IN SLOVENIA: A CROSS-SECTIONAL SURVEY REVEALS KNOWLEDGE–PRACTICE GAPS

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Introduction and Objectives

The Krškopolje pig is the only preserved indigenous pig breed in Slovenia. The aim of this study was to assess current practices, knowledge, and diagnostic behavior related to parasitic infections among farmers raising the Krškopolje pig breed.

Materials and Methods

A cross-sectional survey was conducted among 33 pig farmers. Data were collected across nine thematic domains: farmer demographics, farm characteristics, parasite occurrence and severity, treatment practices, diagnostic approaches, awareness of anthelmintic resistance, veterinary involvement, seasonal patterns, and farmers' knowledge and perceptions.

Results and Discussion

Respondents were predominantly male (81.8%), aged 40–60 years (51.5%), with varying levels of farming experience. The primary sources of information were personal experience (54.5%) and veterinarians (63.6%). Most farms were intensive (51.5%) or ecological (30.3%), with 39.4% keeping 31 - 100 pigs and 54.5% maintaining 1 - 5 breeding sows. Clinical signs of parasitic infection in the past 12 months were observed by 18.2% of farmers. Parasites were considered a non-serious problem by 51.5% of respondents, while 27.3% reported never detecting parasitic issues. Regular scheduled deworming was practiced by 54.5% of respondents, mainly using macrocyclic lactones (24.2%), followed by piperazine (18.2%), benzimidazoles (9.1%), and levamisole (3.0%); however, 45.5% of respondents did not specify the active substance used. Regarding perceptions of antiparasitic drug efficacy, 51.5% of respondents believed these drugs are less effective today, 36.4% considered them as effective as in the past, and 12.1% did not express an opinion. Pre-farrowing deworming was performed in only 36.4% of herds. Laboratory diagnostics prior to treatment were considered necessary by 51.5% of respondents. Parasitological fecal examinations were conducted by 24.3% of farmers, while post-treatment efficacy monitoring was reported by 42.4%. Seasonal variation in parasite pressure was not perceived by 33.3% of farmers. Education and training (24.2%), professional consulting (27.3%), and diagnostic support (21.2%) were identified as priority needs.

Conclusion

Although farmers demonstrate a strong theoretical understanding of parasite management principles and antiparasitic resistance, systematic diagnostic practices are largely lacking. This discrepancy between knowledge and practice, combined with reliance on empirical treatment and limited efficacy monitoring, represents a substantial risk for the development and spread of anthelmintic resistance.

Keywords: Anthelmintic resistance, Farm management, Krškopolje pig, Parasitic infections, Parasite control.

MYCOPLASMA HYOPNEUMONIAE QUANTIFICATION DEPENDING ON THE VACCINATION STATUS OF PIGS

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Introduction and Objectives

Mycoplasma hyopneumoniae (*M. hyo*) is a dose dependent pathogen (Marois et al., 2010), making its quantification a useful information for veterinarians. Therefore, this work aims to report a descriptive Mhyo quantification study depending on the pig vaccination status.

Materials and Methods

This work was conducted within the context of two parallel randomized field trials designed to compare a new PCV2-*M. hyo* combination vaccine, CIRBLOC M Hyo (A), with competitor vaccines (B or C). Five batches (F1α/F1β/F1γ/F2α/F2β) of piglets individually ear tagged from two farms (F1, F2) were included. To document those trials, a focus population of 40 piglets per batch have been randomly selected at weaning (10 non-vaccinated (NV), 15 vaccinated with A, 15 with B or C) and sampled four times using deep tracheobronchial swabs (TBS) to describe *M. hyo* infection dynamic. This work focused on the final sampling at 22 weeks of age (woa) with individual *M. hyo* qPCR quantification. The selected criteria were the average *M. hyo* load expressed in $\log_{10}$ *M. hyo* copies/ml. Although the study involved 40 pigs per batch, statistical power was limited due to cost and ethical constraints on increasing sample size.

Results and Discussion

At weaning, all pools of 3 TBS samples were negative. At 22 woa, Mhyo presence varied a lot depending on farm and batch, from one batch nearly negative (F1γ; 0.1 Log_{10} copies; excluded from study) to a fully positive one (F2β; 6.5 Log_{10} copies). F1α-F1β batches showed similar load and were aggregated for analysis: A 2.32 Log_{10} copies / B 3.05 Log_{10} copies / NV 3.36 Log_{10} copies. F2 batches displayed greater heterogeneity. F2α: A 3.72 Log_{10} copies / C 4.20 Log_{10} copies / NV 4.17 Log_{10} copies. F2β : A 5.79 Log_{10} copies / C 6.83 Log_{10} copies / NV 7.24 Log_{10} copies. As expected, differences were not significant, but it is noticeable that each time the quantification of A group was 0.5 to 1 Log lower than the competitor vaccinated group and NV group showed the highest loads.

Conclusion

This work highlights variation of Mhyo batch loads and argues for the benefit of vaccination to reduce it.

Keywords: *Mycoplasma hyopneumoniae*, quantification, vaccination

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SEASONALITY OF *MYCOPLASMA HYOPNEUMONIAE* AND *ACTINOBACILLUS PLEUROPNEUMONIAE* LUNG LESIONS IN TAIWANESE SWINE FARMS: A 2021–2024 LONGITUDINAL SLAUGHTERHOUSE SURVEY

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Introduction and Objectives

Respiratory diseases, particularly those associated with *Mycoplasma hyopneumoniae (M. hyo)* and *Actinobacillus pleuropneumoniae* (APP), remain a primary cause of economic loss in Taiwan. While pathogen prevalence is documented, seasonal dynamics in this subtropical climate remain less defined. This study evaluated seasonal fluctuation of Enzootic Pneumonia (EP) and APP-indices in central and southern Taiwan from 2021 to 2024.

Materials and Methods

Slaughterhouse lung scoring followed the Ceva Lung Program (CLP) methodology. Data (2021 - 2024) from 12 central and southern Taiwanese farms were analyzed. To minimize variation, specific farm audits were performed by the same auditor. In total, 2,746 lungs were audited (minimum 14/farm/season). Seasons were defined as Winter (Dec - Feb), Spring (Mar - May), Summer (Jun - Aug), and Autumn (Sep - Nov). EP (Mhyo-like) and APP (APP-like) indices were calculated.

Results and Discussion

The aggregated data revealed distinct seasonal patterns. The EP Index peaked in Winter (Mean = 7.03), declining through Spring (5.67) and Summer (4.99) to an Autumn nadir (4.48). Notably, high-challenge farms (e.g., Farm 9 and 11) showed Winter EP indices > 10.0. Seven farms conformed to this winter-peak EP decline; the other five showed counter-seasonal patterns, peaking in Spring/Summer or rebounding later. Conversely, the APP Index (APPI) peaked in Spring (Mean = 1.09) and Winter (1.02), with lower pressures in Summer (0.88) and Autumn (0.74). The APPI showed greater farm-to-farm variability than the EP index.

Conclusion

This study confirms a strong seasonality for respiratory lesions in Taiwanese herds. Mhyo pressure is most severe during Winter, likely driven by ventilation challenges and temperature fluctuations. APP pressure persists longer, peaking in Spring. These findings suggest that optimal climatic control and vaccination programs would be key to prevention of respiratory disease.

Keywords: *Actinobacillus pleuropneumoniae,* Lung lesions, *Mycoplasma hyopneumoniae*, Seasonality, Slaughterhouse survey.

DEVELOPMENT OF AN ENZYME-LINKED IMMUNOSORBENT ASSAY FOR SEROLOGICAL EVALUATION OF *MYCOPLASMA HYORHINIS* ANTIBODY

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Introduction and Objectives

Mycoplasma hyorhinis (Mhr) is a pathogen causing polyserositis and arthritis in afflicted pigs, resulting in retarded growth and low feed efficiency. Currently quantitative polymerase chain reaction (qPCR) remains a commonly used method for Mhr diagnosis. While an indirect enzyme-linked immunosorbent assay (ELISA) kit using Mhr whole bacteria as coated antigen was previously developed, its sensitivity in sera collected from pigs immunized with Mhr subunit vaccine was low. In the present study, the sensitivity and specificity of a recombinant protein-based ELISA, MHR-K1 ReberLISA, for Mhr-infected and subunit vaccine-immunized pigs were evaluated.

Materials and Methods

A recombinant protein MHR0625 was expressed in E. coli and used as coated antigen in MHR-K1 ReberLISA. A total of 49 samples (n = 18 for known Mhr negative samples; n = 38 for known Mhr positive samples) were analyzed to determine the S/P cut-off value. To test the sensitivity of this ELISA method, sera samples collected from clinically Mhr-infected pigs (n = 13) and pigs vaccinated with MRQ, a Mhr subunit vaccine, (n = 20) were analyzed.

Results and Discussion

Data from analyzing known Mhr negative and positive sera samples showed two distinct clusters, separating negative samples from the positive samples. After ROC curve analysis, setting S/P cut-off value at 0.3 yielded 100% sensitivity and specificity. All samples obtained from pigs vaccinated with MRQ were sero-positive 4 weeks after immunization and 12 known Mhr-infected samples were sero-positive. The specificity for testing clinical samples was 100% while the specificity was 95%. The one known Mhr-infected sample that did not sero-convert may also be due to unsuccessful infection.

Conclusion

Compared to whole bacteria-based ELISA kit, this recombinant protein-based MHR ELISA kit, MHR-K1 ReberLISA, should contribute to more sensitive detection of Mhr antibody associated with vaccination and Mhr infection.

Keywords: Antibody detection, ELISA, *Mycoplasma hyorhinis*, Recombinant protein.

EFFECT OF THE VACCINATION AGAINST SHIGA TOXIN 2E IN A PIGLET PRODUCING FARM WITH SUBCLINICAL OEDEMA DISEASE (OD) IN JAPAN

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Introduction and Objectives

Oedema disease (OD) of weaned piglets is caused by shigatoxigenic *Escherichia coli* (STEC), typically harbouring the stx2e gene and F18 adhesins. Aim of this study was to assess the effect of a commercially available oedema disease vaccine on zootechnical performance and mortality in a herd, in which circulation of STEC strains and subclinical form of OD have been identified.

Materials and Methods

Zootechnical performance (weight gain, kg) and mortality were compared between vaccinated and non-vaccinated control piglets in monocentric field efficacy study, which was performed using parallel, randomized design (within the litter randomization according to the birth order). In total, 11 litters were included, vaccinated group V (63 piglets), vaccination on 3.0 ± 1.4 days of age (DOA) by inactivated toxoid vaccine (Ecoporc Shiga®, Ceva Sante Animale, France) and control C, (64) piglets. Body weight was measured in 5-time intervals (at the start of the study (T0), 19 DOA (T1), 40 DOA (T2), 65 DOA (T3), 79 DOA (T4)). Circulation of STEC *E. coli* was confirmed just before the start of the study by isolation and strain characterization by PCR. Results were compared using Pearson Chi-square test or t-Student test. Significant differences were considered when $P < 0.05$.

Results and Discussion

Piglet weight in both groups did not differ at the start of the study and at weaning (T1) thus effect of vaccination can be evaluated for STEC *E. coli* sensitive period. Weight gain did not differ significantly at T2 and T3 time points. The significantly different weight gain (1.49 kg) was observed in favor of vaccinated group in the last period (T4) ($P < 0.05$), with trend in favor for vaccinated piglets in the entire study period (1.37 kg; $P = 0.09$). No clinical signs of OD or mortality related to the disease were observed during the study.

Conclusion

Positive effect of vaccination on zootechnical performance was confirmed in the herd without clinical form of OD and mortality associated with disease during the period of the late nursery, where negative effect of Stx2e toxin is expected. The vaccine was therefore effective also against subclinical OD under the conditions of this study.

Keywords: Oedema disease, STEC *E. coli*, Vaccination.

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EVOLUTION OF THE PREVALENCE AND SEVERITY OF LUNG LESIONS ASSESSED IN SLAUGHTERHOUSES IN SPAIN FROM 2016 TO 2025

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Introduction and Objectives

Slaughterhouse lung lesion scoring helps estimate respiratory disease prevalence. Common lesions include cranioventral bronchopneumonia linked to *Mycoplasma hyopneumoniae*, cause of Enzootic Pneumonia (Ep), and dorso-caudal pleuritis associated with any subclinical, subacute, acute, or chronic pleuropneumonic manifestation of *Actinobacillus pleuropneumoniae* (App). This study examines trends in prevalence and severity of Ep-like and App-like lesions in Spain since 2016.

Materials and Methods

A total of 1.309.726 lungs from 8.187 batches from farms across Spain were evaluated between 2016 and October 2025 using the Ceva Lung Program methodology, scoring for Ep-like lesions using modified Madec grid, and dorso-caudal pleurisy to evaluate App-like lesions. The following parameters were calculated at batch level:

Ep-like lesions: broncho-pneumonic lungs (BPL), and average affected surface (AAS).

Ap-like lesions: dorso-caudal pleuritis (DCP), and App index (APPI)

Trends were analysed using Spearman's correlation coefficient (r_s). Statistical difference was set at 0.05.

Results and Discussion

Prevalence (BPL) and severity (AAS) of Ep-like lesions showed a progressive negative correlation over the years (r_s = -0.28; $P < 0.001$) (r_s = -0.23; $P < 0.001$), respectively. BPL decreased from 49.96% (CI 95% = 47.91 - 52.01%) in 2016 to 29.78% (CI 95% = 28.43 - 31.13%) in 2025, while AAS declined from 3.8% (IC95% = 3.51 - 4.15%) to 1.93% (IC95% = 1.76 - 2.10%) over the same period.

In contrast, App-like lesions showed no consistent trend in either prevalence (r_s = 0.002; P = 0.87) or severity (r_s = 0.007; P = 0.55). Prevalence (DCP) fluctuated between 10.02% (CI 95% = 9.26 - 10.78%) and 23.22% (CI 95% = 22,27 - 24,17%), and severity (APPI) ranged from 0.29 (CI 95% = 0.27 - 0.31) to 0.60 (CI 95% = 0.58 - 0.63) without a clear pattern.

Conclusion

EP control has improved over time, likely reflecting more effective prevention strategies. A temporary increase in EP-like lesions during 2021 - 2022 may relate to severe PRRS outbreaks caused by the Rosalia strain, which strongly affected farms in North-East Spain, the country's region with the highest pig density. In contrast, no consistent trend was observed for DCP, possibly due to the wide diversity of App serotypes and their variable control measures, highlighting the need for continuous surveillance, and improved preventive measures, better vaccination protocols.

Keywords: *Actinobacillus pleuropneumoniae*, CLP, Lung lesions, *Mycoplasma hyopneumoniae*, vaccination.

SEASONALITY AND INCIDENCE OF SLAUGHTERHOUSE-ASSESSED LUNG LESIONS IN SPAIN

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Introduction and Objectives

Respiratory diseases in pigs are multifactorial. Slaughterhouse lung lesion scoring provides insights into the incidence and severity of Enzootic pneumonia (Ep)-like lesions, and dorso-caudal pleurisy, associated with any pleuropneumonic manifestation of *Actinobacillus pleuropneumoniae* (App). This study aimed to evaluate the influence of seasonality on lung lesions detected at slaughter.

Material and methods

A total of 8,187 batches, 1,309,726 lungs, were assessed in slaughterhouses across Spain between January 2016 and October 2025. Four seasonal groups were defined based on slaughtering period: 1. January - March (n = 2189), 2. April - June (n =1709), 3. July - September (n = 1742), 4. October - December (n = 2547).

Lungs were scored using Ceva Lung Program methodology. The following parameters were calculated at batch level. Ep-like lesions: broncho-pneumonic lungs (BPL), average affected surface (AAS); Ap-like lesions: dorso-caudal pleurisy (DCP), severity index (APPI).

Statistical comparisons were performed using the Kruskal-Wallis test with pairwise comparisons; significance was set at $P < 0.05$.

Results and Discussion

In seasonal group-1 was determined a BPL prevalence of 36.35% (Confidence Interval 95% (CI 95%) = 35.00 - 36.35%); with AAS of 2.41% (CI95% = 2.30 - 2.53%); DCP prevalence of 19.88% (CI 95% = 19.18 - 20.58%); and APPI of 0.54 (CI95% = 0.52 - 0.56)). In seasonal group-2 was determined a BPL prevalence of 33.40% (CI 95% = 32.34 - 34.46%); with AAS of 2.17% (CI 95% = 2.04 - 2.29%); DCP prevalence of 15.82% (CI 95% = 15.15 - 16.48%); and APPI of 0.44 (CI 95% = 0.42 - 0.46)). In seasonal group-3 was determined a BPL prevalence of 34.4% (CI 95% = 32.97 - 35.11%); with AAS of 2.57% (CI 95% = 2.43 - 2.72%); DCP prevalence of 15.82% (CI 95% = 15.17 - 16.46%); and APPI of 0.45 (CI 95% = 0.43 - 0.46). Finally, in seasonal group-4 was determined a BPL prevalence of 37.83% (CI95% = 36.90 - 38.75%); with AAS of 2.61% (CI 95% = 2.50 - 2.72%); DCP prevalence of 17.28% (CI 95%= 16.67 - 17.90%); and APPI of 0.46 (CI 95% = 0.44 - 0.47)). Statistically significant differences in BPL prevalence were found between groups 1 and 2 ($P < 0.001$), groups 1 and 3 ($P < 0.05$) and group 4 versus groups 2 and 3 ($P < 0.001$). For AAS, significant differences were observed between group 4 and groups 1 ($P < 0.05$) and 3 ($P < 0.001$). Regarding App-like lesions, both prevalence and severity were significantly higher ($P < 0.001$) in group 1 compared to groups 2, 3 and 4.

Conclusion

EP-like lesions were more prevalent in colder months; severity peaked mid-year. App-like lesions were highest early in the year. However, seasonal differences were minimal and clinically irrelevant.

Keywords: *Actinobacillus pleuropneumoniae*, CLP, Lung lesions, *Mycoplasma hyopneumoniae,* vaccination.

RELATIONSHIP BETWEEN ANTIBODIES AGAINST *ACTINOBACILLUS PLEUROPNEUMONIAE* TOXINS IN SOWS AND THEIR PIGLETS AT 24 HOURS OF LIFE

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Introduction and Objectives

Swine pleuropneumonia, caused by *Actinobacillus pleuropneumoniae* (App), involves several virulence factors, notably the ApxI–IV toxins. This study aimed to assess, in an App-positive herd, the antibody levels and distribution against these toxins in 24-hour-old piglets, and their correlation with maternal antibody levels.

Materials and Methods

In an App-endemic commercial farm, 42 piglets from 7 different parity sows were randomly selected and ear tagged. Blood serum samples were taken from piglets at 24 hours of life and from their respective mothers. These samples were analysed through four enzyme-linked immunosorbent assay (ELISA) tests against Apx toxins I, II, III (in-house ELISA), and IV (IDEXX APP-ApxIV Ab, Idexx, USA), expressing the results in S/P value. Correlations were analysed using Spearman's correlation coefficient (rs), and statistical difference was set at 0.05.

Results and Discussion

In piglets at 24 hours of life, S/P ratios were detected at the following values for ApxI: 0.733 (IC 95% = 0.505 - 0.960), ApxII: 2.907 (IC 95% = 2.654 - 3.160), ApxIII: 1.098 (CI 95% = 0.956 - 1.241), ApxIV: 1.677 (CI 95% = 1.555 - 1.800). In their mothers, S/P ratio values were ApxI: 0.541 (CI 95% = 0.126 - 0.956), ApxII: 2.377 (CI 95% = 1.717 - 3.037), ApxIII: 0.913 (CI 95% = 0.425 - 1.402), and ApxIV: 1.412 (CI 95% = 0.965 - 1.859). The first parity sow was seronegative for ApxI and ApxIV in these tests. A positive correlation was determined for all types of antibodies ($P < 0.001$): ApxI (rs = 0.696), ApxII (rs = 0.738), ApxIII (rs = 0.613), and ApxIV (rs = 0.496).

Conclusion

In all cases, differences in maternal antibody levels determined the concentration and uniformity of antibodies in 24-hour-old piglets, reflecting the sow's exposure to *A. pleuropneumoniae* and its toxins. The ApxI, -II, and -III anti-toxin antibodies may also originate from bacteria other than App. A seronegative sow was detected at her first farrowing, resulting in piglets with very low antibody titers against *A. pleuropneumoniae* and an increased risk of early clinical outbreaks.

Keywords: App, Apx, *Actinobacillus pleuropneumoniae,* Colostral antibodies, MDA.

DETECTION OF APXII-TOXIN ANTIBODIES IN A FARM NEGATIVE TO *ACTINOBACILLUS PLEUROPNEUMONIAE*

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Introduction and Objectives

Swine pleuropneumonia is caused by *Actinobacillus pleuropneumoniae* (App) through different toxins and other virulence factors. Among toxins, ApxI-III toxins are considered the most relevant virulence factors of this pathogen. ApxIV is mainly used for diagnostic purposes. The objective of this work was to determine in a negative herd the presence of antibodies against the different Apx toxins of App, given that ApxI-III are non-App specific, while ApxIV has been described as App-specific.

Materials and Methods

In a negative commercial farm, 42 piglets were randomly selected and ear tagged. Blood serum samples were taken in the 4th and 10th weeks of life. These samples were analysed through four enzyme-linked immunosorbent assay (ELISA) tests against Apx toxins I, II, III (in-house ELISA), and IV (IDEXX APP-ApxIV Ab (Idexx, USA)), expressing the results in S/P value and positive frequency (%). The cut-off value for ApxI-III ELISA was set up at 0.3 and for ApxIV at 0.5.

Results and Discussion

In S/P ratio, at 4 weeks of life were detected the following values for ApxI: 0.000 (CI 95% = 0.000 - 0.000), ApxII: 0.416 (CI 95% = 0.229 - 0.604), ApxIII: 0.007 (CI 95% = 0.001 - 0.013), and ApxIV: 0.002 (CI 95% = 0.000 - 0.006). At 10 weeks of life were detected the following values for ApxI: 0.011 (CI 95% = 0.000 -0.021), ApxII: 0.596 (CI 95% = 0.365 - 0.827), ApxIII: 0.038 (CI 95% = 0.011 - 0.064), and ApxIV: 0.011 (CI 95% = 0.000 - 0.025). All animals were considered to be negative for Apx-I, -III and -IV antibodies; however, 51.3% of samples resulted positive for ApxII-toxin antibodies. The negative results obtained for ApxIV-toxin antibodies in all samples classify the farm as being negative for App. However, the presence of a high prevalence of ApxII-positive animals suggests that this farm could have been infected by other Apx toxin-producing bacteria, as *Actinobacillus porcitonsillarum*, given that it is the only known bacterium producing ApxII toxin without ApxI or III production.

Conclusion

These results also suggest a low specificity of ApxI-III ELISAs to define the App status of a farm, given that the presence of other ApxI-III producing bacteria could show false-positive results.

Keywords: ApxI, ApxII, ApxIII, ApxIV, App.

CONTROL OF EDEMA DISEASE IN PIGS BY SODIUM BENTONITE

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Introduction and Objectives

Edema disease (ED) caused by Shiga toxin-producing *Escherichia coli* (STEC) remains a significant cause of post-weaning mortality in pig farms. This study evaluated the efficacy of sodium bentonite (SB) supplementation for controlling ED in a farrow-to-finish farm (480 sows) where multiple feed additives had previously failed to reduce mortality. Prior to the ED outbreak, average piglet mortality was approximately 1%; after onset, mortality repeatedly exceeded 6% despite supplementation with probiotics (*Bacillus subtilis* C-3102; *Enterococcus faecium* T-110; *Clostridium butyricum* TO-A; *Bacillus subtilis* TO-A), antibacterial agents (Colistin and Tilmicosin), formic acid, alfalfa meal, and zinc oxide. SB is Na-type bentonite containing abundant Na^+ ions in the interlayer cations of montmorillonite. The objective of this study was to determine whether dietary SB could reduce mortality and growth retardation associated with ED.

Materials and Methods

After weaning, 672 piglets (223 test, 449 control) and 500 fattening pigs (212 test, 288 control) were included. The test group received feed supplemented with 0.4% SB from the weaning stage. Mortality during the fattening period and the incidence of stunted pigs (not reaching 115 kg at shipment) were recorded. STEC detection was performed using rectal feces from dead pigs and environmental samples. Mortality and stunting rates were compared between groups using chi-square or Fisher's exact tests ($P < 0.05$).

Results and Discussion

Mortality in the fattening barn was significantly lower in the SB group than in controls (2.4% [5/212] vs. 13.9% [40/288]; $P < 0.001$). The incidence of stunted pigs was reduced in the SB group (3.8% [8/212] vs. 7.3% [21/288]), although the difference was not statistically significant ($P > 0.05$). STEC was not isolated from diarrheic feces but was detected in rectal and floor fresh feces of dead pigs ($2.50 \times 10^5 \sim 1.50 \times 10^6$ cfu/g). These findings suggest that dietary SB supplementation from the post-weaning stage significantly reduces mortality associated with ED and may contribute to disease control in affected farms.

Keywords: Edema disease, Feed additives, Mortality rate, Shiga toxin-producing *Escherichia coli*, Sodium bentonite.

APPLICATION OF ORAL FLUIDS FOR SALMONELLA CHARACTERIZATION AND SURVEILLANCE IN COMMERCIAL FINISHER PIGS

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Introduction and Objectives

Salmonella is a widespread pathogen in swine populations and remains a challenge for herd health, productivity, and food safety (Schwartz et al., 2021). Although fecal culture is considered the standard diagnostic approach, oral fluids (OF) represent a practical, non-invasive, aggregated sample type that may enhance population-level surveillance (Prickett et al., 2010). The objectives of this study were to compare the probability of Salmonella detection between oral fluids and pooled pen-floor fecal (FP) samples under commercial field conditions, assess the feasibility of culturing Salmonella from OF, and compare serotypes recovered from both sample types.

Materials and Methods

The study was conducted on three commercial finisher sites in Iowa, each housing approximately 1,000 pigs across 48 pens. Seventeen pens per site (51 total) were randomly selected at approximately 11 weeks of age. Paired OF and FP samples were collected from each pen. OF samples were obtained using suspended cotton ropes exposed to pigs for 30 - 45 minutes, while FP samples consisted of composite material collected from five fresh floor locations per pen. All samples were cultured following sequential enrichment using Tetrathionate (TTB) and Rappaport–Vassiliadis (RV) broths and tested by real-time PCR (Naberhaus , et al., 2019). Agreement between sample types and between culture and enriched PCR was assessed, and detection probabilities were compared.

Results and Discussion

Culture detected Salmonella in 66.7% (34/51) of OF samples and 74.5% (38/51) of FP samples. Detection probabilities were 81% (95% CI: 44 - 96%) for FP and 66% (95% CI: 28 - 91%) for OF, with no statistical difference between sample types (P = 0.13). Sample types showed fair agreement (κ = 0.37; overall agreement = 72%). Direct PCR testing of raw samples was negative for both sample types (Ct > 34). PCR following enrichment showed substantial agreement with culture for FP samples (κ = 0.73; 92%) and near-perfect agreement for OF (κ = 0.91; 96%). Five Salmonella enterica serotypes were identified across sites.

Conclusion

OF demonstrated a comparable ability to detect and culture Salmonella at the pen level when compared with FP samples. These findings support OF as an alternative for Salmonella surveillance in commercial finisher pig populations when enrichment is incorporated into diagnostic workflows.

Keywords: Fecal samples, Oral fluids, Salmonella, Swine, Surveillance.

Acknowledgements: The authors acknowledge Boehringer Ingelheim Animal Health for supporting this study.

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REDUCING ANTIMICROBIAL RELIANCE AND ENHANCING GROWTH IN PRDC-AFFECTED PIGS THROUGH A COMPREHENSIVE MULTIVALENT VACCINATION STRATEGY

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Introduction and Objectives

PRDC is a major challenge in Mexican swine production due to pathogen co-circulation. This field trial evaluated the comparative performance of two immunization strategies in a commercial setting naturally challenged by multiple respiratory agents.

Materials and Methods

The study was conducted on a 1,500-sow farrow-to-finish farm positive for PRRSV, PCV2, SIV, *Glaesserella parasuis* (Gps), and *Actinobacillus pleuropneumoniae* (App). 475 weaned piglets were litter-matched into a Test (T) or Control (C) group. Group T was vaccinated at 5 and 8 weeks of age (WOA) with a multivalent vaccine (Suigen® Donoban 10) targeting *Mh, S. suis, P. multocida, B. bronchiseptica, Gps,* and *App* (serotypes 2, 5). Group C received a conventional protocol: Gps (2 and 4 WOA) and App (7 and 10 WOA). Both groups received a PCV1-2a/b + Mh vaccine at 3 WOA. Respiratory mortality, antimicrobial treatments, and weights (3 and 20 WOA) were recorded. Serology for ApxIV antibodies was performed at weaning and 20 WOA. Data were analyzed via Fisher's exact and t-tests.

Results and Discussion

Growth significantly improved in Group T, reaching 86.4 ± 9.3kg at 20 WOA vs 80.5 ± 13.4 kg in Group C ($P = 0.005$). Respiratory mortality showed a numerical reduction in Group T (11.1 vs 16.7%; $P = 0.085$), while antibiotic interventions decreased by 60% (93 vs 223 injections). Serologically, Group T exhibited significantly lower ApxIV titers at finishing (11.9 ± 13.3) than Group C (25.0 ± 23.1; $P = 0.01$), indicating superior App control. The broad-spectrum coverage of this multivalent strategy effectively mitigated poly-microbial impacts, outperforming the narrower protocol. Beyond clinical outcomes, consolidating protection into a single multivalent solution optimizes labor efficiency, enhances animal welfare by reducing handling stress, and strengthens on-farm biosecurity.

Conclusion

Implementing a comprehensive multivalent vaccine significantly improves weight gain and drastically reduces reliance on antimicrobials. Aligning the vaccination spectrum with the specific pathogen profile of Mexican field conditions is a critical factor for optimizing swine health and sustainable farm productivity.

Keywords: *Actinobacillus pleuropneumoniae*, Antimicrobial reduction, Growth performance, Multivalent vaccine, PRDC.

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PRELIMINARY STUDY OF ANTIMICROBIAL RESISTANCE OF *STAPHYLOCOCCUS HYICUS* ISOLATES ASSOCIATED WITH SWINE EXUDATIVE EPIDERMITIS IN QUEBEC, CANADA

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Introduction and Objectives

Staphylococcus hyicus is the etiological agent of exudative epidermitis (EE, Greasy pig disease) in suckling and weaned piglets. It is characterized by reddening and exfoliation of the skin, exudative pustules and crusts which may lead to mortality in severely affected pigs. Antimicrobial-resistant (AMR) strains could explain treatment failures reported by veterinarians. The objective of this study was to characterize AMR in *S. hyicus* isolates from EE clinical cases.

Materials and Methods

S. hyicus isolated in bacteriological culture from samples submitted by veterinarians between March 2021 and June 2023 in the two provincial laboratories were included. The reason for submission, the age category of the pig sampled, and *S. hyicus* Kirby-Bauer disc diffusion susceptibility results were extracted from the initial laboratory results form. In the presence of multiple isolates per production site, only the first was analyzed. The proportions of resistant isolates by antibiotic and of multidrug-resistant (≥ 3 antibiotic classes) were evaluated.

Results and Discussion

Antimicrobial resistance profiles of 28 EE *S. hyicus* isolates originating from sucking (64%) or weaned (36%) piglets of distinct production sites were described. Resistance to penicillin, ampicillin and tetracycline was observed in ≥ 50% and ≥ 80% of isolates from suckling and weaned piglets, respectively. In weaned piglets, 80% of isolates were resistant to clindamycin. Overall, 54% of the isolates were multidrug-resistant. No resistance was observed for enrofloxacin and ceftiofur. Intermediate susceptibility for neomycin, novobiocin and trimethoprim-sulfamethoxazole was observed on < 30% of the isolates.

Conclusion

Although only a few isolates exhibited intermediate susceptibility to antimicrobials commonly used for treatment of EE (e.g., neomycin), half isolates were multidrug-resistant, underscoring the need to develop alternative control strategies such as autogenous vaccine or phage therapy.

Keywords: Antimicrobial resistance, Canada, Exudative epidermitis, *Staphylococcus hyicus*.

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ORAL SALMONELLA VACCINATION: PRODUCTIVITY IMPROVEMENTS IN A WEAN TO FINISH SYSTEM IN COLOMBIA

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Introduction and Objectives

Porcine salmonellosis is a zoonotic disease of great global importance. It is caused by Salmonella and clinically manifests in pigs in two forms: the systemic presentation and the enteric presentation. The disease causes considerable production and economic losses to mitigate these losses; this study aims to demonstrate the efficacy of vaccination (Enterisol®Salmonella T/C) in a Wean-To-Finish production system in Colombia.

Materials and Methods

A total of 26 batches of 1400 piglets, 21 days old, were randomly assigned to vaccinated and unvaccinated groups for 2.2 years. Production data were collected from 13 unvaccinated batches (control group) and compared with the results from 13 batches vaccinated with a single 2 mL dose of Enterisol® Salmonella T/C (Boehringer Ingelheim) administered at 14 days of age (live attenuated vaccine administered by oral drench). The selected batches were kept under the same management and production conditions. Statistical analysis of the data was performed using Stata 17 software, employing the Student t-test or the Mann-Whitney U test to assess differences between the two treatment groups, and a $P < 0.05$ was reported.

Results and Discussion

The vaccinated group showed a final weight gain of 2.17 kg in the crude analysis. Adjusting the initial weight between the experimental groups to 5.97 kg and the number of days on the farm to 133 days, the vaccinated group was able to increase its final weight by 4.58 kg, showing a statistically significant difference in weight ($P < 0.042$) and days from Wean-To-Finish ($P < 0.008$). The feed conversion ratio (FCR) was 1.97 for the vaccinated pigs and 2.01 for the control group, with a numerical difference of -0.04, which may represent lower production costs.

Conclusion

The results obtained in this study, conducted under field conditions in Colombia, demonstrate that vaccination with Enterisol® Salmonella T/C improved production parameters such as average daily gain (+30 g/day), final weight (+2.17 kg), and feed conversion ratio (-0.04). These benefits, observed on the farm, translate into a positive return on investment for the producer. Through a holistic approach, it will be possible to achieve a sustainable impact, improving productivity and mitigating risks to public health.

Keywords: One health, Performance, Salmonella, Swine, Vaccine.

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COMPARISON OF MONOVALENT AND DIVALENT COPPER SOURCES ON IN VITRO ANTIBACTERIAL ACTIVITY AGAINST HEMOLYTIC *ESCHERICHIA COLI*

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Introduction and Objectives

Copper has long been recognized for its antimicrobial properties, yet the influence of copper valence on antibacterial efficacy remains insufficiently characterized in animal nutrition. Monovalent copper (Cu^{+}) has been suggested to exert stronger antimicrobial activity than divalent copper (Cu^{2+}), potentially offering improved control of enteric pathogens (Borkow, 2014). The objective of this study was to compare the in vitro antibacterial activity of a monovalent copper source with three different sources of divalent tribasic copper chloride (TBCC) against hemolytic Escherichia coli strains isolated from pigs.

Materials and Methods

The trial was conducted at IMUNOVA (Brazil) using a modified antimicrobial disk susceptibility test based on the Kirby–Bauer disk diffusion methodology. Hemolytic E. coli, a pathogenic strain associated with hemorrhagic diarrhea in swine, was cultured on Mueller - Hinton agar (pH 7.2 - 7.4). Plates were incubated for 16 - 18 hours at 35 ± 2°C. Standardized agar wells were prepared using a calibrated agar punch, which allowed a maximum and reproducible loading of 0.2 g of product per well; this amount was therefore used for all copper compounds. Three replicates were performed per treatment. Antibacterial efficacy was assessed by measuring the diameter of the inhibition zone, defined as the area showing no visible bacterial growth, using a pachymeter. Results were analyzed by one-way ANOVA using R studio.

Results and Discussion

The three divalent TBCC sources produced inhibition zones ranging from 13.8 to 16.2 mm, whereas monovalent copper generated the largest zone (18.1 mm). Treatment differences were significant ($P < 0.01$; RSEM = 1.08). Monovalent copper showed significantly greater inhibition than one TBCC source (TBCC 2), while the remaining TBCC sources were intermediate and did not differ statistically from either treatment. The enhanced antibacterial activity of monovalent copper may be associated with its higher redox reactivity and stronger interaction with bacterial membranes, promoting oxidative stress and cellular damage.

Conclusion

Monovalent copper demonstrated superior or comparable in vitro antibacterial activity against hemolytic *E. coli* compared with multiple TBCC sources, supporting its potential as a pathogen-control strategy in animal nutrition. Further in vivo validation is warranted.

Keywords: Antibacterial, Copper source, *E. coli*.

Acknowledgements: We gratefully acknowledge IMUNOVA (Brazil) for conducting the antimicrobial analyses.

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DEVELOPMENT AND APPLICATION OF A BLOCKING ELISA KIT FOR DETECTING ANTIBODIES AGAINST *LAWSONIA INTRACELLULARIS*

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Introduction and Objectives

Lawsonia intracellularis (LI) is the key pathogen causing Porcine Proliferative Enteropathy (PPE), which severely endangers the development of the swine industry (Arnold et al., 2019; Jensen et al., 2006). There is a lack of commercial blocking ELISA kits in China. This study aimed to develop an efficient and accurate blocking ELISA kit for detecting LI antibodies.

Materials and Methods

LI-OmpA recombinant protein, prepared and purified via a prokaryotic expression system as high-purity coating antigen, was used to immunize BALB/c mice. Positive hybridoma cell line 5F2 was established by cell fusion, screening and subcloning. HRP-labeled specific monoclonal antibody was prepared through periodate oxidation. The kit contained full components (antigen-coated plates, enzyme-labeled antibodies, controls, sample diluent etc.), with key parameters (coating concentration, reaction temperature/time) optimized.

Results and Discussion

This kit adopts a 2-fold diagnostic starting dilution for clinical sample detection. For sensitivity evaluation, positive serum after 2-fold initial dilution was further serially diluted, and the kit stably detected positive signals at a 8-fold secondary dilution. It had no cross-reactivity with positive sera of various common pathogens such as Classical Swine Fever Virus (CSFV) and Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), indicating strong specificity; Intra-batch CVs (0.8% ~ 9.8%) were < 10% and inter-batch CVs (1.0% ~13.56%) < 15%, reflecting excellent repeatability. When testing 150 clinical serum samples, the developed kit showed a concordance rate of 85.33% (128/150) with a commercially available indirect ELISA kit, with partial results exhibiting inter-assay variation between the two detection methods. The application of this test kit for dynamic detection of serum antibody levels in LI-challenged pigs demonstrated that antibodies started seroconversion to positive at 14 days post-challenge, and by day 28, all challenged pigs exhibited positive serum antibody results. These findings showed high concordance with IFA results (19/20) and indicated superior sensitivity compared to indirect ELISA (15/20).

Conclusion

The blocking ELISA kit developed in this study fills the gap in related fields in China, featuring simple operation and rapid detection, and provides a reliable tool for the serological diagnosis and immune prevention and control of LI infection.

Keywords: Blocking ELISA, *Lawsonia Intracellularis*, Monoclonal Antibody, OmpA, Serological Diagnosis.

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RAPID ASSESSMENT OF *CLOSTRIDIUM PERFRINGENS* INFECTION RISK IN PIG FARMS BY A HYDROGEN SULFIDE-BASED MEDIUM

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Introduction and Objectives

Clostridium perfringens is an important pathogen causing intestinal diseases in pigs, including necrotic enteritis in piglets and gas-bloating sudden death in sows, seriously affecting production efficiency (Liu et al., 2016; Zhang et al., 2022). Traditional detection relying on bacterial isolation and laboratory identification is cumbersome and time-consuming (2 - 3 days), failing to meet rapid assessment needs (Wu et al., 2023). Therefore, developing simple and rapid detection tools is of great significance. This study developed a selective medium based on *C. perfringens* metabolism of sulfur-containing compounds to produce hydrogen sulfide, which reacts with ferrous ions to form black ferrous sulfide precipitate. Bacterial load was quantified by precipitate formation time and intensity. Laboratory sensitivity tests, temperature optimization, and field validation were performed to establish a rapid detection method for clostridial infection.

Materials and Methods

Medium Preparation: The selective medium was formulated with sulfur-containing substrates and ferrous salts. 2) Sensitivity Testing: Ten-fold serial dilutions of C. perfringens (ATCC 13124) were inoculated to determine minimum detection limit. 3) Temperature Optimization: Cultures were incubated at 25°C, 37°C, 42°C, and 45°C to identify optimal conditions. 4) Field Validation: Fresh fecal samples from three pig farms (A, B, C) were cultured at 45°C and compared with PCR identification.

Results and Discussion

Laboratory sensitivity tests showed that the minimum detection limit of the medium was 1 - 5 CFU per inoculum, and 45°C was the optimal culture temperature. In pig farm validation, samples from Farm A showed no black precipitate at 6h (PCR-negative), while samples from Farms B and C produced precipitation at 2h (PCR-positive), confirming the detection sensitivity of the medium.

This medium enables rapid detection through the hydrogen sulfide-ferrous ion color reaction. Results can be determined within 2 - 6 hours at 45°C, providing technical support for pig farms to implement timely prevention and control measures.

Conclusion

This hydrogen sulfide-based medium enables rapid, sensitive, and cost-effective detection of *C. perfringens* in pig feces when cultured at 45°C. and assess clostridial infection risk in pig farms. It is easy to operate, and suitable for on-site screening in pig farms.

Keywords: *Clostridium perfringens,* Hydrogen sulfide-based medium, Pig farms, Rapid detection, Risk assessment.

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MOLECULAR CHARACTERIZATION AND ANTIMICROBIAL SUSCEPTIBILITY PROFILE OF CLINICAL STRAINS OF *STREPTOCOCCUS SUIS* ISOLATED IN BRAZIL

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Introduction and Objectives

Streptococcus suis colonizes the upper respiratory tract of pigs, but virulent strains can cause severe systemic disease and high mortality. In Brazil, outbreaks associated with serotype 9 have been increasingly reported since 2018 (Hammerschmitt et al., 2022). This study aimed to determine the serotype distribution of *S. suis* strains isolated from nursery piglets with clinical disease and to characterize their antimicrobial susceptibility profiles.

Materials and Methods

A total of 594 *S. suis* isolates obtained from systemic organs of 32 - 63-day-old piglets were analyzed. Isolates were collected between 2021 and 2024 from ten Brazilian states (Bahia, Espírito Santo, Goiás, Mato Grosso, Mato Grosso do Sul, Minas Gerais, Paraná, Rio Grande do Sul, Santa Catarina, and São Paulo). Colonies grown on blood agar were confirmed by PCR for genus and species (Ishida et al., 2014) and capsular type (Kerdsin et al., 2014). Antimicrobial susceptibility testing was performed in 374 isolates by disk diffusion against up to 12 antimicrobial agents, including amoxicillin, ceftiofur, doxycycline, tetracycline, florfenicol, fosfomycin, sulfamethoxazole-trimethoprim, tilmicosin, and tulathromycin.

Results and Discussion

Twenty-two serotypes were identified, representing 93.3% of isolates; 6.7% were non-typeable (NT). Serotype 9 was the most prevalent (55.7%), followed by serotypes 2 (8.6%), 14 (5.6%), and 7 (5.2%). The remaining serotypes (1, 1/2, 3, 4, 8, 11, 12, 15, 16, 18, 19, 21, 23, 24, 27, 28, 29, 31) were each detected at frequencies below 3%. Amoxicillin (79.7%) and fosfomycin (80.1%) showed the highest *in vitro* susceptibility rates. In contrast, high resistance rates were observed for tetracycline (93.4%), lincomycin (96.8%), tulathromycin (95.6%), tilmicosin (96.5%), and sulfamethoxazole-trimethoprim (83.3%), indicating widespread multidrug resistance.

Conclusion

Clinical *S. suis* infections in Brazilian nursery piglets are predominantly associated with serotype 9. The high frequency of antimicrobial resistance, including multidrug-resistant phenotypes, highlights the need for continuous molecular surveillance and improved preventive strategies.

Keywords: Antimicrobial resistance, Serotype, *Streptococcus suis*, Systemic disease.

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SEROVAR DISTRIBUTION, VIRULENCE, AND ANTIMICROBIAL SUSCEPTIBILITY OF *GLAESSERELLA PARASUIS* CLINICAL STRAINS FROM BRAZIL (2021–2024)

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Introduction and Objectives

Glaesserella parasuis is transmitted to piglets early in life (Cerdà-Cuéllar et al., 2010) and is the etiological agent of Glässer's disease (GD), a major cause of systemic infection and mortality in swine herds. Continuous surveillance is essential due to serovar diversity and increasing antimicrobial resistance. This study aimed to determine serovar distribution, assess the presence of the virulence-associated *vtaA* gene, and characterize antimicrobial susceptibility profiles of clinical *G. parasuis* strains isolated in Brazil between 2021 and 2024.

Materials and Methods

A total of 518 *G. parasuis* isolates were obtained from systemic sites of piglets diagnosed with GD in eight Brazilian states (Santa Catarina, Rio Grande do Sul, Paraná, Minas Gerais, Mato Grosso do Sul, São Paulo, Goiás, and Bahia). Samples were cultured on chocolate agar plates supplemented with NAD and glucose and incubated at 37°C under microaerophilic conditions. DNA was extracted after 24 - 48 hours and analyzed by PCR to confirm genus, species, and capsular type (Howell et al., 2015; Jia et al., 2017). All isolates were screened for the *vtaA* gene (Galofre-Mila et al., 2017) and tested for susceptibility to the main antimicrobials used in swine production.

Results and Discussion

Among typable isolates, serovar 12 was the most prevalent (29.3%), followed by serovars 4 (16%), 13 (8.5%), 5 (6.2%), 14 (6%), and 7 (4.6%). Serovars 1 (3.5%) and 2 (3.3%) were less frequent, whereas the remaining serovars (3, 6, 9, 10 and 11) were each detected at frequencies below 1%. Non-typeable (NT) strains accounted for 20.5% of isolates. The *vtaA* gene was detected in 87.5% of strains, supporting their association with systemic disease. Fosfomycin exhibited the highest in vitro susceptibility rate (94.6%), followed by spectinomycin (87.6%), florfenicol (85.6%), ceftiofur (78%), and tiamulin (75.8%). High resistance rates were observed for lincomycin (75.3%) and sulfamethoxazole–trimethoprim (71.9%), indicating substantial antimicrobial resistance among clinical isolates.

Conclusion

Clinical GD cases in Brazil are predominantly associated with serovars 12, 4, 13, and 5, which together account for approximately 60% of typable isolates. The significant resistance to commonly used antimicrobials underscore the need for continuous molecular surveillance and improved preventive strategies.

Keywords: Antimicrobial susceptibility, *Glaesserella parasuis,* Serovar, Virulence.

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HIGH PREVALENCE OF *MYCOPLASMA SUIS* IN A SOW FARM: HEMATOLOGICAL FINDINGS AND ABSENCE OF ARTHROPOD-ASSOCIATED TRANSMISSION

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Introduction and Objectives

A sow farm in northern Italy recurrently experienced pale mucous membranes, lethargy, vulval and mammary edema. Hypogalactia was suspected due to the recurrent premature transfer of undernourished piglets (1.94 ± 0.92 per litter) to nurseries during mid-lactation. Additionally, a pre-weaning mortality rate of 26.84 ± 4.21% was observed. Previous diagnostic investigations for PRRSV, PCV2 and Leptospira *spp.* yielded negative results. An investigation was conducted to detect *Mycoplasma suis* and assess its effects on sow hematological parameters. Furthermore, entomological surveillance was conducted to explore the potential role of arthropods as vectors.

Materials and Methods

A total of 237 sows (parity 1 - 8) were enrolled during the summer period, and blood samples were collected at day 110 of gestation. Hemoglobin concentration (HGB) and serum fructosamine were determined. Entomological surveillance consisted of a total of 10 samples using CDC-like traps (Italian Mosquito Trap IMT®; PeP, Italy), allocated in the gestation rooms and outside the herd. A real-time SYBR-green PCR targeting M. suis was performed on arthropod pools and on a subsample of 50 sows.

Results and Discussion

M. suis was detected in 100% of the sows, a prevalence markedly higher than that reported in comparable European studies. Mean HGB was 11.48 ± 1.04 g/dL (min: 7.80; max: 14.10 g/dL), slightly below literature references (11.6 - 12.6 g/dL). However, only 16,8% sows were below the threshold for severe anemia (10.5 g/dL), suggesting a predominantly chronic infection pattern. Mean fructosamine concentration was 282.4 ± 19.4 µmol/L (min: 233; max: 392 µmol/L), supporting the absence of subclinical hypoglycemia. All arthropod samples tested negative, suggesting no pathogen detection within the sampled insect population and indicating that transmission dynamics in this herd may be largely independent of seasonal arthropod vectors.

Conclusion

The high prevalence of *M. suis* highlights the need to investigate management-related factors potentially contributing to the persistence and spread of infection within the herd, particularly iatrogenic transmission routes. Herd health strategies should include the strengthening of internal biosecurity protocols to limit within-herd transmission.

Keywords: Anemia, Fructosamine, *Mycoplasma suis*, Vector transmission.

MOLECULAR EPIDEMIOLOGY OF *STREPTOCOCCUS SUIS* IN BELGIAN AND DUTCH PIG FARMS

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Introduction and Objectives

Streptococcus suis is a major bacterial pathogen in pig production and a frequent cause of meningitis, polyserositis, arthritis and septicemia. Its marked genetic variability complicates epidemiological interpretation and poses challenges for effective disease control, emphasizing the need for continuous molecular characterization of circulating strains. The aim of this study was to describe the molecular epidemiology, intra-farm diversity and virulence-associated gene profiles of *S. suis* isolates from Belgian and Dutch pig farms using whole genome sequencing (WGS).

Materials and Methods

Sixty-seven *S. suis* isolates from 21 pig farms in Belgium and the Netherlands were included. Isolates originated from CNS, joints, polyserositis, endocarditis, lung, liver and spleen samples submitted for routine diagnostic investigation. WGS was performed to determine serotype, sequence type (MLST) and the presence of *epf, mrp* and *sly*. Distribution of serotypes and ST`s was assessed at regional and farm level, and shared serotype-ST combinations across farms were identified.

Results and Discussion

Sixteen serotypes were identified across 12 sequence types, confirming high genetic heterogeneity. Serotypes 9 (25.7%), 7 (20%) and 2 (14.3%) accounted for 60% of isolates. Considerable intra-farm diversity was observed, with up to seven serotypes detected within a single farm. Identical serotype-ST combinations were found in multiple farms, including serotype 7 ST29 (five farms) and serotype 9 ST16 (four farms), supporting regional circulation of specific lineages. Classical disease-associated profiles were confirmed (serotype 2 ST1, serotype 9 ST16 and serotype 7 ST29). In addition, serotypes 16 and 19 were repeatedly isolated from multiple farms and anatomical sites, despite lacking the classical virulence genes (*epf, mrp, sly*), suggesting that clinically relevant strains may not always fit the traditional virulence model and that *S. suis* pathogenesis remains incompletely understood.

Conclusion

Streptococcus suis circulating in Belgian and Dutch pig farms shows marked genetic heterogeneity together with regional dissemination of dominant lineages. The coexistence of classical virulent clones and less common serotypes lacking traditional virulence markers underscores the complexity of its epidemiology. Regular WGS-based characterization is essential to support informed control strategies and rational vaccine composition.

Keywords: Strain diversity, Streptococcus suis, Swine health, WGS.

MACROEPIDEMIOLOGICAL PATTERNS OF *MYCOPLASMA HYOPNEUMONIAE* INFECTION IN SWINE HERDS IN BRAZIL

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Introduction and Objectives

Mycoplasma hyopneumoniae is a primary etiological agent of enzootic pneumonia in swine and a key component of the porcine respiratory disease complex, causing substantial economic losses worldwide. Transmission occurs mainly via aerosolized droplets and is influenced by herd density and environmental stressors (Sibila et al., 2009; Maes et al., 2018). This study presents the first nationwide analysis of diagnostic data from Brazilian veterinary laboratories within the Central Intelligence in Swine Health (CISS) project.

Materials and Methods

CISS integrates voluntary, anonymized PCR diagnostic data from two Brazilian veterinary diagnostic laboratories. Each record represents samples collected from the same farm on a single date and was considered positive if at least one sample tested positive. Monthly time-series analyses and logistic regression models were used to assess temporal patterns and risk factors for record positivity.

Results and Discussion

From October 2019 to December 2025, CISS consolidated 14,835 PCR submissions for *Mycoplasma hyopneumoniae*, generating 1,770 records. The overall record positivity rate during was 19.01% (338/1,770). Although a statistically significant increasing trend was detected ($P = 0.005$), annual changes were small, except for a marked increase in 2025. Notably, during the second half of 2025, between June and September, positivity rates ranged from 40% to 50%. Record positivity showed significant seasonality ($P = 0.01$), with the Average Seasonal Index indicating peaks in February, June, and December. June may be associated with winter in Brazil, especially in the South region, whereas February and December coincide with periods of high temperature and thermal stress combined with elevated humidity. Growing and finishing animals showed higher odds of positivity (OR = 3.01; 95% CI: 1.95 - 4.77) compared with nursery animals, whereas suckling piglets and breeding males presented the lowest positivity rates. This finding aligns with reports of increased enzootic pneumonia prevalence from mid-finishing to slaughter age (Sibila et al., 2009).

Conclusion

CISS captured clear temporal, seasonal, and production-stage patterns. Despite a modest long-term increase, pronounced seasonal peaks - particularly in 2025 - and higher risk in growing and finishing pigs underscore the value of continuous diagnostic surveillance for risk-based enzootic pneumonia control.

Keywords: Brazil, Diagnostic, Herd Health, Risk Analysis, Surveillance.

Acknowledgements: The authors thank the collaborating veterinary diagnostic laboratories for voluntarily sending the results of the tested samples.

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FIRST WHOLE GENOME-LEVEL CHARACTERIZATION OF *GLAESSERELLA PARASUIS* IN THE PHILIPPINES

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Introduction and Objectives

Glässer's disease remains a persistent infectious disease affecting the Philippine swine industry, causing significant economic losses in pig production, particularly among pre- and post-weaning populations. Although the disease has been recognized as a major farm health concern since 2004, comprehensive data on the circulating strains of its causative agent, *Glaesserella parasuis* (GPS), remain limited. Specifically, information regarding serovar, potential virulence determinants, antimicrobial resistance genes (ARGs), and the genetic diversity of local isolates is lacking. To address this, we generated and analyzed the first whole genomes of local isolates of GPS.

Materials and Methods

We studied three bacterial isolates (isolates Iris, Jenna and Ella) which came from porcine lung samples exhibiting respiratory lesions. The samples came from a pig farm located in the Visayas islands. Isolate Iris was isolated in 2024 while isolates Jenna and Ella were isolated in 2025. The bacterial isolates underwent initial morpho-biochemical characterization, 16S rRNA gene sequencing, and nanopore-based whole genome sequencing.

Results and Discussion

Genome-based species identification confirmed that the isolates belong to GPS. *In silico* capsular serotyping showed that isolate Iris belonged to serovar 7 while isolates Jenna and Ella belonged to serovar 4. Putative virulence factors were identified through comparative screening against established virulence gene databases and group 1 *vtaA* genes, known as good predictors of clinical disease, were detected in each isolate. Mutated *tuf* and *ftsI* genes and the presence of *crp* gene were the potential ARGs detected. Cluster analysis showed that the three Philippine GPS isolates are unrelated to other global isolates, with isolates Jenna and Ella forming a distinct genetic cluster while isolate Iris forming a singleton cluster.

Conclusion

This study provides the first whole-genome–based characterization of GPS in the Philippines, demonstrating the value of integrating whole-genome sequencing into routine diagnostic workflows. The generated genomic data offers important insights into local GPS strain diversity, virulence potential, antimicrobial resistance, and possible transmission dynamics. This essential baseline genomic information can support enhanced surveillance, prevention, and control strategies for Glässer's disease in the Philippine swine industry.

Keywords: Antimicrobial Resistance Genes, Cluster Analysis, *Glaesserella parasuis*, Serovars, Whole Genome Sequencing.

TOWARD A STANDARDIZED CLASSIFICATION OF *STREPTOCOCCUS SUIS* STRAINS: INSIGHTS FROM A LARGE-SCALE GENOMIC ANALYSIS

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Introduction and Objectives

Streptococcus suis shows marked genetic diversity and a wide virulence spectrum, yet a standardized approach to assess pathogenic potential is lacking. We analyzed the genomic diversity and virulome of 1,349 isolates from > 600 swine farms across North America (n = 1071; 79.4%), Latin America (n = 165; 12.2%), and Spain (n = 113; 8.4%) collected between 2014 - 2024. Our objective was to develop a biologically meaningful classification system based on phylogenomics, supported by virulence gene content and clinical-pathological metadata.

Materials and Methods

Genetic diversity was assessed using in-silico serotyping, MLST, and whole-genome clustering to assign phylogenomic lineages (PLs), expanding the framework of Murray et al. (2023). A core-genome phylogeny identified a distinct pathogenic clade. We defined three pathotypes: putatively pathogenic (PL1 - PL10), potentially pathogenic (novel/less-characterized PLs clustering within the pathogenic clade), and potentially commensal (PLs in a genetically distinct central population clade). Virulome patterns were evaluated using multiple correspondence analysis and hierarchical clustering of principal components across 58 virulence-associated genes. Associations between histopathological lesions and pathotypes were tested using multinomial logistic regression ($P \leq 0.05$).

Results and Discussion

Regional composition and temporal dynamics revealed substantial heterogeneity in circulating genotypes. Predominant sequence types differed by region, with ST1, ST28, ST108, ST977, and ST94 most common in NA; ST28, ST94, ST2487, ST87, and ST790 in LA; and ST1, ST123, ST3, ST29, and ST16 in Spain. NA also showed marked temporal turnover, with ST1/CC1 declining (33.9% in 2020 to 8.5% in 2023) while ST28/CC28 increased (10.7% in 2019 to 21.5% in 2023). Overall, 74.2% of isolates were classified as putatively pathogenic, 4.9% as potentially pathogenic, and 20.9% as potentially commensal. Putatively pathogenic isolates were enriched for recognized virulent clones (ST1, ST3, ST28, ST29, ST94, ST108) and showed significantly higher odds of meningitis, sepsis, arthritis, serositis, and bronchopneumonia (OR 9.1 - 15.6; $P \leq 0.05$). Virulence markers *mrp* and the *SSU_RS01130-SSU_RS01140-SSU_RS01170* cluster were highly prevalent among putatively pathogenic isolates but rare in commensals, supporting the proposed pathotype framework for surveillance and prevention.

Conclusion

This phylogenomics- and virulome-supported pathotype framework links molecular features to disease potential and can support targeted surveillance, prevention, and control strategies in swine populations.

Keywords: *Streptococcus suis*, pathotype classification, phylogenomics, swine, virulome.

Acknowledgements: The authors thank the Iowa State University Veterinary Diagnostic Laboratory and the swine practitioners who contributed the isolates and metadata for this study.

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IMPROVED PMA-QPCR VIABILITY DISCRIMINATION ENABLES ROBUST MIC DETERMINATION FOR THE INTRACELLULAR BACTERIUM *LAWSONIA INTRACELLULARIS*

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Introduction and Objectives

Lawsonia intracellularis is an obligate intracellular bacterium, making plate-based MIC testing impractical and slow. Viability PCR using propidium monoazide (PMA)-qPCR suppresses amplification from membrane-compromised cells, enabling rapid live/dead discrimination. However, PMA primarily reflects membrane integrity; thus bacteriostatic antibiotics such as macrolides can leave intact but growth-arrested organisms PMA-negative and qPCR-positive, and membrane-intact inactivated "ghost" cells may also persist. We aimed to develop a PMA-qPCR workflow that improves dead/ghost signal suppression and supports quantitative MIC determination for *L. intracellularis* in cell culture.

Materials and Methods

L. intracellularis was recovered from infected monolayers and standardized by genome-copy quantification. Samples were processed with PMAxx (± Gram-negative enhancer) in the dark, followed by photoactivation. Immediately before photoactivation, we applied a brief, titrated membrane-destabilization step (chemical micro-permeabilization and/or controlled physical micro-disruption) to promote PMA entry into compromised or inactivated cells while preserving amplification from intact viable organisms. Where needed, a two-round PMA treatment (PMA→ light repeated) was evaluated to further suppress residual dead-cell signals. Performance was assessed using live/dead mixing series (including isopropanol-killed controls), macrolide and bactericidal antibiotic exposures, and a time-course framework. MIC_vPCR was defined as the lowest antibiotic concentration preventing an increase in genome copy number from baseline (T0) to a fixed endpoint (T48 or T72). Because plating is not feasible, infectivity readouts (immunostaining-based infection indices) served as plating-equivalent viability references.

Results and Discussion

The optimized workflow increased ΔCt separation between viable and inactivated controls compared with standard PMA-qPCR, indicating stronger suppression of dead/ghost signals with minimal impact on live controls. Under conventional PMA processing, macrolide-treated samples frequently remained PMA-qPCR positive despite growth inhibition; using the time-course "no-growth" endpoint, MIC_vPCR calls remained interpretable under bacteriostatic conditions. Across antibiotic concentration series, the method reduced carryover positivity consistent with membrane-intact ghosts and improved concordance with infectivity-based references, while retaining sensitivity to detect true viable intracellular bacteria overall.

Conclusion

This post-PMA enhanced discrimination method provides a rapid, culture-agnostic framework for MIC determination of antibiotics against *L. intracellularis* and improves robustness for bacteriostatic agents.

Keywords: Intracellular bacterium, MIC, Macrolides, *Lawsonia intracellularis*, PMA-qPCR.

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INTEGRATED QPCR, TARGETED CULTURE, AND WHOLE-GENOME SEQUENCING REVEAL TRANSMISSION PATTERNS OF DISEASE-ASSOCIATED *STREPTOCOCCUS SUIS*

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Introduction and Objectives

Disease-associated Streptococcus suis (DASS) is a driver of antimicrobial use and production losses in swine systems, yet effective surveillance is limited by its commensal ecology and diagnostic difficulties. We investigated the infection dynamics of DASS in dams and piglets in a prospective longitudinal farm study using a qPCR targeting a virulence-associated marker to improve detection sensitivity. Objectives were (i) describe DASS colonization dynamics from birth through post-weaning, (ii) compare nasal versus tonsillar sampling for antemortem surveillance, and (iii) assess the feasibility of isolating DASS for genotyping to inform transmission hypotheses.

Materials and Methods

Forty dams (20 gilts, 20 parity-3+ sows) were sampled at farrowing using tonsil and nasal swabs; udder wipes, vaginal swabs, and farrowing-crate environmental swabs. Dams were resampled at weaning. Piglets were sampled with tonsils and nasal swabs at days 1, 7, 21 and 35. Statistical models were used for repeated-measure comparisons. Culture was attempted on a subset of high-probability samples followed by PCR confirmation. Isolates underwent whole-genome sequencing.

Results and Discussion

Most dams (87.5%) were DASS-positive at least once in upper respiratory samples; 70% were positive at farrowing, weaning, or both, but only 8/28 were positive at both timepoints, indicating intermittent detection. At farrowing, DASS positivity was 45% in nasal and 50% in tonsil samples, while environmental (75%) and udder (65%) samples were frequently positive and vaginal samples least positive (12.5%), supporting multiple exposure routes. No parity effect was detected. In piglets, prevalence was highly dynamic: ≤ 22% positive at birth, < 40% at day 7 and weaning, then increasing post-weaning (≥ 56%; $P < 0.05$). Nasal detection increased more steadily over time than tonsil detection. Culture success was higher in dams than piglets. ST1 and ST969 were found in dams and ST28 in piglets, with minimal dam-piglet sequence-type overlap.

Conclusion

DASS colonization is intermittent in dams and intensifies after weaning in piglets, underscoring the importance of sampling timing and post-weaning surveillance. Environmental and udder reservoirs likely contribute to exposure, and nasal swabs represent a practical surveillance option in growing pigs. Culture-based strain tracking in piglets remains challenging, supporting the need for culture-independent strain-resolution approaches to clarify transmission.

Keywords: Disease associated *Streptococcus suis*, epidemiology, swine, virulence qPCR.

Acknowledgements: The authors would like to thank the dedicated staff at the Pipestone farm for their invaluable support throughout the study.

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GENOMIC INSIGHTS OF *SALMONELLA* ISOLATES ASSOCIATED WITH SWINE DIAGNOSTIC CASES

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Introduction and Objectives

Salmonella is a bacterial pathogen which can affect both human and swine health. Changes in the prevalence of different disease-causing serotypes and in patterns of antimicrobial resistance (AMR) are known to occur (Bearson, 2021). Tracking epidemiologic changes by monitoring isolates infecting pigs is critical to inform the control and management strategies of this important pathogen. Whole genome sequencing (WGS) is a tool that allows for a robust characterization of Salmonella, allowing for the evaluation of virulence factors, antimicrobial resistance, and relation among isolates beyond serotyping (Bearson, 2021). This study has the objective of characterizing three most important Salmonella enterica serotypes associated with swine disease (*S. typhimurium, S. choleraesuis, S. typhimurium* monophasic 1,4,[5],12:i:-) to investigate current trends and evaluate if relevant changes are occurring to Salmonella leading to infection in the field.

Materials and Methods

A total of 28 isolates of isolates were selected based on the association between bacterial isolation and lesions consistent with salmonella infection: *S. Typhimurium* (n = 8), *S. monophasic* 1,4,[5],12:i:- (n = 10) and *S. choleraesuis* (n = 10). Isolates were from 2024 - 2025 and serotyped in the National Veterinary Services Lab. WGS data were analyzed using open-source bioinformatics tools for taxonomic classification, de novo assembly, MLST typing, antimicrobial resistance and virulence factors analysis.

Results

S. Choleraesuis and I 4,[5],12:i:- each had distinct patterns of shared virulence factors, while *S. Typhimurium* isolates were more variable and greater number of virulence factors overall. Serotype I 4,[5],12:i:- had the highest number of AMR genes. Three AMR genes for tetracycline and aminoglycoside resistance were found in all 28 isolates: tet(34), mdf(A), and aac(6')-Iaa. Further isolates from 2020–2026 are being analyzed to be presented at the conference.

Discussion and Conclusion

This report shares trends of recent Salmonella isolates from swine clinical cases. Serotype I 4,[5],12:i:- is considered the most prevalent serotype with importance in swine disease and harboring emerging AMR genes (Elnekave et al, 2018). Multidrug resistance was also prevalent among isolates highlighting the importance of continuing monitoring of this important pathogen.

Keywords: *Salmonella,* Swine disease, Whole genome sequencing.

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COMPARATIVE FIELD STUDY ON A PIG FARM IN MEXICO, BETWEEN TWO VACCINES (COMMERCIAL VS AUTOGENOUS) FOR THE *GLASERELLA PARASUIS*

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Introduction and Objectives

The prevalence of *Glaserella parasuis* in pig farms is very high, especially when PRRSv is present. Furthermore, its relevance lies in its interaction with the porcine respiratory complex (PRC). Several alternatives exist to control these agents, such as reducing the mobility of the PRRS virus; implementing strict management and hygiene measures in farrowing and weaning areas; using antibiotics; and using bacterins. Commercial bacterial products are available in Mexico and the Americas for the control of *Glaserella parasuis*. They primarily contain serotype 5. In Mexico, after several epidemiological studies, a prevalence of serotype 4 of 48% was detected), which led to the development of a bacterial product called Suisbact.

Materials and Methods

A comparative trial was conducted on a pig farm in central Mexico with a total of 14 groups (7 control groups (1285 piglets) and 7 treated groups (1277 piglets)). The control group received a commercial bacterin (containing primarily serotype 5 of *G. parasuis*), and the treated group received the Suisbact bacterin (containing primarily serotype 4 of *G. parasuis*).

Results and Discussion

The overall mortality rate in the treated groups was 3.05% (39 piglets) compared to 6.9% (89 piglets) in the control group, representing a 57% reduction in mortality. Mortality caused by *Glaserella parasuis* in the treated piglets was 0.5% (6 piglets) compared to 1.71% (22 piglets) in the control group, representing a 72% reduction. The results show that the use of the bacterin (Suisbact) is an excellent alternative for controlling this problem in the Mexican market, according to the findings of Huerta (2003).

Conclusions

For the Mexican market, the use of the bacterin (Suisbact) with a higher concentration of serotype 4 reduced mortality caused by this bacterium. I believe it is necessary to conduct epidemiological studies in each country to identify the prevalence of the serotypes, and if the findings are the same as those of Huerta (2002), I suggest developing a bacterin (Suisbact) like the one used in this study.

Keywords: *Glaserella parauis.*

SURVEILLANCE OF *LAWSONIA INTRACELLULARIS* IN GROWING PIGS: DIAGNOSTIC PERFORMANCE OF ORAL FLUIDS AND FECAL SAMPLES

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Introduction and Objective

Lawsonia intracellularis, the causative agent of porcine proliferative enteropathy (ileitis), is a persistent challenge for pig producers globally (Paradis et al., 2012). The optimal diagnostic sample for *L. intracellularis* surveillance in pigs is still under debate (Arnold et al., 2019). This study aimed to describe the proportion of *L. intracellularis*-positive samples in unvaccinated and vaccinated growing pig herds during mid and late-finishing phases, and to compare detection rates using quantitative PCR (qPCR) on fecal samples (FS) versus oral fluids (OF).

Materials and Methods

A prospective cohort study enrolled 40 wean-to-finish growing pig production sites across three provinces in Canada. Half of the sites were actively vaccinated with an inactivated *L. intracellularis* vaccine, while the remainder were unvaccinated. Each site was visited twice, during the mid-finisher (15 - 17 weeks) and late-finisher (20 - 22 weeks) phases. At each visit, three pens per site were sampled. For each pen, a pooled fecal sample was collected from fresh droppings on the pen floor, and an oral fluid sample was obtained by suspending a cotton rope for 20 - 30 minutes, after which fluid was extracted and stored. In total, 440 samples (205 oral fluids and 235 fecal samples) were analyzed by qPCR for *L. intracellularis* DNA. Statistical analyses compared detection rates between OF and FS using multivariable logistic regression.

Results and Discussion

Overall, 50% of sites tested positive for *L. intracellularis*, with a mean detection risk of 18.7% across all samples. Oral fluids demonstrated a two-fold higher detection rate compared to fecal samples (OR = 2.36; 95% CI, 1.24 - 4.49; $P = 0.009$). Detection rates varied by vaccination status and production phase, but oral fluid sampling consistently outperformed fecal sampling in both groups.

Conclusion

Oral fluid sampling is a sensitive and practical method for detecting *Lawsonia intracellularis* in growing pig herds. These findings support the use of oral fluids for routine surveillance and monitoring of *L. intracellularis* in pig production systems.

Keywords: Growing pigs, *Lawsonia intracellularis*, Surveillance, Vaccination.

Acknowledgements: The authors thank collaborating Canadians veterinarians and producers for their support

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ASSESMENT OF COCCIDIAL INFECTION IN PIGLETS FOLLOWING TOLTRAZURIL ADMINISTRATION ON SELECTED FARMS IN NORTHERN VIETNAM

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Introduction and Objectives

Piglet coccidiosis is a host-specific protozoan disease caused by Isospora suis (*Cystoisospora suis*) and *Eimeria* spp., leading to diarrhea during lactation or subclinical infections that impair growth performance. First described in 1878, the disease occurs worldwide (Gong et al., 2021). In Vietnam, it has been reported since 2004 (Lam, 2004), with a high prevalence (63.3%) in Tra Vinh province (Nguyen, 2009), particularly among suckling and weaning piglets. This study aimed to compare the efficacy of intramuscular (IM) versus oral (PO) administration of toltrazuril in reducing the prevalence of coccidial infection across multiple pig farms in Northern Vietnam.

Materials and Methods

The study included 1,500 piglets (48 h old) from uniform L0 - L5 litters on farms in Northern Vietnam. Piglets with similar birth weights and litter sizes were assigned to IM (67.5 mg toltrazuril injection) or PO (100 mg oral toltrazuril) at 48 h. Coccidial prevalence, oocysts per gram (OPG), and body weight were assessed at 48 h and 14 and 21 days. Fecal samples were examined using Fülleborn flotation and McMaster techniques. Weaning weight and post-weaning growth were recorded. Significance was set at $P < 0.05$.

Results and Discussion

At 14 days, coccidiosis prevalence was 10% in the IM group versus 70% in the PO group, with infection intensities of 100 and 9,580 oocysts/g, respectively. At 21 days, prevalence decreased to 4% (IM) and 50% (PO), with 50 and 8,580 oocysts/g; infection intensity was 171-fold lower in the IM group ($P < 0.05$). Average daily gain was 378 g higher in piglets treated with 67.5 mg toltrazuril intramuscularly than in those receiving 100 mg orally.

Conclusion

The results demonstrated that prevalence and intensity of coccidiosis were significantly lower in suckling piglets treated with intramuscular (IM) Toltrazuril than in those receiving oral (PO) Toltrazuril. Based on our findings, we strongly recommend the administration of a 65.5 mg dose of Toltrazuril via intramuscular (IM) injection to piglets at 48 hours post-partum in piglet production systems, as this protocol provides superior control of coccidiosis and significantly improves average daily gain (ADG).

Keywords: Coccidiosis, Piglets, Toltrazuril.

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EFFICACY OF A ONE-SHOT MARBOFLOXACIN TREATMENT IN NURSERY PIGS WITH EXPERIMENTAL *ACTINOBACILLUS PLEUROPNEUMONIAE* INFECTION

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Introduction and Objectives

Porcine pleuropneumonia caused by *Actinobacillus pleuropneumoniae* is a severe respiratory disease associated with high mortality and substantial economic losses in swine production. Parenteral antimicrobial treatment is often required during acute outbreaks. Considering the concentration-dependent activity of fluoroquinolones, a single high-dose regimen may offer effective therapy while reducing handling stress and administration errors. This study evaluated the efficacy and safety of a one-shot 8 mg/kg marbofloxacin treatment compared with a standard three-day 2.5 mg/kg enrofloxacin regimen in nursery pigs experimentally infected via aerosol inoculation.

Materials and Methods

A blinded, randomized, controlled dose-confirmation study was conducted using 36 eight-week-old nursery pigs. Animals were experimentally inoculated with *A. pleuropneumoniae* serotype 2 via aerosol exposure. Clinical monitoring began 4 hours post inoculation and was performed every 2 hours thereafter. Pigs meeting predefined clinical inclusion criteria were immediately randomized and treated. The median time from challenge to treatment initiation was approximately 6 hours (5.9 - 6.6 hours, depending on group). Eligible pigs were allocated to receive marbofloxacin (8 mg/kg, single intramuscular injection), enrofloxacin (2.5 mg/kg intramuscularly for three consecutive days), or saline control. Primary efficacy was assessed by lung lesion score at necropsy. Secondary endpoints included clinical cure on Day 6, bacteriological clearance, mortality, and average daily weight gain. Statistical significance was defined as $P < 0.05$.

Results and Discussion

Both antimicrobial treatments significantly reduced lung lesion scores compared with controls ($P < 0.0001$). Mean lung lesion scores were 3.9 (marbofloxacin), 6.0 (enrofloxacin), and 21.1 (control). Clinical cure rates were 90.9, 83.3, and 9.1%, respectively. Mortality was markedly lower in treated groups (8.3% and 0%) than in controls (66.7%). Bacteriological clearance was achieved in all marbofloxacin-treated pigs and in 91.7% of enrofloxacin-treated pigs. No treatment-related adverse effects were observed. No statistically significant differences were detected between antibiotic regimens.

Conclusion

A single 8 mg/kg marbofloxacin injection was safe and effective for treating acute porcine pleuropneumonia under experimental conditions. Its efficacy was comparable to a three-day enrofloxacin regimen while reducing handling and treatment frequency. This one-shot approach represents a practical therapeutic alternative during acute outbreaks.

Keywords: *Actinobacillus pleuropneumoniae*, Enrofloxacin, Marbofloxacin, Respiratory disease, Swine.

Acknowledgements: The authors would like to thank M. Homuth (IVD GmbH, Hannover, Germany) for conducting the serological examinations and P. Klein for the statistical analyses (dsh statistical services, Pfaffenhofen, Germany).

ASSOCIATION OF MYCOPLASMA HYOPNEUMONIAE ELISA S/P VALUES WITH LUNG LESIONS AND CARCASS PERFORMANCE IN SLAUGHTER PIGS

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Introduction and Objectives

Respiratory diseases caused by *Mycoplasma hyopneumoniae* are a major concern in the pig industry. Understanding the relationship between antibodies against *M. hyopneumoniae* at slaughter, lung lesion scores, and production parameters could improve disease control strategies.

Materials and Methods

This study was conducted at slaughterhouse from nine farms in five provinces in Southeast Vietnam. All piglets were routinely vaccinated against *M. hyopneumoniae* at 3 weeks of age. 700 pigs were sampled for blood collection. Lung lesions were evaluated by estimating the percentage of damage in each lung lobe according to the method described by Madec (Madec, 1982; Bui et al., 2020). Blood samples were analyzed for antibodies against *M. hyopneumoniae* using IDEXX ELISA test kit. Production performance was assessed by calculating carcass percentage (carcass weight/live weight) and measuring backfat thickness at the P2 position. STATA 14.2 was used to evaluate relationships between antibody levels, lung lesions, and production parameters

Results and Discussion

Due to vaccination, the seropositivity rate for *M. hyopneumoniae* antibodies was high (96.2%). The mean lung lesion score was 5.6 (SD = 4.2). A negative association was observed between the S/P ratio and lesions in the left caudal lung lobe (coefficient = -1.64, $P = 0.038$). In contrast, the S/P ratio showed a positive association with carcass percentage (coefficient = 0.013, $P < 0.001$), suggesting that higher antibody levels may be associated with improved production performance. The regression analysis was repeated using two scenarios: S/P > 1.4 (possible natural infection) and S/P < 1.4 (likely absence of current infection). The cutoff value of 1.4 was based on the dataset median and supported by previous studies on post-vaccination antibody levels (3). The results showed similar but stronger associations. In pigs with S/P >1.4, a stronger negative association was found with lesions in the left caudal lung lobe (coefficient = -5.21, $P = 0.012$). In pigs with S/P < 1.4, the association with carcass percentage was stronger (coefficient = 0.031, $P < 0.001$).

Conclusion

These findings indicate that ELISA is useful for monitoring antibodies against *M. hyopneumoniae* in pigs. The S/P ratio may also serve as an indicator of production performance and lung lesion severity.

Keywords: ELISA, Lung score, *Mycoplasma hyopneumoniae*, S/P.

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PCR-BASED DETECTION AND PREVALENCE OF *SALMONELLA* SPP., *HELICOBACTER* SPP., AND *STAPHYLOCOCCUS AUREUS* IN PIG FECES ACROSS GROWTH STAGES IN VIETNAM

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Introduction and Objectives

Bacterial pathogens in pigs pose a significant concern for both animal health and public safety due to their potential transmission through the food chain. Bacterial infections such as *Salmonella* spp., *Helicobacter* spp., and *Staphylococcus aureus* significantly impact growth performance and cause economic losses (Meurens et al., 2008, Kumar et al., 2014, Zheng et al., 2023). Traditional culture methods have limitations, making PCR a more accurate approach. This study aimed to detect and compare the prevalence of *Salmonella spp., Helicobacter spp.,* and *S. aureus* in fecal samples collected from pigs at different growth stages.

Materials and Methods

A total of 324 fecal samples were collected from 18 commercial pig farms in Vietnam, with 108 samples per growth stage (weaned, grower, and finisher). At each farm and stage, six pooled samples (three diarrheic and three non-diarrheic) were collected, each representing five pigs. Detection was performed using PCR with three species-specific primer pairs targeting *Salmonella* spp*., Helicobacter* spp*.,* and *Staphylococcus aureus*, based on 16S rRNA gene regions. Annealing temperatures were optimized, and primer specificity and sensitivity were validated. The assay was then applied to field samples, and prevalence was calculated based on PCR results.

Results and Discussion

All three bacterial groups were detected across all farms, with overall prevalence rates of 10.49% for *Salmonella* spp*.,* 34.56% for *Helicobacter* spp*.,* and 24.69% for *Staphylococcus aureus*. Significant differences were observed in the prevalence of Salmonella spp. and Helicobacter spp. among growth stages ($P < 0.05$), with the highest rates in weaned pigs. In contrast, *S. aureus* showed no significant variation across growth stages. No significant differences were found between diarrheic and non-diarrheic pigs for any bacteria. These findings indicate that the presence of these pathogens is not necessarily associated with clinical symptoms, suggesting pigs may serve as asymptomatic carriers and contribute to pathogen persistence and transmission within herds and along the food chain.

Conclusion

The findings highlight pigs as reservoirs of zoonotic pathogens and emphasize the need for early control and monitoring. Despite some limitations, the PCR method proved to be a rapid and effective tool for field surveillance.

Keywords: *Helicobacter* spp., *Salmonella* spp., *Staphylococcus aureus*, PCR detection, Pig feces.

Acknowledgements: The authors thank the Faculty of Animal Science and Veterinary Medicine, Nong Lam University HCMC, Vietnam for the support with providing samples.

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POSTERS

TOPIC 3: COMBATING AFRICAN SWINE FEVER (ASF)

DURABILITY OF PROTECTIVE IMMUNITY INDUCED BY AN ASF-G-ΔI177L/ΔLVR VACCINE: EFFICACY AND SAFETY IN A TWO-CONSECUTIVE-CHALLENGE MODEL AND IN A DELAYED PRIMARY CHALLENGE AT 3 MONTHS POST-VACCINATION

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Introduction and Objectives

Live-attenuated African swine fever (ASF) vaccine candidates can provide strong protection, but data on the durability of protection and persistence of vaccine genome detection over time remain limited. We evaluated protective durability, clinical safety, and ASFV genome detection after intramuscular vaccination with ASF-G-ΔI177L/ΔLVR under ABSL-3 containment.

Materials and Methods

Eighteen 6-week-old pigs were assigned to vaccinated (n = 12) or unvaccinated controls (n = 6). Vaccinated pigs received ASF-G-ΔI177L/ΔLVR intramuscularly at 10^3 $TCID_{50}$ per pig. Virulent challenge inoculum was 10^2 HAD_{50} of a Korean field isolate (ASFV Hwacheon/2020). Three challenge models were tested (each model: 4 vaccinated + 2 controls): Model 1, challenges at 4 and 8 weeks post-vaccination (wpv); Model 2, challenge at 8 wpv; Model 3, delayed primary challenge at 12 wpv. Rectal temperature and clinical signs were monitored throughout. Whole blood, oral swabs, and rectal swabs were collected at predefined timepoints (twice per week) for antibody detection by competition ELISA (ID Screen® ASF Competition, ID.vet) and ASFV genome detection by real-time PCR (VetMAX™ ASFV Detection Kit, Thermo Fisher Scientific).

Results and Discussion

No vaccine-associated fever or other adverse clinical reactions were observed after vaccination. All vaccinated pigs seroconverted by day 10 post-vaccination and maintained high ASF-specific antibody levels through the final observation period. ASF vaccine genome was repeatedly detectable in whole blood after vaccination. In contrast, detection in oral/rectal swabs was limited (App. 5% positive through week 4) and sporadic through week 8; all swabs were qPCR-negative from week 10 onward. Following virulent challenge, all vaccinated pigs remained clinically healthy and survived in all three models, including after two consecutive challenges (4 and 8 wpv) and after delayed primary challenges at 8 or 12 wpv, whereas unvaccinated controls developed acute ASF-compatible disease after challenge.

Conclusion

A single intramuscular dose of ASF-G-ΔI177L/ΔLVR provided sustained protection through 12 wpv (approaching market age), with an excellent safety profile and limited, transient qPCR detection in secretions.

Keywords: African swine fever, Delayed challenge, Live-attenuated vaccine, Second challenge protection.
Acknowledgements: We thank the National Institute of Wildlife Disease Control in the Republic of Korea for their support.

AFRICAN SWINE FEVER VACCINE ASFV-G-ΔI177L/ΔLVR CONFERS PROTECTION AGAINST HOMOLOGOUS CHALLENGE AND INDUCES SUSTAINED ASFV-SPECIFIC ANTIBODY RESPONSES

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Introduction and Objectives

African swine fever virus (ASFV) continues to cause major economic losses in global pig production. Despite extensive research, live attenuated vaccines remain among the most advanced candidates for ASF control. ASFV-G-ΔI177L/ΔLVR has previously shown protective outcomes against homologous challenge under controlled conditions. This laboratory-based study evaluated survival and clinical outcomes following homologous virulent challenge, described vaccine virus genome detection in blood and secretions, and characterized ASFV-specific antibody kinetics without assuming an immunological correlate of protection.

Materials and Methods

This study was conducted in an ABL3 laboratory under controlled conditions. Domestic pigs (YLD), 8 weeks and ASFV-seronegative, were randomly assigned to experimental groups (four pigs per group). Pigs were vaccinated intramuscularly with ASFV-G-ΔI177L/ΔLVR at 10^3 $TCID_{50}$/dose. Vaccinated pigs were assigned to vaccinated-challenged or vaccine-only groups, and an unvaccinated challenged control group was included. At 28 days post-vaccination, vaccinated–challenged and control pigs were challenged intramuscularly with a homologous highly virulent ASFV field strain at 10^2 HAD_{50}/dose. Blood and oral and rectal swabs were collected at predefined time points. Viral genome detection was assessed by qPCR and ASFV-specific antibodies by ELISA. Results are presented descriptively without formal statistical analysis.

Results and Discussion

All vaccinated pigs survived homologous challenge and remained free of clinical signs for up to 60 days post-vaccination, whereas unvaccinated control pigs developed acute disease consistent with highly virulent ASFV infection. ASFV-specific antibodies were detected prior to challenge and remained detectable for approximately two months in the vaccine-only group. Antibody levels were not interpreted as a correlate of protective immunity but as evidence of immunological recognition of the vaccine virus. Vaccine virus genome was detected in whole blood for an extended period, while detection in oral and fecal swabs was transient and became qPCR-negative within approximately two months.

Conclusion

Under controlled ABL3 conditions, intramuscular administration of ASFV-G-ΔI177L/ΔLVR resulted in 100% survival following homologous virulent challenge and absence of clinical signs for up to 60 days post-vaccination. ASFV-specific antibodies persisted for approximately two months; however, no causal relationship between antibody levels and protective immunity is inferred. Further studies are required to define safety, viral kinetics, and duration of protection.

Keywords: ASFV-G-ΔI177L/ΔLVR vaccine, Antibody persistence, Homologous challenge.

Acknowledgements: We thank the National Institute of Wildlife Disease Control and the Institute of Zoonotic Diseases at Jeonbuk National University in the Republic of Korea for their support.

PRELIMINARY EVALUATION OF LIVE-ATTENUATED ASFV-G-ΔI177L/ΔLVR VACCINATION IN LATE-GESTATION SOWS AND MATERNAL ANTIBODY TRANSFER TO PIGLETS

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Introduction and Objectives

This pilot study evaluated the immunogenicity and preliminary safety of the live-attenuated ASFV-G-ΔI177L/ΔLVR vaccine administered to late-gestation sows under high-containment conditions.The objectives were to assess clinical tolerance and farrowing performance in pregnant sows, determine vertical (transplacental) transmission of the attenuated vaccine genome, and evaluate transfer of maternally derived antibodies to piglets before and after colostrum intake.

Materials and Methods

Safety was evaluated in five late-gestation sows housed in a restricted BSL-3 facility. Three sows were vaccinated intramuscularly with 1 mL of ASFV-G-ΔI177L/ΔLVR ($10^{3.5}$ $TCID_{50}$), and two sows received a mock vaccine. Clinical signs and rectal temperatures were monitored daily. Blood samples were collected at 11 days post-vaccination and at 20 dpv (post-farrowing) for ASFV P72 gene detection and antibody analysis. Piglet sera were collected before and after colostrum intake to assess maternal antibody transfer, and selected major organs were examined for detection of the vaccine genome to evaluate transplacental transmission.

Results and Discussion

All sows in both vaccinated and control groups farrowed normally, with no miscarriages or clinically significant adverse events. Vaccinated sows developed strong ASFV-specific antibody responses by 11 dpv, and no increase in reproductive failure was observed compared with controls. More than 90% of piglets showed ASFV-specific antibodies after colostrum intake from vaccinated sows, indicating efficient maternal antibody transfer. ASFV-G-ΔI177L/ΔLVR genome was detected at low levels in selected piglet organs regardless of colostrum intake, consistent with transplacental passage of the attenuated vaccine virus. No clinical abnormalities were observed in piglets with detectable vaccine-derived genomes, suggesting limited replication and absence of overt pathogenicity.

Conclusion

In this preliminary study, intramuscular administration of ASFV-G-ΔI177L/ΔLVR to late-gestation sows was well tolerated and did not adversely affect sow health or farrowing outcomes. Vaccination induced robust antibody responses and effective transfer of maternal immunity to piglets via colostrum. Although low-level transplacental transmission of the attenuated vaccine genome was detected, no evidence of clinical disease or reproductive impairment was observed. Further studies with larger sample sizes are warranted to confirm safety and clarify the biological significance of fetal exposure to the attenuated vaccine virus.

Keywords: ASFV-G-ΔI177L/ΔLVR, African swine fever virus, Maternal antibodies, Pregnant sows, Transplacental transmission.

Acknowledgements: We thank the Animal and Plant Quarantine Agency, the Ministry of Agriculture, the National Institute of Wildlife Disease Control in the Republic of Korea, and all technical staff and veterinarians who supported animal care, sampling, and laboratory analyses during this experiment.

RAPID SPREAD OF RECOMBINANT AFRICAN SWINE FEVER VIRUS GENOTYPES I AND II IN VIETNAM DURING 2023 - 2025

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Introduction and Objectives

African swine fever (ASF) is a highly lethal viral disease of pigs, caused by the African swine fever virus (ASFV). Since 2023, recombinant ASFV strains containing genetic elements from both genotypes I and II (rASFV I/II) have emerged in Vietnam (Le et al., 2024), posing a serious threat to the effectiveness of current genotype II-based vaccines (Diep et al., 2024). This study aimed to investigate the genetic characteristics, prevalence, and distribution of ASFV strains circulating in northern and central Vietnam during 2023 - 2025, focusing on the emergence and spread of rASFV I/II.

Materials and Methods

A total of 359 clinical samples from suspected ASF outbreaks were collected from 26 provinces in northern and central Vietnam during 2023 (n = 99), 2024 (n = 83), and 2025 (n = 177). Samples were tested by real-time PCR targeting the B646L (p72) gene, with genotypes I and II differentiated using genotype-specific real-time PCR assays (Phan G1 and G2) (Diep et al., 2024). Selected positive samples were further characterized by sequencing the B646L, E183L, EP402R, intergenic region (IGR), and central variable region (CVR). Phylogenetic and diversity analyses were performed using Geneious Prime, MEGA11, and iTOL software.

Results and Discussion

All samples were positive for ASFV DNA. Among the 182 samples collected in 2023 - 2024, 133/182 (73.1%) were genotype II and 49/182 (26.9%) were genotype I based on p72 genotyping. However, sequence analysis revealed that the p72 genotype I-positive strains carried genotype II p54 and CD2v genes, confirming their recombinant nature (rASFV I/II) (Le et al., 2024). These recombinant strains were detected in 17 of 26 provinces, with prevalence increasing from 14.1% in 2023 to 42.2% in 2024. In 2025, the prevalence of rASFV I/II continued to rise, accounting for 48.0% (85/177) of all cases and being identified in all 26 provinces. Notably, monthly analysis showed a rapid increase in rASFV prevalence from 12.5–22.2% (January - March) to 59.5 - 77.4% (June - July), indicating progressive spread and potential dominance.

Conclusion

This study provides molecular evidence that rASFV I/II strains are rapidly spreading in Vietnam and may be replacing classical genotype II viruses, highlighting the urgent need for enhanced surveillance, improved diagnostics, and next-generation vaccines

Keywords: African swine fever, Genetic diversity, Recombinant, rASFV I/II, Vietnam.

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INTERACTIONS WITH ORGANIC SOILING ON VIRUCIDAL ACTIVITY DIFFER BETWEEN OXIDATIVE AND NON-OXIDATIVE DISINFECTANTS

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Introduction and Objectives

Enveloped viruses, such as the African Swine virus, are generally easier to inactivate than non-enveloped viruses. In practice, however, the actual efficacy of disinfectants against an enveloped virus depends on several interacting factors, including the concentration, contact time, temperature and pH or the presence of organic/soil load (Allingham et al, 2024; Gerba et al, 2024). The current study investigates the influence of organic soiling on the quality of virus inactivation by oxidative and non-oxidative disinfectants.

Materials and Methods

Virucidal suspension tests were conducted with three enveloped viruses (African Swine Fever, Vaccinia virus, PEDv). In these tests, the soiling with bovine serum albumin was varied from 0 to 3 g/L. Oxidative (based on potassium peroxymonosulfate, sodium dichloroisocyanurate) and non-oxidative disinfectants (based on glutaraldehyde, quaternary ammonium compounds) were compared. Log reductions were measured in standardized tests according to EN 14675, ASTM and lab-specific protocols.

Results and Discussion

The increase in organic load strongly reduced the virus inactivation by the oxidative disinfectant for ASF (log 5.12 to log 2.28), the Vaccinia virus (log 4.83 to log 2.87), and PEDv (log 4.71 to log 3.22). For the non-oxidative disinfectant, the decrease in virus inactivation with increasing organic soiling was less pronounced. Virus inactivation decreased, however, for ASF (log 4.85 to log 4.05), Vaccinia virus (log 5.10 to log 4.29) and PEDv (log 4.71 to log 3.95).

Conclusion

Organic soiling negatively impacts the activity of disinfectants against enveloped viruses (ASF, Vaccinia and PEDv), but this effect is significantly stronger for oxidative than for non-oxidative disinfectants. In practice, the effect of (mainly oxidative) disinfectants against viruses is often quantified by PCR-testing for monitoring purposes. Hence, adequate cleaning procedures are instrumental to secure the efficacy of disinfectants against viruses, especially when using oxidative disinfectants.

Keywords: ASF, Cleaning, Disinfectants, Enveloped viruses, Organic soiling.

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NATURALLY OCCURRING AFRICAN SWINE FEVER CASES FOLLOWING LIVE-ATTENUATED VACCINATION AT A COMMERCIAL PIG FARM

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Introduction and Objectives

African-swine-fever (ASF) remains endemic in the Philippines, causing recurrent outbreaks despite strengthened biosecurity. We report a naturally occurring ASF outbreak during a field evaluation of the live-attenuated ASFV-G-ΔI177L/ΔLVR vaccine on a commercial farm. This unexpected event enabled assessment of vaccine performance under routine production conditions.

Materials and Methods

The study was conducted on a commercial pig farm in the Philippines. One hundred growing pigs housed under identical management conditions were enrolled (50-vaccinated, 50-non-vaccinated controls). Vaccinated pigs received a single intramuscular dose of 10^3 TCID50/mL ASFV-G-ΔI177L/ΔLVR. Blood, oral and rectal swabs were collected at regular intervals up to 17 weeks post-vaccination (WPV) for antibody and vaccine genome (p72) detection. Pigs were monitored daily for fever, clinical signs and mortality. Carcasses from initial deaths underwent necropsy, and ten organs per pig were submitted to the Animal Disease Diagnosis and Reference Laboratory for ASFV diagnosis. The VetMAX™ ASFV I177L DIVA real-time PCR assay differentiated field virus from the vaccine strain.

Results and Discussion

The index case (first mortality) occurred at approximately 3 WPV. All tested carcasses were positive for field ASFV by DIVA testing, confirming natural infection and excluding vaccine-derived disease. Both groups showed mild, fluctuating fever after vaccination; however, from around 4 WPV all control pigs developed sustained high fever (> 41°C) and increasing daily mortality. The first death in the vaccinated group occurred at 21 days post-vaccination. ASF vaccine antibodies were detected in 60% and 80% of vaccinated pigs at 2 and 3 WPV, respectively, lower than in previous controlled trials, and vaccine genome detection in blood declined to about 50% by 2 - 3 WPV. Overall survival was ~90% in vaccinated pigs, whereas more than 80% of controls died; all remaining pigs were culled according to national policy.

Conclusion

Under the severe challenge of an unplanned natural ASF outbreak, ASFV-G-ΔI177L/ΔLVR vaccination markedly reduced mortality compared with non-vaccinated controls. Incomplete protection was likely associated with field exposure before full development of vaccine-induced immunity. These findings highlight the complementary roles of vaccination and biosecurity in ASF-endemic regions and support ASFV-G-ΔI177L/ΔLVR as a promising tool for ASF control in the Asian swine industry.

Keywords: African swine fever, DIVA test, live-attenuated vaccine, naturally occurring ASFV.

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STABILITY AND INACTIVATION OF AFRICAN SWINE FEVER VIRUS IN FEED AND WATER

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Introduction and Objectives

African swine fever (ASF) poses a major biosecurity threat to the global pig industry. Contaminated water and feed are increasingly recognized as important routes for African swine fever virus (ASFV) transmission. This study aimed to systematically evaluate the stability of ASFV in feed and water under different environmental conditions, and to assess the inactivation efficacy of thermal treatment and drinking water disinfectants, thereby providing a scientific basis for strengthening ASF prevention and control strategies

Materials and Methods

ASFV was inoculated into feed, drinking water collected from pig farms, and pure water supplemented with 0–20% fetal bovine serum (FBS) as organic matter. Samples were stored at 4°C, 15°C, and 25°C, and collected at predefined time points for quantification of viral genome copy numbers and assessment of viral infectivity. For thermal inactivation, ASFV-contaminated feed was heated at 60°C, 70°C, and 85°C for different durations. In addition, the virucidal efficacy of sodium dichloroisocyanurate was evaluated at different concentrations and exposure times.

Results and Discussion

ASFV remained infectious in feed for 28 - 42 days at 4°C. In drinking water from pig farms, ASFV maintained infectivity for at least 42 days at 4, 15, and 25°C. In pure water supplemented with 0%–20% FBS, the virus remained infectious for at least 154 days at 4°C and 15°C, with higher organic matter levels significantly prolonging virual persistence. Overall, increasing temperature reduced the duration of detectable infectious virus, whereas viral nucleic acid exhibited minimal degradation over time. Regarding inactivation, complete inactivation of ASFV in feed required heat treatment at 70°C for ≥ 6 min or 85°C for ≥ 3 min. Sodium dichloroisocyanurate effectively inactivated ASFV (> 4 log reduction) at concentrations ≥ 2.75 g/L and markedly degraded viral nucleic acid.

Conclusion

ASFV shows high environmental stability in feed and water, especially at low temperatures and high organic matter, posing a substantial risk for indirect transmission. Thermal treatment and appropriate concentrations of sodium dichloroisocyanurate are effective mitigation measures. These findings support strengthening biosecurity in feed processing and drinking water disinfection to prevent and control ASF.

Keywords: African swine fever virus, Disinfectants, Stability, Thermal treatment.

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LOSS OF RIBOSOMAL PROTEIN RPL22 RESTRICTS AFRICAN SWINE FEVER VIRUS REPLICATION BY INDUCING PERK-DEPENDENT ER STRESS

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Introduction and Objectives

African swine fever virus (ASFV) is a large DNA virus that causes highly lethal disease in domestic pigs and wild boars, posing a significant threat to the global swine industry. The inner envelope protein p54 is essential for multiple stages of the viral life cycle, including attachment, entry, and replication. However, the mechanisms by which p54 influences host cellular processes remain poorly understood. In this study, we employed TurboID-based proximity labeling systematically map the host protein interactome of ASFV p54 and investigated the functional role of the ribosomal protein RPL22 in viral replication and the endoplasmic reticulum stress (ERS) response.

Materials and Methods

Proximity labeling was performed in HEK-293T cells expressing p54-TurboID to identify biotinylated host proteins via mass spectrometry. Candidate interactions were validated using co-immunoprecipitation (Co-IP), confocal microscopy, and bimolecular fluorescence complementation (BiFC) assays. To assess functional significance, RPL22-knockout (RPL22-KO) and overexpression cell lines were generated using CRISPR-Cas9 and lentiviral transduction, respectively. The role of the ERS pathway was evaluated using Quantitative RT-PCR, Western blotting, and pharmacological modulation with specific PERK inhibitors (AMG-PERK-44) and activators (CCT020312) in LLC-PK1 cells and porcine alveolar macrophages (PAMs).

Results and Discussion

Our screen identified 257 high-confidence host interacting partners of p54. Among these, the interaction between p54 and RPL22 was confirmed by Co-IP and confocal microscopy. Functional studies revealed that RPL22 serves as a significant regulatory host factor; RPL22 knockout significantly reduced ASFV replication, whereas its overexpression did not enhance it. Mechanistically, the loss of RPL22 significantly inhibited ASFV replication through the activation of the PERK signaling pathway, a key branch of the ERS response. This was evidenced by elevated phosphorylation of PERK and eIF2α in infected RPL22-KO cells. Furthermore, inhibition of PERK using AMG-PERK-44 rescued viral replication in RPL22-KO cells, while PERK activation using CCT020312 potently suppressed viral replication.

Conclusion

We demonstrated that RPL22 interacts with p54 and modulates ASFV replication via the PERK signaling pathway of the ERS response. Furthermore, we show that pharmacological modulation of this pathway significantly alters viral replication, highlighting the ERS-PERK axis as a promising antiviral target.

Keywords: ASFV, ER stress, p54, Proximity labeling, RPL22.

Acknowledgements: This project was funded by the National Key Research and Development Program of China (2023YFF1000901).

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IN VIVO STUDY OF INOCULATION APPROACHES AND PATHOGENICITY IN AFRICAN SWINE FEVER

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Introduction and Objectives

Most experimental African swine fever virus (ASFV) infection studies rely on intramuscular (IM) inoculation, which does not accurately reflect the natural routes of transmission and may bypass early host-virus interactions at mucosal surfaces. In this study, a genotype II ASFV strain (HB31A) was used to compare intramuscular and oronasal (ON) inoculation in pigs. The objective was to evaluate the impact of inoculation route on viral dynamics, pathogenicity, and host responses, thereby improving experimental models that represent natural infection and support vaccine and pathogenesis research.

Materials and Methods

Nine healthy pigs were randomly assigned to intramuscular, oronasal, or control groups. Pigs were inoculated with 200 TCID50 of ASFV strain HB31A via the IM or ON route. Clinical signs and rectal temperatures were monitored daily for 28 days post-inoculation (dpi). Swab samples were collected daily for viral genome detection by qPCR, and blood samples were collected at predefined intervals to assess viremia and IgG responses. All pigs underwent necropsy, and tissues were subjected to histopathological examination and viral load quantification.

Results and Discussion

All pigs inoculated with HB31A developed fever, anorexia, and lethargy. Pigs in the IM group exhibited shorter incubation period (4.33 ± 0.47 d), earlier viral detection in swabs (1 - 3 dpi) and blood (2 dpi), and uniform acute disease course, with all animals succumbing by 6.67 ± 0.47 dpi. In contrast, the ON group showed delayed virus detection, a longer incubation period (6.00 ± 0.82 d), and heterogeneous disease outcomes. Two pigs died at 8 and 10 dpi, while one pig survived, developing a chronic infection characterized by low-level viremia, intermittent viral shedding, and seroconversion at 14 dpi. Acute fatal cases lacked detectable antibody responses and presented severe hemorrhagic lesions, whereas the surviving pig exhibited mild lesions.

Conclusion

ASFV strain HB31A is highly virulent in domestic pigs. IM inoculation resulted in rapid, uniform and lethal disease, whereas ON inoculation more closely mimicked natural infection, revealing variable disease outcomes including persistent infection with intermittent viral shedding. These findings enhance understanding of ASFV pathogenesis and have important implications for ASFV diagnosis, surveillance, vaccine evaluation, and experimental model selection.

Keywords: African swine fever virus, Intramuscular inoculation, Oronasal inoculation, Pathogenicity.

A SIMULATION-BASED DECISION SUPPORT TOOL FOR EMERGENCY RESPONSE PLANNING IN SWINE POPULATIONS IN EXPORT-ORIENTED COUNTRIES

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Introduction and Objectives

Contagious diseases in swine populations can disrupt production and animal movements in export-oriented countries. A foreign animal disease (FAD) incursion would necessitate control measures by competent veterinary authorities, including movement controls, depopulation, and compensation for affected premises. Experience during the SARS-CoV-2 pandemic, illustrated how disruptions related to human populations can affect herds beyond regulated control zones. In an FAD event, such impacts would be expected to be more extensive, particularly for herds outside disease control and compensation frameworks. This study reports on the development of a simulation-based decision support tool and evaluates the impact of selected mitigation strategies on swine herds outside government compensation systems in Ontario, Canada, under assumed FAD-related disruptions.

Materials and Methods

A discrete-event simulation tool was developed using AnyLogic to represent swine production in Ontario at a weekly time step. The model includes an open sow population with user-modifiable parameters and growing pig cohorts produced weekly and marketed 27 weeks later, which are allocated to multiple processing routes. Processing streams convert marketed pigs into consumable pork, further divided into primal cuts for domestic use or export. A range of mitigation strategies and baseline control scenarios were evaluated through repeated simulation runs. A Shiny-based application was developed to enable interactive, head-to-head comparison of model outputs.

Results and Discussion

The baseline model with no disruptions was validated against Statistics Canada census and other data, confirming that performance was in line with observed population, and weekly marketing levels. Simulation results indicated that strategies applied simultaneously across multiple production stages, including the sow herd, were more effective than single-stage approaches in reducing surplus market hogs and pork volumes. Under assumed resource constraints and domestic consumption targets, achieving provincial production levels aligned with internal demand required sustained implementation over a minimum of 21 weeks. These results highlight structural limitations in processing and animal management capacity during prolonged disruptions.

Conclusion

The mitigation strategies evaluated in this study represent a sample of possible response options rather than definitive solutions to an FAD-related disruption. The findings underscore the need for advance planning and targeted investment in surge capacity and response options.

Keywords: African swine fever, Decision support system, Foreign animal disease.

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TRANSCRIPTIONAL ARCHITECTURE OF AFRICAN SWINE FEVER VIRUS

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Introduction and Objectives

African swine fever virus (ASFV), a large double-stranded DNA virus, poses one of the most significant infectious disease threats to the global swine industry. The transcriptional mechanism of ASFV is particularly complex because of its unique host-independent transcription system. Using nanopore sequencing, we discovered that the virus produces long-chain RNAs as well as multiple transcription start and end sites. Combined with direct RNA sequencing revealed that the presence of long polycistronic co-transcribed RNA is confirmed. By combining this information with the viral genome annotation, we identified four novel transcriptional genes with potential functions. We also observed transcriptional "read-through" events, where transcription continues past typical termination sites at the same transcription start site, producing multiple RNA transcripts of different lengths. Additionally, nanopore direct RNA sequencing to compared with unmodified transcripts, modified mRNAs presented shorter poly(A) tails, suggesting a relationship between RNA modification and poly(A) tail length.

Materials and Methods

Porcine alveolar macrophages (PAMs) were retrieved from liquid nitrogen storage and cultured in RPMI 1640 medium (Gibco, USA) supplemented with 10% fetal bovine serum (FBS; Gibco, USA) at 37°C in a 5% CO_2 humidified incubator. Cultured cells were washed once with PBS before the addition of TRIzol reagent (Invitrogen).

Results and Discussion

At 24 and 36 hours post-infection (MOI 0.5), we generated over 15 million reads (16 Gb), with 7.4% mapping to the ASFV genome. We identified a positive-strand transcriptional bias, 236 viral transcripts, 198 transcription start sites (TSSs), 259 transcription termination sites (TTSs), and 26 putative novel genes-four validated via immunoprecipitation with convalescent pig serum.

Conclusion

Our data reveal transcriptional read-through events producing long-chain mRNAs, potentially enhancing gene expression. Promoter analysis identified conserved A-T-rich motifs, while TTS regions contained poly(A/T) stretches suggestive of RNA polymerase III-like termination signals. DRS detected RNA modifications, with modified transcripts having distinct poly(A) tail lengths. Functional assays confirmed that disrupting specific TSS regions impairs downstream gene expression and viral replication.

Keywords: Nanopore sequencing, Potential novel genes, Polycistronic transcription mRNA, RNA modification.

Acknowledgements: This work was supported by the biosafety level 3 (BSL-3) core facility at Huazhong Agricultural University.

EVALUATION OF SAFETY, IMMUNOGENICITY, AND PROTECTIVE EFFICACY OF AN ORALLY ADMINISTERED AFRICAN SWINE FEVER VACCINE CANDIDATE ASFV-G-Δ177LΔLVR

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Introduction and Objectives

African swine fever (ASF) is a highly contagious viral disease affecting domestic pigs and wild boars, causing severe economic losses. Although commercial ASF vaccines have recently been approved in Vietnam, controlling ASF transmission remains challenging, particularly in wild boar populations. Because injection-based vaccination is impractical for wild boars, oral vaccination is considered essential. This study evaluated the safety, immunogenicity, and protective efficacy of an orally administered live attenuated ASF vaccine candidate, ASFV-G-ΔI177LΔLVR.

Materials and Methods

Conventional pigs were orally inoculated with ASFV-G-ΔI177LΔLVR (obtained from the USDA) at three dose levels ($10^{2.25}$, $10^{5.0}$ and $10^{6.0}$ $TCID_{50}$/dose). At 28 days post-vaccination, pigs were challenged intramuscularly with a virulent ASFV field strain at $10^{2.0}$ HAD_{50}/mL, with virulence confirmed in preliminary experiments. Animals were monitored for clinical signs and lesions. Protection was assessed by viremia (p72) and ASFV-specific antibody responses (p32).

Results and Discussion

Oral immunization was well tolerated, with no vaccine-associated clinical signs prior to challenge. After challenge, vaccinated pigs showed dose-dependent protection with survival rates of 1/4 ($10^{2.25}$ $TCID_{50}$), 4/4 ($10^{5.0}$ $TCID_{50}$), and 3/4 ($10^{6.0}$ $TCID_{50}$). Notably, pigs that succumbed to infection showed no detectable viremia or ASFV-specific antibodies prior to challenge, suggesting insufficient vaccine take rather than vaccine-associated enhancement. In contrast, pigs that showed complete seroconversion prior to challenge were fully protected and had reduced viral loads compared with controls. These results highlight the importance of effective vaccine exposure for successful oral immunization.

Conclusion

ASFV-G-ΔI177LΔLVR is a safe oral live attenuated vaccine candidate that induces dose-dependent protection against ASFV. Oral administration at $10^{5.0}$ $TCID_{50}$ provided complete protection, supporting this dose as a practical target for oral vaccination. Overall, these results highlight the feasibility of ASFV-G-ΔI177LΔLVR as a tool for ASF control, particularly in wild boar populations.

Keywords: African swine fever virus, Live-attenuated vaccine, Oral administration, Protective efficacy.

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DIAGNOSIS AND PREVENTION OF AN AFRICAN SWINE FEVER GENE-DELETED STRAIN OUTBREAK

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Introduction and Objectives

Low-virulence African Swine Fever Virus (ASFV) poses challenges due to prolonged incubation, atypical signs, and intermittent shedding. This study reports controlling an ASFV low-virulence strain outbreak in a 1,800-sow farm via on-site rapid diagnosis and targeted culling, exploring effective prevention and control strategies for such infections.

Materials and Methods

Sample collection & diagnosis: Oropharyngeal and tail-root blood swabs were collected from symptomatic sows; differential diagnosis was performed using ASFV triple real-time qPCR (P72/MGF/CD2v) assay. Zoned management: Farm was divided into low/medium/high-risk zones based on herd spread and personnel movement; cross-zone personnel flow was blocked. Disinfection protocol: Alternating disinfection with 3 - 5% caustic soda and 1:200 potassium peroxymonosulfate. Screening & culling: ASFV antigen-antibody testing was conducted for sows in medium/high-risk zones with individual screening; positive and associated pigs were culled. Clearance verification: Continuous PCR testing was performed until 21 consecutive negative results were achieved, followed by two rounds of ASFV antibody testing at 10-day intervals prior to production resumption.

Results and Discussion

QPCR confirmed the pathogen as genotype II ASFV MGF-deleted strain. Initial screening of 20 samples yielded 3 PCR-positive and 6 antibody-positive results. After 18 days of continuous testing, 176 PCR-positive and 83 antibody-positive pigs were identified; 619 positive/associated pigs were culled, achieving a 64% sow preservation rate (1,147/1,800). Continuous negative PCR results were obtained from day 19 (sustained for 21 days), with two consecutive negative antibody rounds initiated on day 39. Production resumed on day 50, followed by 750 days of stable operation. Combining dual testing (PCR + rapid antibody), zoned management, and targeted culling minimized losses and enabled rapid recovery for ASFV MGF-deleted strain-infected farms.

Conclusion

Integrating on-site rapid diagnosis (PCR & antibody testing), zoned management, and targeted culling effectively controls ASFV low-virulence strain outbreaks, preserving core herds, minimizing economic losses, and facilitating rapid production resumption in large-scale sow farms.

Keywords: African Swine Fever; Antibody Detection; Gene-deleted Strain; Targeted Culling; Zoned Management.

Acknowledgements: The authors thank the farm team for their diligent implementation of sampling and biosecurity procedures.

PRECISION ERADICATION OF ASF THROUGH ACCURATE DIAGNOSIS - A SUCCESSFUL FIELD-OUTBREAK RESPONSE

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Introduction and Objectives

African Swine Fever (ASF) inflicts devastating losses on the global pig industry. Accurate diagnosis underpins targeted pathogen elimination and loss reduction. By employing a parallel nucleic acid-antibody testing approach for precision diagnosis, this study presents a field case of ASFV eradication in a 2,500 - head finishing farm, demonstrating how this combined diagnostic tool, together with reinforced biosecurity protocols, facilitates reliable outbreak assessment, targeted culling and rigorous efficacy validation.

Materials and Methods

Precision detection: Under silent production, environmental (fans, wet curtains, tools, pens) and abnormal pig samples (tail-root blood, saliva, pen composites) were collected; ASFV real-time PCR delineated the infection scope. Strain characterization: Fluorescent PCR kits differentiated full/deletion strains and genotyped the virus. Source/timing tracing: Pen-by-pen sampling in the affected barn; PCR (Ct documented) and antibody strips for serological assessment of PCR-positive pigs. Precision culling: PCR-positive pigs and direct/indirect contacts were identified and euthanized. Enhanced biosecurity: On-farm: transmission interruption, vector control, airflow regulation. Off-farm: zoned management, intensified disinfection, equipment retrofitting to mitigate biosecurity vulnerabilities. Continuous monitoring: 30-day daily PCR (oral fluid, abnormal pig tail-root blood, composites) and weekly antibody testing; prompt euthanasia/decontamination for positives. Genomic confirmation: Positive samples underwent third-party sequencing, aligned with GenBank reference strains.

Results and Discussion

ASFV infection localized to Barn A3 (recombinant genotype I/II wild-type strain). Tracing detected 4 PCR-positive pigs and 1 seropositive pig, confirming early infection; 20 pigs euthanized. Two additional positives (day 7 PCR; days 7 ~ 14 sero) were promptly managed. All samples negative by day 14; farm resumed production on day 31 (120 days no recurrence). Culling losses reduced by 95% vs. full-herd depopulation. Sequencing confirmed 99.96% nucleotide homology with ASFV OQ504954. Integrating precision detection (real-time PCR and serology), targeted culling, and enhanced biosecurity effectively constrains ASF outbreaks, minimizing losses and sustaining production in intensive farms.

Conclusion

Accurate diagnosis combined with biosecurity enables early detection, rapid localization and targeted eradication of ASFV. The parallel use of nucleic acid and antibody testing ensures comprehensive precision diagnosis. This provides a cost-effective protocol for large-scale pig farms to maintain production continuity against ASF.

Keywords: African swine fever, Accurate diagnosis, Biosecurity, Precision eradication.

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GENOMIC EVOLUTION OF AFRICAN SWINE FEVER VIRUS IN VIETNAM: COMPARATIVE ANALYSIS OF GENOTYPE II STRAINS FROM THE INITIAL 2019 OUTBREAK THROUGH 2022

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Introduction and Objectives

African swine fever (ASF) was first reported in Vietnam in February 2019, causing significant economic losses. This study characterizes complete genome sequences of ASFV genotype II strains circulating from the initial 2019 outbreak through 2022, predating the emergence of genotype I & II recombinant strains reported in China. We aimed to establish baseline genomic data and track evolutionary changes over this three-year period.

Materials and Methods

ASFV-infected spleen tissues were collected from Hung Yen province and Quynh Phu district (Thai Binh province) in 2019, and whole blood samples from Hung Yen in November 2022. Next-generation sequencing was performed using Illumina HiSeq 4000. Complete genomes were compared with 25 ASFV strains representing the first outbreak reports from various countries by 2019. Average nucleotide identity (ANI), phylogenetic analysis, intergenic region (IGR) characterization, and direct comparison between 2019 and 2022 strains were performed.

Results and Discussion

Three complete genomes were obtained: VN/HY/2019-ASFV1 (189,113 bp), VN/QP/2019-ASFV1 (189,081 bp), and VN/HY/2022-ASFV2 (189,607 bp). All belonged to p72 genotype II and CD2v serotype 8. Direct comparison revealed evolutionary changes: VN/HY/2022-ASFV2 exhibited variations in 16 ORFs, including MGF_360-21R (19 nt mutations), I196L (66 nt insertion), and H233R (11 nt deletion), demonstrating viral evolution in virulence-related genes. The 2019 strains were classified as IGR II variants and showed 99.99% ANI with the Estonia 2014 strain, suggesting European origin. Variations in 28 ORFs were identified in multigene families (MGF360, MGF110, MGF505) and virulence-associated genes (EP153R, I196L, KP177R). These findings represent specific outbreak cases and emphasize the need for continued surveillance.

Conclusion

This study provides the first complete genomic characterization of ASFV genotype II strains from Vietnam's initial 2019 outbreak and demonstrates measurable viral evolution through 2022. The identification of 16 ORF variations between 2019 and 2022 strains highlights ongoing ASFV evolution. These baseline genomic data provide crucial reference for comparison with emerging variants, including genotype I & II recombinants.

Keywords: African swine fever virus, Genotype II, Vietnam, Viral evolution, Whole-genome sequencing.

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A ROBUST QUADRUPLE PROTEIN-BASED INDIRECT ELISA FOR DETECTION OF ANTIBODIES TO AFRICAN SWINE FEVER VIRUS IN PIGS

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Introduction and Objectives

African swine fever (ASF) threatens global swine production with no vaccines or diagnostics available. This study developed a quadruple recombinant protein-based indirect ELISA (QrP-iELISA) using four antigenic proteins (CD2v, CAP80, p54, and p22) to detect ASFV antibodies and compare its performance with a commercial kit.

Materials and Methods

Four recombinant proteins from ASFV genotype II were expressed and purified. QrP-iELISA was optimized with a coating concentration of 1 µg/mL (25 ng each) and a serum dilution of 1:100. Seventy ASFV-positive and 26 negative samples from Vietnam and Korea were tested. Experimental infections with ASFV I (OURT 88/3) and II (Korea/Pig/Paju1/2019) strains compared QrP-iELISA with single-protein ELISAs and the IDvet kit.

Results and Discussion

QrP-iELISA detected all 70 ASFV-positive samples (100% sensitivity) compared to 14 by IDvet (20% sensitivity), both with 100% specificity. The maximum P/N ratio was 24.033. Individual protein ELISAs showed 92.9 - 100% sensitivity, with p22-iELISA enabling earliest detection. In experimental infections, QrP-iELISA detected antibodies at 5 DPI in ASFV I-infected pigs and 3 DPI in ASFV II-infected pigs, earlier than IDvet. QrP-iELISA demonstrated superior sensitivity for both genotypes with high OD450 values (> 1.0). Combining four proteins representing different infection stages enabled comprehensive antibody detection throughout the post-infection period.

Conclusion

QrP-iELISA demonstrated superior performance with 5-fold higher sensitivity and earlier detection than commercial kits. This tool is essential for large-scale ASF surveillance, enabling early infection detection, which is critical for preventing virus spread.

Keywords: African swine fever virus, ELISA, Quadruple recombinant protein.

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ENVIRONMENTAL IMPACTS OF PIG DISEASES AND DISEASE CONTROL STRATEGIES IN ASIAN PRODUCTION SYSTEM - INTEGRATING ANIMAL HEALTH INTO A LIFE CYCLE ASSESSMENT

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Introduction and Objectives

Infectious diseases remain a critical challenge for pig production systems, particularly in Asia, where high animal densities, diverse production structures, and recurrent transboundary disease incursions place sustained pressure on animal health management. Diseases such as African swine fever (ASF), porcine reproductive and respiratory syndrome (PRRS), porcine epidemic diarrhea (PED), and porcine circovirus type 2 (PCV2) are well recognized for their adverse effects on herd productivity through increased mortality, compromised growth performance, and reduced reproductive output. African swine fever outbreaks further necessitate extensive control measures, including mass culling, carcass disposal, heightened biosecurity, and prolonged production downtime. While the epidemiological and economic dimensions of these diseases are extensively documented in veterinary science, their environmental consequences remain insufficiently quantified within environmental assessment frameworks. This study aims to bridge animal health and environmental science by evaluating the environmental impacts of pig diseases and associated control strategies using life cycle assessment (LCA), thereby addressing a key gap in sustainability assessment of livestock systems.

Materials and Methods

Life cycle assessment is applied as a systems-based analytical framework to representative pig production systems in Taiwan, the Philippines, and Malaysia, selected to reflect contrasting disease burdens and levels of management input. The assessment adopts a cradle-to-farm-gate system boundary and a functional unit of per kilogram of carcass weight. Disease effects are incorporated by systematically modifying production parameters commonly used in veterinary epidemiology, including mortality rates, feed conversion ratios, growth performance, sow productivity, culling intensity, carcass disposal pathways, and restocking delays.

Analysis and Significance

Scenario-based analyses compare healthy production baselines with endemic disease conditions associated with PRRS, PED, and PCV2, as well as ASF outbreak response strategies. Uncertainty and sensitivity analyses are conducted to identify key drivers of environmental outcomes and assess robustness. By explicitly integrating animal health dynamics into environmental assessment, this research provides evidence-based insights to support sustainable livestock development and One Health oriented decision making at the interface of veterinary medicine and environmental science in Asia.

Keywords: African swine fever, Disease control strategies, Environmental sustainability, Life cycle assessment, Pig production systems.

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UNIQUE CHARACTERISTICS OF THE 2023 AFRICAN SWINE FEVER OUTBREAK IN CROATIA

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Introduction and Objectives

African swine fever (ASF) has affected Europe since the introduction of ASFV genotype II in 2007 and remains a serious threat to pig production. After entering the European Union ASF spread with diverse epidemiological patterns. Despite reduced incidence or temporary elimination in some countries, the disease continues to emerge in new areas and reappear in affected regions. In 2023, a notable proportion of European ASF outbreaks occurred in Croatia. Therefore, this study describes the 2023 ASF outbreak in domestic pig establishments in Croatia.

Materials and Methods

Data for this study consisted of laboratory records and data collected during field investigations. Laboratory data consisted of results of PCR testing on samples collected on the affected or suspected establishments and conducted in the Croatian Veterinary Institute (CVI, Zagreb, Croatia). Epidemiological data were provided by the Veterinary and Food Safety Directorate of the Ministry of Agriculture, Forestry and Fisheries (MAFF) of the Republic of Croatia. The unit of analysis in this study was a unique establishment. Inclusion criteria were establishments keeping domestic pigs, with a study period between June 2023 and December 2023. Start of the outbreak was the date of clinical signs, if applicable, or date of sampling for a laboratory confirmed case.

Results and Discussion

1124 unique establishments were detected as positive. First clinical signs were noted on June 17, 2023, with laboratory confirmation on June 26, with the last outbreak reported in November of 2023. Only establishments in the 3 eastern counties were affected. Outbreaks mostly affected small establishments, which varied in size (1 - ~1200 pigs), and median of 9 pigs. Outbreak exhibited strong space-time clustering, with most outbreaks classified into distinct space-time clusters. Mortality varied between three established herd-size categories and the method of estimation; with the median mortality rate of 12.1 cases per 100-pig-weeks-at-risk (pw) (IQR = 43.7), and 24.4 cases pw (IQR = 50.9) in establishments with mortality.

Conclusion

The 2023 ASF outbreak was limited in geographical scope, with strong spatio-temporal clustering affecting small establishments. Findings of this study illustrate unique spread in a dense population of establishments and could inform control measures in this and similar populations.

Keywords: African swine fever, Croatia, outbreak investigation.

Acknowledgements: The authors thank all experts contributing to generating these data in the field and in laboratory, and swine producers for taking time to provide recall and valuable insights during emergency situation.

IMMUNOINFORMATICS-BASED DESIGN OF A MULTI-EPITOPE VACCINE AGAINST AFRICAN SWINE FEVER VIRUS

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Introduction and Objectives

African swine fever (ASF) is a fatal haemorrhagic disease affecting domestic and wild pigs. The lack of an effective vaccine has hindered global ASF control efforts, leading to devastating economic losses in the swine industry. Traditional vaccine development approaches have faced challenges due to ASFV's genetic complexity and immune evasion strategies. Therefore, this study aims to design a multi-epitope vaccine against ASFV using immunoinformatics approach incorporating epitopes from conserved ASFV genes.

Materials and Methods

Antigenic and non-allergenic epitopes were selected and assembled into a multi-epitope vaccine construct using suitable linkers and an adjuvant. The physico-chemical properties of the construct were analyzed, followed by secondary and tertiary structure prediction and validation. Molecular docking was performed between the vaccine construct and SLA-1*0401, and the stability of the docked complex was evaluated through molecular dynamics simulations. Normal mode analysis was conducted to assess the structural flexibility of the construct. Immune simulations were carried out to predict the adaptive immune response. The vaccine sequence was further codon optimized to improve CAI and GC content for enhanced expression in Sus scrofa, and the optimized sequence was cloned in silico into the pVAX1-eGFP expression vector (Simbulan et al., 2024).

Results and Discussion

The selected epitopes were confirmed to be antigenic and non-allergenic, and the vaccine construct exhibited favorable physico-chemical properties. Structural analysis indicated a stable and well-folded protein model. Docking results demonstrated strong binding affinity between the vaccine construct and SLA-1*0401, which was further supported by molecular dynamics simulations confirming the stability of the complex. Normal mode analysis indicated structural balance and acceptable flexibility. Immune simulations predicted strong humoral and cell-mediated immune responses. Codon optimization significantly improved CAI and GC content, and successful in-silico cloning into the pVAX1-eGFP vector was achieved, indicating the feasibility of downstream experimental validation.

Conclusion

These in-silico results prove that the designed multi-epitope vaccine is potentially effective and warrants for further in vitro and in vivo studies to confirm the efficiency of the vaccine against ASFV.

Keywords: African swine fever virus, Immunoinformatics, In-silico approach, Multi-epitope, Vaccine.

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IMMUNOINFORMATICS-BASED COMPARATIVE ANALYSIS OF STRUCTURAL DESIGNS OF MULTI-EPITOPE VACCINE CONSTRUCTS AGAINST ASFV

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Introduction and Objectives

Multi-epitope vaccines (MEVs) are a promising strategy to induce broad humoral and cellular immune responses, against various pathogens, including African Swine Fever Virus (ASFV). A critical challenge in multi-epitope vaccine design is the optimal positioning of linker sequences, which can influence antigen processing, structural stability, and epitope presentation. Linker placement strategies vary widely across studies and host systems, with no standardized protocol. Here, we present the first comparative investigation of linker positioning in MEV constructs targeting ASFV, with evaluation in the context of the swine immune system.

Materials and Methods

Conserved, antigenic, and non-allergenic CTL, HTL, and B-cell epitopes were identified and assembled into four constructs with identical epitope and adjuvant composition, differing only in linker arrangement. Each construct was evaluated through physicochemical characterization, structural modelling and validation, molecular docking with SLA-1*0401, and molecular dynamics simulations to assess complex stability and binding affinity. Immune simulations predicted the capacity of each construct to elicit coordinated humoral and cellular responses (Venkateswaran et al., 2025).

Results and Discussion

Comparative analysis showed that Construct 4, designed with a linker placed between each individual epitope, consistently exhibited the strongest stability, highest binding affinity, and most robust immune response. This epitope-by-epitope linker arrangement enhanced antigen processing and presentation, improving predicted immunogenicity compared to group-based linker placements. These findings highlight construct-level optimization of linker positioning as a critical determinant of MEV performance and establish the epitope-by-epitope linker strategy as a promising design principle for MEV development, demonstrated in the present study against ASFV.

Conclusion

This study provides a rational framework for optimizing MEV structural organization, translatable to experimental vaccine development against ASFV. Given the limited number of structural vaccinology studies in this field, further research is strongly recommended to explore alternative linkers, adjuvants, and epitope combinations to refine MEV design and improve immunogenicity across diverse pathogens.

Keywords: African swine fever virus, In-silico approach, Linkers, Multi-epitope vaccine.

Acknowledgements: This work was funded by The Second Century Fund (C2F), Chulalongkorn University, and Agricultural Research Development Agency (ARDA).

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THE PROSPECTS AND CHALLENGES OF LIVE ATTENUATED VACCINES AGAINST AFRICAN SWINE FEVER VIRUS IN VIETNAM

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Introduction and Objectives

African swine fever (ASF) has become endemic in Vietnam since its introduction in 2019, causing severe and persistent impacts on the swine industry. Although early outbreaks were dominated by African swine fever virus (ASFV) genotype II strains, recent molecular surveillance has revealed increasing genetic variability. These genetic changes raise important concerns regarding virus evolution and the performance of live attenuated vaccines (LAVs) currently deployed in Vietnam. This review aims to summarize the genetic evolution and discuss the prospects and challenges of live attenuated vaccines against ASFV in Vietnam.

Materials and Methods

A structured literature review was conducted using major scientific databases, including PubMed, Web of Science, and Scopus, supplemented by national surveillance reports and official technical documents. A total of 121 papers were identified, and available information on ASFV genomic variation, including mutations, multigene family (MGF) deletions, and recombination events, was synthesized and analyzed in relation to vaccine strain design, attenuation mechanisms, and post-vaccination observations.

Results and Discussions

Between 2019 and 2021, ASFV strains circulating in Vietnam showed high genetic similarity to the Georgia 2007/1 genotype II strain. Genomic analyses indicate that ASFV circulating in Vietnam has undergone progressive genetic diversification since 2022. Increasing genomic variation, including mutations and deletions in multigene family regions, and the emergence of recombinant genotype I/II strains have reshaped ASF molecular epidemiology and complicated surveillance, diagnostics, and control. Vietnam has become the first country to commercialize live attenuated ASF vaccines based on genotype II gene-deleted strains, representing a major milestone in ASF control. Experimental and field studies demonstrate that these vaccines can induce protective immunity; however, concerns remain regarding genetic stability, reversion to virulence, viral persistence, recombination with field strains, and reduced efficacy against emerging variants. Post-vaccination surveillance has revealed co-circulation of vaccine-like and recombinant viruses.

Conclusion

Rapid ASFV genetic evolution has increased molecular epidemiological diversity in Vietnam, highlighting the need for comprehensive genotype-phenotype surveillance. While biosecurity remains the primary control measure, hesitancy toward vaccination persists. Live attenuated vaccines are promising but require stringent assurance of safety and robust protective efficacy for wider adoption.

Keywords: African swine fever virus, Genetic evolution, Live attenuated vaccine, Recombinant strains, Vietnam.

EVALUATION OF MEMBRANE FILTRATION–BASED METHOD FOR DETECTING AFRICAN SWINE FEVER VIRUS IN WATER BY REAL-TIME PCR

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Introduction and Objectives

African swine fever virus (ASFV) is a highly contagious and environmentally stable pathogen that poses a significant threat to swine production. Contaminated water has been recognized as a potential transmission route, highlighting the need for sensitive methods to detect low concentrations of ASFV in water matrices.

Materials and Methods

ASFV suspensions with initial concentrations ranging from 3.3×10^4 to 3.3×10^0 HAD_{50}/mL were diluted 1:1000 by mixing 1 mL of virus with 999 mL of ASFV-free water. The diluted samples (1L each) were filtered under vacuum through 0.1 µm membrane filters at a stable negative pressure of approximately 600 mbar. Viruses retained on the membrane were eluted using 500 µL sterile PBS, followed by vortexing to release viral particles. The recovered volume (~ 200 µL) was subjected to DNA extraction and ASFV detection using a laboratory-validated real-time PCR assay. Each viral concentration was analyzed in triplicate. Recovery efficiency was estimated based on Ct value differences between treated samples and a reference virus control, assuming near-100% PCR amplification efficiency.

Results and Discussion

The reference control containing 6.6×10^3 HAD_{50} per 200 µL yielded a mean Ct value of 31.82. After dilution, filtration, and recovery, the corresponding samples showed a mean Ct of 33.05 ± 0.24, corresponding to a ΔCt of 1.235 and an estimated ASFV recovery efficiency of approximately 42.4%. ASFV was consistently detected (100%, 3/3) in samples with initial virus concentrations from 3.3×10^4 to 3.3×10^2 HAD_{50}/mL after membrane filtration, whereas diluted samples without filtration were PCR-negative. Detection became inconsistent at 3.3×10^1 HAD_{50}/mL (33.3%), and all samples at 3.3×10^0 HAD_{50}/mL were negative. The LOD and LOQ were both determined to be 3.3×10^{-1} HAD_{50}/mL, corresponding to a mean Ct of approximately 34.69.

Conclusion

The membrane filtration method using a 0.1 µm filter effectively concentrates ASFV from water samples, enabling sensitive and reproducible detection by real-time PCR. With a recovery efficiency of approximately 42.4% and a low LOD, this approach represents a practical tool for ASFV environmental surveillance and water biosecurity monitoring

Keywords: African swine fever virus, Membrane filtration, Water samples, Real-time PCR, Virus recovery.

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COMPARATIVE EVALUATION OF REAL-TIME PCR AND DROPLET DIGITAL PCR TARGETING P72 GENE FOR EARLY AND ACCURATE DETECTION OF AFRICAN SWINE FEVER VIRUS

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Introduction and Objectives

African swine fever (ASF) is a highly contagious viral disease with devastating economic impacts, requiring rapid and accurate diagnostic tools due to the lack of effective vaccines or treatments. Real-time PCR (qPCR) targeting the B646L (p72) gene is recommended by the World Organization for Animal Health (WOAH) as the reference diagnostic method. Droplet digital PCR (ddPCR), a third-generation PCR technology, enables absolute quantification without the need for standard curves and demonstrates greater tolerance to inhibitors. This study aimed to evaluate and compare the diagnostic performance of p72-based qPCR and ddPCR for the detection of African swine fever virus (ASFV), with a particular focus on early-stage and low-viral-load infections.

Materials and Methods

A total of 120 samples were analyzed, including 60 samples obtained from experimentally infected 8-week-old crossbred pigs (Landrace × Yorkshire × Duroc) challenged with ASFV genotype II (tissue and whole blood samples obtained at multiple time points post-infection) and 60 samples from healthy control pigs. Both qPCR and ddPCR assays targeted the ASFV p72 gene using identical primer–probe sets (King et al., 2003). qPCR was performed on a QuantStudio 5 system, while ddPCR was conducted using the QX200 Droplet Digital PCR platform.

Results and Discussion

All 60 samples from healthy control pigs tested negative by both assays, demonstrating 100% analytical specificity. Among samples from infected pigs, p72-ddPCR detected ASFV DNA in 58/60 samples (96.67%), whereas p72-qPCR identified 51/60 positive samples (85.00%). Seven samples that were negative or inconclusive by qPCR were confirmed positive by ddPCR, including three blood samples collected as early as 3 days post-infection. Absolute quantification showed that 6/7 discordant samples contained low viral copy numbers, likely below the detection threshold of conventional qPCR. These findings confirm the superior analytical sensitivity of ddPCR for early and low-level ASFV genotype II detection.

Conclusion

While p72-based qPCR remains a reliable and widely used method for routine ASFV diagnosis, p72-ddPCR provides enhanced analytical sensitivity, particularly for samples with low viral loads. The complementary use of ddPCR as a confirmatory tool can improve diagnostic accuracy, support early detection, and strengthen ASF surveillance and control programs.

Keywords: African swine fever virus, droplet digital PCR, early detection, p72 gene, real-time PCR.

Acknowledgements: The authors thank Nong Lam University HCMC, Vietnam and United Scientific Company (United Scientific), Vietnam for the support with providing testing facilities.

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POSSIBILITIES FOR THE REDUCTION OF AFRICAN SWINE FEVER VIRUS IN FEED THROUGH BIOACTIVE PLANT SUBSTANCES

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Introduction and Objectives

African swine fever remains one of the highest threats to global pork production. Although feed is not the main route of transmission, it is still a risk. Feed mitigants based on chemicals are already used (Niederwerder et al., 2021) but plant bioactives with antiviral activity could be a natural and environmentally friendly alternative. The objective of this study was the evaluation of plant-based ingredients (Phyt.A04, Phyt.B) for the development of a phytogenic feed mitigant (Anta®Shield, Dr. Eckel Animal Nutrition GmbH & Co. KG, Germany).

Materials and Methods

Two plant substrates (Phyt.A04, Phyt.B), either individually or in combination, were tested for their effect against ASFV in feed and compared to an organic acid blend (OAB). Untreated feed with ASFV was used as positive and just untreated feed as negative control. In total there were 14 groups. Commercial industrial pig feed spiked with ASFV (strain VNUA/HY/ASFI/Vietnam/2019) was treated with the test substances and inactivation of the virus was evaluated by cell culture test.

Results and Discussion

The ASFV titration assay showed that OAB and plant-based additives both reduced viral load of ASFV in the feed from day one to day seven. A dose-dependent decrease in viral HAD50 titers could be observed for all treatments already within 24 hours. The viral HAD50 titers in all samples treated with either the individual plant extracts or combinations thereof were below the detection limit of 1.5 $\log_{10}$ HAD50/ml by day three, while it took seven days for the OAB treatment. A combination of plant-based additives seemed to have better efficacy at lower dosage than OAB.

Conclusion

The feed additives used could inactivate ASFV in feed. The study showed that by adding certain bioactive substances derived from plants to the feed, the risk of ASFV transmission through the feed can be mitigated. Phytogenic additives can potentially reduce the viral load in feed and improve feed security. Suitable plant extracts can therefore be part of a comprehensive biosecurity concept to control the spread of ASFV.

Keywords: African swine fever, Antiviral activity, Phytogenics, Plant-based additives.

Acknowledgements: The authors thank the College of Veterinary Medicine, Vietnam National University of Agriculture (VNUA), Vietnam for the support.

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AFRICAN SWINE FEVER VIRUS DP71L SUPPRESSES STING - MEDIATED TYPE I INTERFERON SIGNALING

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Introduction and Objectives

African swine fever virus (ASFV) is a lethal virus that infects pigs. This large double-stranded DNA virus encodes 150 to 167 proteins, the functions of most of which remain unknown. Hence, the primary aim of this study was to elucidate the role of the ASFV DP71L protein in antiviral immunity, specifically focusing on its impact on type I interferon (IFN-I)-mediated responses. These responses play a critical role in the early defense against viral infections, and the cGAS-STING signaling pathway, often targeted by DNA viruses for immune evasion, is a key player in this process.

Materials and Methods

In this study, DP71L was identified as an IFN-I antagonist in STING-mediated IFN-β luciferase activity. We explored the antiviral role of DP71L in PK15, stable PAM, PIB, and MA-104 cells during GFP-tagged DNA virus infections, employing fluorescence microscopy and cytokine ELISA kits. The phosphorylation status of IFN-I molecules was evaluated through immunoblotting. Confirmation of the STING and DP71L interaction encompassed luciferase assays, mass spectrometry, and binding assays in HEK293T, PK15, and PAM-stable cells. Confocal imaging enabled the visualization of co-localization and STING/TBK1 puncta formation in HeLa and PK-15 cells. Immunoprecipitation of STING and DP71L domain constructs was conducted to pinpoint the interaction interface. Mutation analysis pinpointed crucial binding residues on STING.

Results and Discussion

Results revealed that DP71L specifically impeded the production of IFN-I induced by DNA viruses and the subsequent downstream signaling. The conserved protein phosphatase 1 motif of DP71L competed with the C-terminal tail of STING for interaction. This interaction was contingent on specific amino acids, namely P371Q, L374, and R375. Consequently, this interaction disrupted the binding of STING and TBK1, thereby inhibiting downstream antiviral signaling events involving IRF3.

Conclusion

The study underscores the importance of early antiviral defense through IFN-I-mediated responses and the cGAS-STING signaling pathway. Targeted by DNA viruses like ASFV, this pathway is crucial for immune evasion. ASFV DP71L inhibits IFN-I signaling via STING, revealing its role in suppressing IFN-I responses and providing insights for developing live-attenuated ASFV vaccines.

Keywords: ASFV DP71L, STING, Type-I interferon.

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AFRICAN SWINE FEVER VIRUS DP96R SUPPRESSES INTERFERON AND CYTOKINE PRODUCTION BY TARGETING IRF3 AND IKKA

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Introduction and Objectives

DP96R of African swine fever virus (ASFV), also known as uridine kinase (UK), encodes a molecularly uncharacterized protein. Researchers have been examining DP96R alongside other genes to create live attenuated vaccines. While experiments in pigs have explored the impact of DP96R on the pathogenicity of ASFV, the precise molecular mechanism underlying this phenomenon remains unknown. Here, we describe a novel molecular mechanism by which DP96R suppresses IRF3- and IKKα-mediated antiviral responses.

Materials and Methods

A large-scale pull-down and mass spectrometry analysis, interferon β (IFN-β), and NF-κB luciferase assays were conducted to determine the target of the ASFV DP96R protein in host immune response. Immunoprecipitation and immunofluorescence assays confirmed the ASFV DP96R protein interaction with IRF3 and IKKα. DNA virus replication was evaluated by infecting GFP-tagged ADV, HSV, and VACV viruses into DP96R stably expressing porcine macrophages (PAMs and PIBs), MA104 cells, and transiently transfected PK-15 cells. IFN-β, pro-inflammatory cytokine and chemokine secretion were assessed by ELISA. A mutation assay kit was used to construct different IRF3 mutations.

Results and Discussion

DP96R reduced cGAS-STING signaling and anti-viral gene transcription, enhancing DNA and RNA virus replication. Most notably, the ASFV DP96R is associated with the major karyopherin alpha (KPNA) binding residues of IRF3, inhibiting KPNA-activated IRF3 interaction and leading to inhibition of activated IRF3 nuclear translocation, which in turn reduces IFN production. Furthermore, DP96R specifically interacted with and inhibited the phosphorylation of IKKα, hampering the activation downstream of NF-κB. HSV-GFP induced transcription and translation of pro-inflammatory cytokines, and the chemokine was significantly decreased by DP96R protein. In particular, we discovered that the ASFV DP96R central region is crucial in suppressing IFNs and pro-inflammatory cytokine production.

Conclusion

Collectively, these findings underscore the pivotal role of DP96R in inhibiting IFN responses and increase our understanding of the relationship between DP96R and the virulence of ASFV.

Keywords: ASFV DP96R, IRF3, IKKα, KPNA.

Acknowledgements: This study was supported by the National Research Foundation (RS-2021-NR060136), Ministry of Food, Agriculture, Forestry and Fisheries (RS-2024-00402146), and Ministry of Environment (NIWDC-2024-SP-04).

AFRICAN SWINE FEVER VIRUS B354L INHIBITS THE CGAS–STING PATHWAY BY TARGETING CYCLIC GMP-AMP

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Introduction and Objectives

African swine fever virus (ASFV) is a highly contagious DNA arbovirus responsible for African swine fever (ASF). While some ASFV-encoded proteins have been characterized by their roles, the functions of many remain unexplored. B354L is one such protein predicted to possess ATPase activity, however, its specific role in the regulation of host immune responses has not yet been investigated. During DNA virus infection, the cytosolic DNA sensor cyclic GMP-AMP synthase detects viral DNA and catalyzes the synthesis of the second messenger 2'3'-cyclic GMP-AMP (cGAMP), which serves as a crucial signal for the activation of the host antiviral defense.

Materials and Methods

Screening of the ASFV gene library by adenovirus replication assay found B354L as a gene involved in promoting virus replication. This effect was further evaluated in B354L stably expressing PK-15 and PAM cells upon infecting GFP-tagged ADV, HSV, and VACV viruses. IFN-β, pro-inflammatory cytokine, chemokine, and cGAMP levels were assessed by ELISA. ATPase activity of B354L and its mutations were assessed using an ATPase assay kit. Immunoprecipitation assay confirmed the interaction between B354L and cGAMP.

Results and Discussion

Results revealed that B354L inhibits IFN responses by directly targeting cGAMP. B354L interacts with cGAMP and removes its phosphate groups via its intrinsic ATPase activity, thereby disrupting 2'3'-cGAMP structural integrity and impairing downstream immune signaling. ASFV lacking functional B354L exhibited diminished cGAMP degradation and reduced suppression of antiviral gene expression compared to wild-type virus. Additionally, we show that ATPase activity of B354L is essential for its immune antagonistic function, as treatment with ATPase inhibitors or mutation of ATPase motifs abolished its ability to degrade cGAMP. Moreover, three homologous viral proteins, Vaccinia virus A32L, Molluscum contagiosum virus MC140L, and Fowlpox virus FPV197 also exhibited ATPase-dependent degradation of cGAMP.

Conclusion

Our findings uncover a novel immune evasion strategy employed by B354L, in which it degrades cGAMP to suppress host IFN responses. These insights provide a mechanistic basis for ASFV pathogenesis and offer potential targets for the development of effective antiviral strategies and protective vaccines.

Keywords: ASFV B354L, ATPase, 2'3'-cGAMP, IFN.

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A PILOT STUDY OF AN EFFICACY OF INGEZIM® ASFV COMBO CROM AG/AB FOR DETECTION OF ASFV AND ASF-ANTIBODY IN BLOOD BANK SAMPLES AND THORACIC FLUID/ABDOMINAL FLUID IN MUMMIFIED PIGLET

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Introduction and Objectives

ASF is a devastating viral disease caused by ASFV, with nearly 100% mortality in domestic pigs and Eurasian wild boars (Blome et al., 2020). Since, there are currently no commercially available vaccines or effective antiviral drugs to fight ASFV infection. Rapid effective detection methods for clinical and subclinical diseases and strict biosecurity measures are critical for controlling ASF in pig farms. Recently, the emergence of low-virulence-strains-ASFV in recent years has led to false-negative-results of antigen testing, highlighting the importance of detection methods for both antigen and antibody of infected pigs.

Materials and Method

We tested Ag/Ab-lateral-flow-assay in the same cassette for both antigen/antibody detection to ASFV in whole blood. We used rt-PCR as a standard method for antigen detection (King et al., 2003, recommended by WOAH). For antigen detection in blood-samples, a double antibody sandwich assay employing latex nanoparticles was developed (INgezim® ASFV CROM Ag 2.0, GSD Madrid, Madrid, Spain). For antibody detection in blood-samples, a double-antigen-sandwich-assay based on colloidal gold nanoparticles was optimized (INgezim® ASFV CROM Ab 2.0, GSD Madrid, Madrid, Spain) (Aira et al., 2024). We tested known 19-positive-and-2-negative-blood-samples, and 2-unknown-thoracic-and-abdominal fluid bank-samples which were collected from pig farms with high percentage of mummification during 2022. All blood samples were positive by rt-PCR-ASFV-VP72-Ag, their CT-values varied from 21.060 to 26.687.

Results and Discussion

For the antigen test, this Ag/Ab-kit showed positive results in 15/19 blood samples; however, for the antibody test, there were no positive results were found. For thoracic/abdominal fluid samples, Ag/Ab-kit showed both positive results for antigen and antibody in 2/2 samples. Considering CT-values from rt-PCR, Ag/Ab-kit has ability to detect ASFV less than 26.687, indicating a number of virus particles in samples influence the antigen testing. All blood samples were antibody negative might be explained by acute infection in pigs. A positive antibody found in thoracic/abdominal fluid samples, lead to the implication for detection of ASFV circulation in subclinical sow herd.

Conclusion

Ag/Ab-lateral-flow-assay showed compromised results for detecting Ag/Ab of ASFV in pig blood and thoracic/abdominal fluid of mummy, providing a good specific tool for monitoring ASFV particular for Ab detection in mummy.

Keywords: African swine fever, Lateral flow, Mummy, rt-PCR.

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SURVEILLANCE AND BIOSECURITY MEASURES FOR MAINTENING AN ASF-FREE BREEDING FARM IN CHINA

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Introduction and Objectives

Since 2018, African Swine Fever (ASF) has profoundly affected global pig production, particularly in China where it has become endemic in several provinces, such as Henan. Despite this unfavorable environment, the Cooperl breeding farm (1,700 sows) has successfully maintained its ASF-free status. This study aims to show the biosecurity measures that have enabled the control of ASF virus contamination within this high-risk context.

Materials and Methods

The farm is divided by physical and behavioral barriers into three distinct zones: a public zone (visitor parking and sales dock), a professional zone (fenced, accessible via a sanitary lock/SAS and requiring a 72-h quarantine), and a production zone (delimited by building walls, requiring a second SAS). Between 2024 and 2025, 24,529 samples were analyzed. Sampling combined systematic approaches (daily animal checks, personnel tested at every entry, vehicles tested after cleaning) and random environmental swabbing. Samples were distributed across the public (9,563), professional (1,246), and production (>13,000) zones. Viral detection relied on fluorescence-based PCR (Beijing Yisen-Bio, China). Samples were classified as positive (Ct < 36), suspect (Ct 36 - 40), or negative.

Results and Discussion

Of the 24,529 samples tested, 66 were positive and 44 were suspected. In the public zone, 63 positive and 41 suspect cases were detected out of 9,563 samples (1.09% positivity), mainly tracing back to personnel and external trucks. The professional zone yielded 3 positive and 3 suspect cases out of 1,246 samples (0.48%), mostly in the living area. Crucially, zero positive or suspect cases were found among the more than 13,000 production zone samples. Upon detecting the virus, implicated matrices were strictly denied access to subsequent zones without undergoing additional cleaning and disinfection protocols. These results demonstrate the effectiveness of spatial organization into successive barriers (zoning) and the critical importance of cleaning and disinfection protocols.

Conclusion

Maintaining an ASF-free status in endemic regions is achievable through multilayered biosecurity, systematic PCR surveillance, and constant operational vigilance. This success relies on the mobilization of adequate resources and strict adherence by all stakeholders to sanitary prevention principles.

Keywords: African Swine Fever (ASF), Biosecurity, Systematic PCR surveillance, China, Disease prevention.

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DEVELOPMENT AND CHARACTERIZATION OF A HIGH-EFFICIENCY CELL-ADAPTED LIVE ATTENUATED VACCINE CANDIDATE ASFV-MEC-01 AGAINST AFRICAN SWINE FEVER

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Introduction and Objectives

African Swine Fever (ASF) remains one of the most devastating viral diseases affecting domestic pigs and wild boars, posing substantial threats to global food safety. Recently, ASFV has extended its geographical area from Central Europe to East Asia, causing tremendous economic losses to the local swine industry. The absence of a commercial vaccine heightens the vulnerability of swine populations to widespread outbreaks. This study aimed to develop a safe and efficient live attenuated ASFV vaccine that offers protection against ASFV in domestic pigs.

Material and Methods

To develop a cell-adapted live attenuated ASFV genotype II strain that replicates effectively in an established cell line, South Korea/Wild boar/Hwacheon/2020 virus was serially passaged into the CA-CAS-01-A cell line. Replication of ASFV in CA-CAS-01-A cells increased with increasing number of passages, and a specific clone of ASFV-KOR.INJE.MEC-01.2022 (ASFV-MEC-01) was isolated via plaque purification after 18 passages. To assess the genetic changes acquired during the adaptation, next-generation sequencing (NGS) was performed. In order to define the safety and efficacy, the attenuated vaccine candidate ASFV-MEC-01 was administered intramuscularly to 6-week-old piglets. ASFV-specific antibody production, disease severity and survival in lethal parental strain challenge was determined.

Results and Discussion

NGS analysis revealed that ASFV-MEC-01 lacked 12 genes within the multigene family (MGF) region compared with the parental strain. In vivo evaluation demonstrated that the virus was completely attenuated in pigs inoculated with two doses of 10^5 HAD_{50} remained clinically healthy and showed no signs of ASF. Notably, all vaccinated pigs were fully protected against lethal challenge with the parental ASFV strain at dpv 28, achieving 100% survival. This protection correlated with the induction of high ASFV-specific antibody titers. Functional analysis further indicated that the deleted MGF genes are involved in antagonizing the host innate antiviral immune response, supporting their role as key virulence determinants and explaining the observed attenuation phenotype.

Conclusion

These findings demonstrate that ASFV-MEC-01 is a safe and promising live-attenuated vaccine candidate against the current ASFV outbreak. The attenuation of virulence is likely mediated by enhanced activation of host innate antiviral immune responses resulting from the deletion of MGF genes.

Keywords: African swine fever, ASFV-MEC-01, CA-CAS-01-A cell, Live-attenuated virus.

Acknowledgements: This study was supported by the Ministry of Environment (NIWDC-2021-SP-02) and National Research Foundation (RS-2021-NR060136).

EVALUATION OF THE VACCINE CANDIDATE ASFV-MEC-01: SAFETY, EFFICACY, TRANSMISSION DYNAMICS, AND ASSESSMENT OF REVERSION TO VIRULENCE

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Introduction and Objectives

African swine fever (ASF) is a highly lethal transboundary disease that continues to cause severe economic losses worldwide. Live-attenuated virus (LAV) vaccines show the greatest potential for ASF control, but their development is constrained by safety concerns. This study evaluated the safety, efficacy, transmission potential, and phenotypic stability of the live-attenuated African swine fever virus vaccine candidate ASFV-MEC-01.

Materials and Methods

ASFV-MEC-01 was generated by serial passaging of a virulent field isolate in the CA-CAS-01-A cell line. Safety and protective efficacy were assessed in piglets challenged with a highly virulent Vietnamese ASFV strain. Vaccine safety in pregnant sows was evaluated through clinical observation, virological testing, and assessment of reproductive outcomes. Horizontal and vertical transmission were examined by commingling vaccinated animals with naïve sentinel pigs under standard and high-dose vaccination conditions. Reversion to virulence was assessed through consecutive in vivo passages.

Results and Discussion

ASFV-MEC-01 vaccination provided complete protection against lethal ASFV challenge, with all vaccinated piglets surviving without clinical disease or persistent viremia. Vaccinated pregnant sows remained clinically healthy and produced normal fetuses, with no evidence of vertical transmission. No viral shedding, ASFV genome detection, or seroconversion was observed in sentinel pigs, indicating the absence of horizontal transmission. Importantly, ASFV-MEC-01 maintained a stable attenuated phenotype during serial in vivo passages, showing no evidence of reversion to virulence. Vaccinated pigs developed robust and sustained ASFV-specific antibody responses without signs of chronic infection.

Conclusion

ASFV-MEC-01 demonstrates strong protective efficacy, an excellent safety profile, and phenotypic stability, supporting its potential as a safe live-attenuated vaccine candidate for African swine fever control.

Keywords: African swine fever, ASFV-MEC-01, Live attenuated virus, Reversion to virulence, Vaccine.

Acknowledgements: This study was supported by the Ministry of Environment (NIWDC-2024-SP-04) and National Research Foundation (RS-2021-NR060136).

PATHOLOGICAL STUDY OF THE FIRST OUTBREAK WITH AFRICAN SWINE FEVER VIRUS IN TAIWAN, 2025

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Introduction and Objectives

African swine fever (ASF) is a highly fatal hemorrhagic disease of domestic pigs and wild boars. On October 21, 2025, African swine fever virus (ASFV) nucleic acid was detected in a domestic pig farm in Wuqi District, Taichung City, Taiwan. Clinical signs, including wheezing, nasal bleeding, and sudden death, were first observed in finishing pigs on October 10, 2025. Between October 10 and 20, 97 pigs died, corresponding to a mortality rate of 30%. This study describes the pathological and immunohistochemical (IHC) features of this index case to provide baseline diagnostic information for ASF in Taiwan.

Materials and Methods

Tissue samples from three pigs including spleen, liver, kidney, lung, and lymph nodes were submitted to the Veterinary Research Institute for diagnostic investigation. All samples handling and processing were conducted in a biosafety level 3 laboratory and collected for molecular detection and histopathological examination. For histological analysis, tissues were fixed in 10% neutral buffered formalin for 48 hours prior to further processing. ASFV was detected in all tissues using real-time polymerase chain reaction (PCR) and conventional PCR assays targeting the p72 gene. Formalin-fixed tissues were examined by histopathology and IHC stain using anti-ASFV p30 monoclonal antibody developed at the Veterinary Research Institute.

Results and Discussion

Gross lesions included red-to-purple skin discoloration, enlargement and hemorrhage of lymph nodes, hemorrhagic kidneys, and splenomegaly. Histopathology revealed severe lymphoid depletion with extensive apoptosis, congestion, and hemorrhage in the spleen and lymph nodes. Additional findings included hepatic portal inflammation, renal hemorrhage with tubular necrosis, and severe pulmonary lesions characterized by interstitial pneumonia, hemorrhage, and edema. ASFV antigen was detected in all examined tissues from all three pigs. Abundant ASFV antigens were detected by IHC predominantly in macrophages within lymphoid tissues and the lung, with only occasional positivity in vascular endothelial cells, hepatocytes and renal tubular epithelial cells.

Conclusion

Consistent lesions and immunoreactivity were observed among the three pigs. Characteristic lesions included severe lymphoid depletion and hemorrhagic lesions with the marked tropism of ASFV for the mononuclear phagocyte system. These findings provide essential baseline pathological evidence to support ASF diagnosis in Taiwan.

Keywords: African swine fever, Histopathological examination, Immunohistochemistry.

ENVIRONMENTAL DETECTION OF AFRICAN SWINE FEVER VIRUS DNA IN VIETNAM: EVIDENCE FROM WASTEWATER AND *AMBLYOMMA JAVANENSE* TICKS

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Introduction and Objectives

African swine fever (ASF) is one of the most devastating transboundary diseases of pigs, causing major economic losses worldwide. ASF virus (ASFV) can persist in environmental matrices, supporting indirect transmission (Mazur-Panasiuk et al., 2019). Although wastewater-based surveillance is increasingly used for early pathogen detection (Ahmed et al., 2020), its application for ASF remains limited. This study aimed to detect ASFV DNA in pig farm wastewater and Amblyomma javanense ticks in Vietnam and to optimize a polyethylene glycol (PEG)-based real-time PCR approach to improve detection sensitivity in low-viral-load samples, building on previously validated methods (Mai et al., 2025).

Materials and Methods

A total of 93 wastewater samples and 40 tick samples were analyzed. Ticks were collected from confiscated Sundapangolins (Manis javanica) temporarily housed at the wildlife rescue center in Northern Vietnam before release. Wastewater samples were concentrated using PEG precipitation before DNA extraction. ASFV detection targeted the p72 gene by real-time PCR. Diagnostic performance of the PEG-based method was compared with conventional extraction.

Results and Discussion

ASFV DNA (Ct ≤ 37.00) was detected in 7.5% (7/93) of wastewater samples and 7.5% (3/40) of tick samples. Median Ct was 32.47 (range 31.09 - 35.51) for wastewater and 35.68 (range 34.66 - 36.80) for ticks. All positive samples were confirmed by repeat qPCR. Virus isolation in PAM cells was attempted for positive wastewater samples, but no infectious virus was recovered, likely due to low viral loads. The PEG-based method improved analytical sensitivity by approximately 100-fold and reduced Ct values by 3–7 cycles, increasing the detection rate from 3.2 to 7.5% compared with the conventional protocol. Diagnostic sensitivity (100%) and specificity (95.6%) were calculated using the conventional method as reference. Wastewater detection preceded clinical outbreaks on certain farms, indicating potential value for early environmental surveillance. Detection of ASFV DNA in A. javanense suggests environmental exposure; biological transmission cannot be inferred.

Conclusion

This study provides molecular evidence of ASFV DNA in pig farm wastewater and in A. javanense ticks in Southeast Asia. The optimized PEG-based qPCR enhances detection sensitivity in environmental matrices and supports environmental surveillance for early ASF warning in endemic settings.

Keywords: African swine fever virus, *Amblyomma javanense*, PEG precipitation, Vietnam, Wastewater surveillance

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AFRICAN SWINE FEVER VIRUS L11L INTERFERES WITH ANTIVIRAL RESPONSES BY TARGETING THE IRF3 AND PKR

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Introduction and Objectives

African Swine Fever Virus (ASFV) is a complex DNA virus causing a highly fatal disease in domestic and wild pigs. While ASFV is known to employ various proteins to subvert host immunity, the specific functions of many viral proteins, including L11L, remain poorly understood. This study aimed to elucidate the molecular mechanisms by which ASFV L11L evades type-I interferon (IFN-I) pathways and protein kinase R (PKR)-mediated antiviral responses.

Materials and Methods

The L11L gene was cloned into Flag-tagged pIRES and GST-tagged pEGB vectors. Host targets were identified using large-scale mass spectrometry and IFN-β reporter assays. Protein interactions were validated via co-immunoprecipitation and immunofluorescence. To assess functional impact, DNA virus replication (ADV-GFP, HSV-GFP, and VACV-GFP) was evaluated in L11L-expressing porcine macrophages, MA104, and PK-15 cells. Cytokine and chemokine secretions were quantified by ELISA.

Results and Discussion

ASFV L11L significantly enhanced DNA and RNA virus replication by suppressing cGAS-STING signaling and subsequent antiviral gene transcription. Mechanistically, L11L directly interacted with the Autoinhibitory Element (AIE) of IRF3, specifically targeting residues S396 and S398 to inhibit its phosphorylation. Simultaneously, L11L interfered with the PKR pathway by binding to the K196 residue, which physically hindered PKR dimerization, autophosphorylation, and the subsequent phosphorylation of eIF2α. This dual-targeting strategy resulted in the profound suppression of IFNs and pro-inflammatory cytokines.

Conclusion

These findings identify ASFV L11L as a critical virulence factor that targets two major immune modulators, IRF3 and PKR, to facilitate a permissive environment for viral growth. By characterizing these novel interactions, this study provides a molecular basis for the strategic deletion of L11L in the development of safe and effective live-attenuated vaccines (LAVs) against ASFV.

Keywords: African swine fever virus, eIF2α, IRF3, L11L, PKR.

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ASFV A238L SUPPRESSES INNATE IMMUNE SIGNALING BY TARGETING STING AND TLR9

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Introduction and Objectives

African swine fever (ASF) is a highly contagious disease caused by the African swine fever virus (ASFV), which exploits various immune evasion mechanisms. ASFV A238L, an early gene, has been identified for its ability to suppress the transcription of immunoregulatory genes. In this study, we identified a dual molecular mechanism by which A238L suppresses the type I interferon pathway.

Materials and Methods

ASFV A238L was identified as a negative regulator of type I interferon pathway by a STING mediated IFN-β luciferase assay. The antiviral role of A238L was explored during DNA virus infections and CpG-DNA treatment, employing fluorescence microscopy and cytokine ELISA in different cells. The phosphorylation status of type I interferon pathway molecules was evaluated through immunoblotting. Large-scale mass spectrometry analysis was conducted to determine the target of A238L. Binding assays and immunofluorescence assays were used to confirm A238L interaction with target host proteins.

Results and Discussion

A238L inhibits DNA virus-induced type I interferon signaling through its interaction with STING. Specifically, A238L interacts with the 330-340 region of STING, a crucial domain for type I interferon induction and cGAMP-induced autophagy through its association with the COPII vesicle component Sec24C. Mutation analysis revealed that A238L interacts with residues L333 and R334 of STING, hindering the STING-Sec24C interaction. This inhibition blocks the formation of STING-containing COPII vesicles and the subsequent translocation of STING into the ERGIC. Consequently, it inhibits IFN-β production and cGAMP-induced autophagy. Furthermore, A238L interacts with 660 - 725 region of TLR9, which is important to CpG binding. Thereby it inhibits type I interferon and pro-inflammatory cytokine production induced by CpG-DNA and DNA virus infection.

Conclusion

Overall, these findings highlight the crucial role of the ASFV A238L in evading the host innate immune response. By inhibiting the cGAS-STING and TLR9 signaling pathways, A238L ensures the effective suppression of the antiviral signaling and promotion of DNA virus replication. This research provides a promising new target to guide the advancement of safe and effective live-attenuated ASFV vaccines.

Keywords: A238L, STING, TLR9, Type I Interferon.

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AFRICAN SWINE FEVER VIRUS MGF505-3R INDUCES MITOCHONDRIAL APOPTOSIS BY TARGETING VDAC3 AND ANT3

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Introduction and Objectives

African swine fever virus (ASFV) causes a highly lethal hemorrhagic disease in domestic pigs and wild boars. ASFV infection is known to trigger host cell apoptosis; however, the viral factors and molecular mechanisms involved are not well characterized. Members of the ASFV multigene family (MGF) are implicated in viral pathogenesis, but their roles in apoptosis remain unclear. This study aimed to identify ASFV proteins that induce apoptosis and to elucidate the molecular mechanism by which MGF505-3R promotes host cell death.

Materials and Methods

An ASFV gene library containing 158 viral genes was screened to identify apoptosis-inducing proteins. MGF505-3R was selected for further analysis. Mass spectrometry was performed to identify host proteins interacting with MGF505-3R. Protein-protein interactions were validated using immunoprecipitation assays. The effects of MGF505-3R on mitochondrial membrane permeabilization were investigated by analyzing its interaction with mitochondrial transition pore complex components. Cytochrome c release was quantified using porcine cytochrome c ELISA in MGF505-3R-overexpressing porcine macrophage (3D4/21) and epithelial (PK-15) cells. Apoptosis was assessed by examining caspase activation and PARP-1 cleavage.

Results and Discussion

Screening of the ASFV gene library identified MGF505-3R as a pro-apoptotic protein. Mass spectrometry analysis revealed that MGF505-3R interacts with mitochondrial transition pore complex proteins, including voltage-dependent anion channel-3 (VDAC3) and adenine nucleotide translocase-3 (ANT3). MGF505-3R interaction with the β-barrel domain of VDAC3 promoted VDAC3 aggregation and pore formation in the outer mitochondrial membrane. In addition, MGF505-3R binding to ANT3 increased mitochondrial membrane permeabilization, resulting in the release of cytochrome c into the cytoplasm. Elevated cytoplasmic cytochrome c levels were confirmed in MGF505-3R-overexpressing cells.

Conclusion

This study demonstrates that ASFV MGF505-3R induces apoptosis through a mitochondria-dependent pathway by targeting key components of the mitochondrial transition pore complex. These findings provide new insights into ASFV-induced apoptosis and highlight MGF505-3R as a potential target for antiviral strategies and vaccine development.

Keywords: ASFV, ANT3, MGF505-3R, VDAC3.

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SINGLE-CELL RNA-SEQ ANALYSIS OF PBMCS FROM PIGS INFECTED WITH VIRULENT AFRICAN SWINE FEVER VIRUS

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Introduction and Objectives

African swine fever virus (ASFV) is the causative agent of a viral hemorrhagic disease. Previous studies have applied single-cell RNA sequencing (scRNA-Seq) to in vitro porcine alveolar macrophage infection and to spleen tissue, revealing profound immune dysregulation. The objective of this study was to characterize peripheral blood mononuclear cell (PBMC) immune responses during virulent ASFV infection, as defining the mechanisms underlying severe disease is essential for guiding vaccine development.

Materials and Methods

An experimental infection of six pigs with the virulent strain ASFV Arm/07/CBM/c2, while six uninfected pigs served as controls. PBMCs were isolated whole blood collected at 0, 1, 2, 3, 4, 5, and 7 days post infection (dpi) and subjected to scRNA-Seq analysis.

Results and Discussion

Viral RNA was mainly detected in a newly recruited $CD14^+$ monocyte population. Immature monocytes appeared during infection consistent with emergency release of immature cells from the bone marrow. Across circulating immune cells, early interferon activity was accompanied by broad suppression of genes involved in cell movement, adhesion, and immune activation. Cytotoxic lymphocytes produced effector molecules but displayed reduced capacity to engage infected targets, indicating functionally limited responses. Reduced expression of homing-related genes across B and T cells suggested impaired migration to lymphoid tissues, where coordinated antibody responses normally develop. These patterns were consistent across all animals, highlighting a coordinated disruption of systemic immune function during virulent ASFV infection.

Conclusion

Virulent ASFV infection establishes early viral replication niches and induces widespread immune dysfunction, limiting cytotoxic responses and driving rapid clinical deterioration. These findings define critical immune failure points, emphasizing that protective strategies must act early to maintain coordinated and effective immune control.

Keywords: African swine fever, Infection, PBMC, scRNA-Seq, Transcriptomics.

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EVALUATION OF THE SAFETY AND EFFECTIVENESS OF THE AVAC ASF LIVE VACCINE FOR PREVENTING AFRICAN SWINE FEVER UNDER FIELD CONDITIONS

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Introduction and Objectives

African swine fever (ASF), caused by the African swine fever virus (ASFV), continues to pose a major threat to global pig production. Among current control strategies, live attenuated vaccines (LAVs) have shown promising protection (Zhang et al., 2023). AVAC ASF LIVE, a gene-deleted live attenuated vaccine, has previously demonstrated safety and efficacy under controlled experimental conditions (Diep et al., 2025). This study aimed to evaluate the safety and protective efficacy of AVAC ASF LIVE under real-world field conditions.

Materials and Methods

A field trial was conducted at four commercial pig farms in Vietnam using healthy crossbred pigs aged 4–13 weeks with no prior ASF vaccination. Pigs received a single dose of live attenuated AVAC ASF LIVE and were monitored daily for clinical signs and rectal temperature. At 28 days post-vaccination, blood samples from ≥30 pigs per farm were collected for ELISA. Five unvaccinated and five seropositive pigs per farm were randomly selected and challenged with a virulent genotype II ASFV strain. Post-challenge, pigs were observed for 21 days for clinical signs, fever, morbidity, and mortality, and blood and oral fluids were collected on days 5, 10, 14, and 21 for ASFV DNA detection by real-time PCR.

Results and Discussion

Vaccination of 4,892 pigs across four commercial farms demonstrated an excellent safety profile, with no post-vaccination adverse reactions observed. On 28 days post-vaccination, 90.1% (range: 88.2 - 91.9%) of tested pigs were seropositive for ASFV antibodies. Following challenge with a highly virulent genotype II ASFV strain, all unvaccinated control pigs developed severe clinical signs and died within 9 days (100% mortality). In contrast, vaccinated pigs showed 80 - 100% survival across farms, with an overall protective efficacy of 95%. Viremia levels in vaccinated animals were markedly lower than in controls, and oral shedding of challenge virus was almost completely prevented, except in one non-protected animal.

Conclusion

AVAC ASF LIVE vaccine was demonstrated to be safe and effective under field conditions, providing strong protection against circulating genotype II ASFV and reducing viral replication and transmission risk. These findings support its use as a practical control tool for African swine fever.

Keywords: African swine fever, ASF live vaccine, Field trials, Vaccination.

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PRELIMINARY EVALUATION OF CROSS-PROTECTIVE EFFICACY OF THE AVAC ASF LIVE VACCINE AGAINST RECOMBINANT RASFV I/II STRAIN IN EXPERIMENTAL PIGS UNDER VARIOUS VACCINATION REGIMENS AND CHALLENGE DOSES

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Introduction and Objectives

The emergence of the recombinant ASFV strain rASFV I/II challenges current vaccine efficacy. Given inconsistent reports on cross-protection and the ability of low viral doses to cause disease, this study evaluated the cross-protective efficacy of AVAC ASF LIVE vaccine against rASFV I/II at 10 - 200 HAD_{50} and assessed whether a two-dose regimen enhances protection.

Materials and Methods

Two independent studies were conducted in 26 healthy 5-week-old crossbred pigs to evaluate the protective efficacy of AVAC ASF LIVE under single- and two-dose regimens. In Experiment 1 (n = 16), pigs received one vaccine dose (n = 10) or PBS (n = 6) and were challenged at 28 days post-vaccination with rASFV I/II at 10 or 100 HAD_{50}. In Experiment 2 (n = 10), pigs received two doses 21 days apart (n = 6) or PBS (n = 4) and were challenged 28 days after the second dose with 20 or 200 HAD_{50}. All pigs were monitored for 21 days post-challenge, and blood samples were collected for antibody and ASFV DNA analysis.

Results and Discussion

Single-dose vaccination: All vaccinated pigs seroconverted by day 14 post-vaccination. After challenge, complete protection was observed at 10 HAD_{50} (100% survival, no viremia), whereas partial protection was recorded at 100 HAD_{50} (40% survival) with detectable viremia in some pigs. All control pigs developed acute ASF and died.

Two-dose vaccination: Seropositivity was maintained at 100% following the second vaccination. Full protection was achieved at a challenge dose of 20 HAD_{50} (100% survival), and 66.7% survival was observed at 200 HAD_{50}. All control pigs succumbed to infection. Overall, AVAC ASF LIVE provided effective cross-protection at lower challenge doses, with improved survival under the two-dose regimen.

Conclusion

This preliminary study suggests that the cross-protective efficacy of the AVAC ASF LIVE vaccine against the recombinant rASFV I/II strain depends on both the vaccination regimen and the challenge dose. The two-dose regimen provided stronger protection than a single dose, and efficacy decreased as the challenge dose increased. Further studies with larger sample sizes are needed to confirm these findings and optimize vaccination strategies for ASF control.

Keywords: African swine fever, ASF vaccine, Cross-protection, Recombinant rASFV I/II strain.

Acknowledgements: The authors would like to thank the AVAC staff for their support in caring for the animals during the experiment.

A NOVEL LIVE ATTENUATED ASF VACCINE CANDIDATE PROVIDING BROAD PROTECTION AGAINST EMERGING RECOMBINANT GENOTYPE I/II AND GENOTYPE II VIRUSES IN ASIA

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Introduction and Objectives

A highly virulent recombinant ASFV strain combining genotypes I and II (rASFV I/II) has recently emerged and spread in several Asian countries, including Vietnam (Le et al., 2023). Commercial live attenuated vaccines (LAVs) developed from genotype II strains have demonstrated limited protection against rASFV I/II infection (Diep et al., 2024). Therefore, there is an urgent need to develop novel vaccines capable of conferring protection against both genotype II and rASFV I/II strains. This study aimed to evaluate the safety and protective efficacy of a novel live attenuated vaccine candidate, AVAC-rASF-9L.

Materials and Methods

AVAC-rASF-9L was generated from a highly virulent recombinant ASFV genotype I/II strain through targeted deletion of nine genes belonging to the MGF360 and MGF505 gene families using CRISPR/Cas12a technology. Fifteen 4-week-old crossbred pigs were inoculated intramuscularly with 10^4 or 10^6 HAD_{50} of AVAC-rASF-9L to evaluate safety and immunogenicity; six controls received PBS. Clinical signs (Gallardo et al., 2015) and seroconversion were monitored post-vaccination (dpv). At 28 dpv, pigs vaccinated with 10^4 HAD_{50} were challenged with 10^2 HAD_{50} of either the parental rASFV I/II or a virulent genotype II strain and observed for 28 days.

Results and Discussion

AVAC-rASF-9L was safely attenuated, as all vaccinated pigs remained clinically healthy without ASF-associated signs across all tested doses. Seroconversion occurred in 100% of vaccinated pigs within three weeks post-vaccination, indicating a robust humoral immune response. The vaccine virus was sporadically detected at low viral loads in fecal or oro-nasal swabs collected at 7, 14, 21, or 28 dpv. Low-level viremia was detected in vaccinated pigs between 7 and 28 dpv. Importantly, while all control pigs died within two weeks post-challenge, 100% of pigs vaccinated with 10^4 HAD_{50} were fully protected against challenge with either the parental recombinant rASFV I/II strain or the virulent genotype II strain, showing complete survival and no clinical signs throughout the 28-day observation period.

Conclusion

AVAC-rASF-9L is a safely attenuated and highly efficacious live vaccine candidate that provides complete protection against both genotype II and recombinant genotype I/II ASFV strains.

Keywords: African swine fever, Genotype II, Live attenuated vaccine, Recombinant genotype I/II, rASFV I/II.

Acknowledgements: The authors would like to thank the AVAC staff for their support in caring for the animals during the experiment

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DEVELOPMENT OF AN INDIRECT ELISA FOR THE DETECTION OF ANTIBODIES AGAINST THE AFRICAN SWINE FEVER VIRUS USING THREE RECOMBINANT P30, P54, AND P72 ANTIGENS

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Introduction and Objectives

African swine fever (ASF) is a highly contagious viral disease causing major economic losses in the pig industry. ASFV induces strong antibody responses, particularly against structural proteins p30, p54, and p72, which are widely used in serological assays. This study aimed to develop an indirect ELISA based on a hybrid antigen combining these proteins to enhance antibody detection and support routine diagnosis and surveillance.

Materials and Methods

A hybrid gene containing ASFV p30, p54, and p72 fragments was constructed and expressed in E. coli BL21. The recombinant protein was induced with IPTG, purified, and confirmed by SDS-PAGE and Western blot using ASFV-positive and negative sera. An indirect ELISA was developed using antigen-coated plates. Optimal conditions were determined by checkerboard titration, and ROC analysis defined the diagnostic cut-off. A total of 378 pig serum samples were tested with both the developed ELISA and a commercial kit to evaluate performance.

Results and Discussion

The recombinant 3WKPSF protein was successfully expressed as a 45 kDa band. Western blot confirmed specific reactivity with ASFV-positive sera. Positive samples showed S/P ratios ≥ 0.402, while negatives were ≤ 0.400. ROC analysis demonstrated excellent diagnostic performance (AUC = 1.00). Comparison with the commercial kit showed high agreement (Kappa = 0.968), indicating comparable accuracy.

Conclusion

The 3WKPSF KU indirect ELISA demonstrated high diagnostic performance comparable to a commercial kit and is appropriate for ASF diagnosis and surveillance.

Keywords: African swine fever, Antibodies, Indirect ELISA, Serum.

Acknowledgements: This research was financially supported by the project of Immune Detection for Swine Disease with ELISA technique, Department of Farm Resource and Production Medicine, Faculty of Veterinary Medicine, Kasetsart University.

DATA ANALYTICS APPLICATIONS FOR AFRICAN SWINE FEVER HEALTH RISK ASSESSMENT IN COLOMBIA

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Introduction and Objectives

African Swine Fever (ASF) poses a critical threat to the swine industry because of its severe impact on productivity and health (Ruiz et al., 2022). Although Colombia remains disease-free, the detection of the virus in the Caribbean underscores the urgent need to implement analytical tools to respond to potential disease introduction (FAO, 2022). This study aims to propose the application of Data Analytics to quantify the Health Risk of ASF introduction into Colombia.

Materials and Methods

A multivariate model integrating the Hazard, Vulnerability, and Exposure components of Health Risk was developed. Following a Systematic Information Review supported by A.I. tools, Risk Categories and Factors were defined, weighted, and prioritized using Expert Criteria. The resulting values were normalized to generate probability indices from 0 to 1, which were then spatialized at the municipal level using map algebra. Through the construction of Hazard and Vulnerability Indices, the probable impact of ASF was established by calculating animal exposure across the 193,361 farms under study.

Results and Discussion

Six Categories comprising 28 Risk Factors were defined, enabling the identification of municipalities at the highest risk of ASF introduction in Colombia based on structural vulnerabilities stemming from deficiencies in human, animal, and product movement control, as well as the absence of swine isolation units. Of the 9, 926, 922 pigs registered on producing farms, 45% face 80 - 100% risk levels and 50% face 40 - 80% risk levels, highlighting the minimum 90% morbidity and high potential lethality of ASF. Strict biosecurity measures and epidemiological surveillance are justified, particularly in border areas.

Conclusion

It is a strategic tool that enables the identification of potential ASF introduction scenarios, thereby optimizing resources and improving response capacity for a potential introduction, an instrument that strengthens and supports strategic decision-making to maintain health status.

Keywords: African Swine Fever, Data Analytics, Health Risk, Quantitative epidemiological surveillance.

Acknowledgements: The authors would like to express their sincere gratitude to DataLab-UNAL (Erika Camacho, David Gonzalez, Andres Torres, Andres Daza, Andres Bermudez and Johanna Avila) and Porkcolombia-FNP (Adriana Deluque and Juan Angulo) for their significant contribution to this project.

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EVALUATION OF PROSIDIUM™: A NOVEL PEROXYPROPIONIC ACID-BASED SOLUTION FOR THE MITIGATION OF AFRICAN SWINE FEVER VIRUS (ASFV) IN FEED

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Introduction and Objectives

African swine fever virus (ASFV) remains one of the most economically devastating pathogens in global swine production. Increasing evidence indicates that contaminated feed and feed ingredients can act as vehicles for viral transmission, complicating farm-level and regional biosecurity programs. Current formaldehyde-free mitigants - particularly short- and medium-chain organic acid-based products - often exhibit inconsistent virucidal activity, slow inactivation kinetics, and reduced efficacy in complex feed matrices. There is a critical need for next-generation feed biosecurity solutions capable of rapid and reliable viral inactivation under commercial conditions. This study evaluated PROSIDIUM™, a novel proprietary peroxypropionic acid (PPA)-based antimicrobial engineered for rapid oxidative viral inactivation and matrix stability.

Materials and Methods

Virucidal activity against ASFV and Modified Vaccinia virus Ankara (MVA), a validated ASFV surrogate, was evaluated in aqueous and feed matrices using 50% hemadsorption (HAD_{50}) and tissue culture infectious dose ($TCID_{50}$) assays. Initial virus titers were 6 $\log_{10}$ HAD_{50}/mL (ASFV) and 5 $\log_{10}$ $TCID_{50}$/mL (MVA). PROSIDIUM™ was tested at multiple concentrations and contact times. Residual infectivity was quantified, with detection limits (LOD) of 1.5 $\log_{10}$ HAD_{50}/mL (ASFV) and 2 $\log_{10}$ $TCID_{50}$/mL (MVA). Treatments were performed in independent replicates and analyzed by one-way ANOVA with Tukey post-hoc tests ($P < 0.05$).

Results and Discussion

PROSIDIUM™ demonstrated rapid, concentration-dependent virucidal activity consistent with strong oxidative inactivation kinetics. In suspension assays, PPA completely inactivated MVA at 500 ppm within one hour, whereas leading organic acid–based mitigants showed only marginal reductions under identical conditions, underscoring the limitations of pH-dependent systems in inactivating enveloped viruses. PROSIDIUM™ reduced ASFV infectivity to undetectable levels at concentrations as low as 200 ppm within 30 minutes, indicating rapid disruption of this notoriously resilient, large DNA virus. Under feed conditions characterized by high organic load and buffering capacity, PROSIDIUM™ maintained robust antiviral efficacy. At 2,500 g/ton, consistent multi-log viral reductions were achieved in complete feed, demonstrating superior matrix penetration and stability compared with both formaldehyde-free organic acid blends and traditional aldehyde systems.

Conclusion

PROSIDIUM™ delivers rapid, broad-spectrum virucidal activity with strong matrix resilience, supporting its potential as a next-generation tool for feed biosecurity against endemic and emerging swine viruses.

Keywords: African Swine Fever, Feed Biosecurity, Peroxypropionic acid, PROSIDIUM, Organic Acids.

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FIELD-DEPLOYABLE CRISPR-GLUCOMETER PLATFORM FOR RAPID GENOTYPE DIFFERENTIATION OF AFRICAN SWINE FEVER VIRUS

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Introduction and Objectives

The emergence of African swine fever virus (ASFV) genotype I - II recombinants has complicated disease control, as genotype II-based vaccines provide limited cross-protection against heterologous strains (Zhao et al., 2023; Lee et al., 2024). Consequently, rapid, field-deployable diagnostics that can differentiate ASFV genotypes are urgently needed. We developed a point-of-care testing platform integrating recombinase polymerase amplification (RPA) with CRISPR-Cas12a for rapid genotype discrimination.

Materials and Methods

Comparative genomic analysis of global ASFV sequences identified genotype-specific diagnostic targets. We specifically targeted genomic regions where genotype I shares sequence homology with recombinant strains but remains distinct from genotype II, and conversely, where genotype II shares homology with recombinants but differs from genotype I. This dual-target strategy identifies recombinant viruses through concurrent positive signals in both regions. The RPA-CRISPR/Cas12a assay utilizes a biotin-single stranded DNA (ssDNA)-invertase conjugate. Upon target recognition, activated Cas12a cleaves the ssDNA linker, releasing invertase to hydrolyze sucrose into glucose, which is quantitatively measured using a commercial handheld glucometer. Reaction parameters were optimized to maximize assay performance.

Results and Discussion

Optimized conditions achieved analytical sensitivities of 3×10^3 copies/μL for genotype I and 3×10^1 copies/μL for genotype II. This discrepancy in sensitivity is primarily attributed to variations in primer and guide RNA amplification efficiency between the two targets. Although the assay exhibits lower analytical sensitivity compared to conventional real-time PCR, it presents a significant advantage for field surveillance by delivering results in a rapid 40-minute turnaround time without the need for bulky thermal cyclers. Cross-reactivity testing against six major swine pathogens demonstrated complete analytical specificity with no false-positive signals. The complete workflow requires only portable heating and a glucometer.

Conclusion

We developed a field-deployable RPA-CRISPR/Cas12a diagnostic platform capable of differentiating ASFV genotype I, genotype II, and recombinant strains. The integration of a consumer glucometer enables practical implementation in resource-limited farm settings. However, further validation is required to establish the clinical limit of detection, diagnostic sensitivity and specificity, and to evaluate performance using actual clinical field samples to fully support field applicability.

Keywords: African swine fever virus, glucometer, point-of-care diagnostics, recombinant strains.

Acknowledgements: This work was supported by the Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET) through the High-Risk Animal Infectious Disease Control Technology Development Program, funded by the Ministry of Agriculture, Food and Rural Affairs (MAFRA) (RS-2024-00399940).

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RAPID ON-SITE DETECTION OF AFRICAN SWINE FEVER VIRUS USING AN EXTRACTION-FREE DNA METHOD COMBINED WITH COLORIMETRIC LOOP-MEDIATED ISOTHERMAL AMPLIFICATION

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Introduction and Objectives

African swine fever (ASF) remains a major threat to the global swine industry, including Vietnam. Rapid on-site detection of African swine fever virus (ASFV) is one of the important components of disease control, especially in resource-limited areas with restricted access to laboratory facilities. Therefore, this study aimed to develop an ASFV detection approach using Alkaline–Glycol Processing (AG) combined with colorimetric loop-mediated isothermal amplification (cLAMP), providing a practical and time-efficient tool for field-applicable diagnosis.

Materials and Methods

PCR-confirmed ASFV-positive blood and tissue samples were processed using an AG lysis protocol adapted from Chomczynski et al. (2021). Samples were mixed with the lysis solution and incubated at 95°C for 10 min to release viral DNA. Direct PCR was performed to evaluate the DNA extraction efficiency of the AG method in comparison with a commercial extraction kit. Subsequently, the lysate obtained from AG processing was used as the template for cLAMP assays, with hydroxy naphthol blue as the indicator. Positive reactions were identified by a color change from violet to sky blue after incubation at 63 °C for 60 min, and amplification was confirmed by agarose gel electrophoresis.

Results and Discussion

DNA release by the AG method was confirmed by PCR amplification, yielding band intensities comparable to those of a commercial extraction kit. The processing generated amplification-ready DNA without purification. Colorimetric amplification produced a clear transition from violet to sky blue for visual detection. Agarose gel electrophoresis confirmed the characteristic ladder-like pattern of LAMP products. The AG method exhibited good compatibility across both PCR and colorimetric LAMP. The sensitivity and specificity of the on-site diagnostic method should be evaluated.

Conclusion

These results demonstrate the developed ASFV on-site detection method using AG processing combined with cLAMP for immediate result interpretation, supporting enhanced ASF surveillance and control. The protocol is particularly suitable for field implementation and resource-limited conditions.

Keywords: African swine fever virus, Extraction free, LAMP, On-site detection.

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PRELIMINARY EVALUATION OF THE SAFETY AND IMMUNOGENICITY OF AVAC ASF LIVE VACCINE IN BREEDING PIGS

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Introduction and Objectives

African swine fever (ASF) remains a major threat to the global pig industry (WOAH, 2020; FAO, 2025). Although live attenuated vaccines (LAVs) have been licensed for use in growing pigs in Vietnam (Diep et al., 2025), their safety and immunogenicity in breeding animals have not been evaluated. This study aimed to preliminarily assess the safety and humoral immune response of the AVAC ASF LIVE vaccine in gilts, sows, and boars.

Materials and Methods

Twenty-four female breeding pigs (25-week gilts, 30 - 32-week gilts, and parity-2 sows) were included; in each category, five animals received a single intramuscular dose of AVAC ASF LIVE and three received PBS. Seven mature boars (4 vaccinated, 3 controls) were enrolled for safety evaluation. Two additional boars were experimentally infected with a virulent ASFV strain to assess reproductive pathology and viral shedding in semen. Clinical signs and rectal temperature were monitored daily. Blood and swab samples (oral-nasal, feces, urine, semen) were tested for ASFV DNA by qPCR, and antibodies were measured by ELISA. Vertical transmission was assessed in fetuses and newborn piglets from vaccinated females.

Results and Discussion

All vaccinated gilts and sows remained clinically normal, with no abortions or reproductive disorders. Mild, transient inappetence or slight fever was observed in a few animals. Low-level viremia was detected mainly at 7 - 14 days post-vaccination and resolved by day 28. Sporadic low-level ASFV DNA was detected in oral - nasal swabs or urine, while fecal samples were negative. No ASFV DNA was detected in fetal tissues, colostrum, umbilical cord blood, or samples from 1-day-old piglets, indicating absence of vertical transmission. All vaccinated females seroconverted by day 14 and remained antibody-positive until farrowing. Vaccinated boars remained healthy, developed strong antibody responses, and showed only transient low-level viremia; viral DNA was not detected in semen. In contrast, virulent ASFV infection caused severe disease, high viremia, viral shedding in semen, and reproductive lesions.

Conclusion

AVAC ASF LIVE is safe and immunogenic in breeding pigs, does not impair reproduction, is not transmitted vertically, and is not shed in semen, supporting vaccination of breeding herds to enhance herd immunity.

Keywords: African Swine Fever, Breeding pigs, Immunity response, Safety, Vaccine.

Acknowledgements: The authors would like to thank the staff for their support in caring for the animals during the experiment.

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AFRICAN SWINE FEVER IN SPAIN: HOW THE OUTBREAK IS MANAGING?

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Introduction

African swine fever (ASF) was confirmed in Spain on 28th November 2025 after detection of the virus in two wild boars found dead in Cerdanyola del Vallès (Barcelona). The carcasses were located within the Bellaterra University Campus, close to the Faculty of Veterinary and the Animal Health Research Centre of IRTA. This detection represents the re-emergence of ASF in Spain since the last outbreak reported in 1994 and constitutes a major epidemiological and economic concern for the Spanish pig sector.

Methods

After confirmation of the outbreak, surveillance and containment measures were implemented. Field activities involved rural agents, local police forces, the Military Emergency Unit, trained canine units, veterinarians and hunters specialized in outbreak control. Passive surveillance was intensified through systematic searches for wild boar carcasses within and around the affected area. Samples collected from wild boars were analysed for ASF virus detection and genomic characterization. Viral genome sequences were compared with the reference Georgia 2007/1 strain. Epidemiological information from wild boar cases and pig farms located in the regionalized area was collected. Control measures were implemented according to European legislation and bilateral regionalization agreements with major trading partners, including China.

Results and Discussion

To date, 216 ASF-positive wild boars have been detected, with all cases restricted to the wild boar population. Additional detections are expected as surveillance continues. Within the regionalized area, 57 pig farms are present, including 46 production farms. Genomic characterization identified the virus as a variant of the Georgia 2007 lineage (genotype II, variant 29). Compared with the Georgia 2007/1 reference genome, several mutations were detected, including a 9.8 kb deletion. This genomic region is associated with virulence modulation, immune evasion mechanisms and cell tropism, suggesting moderate pathogenicity.

Conclusion

The reappearance of ASF in Spain after more than three decades represents a major epidemiological and economic challenge. Although the outbreak currently affects only wild boars, the presence of pig farms within the regionalized zone requires strict surveillance and biosecurity measures. The outbreak has already had a significant economic impact on the Spanish pork sector, with market prices decreasing by approximately 30%.

Keywords: African Swine Fever, Detection, Regionalization, Spain.

APPLICATION OF A MICROFLUIDIC ISOTHERMAL AMPLIFICATION FOR SIMPLE, RAPID AND SENSITIVE DETECTION OF AFRICAN SWINE FEVER VIRUS (ASFV)

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Introduction and Objectives

African swine fever (ASF) is a highly contagious and fatal disease of domestic pigs and wild boar, causing severe economic losses to the global swine industry. Rapid and accurate detection of African swine fever virus (ASFV) is essential for effective disease control and outbreak management, particularly in field and resource-limited settings. In this study, we employed and analyzed the use of Microfluidic Isothermal Amplification for Animal Disease Detection (mFIND) platform for the rapid detection of ASFV in comparison with the traditional real time PCR.

Materials and Methods

The total of 89 blood, oral or nasal swab and meat product samples submitted for routine diagnosis at the Faculty of Veterinary Medicine, Chiang Mai University, Thailand and Laboratory of Animal Virology, Huazhong Agricultural University, China were subjected to test for the presence of p72 African swine fever virus (ASFV) gene by using mFIND and real time PCR. Sensitivity and specificity of the test were analyzed and data were obtained.

Results and Discussion

The mFIND platform, which combined nucleic acid isothermal amplification, CRISPR/Cas12 and microfluidic technology, demonstrated an overall sensitivity of 98.38% and a specificity of 100% when compared with real-time PCR. A single discrepant result was observed in a meat product sample, which exhibited a low viral load as indicated by a high Ct value in the real-time PCR assay. Notably, mFIND testing of blood and nasal or oral swab samples showed complete agreement with real-time PCR, achieving 100% sensitivity and 100% specificity. Furthermore, no cross-reactivity among other pig pathogens, including classical swine fever virus (CSFV), porcine reproductive and respiratory syndrome virus (PRRSV) and porcine circovirus type 2 (PCV2), has been observed. The mFIND assay represents a promising diagnostic approach for rapid and sensitive detection of ASFV.

Conclusion

Microfluidic isothermal amplification, referred to here as mFIND, represents a next-generation diagnostic approach that combines rapid nucleic acid amplification with microscale reaction environments optimized for efficiency and portability. This platform has strong potential to serve as a rapid diagnostic method and a practical on-site detection tool in the future.

Keywords: African swine fever virus, Detection, isothermal amplification, mFIND.

Acknowledgements: The authors thank KP Biomedical Science Co., Ltd, Thailand for the support with providing testing facilities.

A CASE-CONTROL GENOME-WIDE ASSOCIATION STUDY FOR TOLERANCE TO AFRICAN SWINE FEVER OF PIGS IN VIETNAM

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Introduction and Objectives

African Swine Fever (ASF) was first reported in Vietnam in 2019 and later spread across the country (Luc et al., 2022). A few pigs remained survivors after being infected (Oh et al., 2021). This suggests genetic variation in disease tolerance. Therefore, our study aims to identify the Single Nucleotide Polymorphisms (SNPs) associated with the tolerance to ASF of survivor pigs.

Materials and Methods

A Case-Control Genome-Wide Association Study (GWAS) was conducted to compare pigs that died (n = 208) versus survivors (n = 320) following natural ASF outbreak. All pigs were genotyped using a 70K SNP chip array. Logistic regression with adjustment for population structure and principal component was performed for GWAS analysis using PLINK software.

Results and Discussion

After filtering markers with unknown positions, minor allele frequencies (MAF), SNPs and individuals' call rates, only 498 (192 cases and 306 controls) pigs genotyped for 50,048 SNPs. Only markers located on autosomes were used for association analyses. Results show that no SNPs significantly associated with tolerance to ASF in pigs in Vietnam at this stage. These might be due to the limitation of sample size, density of SNP chip array and statistical models. Ogweng et al. (2024) found 48 significant SNPs, and 28 putative candidate genes may imply the possibility of heritability for resistance to ASF virus.

Conclusion

No significant SNPs were observed at this point. Additional work is therefore needed to either enlarge the sample size and/or change the statistical model, such as by using imputation, haplotyping, or adding more factors.

Keywords: GWAS, Survivor pigs, SNPs, Swine.

Acknowledgements: This study was funded by the Ministry of Agriculture and Rural Development, Vietnam under the project "Study on natural resistance to African swine fever of surviving pigs in outbreak areas in Vietnam".

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AN ATTENUATED ASFV VACCINE STRAIN C4N WITH IMPROVED SAFETY AND PROTECTIVE EFFICACY IN PIGS

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Introduction and Objectives

African swine fever (ASF) remains a major threat to global pig production, with no widely available safe and effective vaccine. Attenuated gene-deleted ASFV vaccines have shown promising results in pigs, but achieving an optimal balance between safety and protective efficacy remains a key challenge. In this context, this study evaluated the safety and protective efficacy of an attenuated ASFV vaccine strain (C4N) with three gene deletions derived from the genotype II Armenia07 strain in pigs.

Materials and Methods

Six-week-old ASFV-negative pigs were vaccinated intramuscularly with C4N at doses of 10^2 or 10^4 $TCID_{50}$. Boosters at 2 or 4 weeks were evaluated. Animals were challenged with 10^2 HAD_{50} of a virulent genotype II ASFV Korean isolate (Paju/2019) at 28 days post-vaccination. Clinical signs, body temperature, viral detection in blood, swabs, and tissue samples, and gross lesions were assessed. ASFV-specific antibody responses were measured by ELISA. Back-passage safety was evaluated using blood samples from vaccinated animals.

Results and Discussion

Vaccinated pigs showed no clinical signs, sustained fever, or mortality across all dose levels and booster regimens, indicating a consistent safety profile. The C4N vaccine conferred dose-dependent protection, with 75% survival at 10^2 $TCID_{50}$ and complete protection at 10^4 $TCID_{50}$. Vaccinated-challenged pigs exhibited markedly restricted viral replication. Viral detection in blood was transient and limited to a subset of animals even at the highest dose (10^4 $TCID_{50}$), with peak Ct values of 37–38 or 29 declining to undetectable levels, accompanied by even lower viral shedding, with no detectable virus in nasal samples and reduced lesion scores. ASFV-specific antibodies were induced, with 100% seroconversion at 10^4 $TCID_{50}$ by 28 days post-vaccination. A 2-week booster showed no additional benefit, whereas a 4-week booster resulted in complete protection (2/2) with improved antibody responses. Back-passage evaluation demonstrated no clinical signs, fever, or viremia in recipient animals, with no evidence of reversion or increased virulence after a second passage.

Conclusion

The attenuated ASFV vaccine strain C4N demonstrated a robust safety profile and complete protective efficacy, with minimal viral detection and no evidence of reversion. These results support its potential as a viable ASF vaccine candidate.

Keywords: African swine fever, Live attenuated vaccine (LAV), Immunogenicity, Protection, Safety.

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POSTERS

TOPIC 4: EMERGING DISEASES IN SWINE (EDS)

GENERATION OF A DISEASE INDEX BASED ON DIAGNOSTIC DATA ANALYZED BY DIAGNOSTICIANS TO ASSESS ENDEMIC SWINE PATHOGEN ACTIVITY IN THE UNITED STATES OF AMERICA

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Introduction and Objective

Endemic diseases in pigs continue to pose significant challenges to animal health, productivity, and food security. These diseases affect farm-level performance and have broader implications for swine producers. Many diagnostic cases with tissue samples are submitted to veterinary diagnostic laboratories (VDL) to be analyzed by diagnosticians, and their aggregation may generate insightful information about disease activity. Therefore, this study aimed to develop a disease index using confirmed tissue diagnosis data from the Iowa State University VDL to assess the activity of endemic pathogens nationwide.

Material and Methods

A total of 59,950 porcine cases with tissue submission from 2020 to 2024 were analyzed, focusing on 81 etiologies diagnosed in 42 USA states. Four normalized variables disease occurrence, comorbidity, geographic distribution, and Early Aberration Reporting System alarms - were integrated using the CompidexR package to generate a weighted index ranging from 0.01 to 1. The weights were assigned to variables using a sensitivity index, variance inflation factor, and linear constraints to optimize the calculated weights and generate the final score. Temporal consistency was evaluated using Manhattan distance, Spearman correlation, and Wilcoxon signed-rank tests, while variability was assessed via bootstrap resampling.

Results and Discussion

The index demonstrated strong year-over-year stability, with PRRSV, *Streptococcus suis, Pasteurella multocida,* and Influenza A virus consistently receiving the highest yearly scores. Emerging viruses, such as Porcine Sapovirus and Porcine Astrovirus, exhibited notable increases in index values, reflecting a rise in diagnostic activity and geographic spread. Bootstrap analysis confirmed predictive consistency, with over 55% of etiologies falling within expected confidence intervals. The index summaries were visualized through an interactive dashboard, enabling dynamic exploration of disease trends. This framework offers a scalable and reproducible tool for monitoring endemic diseases, utilizing routine diagnostic data, and has the potential for application across multiple species.

Conclusion

The ability to rank endemic diseases through a diagnosis and geographical composite index generates information that supports decision-makers with evidence-based information for disease management. The developed model has flexibility and can be adapted to other species and disease systems. The index provided a foundation for enhancing surveillance of endemic pathogens in swine populations.

Keywords: Diagnostic codes, Emerging diseases, Surveillance, Score, Rank.

INTEGRATED VISUALIZATION OF TRANSBOUNDARY SWINE DISEASES VULNERABILITY IN JAPAN USING DOMESTIC PIG, WILD BOAR, AND BIOSECURITY INDICATORS

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Introduction and Objectives

Transboundary swine diseases pose continuous threats to pig production through interactions among domestic pigs (DP), wild boars (WB), and human-related biosecurity practices. However, integrated visualization of these multiple risk components at a regional scale remains limited. This study aimed to develop a prefecture-level vulnerability framework for Japan by integrating environmental risks in DP, WB, and farm biosecurity indicators. We also evaluated farm structural determinants associated with estimated biosecurity levels using a mixed-effects modeling approach.

Materials and Methods

Environmental risk indicators for DP and WB were derived from raster-based environmental suitability indices developed in our previous study (Kawaguchi et al., 2025) and aggregated to the prefectural level. Farm biosecurity data were obtained from a nationwide questionnaire survey conducted in 2016 by the Japan Pig Producer Association, with complete responses from 842 farms. Biosecurity practices were recorded as binary variables (yes/no) and summarized at the farm level, following the methodology established in our previous studies (Ito et al., 2020). To account for regional clustering, prefecture-level biosecurity vulnerability was estimated to use a generalized linear mixed-effects model with a logit link, including prefecture as a random effect. Production stage, management type, and number of employees were included as fixed effects to assess farm structural determinants of biosecurity. All components (DP risk, WB risk, and estimated biosecurity vulnerability) were normalized to a 0 - 1 scale. A composite vulnerability index was calculated by integrating the three components using equal weighting. Sensitivity analyses were conducted to assess robustness under alternative weighting scenarios.

Results and Discussion

High-risk prefectures differed across DP, WB, and biosecurity components. The integrated vulnerability index consistently identified Kagoshima, Oita, and Kumamoto as the highest-risk prefectures across weighting scenarios. Mixed-effects modeling showed that organized production systems, corporate or cooperative management, and larger workforce size were significantly associated with higher estimated biosecurity levels ($P < 0.05$).

Conclusion

This study presents an integrated, policy-oriented framework for visualizing transboundary swine disease vulnerability at the prefectural level in Japan. The approach highlights substantial regional heterogeneity and identifies key farm structural determinants of biosecurity, providing practical support for risk-based surveillance and resource prioritization.

Keywords: Biosecurity, Mixed-effects model, Risk mapping, Transboundary swine diseases, Wild boar.

Acknowledgements: This work was supported by JSPS KAKENHI Grant Number 25K18374.

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AUJESZKY'S DISEASE IN ARGENTINA: FROM AN ENDEMIC INFECTION IN SWINE TO A RE-EMERGING INFECTION IN HIGH-HEALTH FARMS

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Introduction and Objectives

Aujeszky's disease (AD), caused by Suid Herpesvirus 1 (SHV-1), remains endemic in Argentina (19.1% prevalence in low-biosecurity farms). However, recent outbreaks in high-health systems - characterized by strict access control, official disease-free certification, and negative status for PRRSV and Brucellosis- suggest SHV-1 is a re-emerging threat. Between late 2024 and early 2025, an outbreak was reported by SENASA in a 7,000-sow indoor farm. This study characterizes the epidemiological, pathological, and molecular features of the infection in this facility, which had been previously certified AD-free.

Material and Methods

The farm maintained its negative status through quarterly official serological monitoring (ELISA gE), with the last negative result obtained 60 days prior to the outbreak. Baseline pre-weaning mortality (PWM) was 6.73%. The investigation (Dec 2024–Jan 2025) included biosecurity audits and PigChamp record reviews. Thirteen piglets (6–24 days old) displaying neurological signs were purposively selected from all affected barns for necropsy. Samples from the CNS and tonsils were processed for histopathology, IHC (targeting SHV-1 antigen), and bacteriology.

Results and Discussion

The epidemic curve identified an exposure window (Dec 30 - Jan 6) coinciding with external vaccination teams (targeting replacement gilts) and pest control visits. Clinical signs initially clustered in five barns at Site 3 (averaging 1,600 - 1,700 animals per room) handled by these personnel. Following a 9-day average incubation, the outbreak peaked on Jan 16. Site 1 (5 km away), with 700 – 800 animals per room, became affected 15 days later. Piglets from multiple litters in Site 1 developed fever and neurological signs, with PWM reaching 70% (morbidity > 40%), suggesting internal transmission via fomites or personnel following the primary introduction at Site 3. Pathology revealed non-suppurative meningoencephalitis and necrotic tonsillitis. IHC confirmed SHV-1 in neurons and glia cells. Molecular analysis identified SHV-1 genotype I.

Conclusion

The outbreak was associated with bio-exclusion failures during external service visits at Site 3. This highlights the vulnerability of certified AD-free farms when biosecurity protocols for external personnel are not strictly enforced, especially in high-density populations where internal dissemination via fomites can be rapid.

Keywords: Endemic infection, Histopathological lesions, Neurological signs, Re-emerging infection, SHV-1.

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FIELD EVIDENCE FOR PRRS PREVENTION: SIXTEEN-YEAR EVALUATION OF AIR FILTRATION AND VENTILATION PRESSURE STRATEGIES IN BREEDING HERDS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) can travel over long distances through aerosols. Air filtration has become a key biosecurity intervention. While the effectiveness of air filtration is well documented, limited research has evaluated its long-term impact while accounting for ventilation pressure and regional pig density. This study estimated the effect of air filtration approach (year-round vs. partial-year) and pressure type (positive vs. negative) on PRRS incidence in U.S. sow herds.

Materials and Methods

This study utilized data from the Morrison Swine Health Monitoring Project (MSHMP), the largest voluntary swine health surveillance project in the U.S. Participating production systems update their PRRS status weekly with MSHMP using the AASV classification (Holtkamp et al., 2021). We analyzed 16 years (2009–2024) of longitudinal data from 25 production systems, representing 1.6 million sows, including 245 non-filtered and 178 filtered farms. Generalized additive models were used to assess the effects of air filtration approach and ventilation pressure type on the PRRSV incidence, incorporating Gaussian process smooths for spatial autocorrelation. The PRRS incidence was defined as the number of outbreaks per farm-weeks-at-risk period, with the farm-weeks-at-risk period determined by the filtration status of each farm.

Results and Discussion

Compared to non-filtered farms, year-round and partial-year (without specifying the filtering months) air-filtered farms showed significantly lower PRRS incidence rates, with 0.494 times ($P < 0.001$) and 0.502 times ($P = 0.006$) the incidence rate of non-filtered farms, respectively. Farms with negative-pressure filtration had 0.492 times ($P < 0.001$) the incidence rate, while positive-pressure farms showed 0.416 times ($P < 0.001$) the incidence rate of non-filtered farms. No significant differences were observed between different filtration approaches and ventilation pressures. Higher regional pig density was associated with increased PRRS incidence rate, whereas herd size remained non-significant. A temporal sub-analysis revealed that the protective effect of air filtration increased over time.

Conclusion

This study offers valuable evidence on the effects of air filtration approaches and ventilation pressure on PRRS occurrence while accounting for regional disease burden. Our findings provide solid long-term, field-based evidence to support air filtration decisions and guide tailored biosecurity planning across diverse production systems.

Keywords: Air filtration, Biosecurity, Disease surveillance, Porcine reproductive and respiratory syndrome, Prevention measure.

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GENETIC STUDY OF THE TRANSCRIPTOME IN PIGLETS WITH PERIWEANING FAILURE TO THRIVE SYNDROME: DIFFERENCES BETWEEN SICK AND HEALTY ANIMALS

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Introduction and Objectives

Periweaning failure to thrive syndrome (PFTS) is a complex, multifactorial disease, including a possible genetic predisposition. It causes nonspecific symptoms and lesions in weaned piglets, such as growth retardation, progressive wasting, gastrointestinal lesions, and thymic atrophy, among others (Rodriguez-Ruiz et al., 2025). The aim of this study was to investigate predisposing genetic factors by studying the gene expression of thymic RNA transcripts in individuals with PFTS and to establish an association with other microbial, environmental, genetic, and physiological factors.

Materials and Methods

Thymus samples were taken from 25 animals (12 healthy and 13 diseased) from five different farms in Spain. Total RNA was extracted, mRNA was purified and after fragmentation, cDNA was synthesized. Quantification of the libraries was performed using Qubit and real-time PCR, and the transcriptome was analyzed by sequencing by synthesis on Illumina platforms. Bioinformatic analysis of the data was performed using the NCBI Sus scrofa reference genome and the clusterProfiler software for functional analysis of the expressed genes.

Results and Discussion

The number of genes with differential expression in the thymus between healthy and diseased animals totals 5641, of which 3985 show positive expression and 1656 negative expression. Previous research has identified a possible genetic predisposition in chromosomal regions that regulate behavioral and neurological changes (Zanella et al., 2016), while in our study, gene enrichment analysis shows significant differential expression (padj < 0.05) in biological processes related to development, vascular morphogenesis, and the circulatory system. The metabolic pathways with the highest differential expression (Padj < 0.05) are responsible for the interaction of cytokine receptors, cell adhesion molecules, hematopoietic cell lineages, and the cytoskeleton in muscle cells.

Conclusion

Animals with PFTS exhibit differentiated gene expression, affecting different biological processes and metabolic pathways that have biological implications in the immune response, inflammatory processes, energy homeostasis, cell growth, as well as in the differentiation and repair of adipose tissue and differentiation of hematopoietic stem cells.

Keywords: Genetics, Piglets, PFTS, Transcriptome, Weaning.

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INFLUENCE OF PIG BREED ON GENETIC PREDISPOSITION TO PERIWEANING FAILURE TO THRIVE SYNDROME

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Introduction and Objectives

Several studies confirm that Peri-weaning Failure to Thrive Syndrome (PFTS) in piglets is a multifactorial disease in which environmental, nutritional, and management factors may be involved (Ramis et al., 2015). Since its first description in Spain (Segalés et al., 2012), a genetic predisposition has been identified (Ramis et al., 2015), but it is unknown whether breed or genetic lines are predisposing factors. The aim of this study was to investigate predisposing genetic factors considering the effect of pig breed by studying the genetic expression of RNA transcripts in individuals with PFTS.

Materials and Methods

Thymus samples were taken from 25 animals from two different breeds in Spain: 12 Iberian pigs (6 healthy, 6 diseased) and 13 Commercial White pigs (6 healthy, 7 diseased). Total RNA was extracted, mRNA was purified and after fragmentation, cDNA was synthesized. Quantification of the libraries was performed using Qubit and real-time PCR, and the transcriptome was analyzed by sequencing by synthesis on Illumina platforms. Bioinformatic analysis of the data was performed using R and the packages affy, DESeq2, GEOQuery, ggplot2, plotly, RMarkdown and the NCBI Sus scrofa reference genome.

Results and Discussion

The total number of genes analyzed in the thymus was 32,057 in healthy pigs and 28,503 in diseased pigs of both breeds. When comparing healthy Iberian and Commercial White piglets, we observed few genes with differential expressions, with *P*adj value < 0.05 (9 overexpressed genes/30 underexpressed genes). However, when comparing both breeds in diseased animals, the difference was greater (121 overexpressed/98 underexpressed) explaining 21% of the variance in PC2 ($P = 0.03$) in ANOVA. To date, we know that there is an individual genetic influence even within the same genetic line (Ramis et al., 2015), but our results suggest that there could also be a clear genetic component to PFTS, with a greater predisposition in some breeds. However, the difference between sick and healthy animals is greater than between breeds (data not shown).

Conclusion

Diseased piglets with PFTS show that they may have a greater genetic predisposition depending on the breed and clearly differing between Iberian and Commercial White pigs.

Keywords: Iberian pigs, genetics, piglets, PFTS, transcriptome.

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ASSESSMENT OF CLEANING AND DISINFECTION EFFICACY IN PIG TRANSPORT VEHICLES BY TOTAL VIABLE COUNT REDUCTION USING SOCK SWAB SAMPLING

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Introduction and Objectives

Transmissible swine diseases remain a major challenge in pig production, with animal transport representing an important pathway for pathogen dissemination. Transport to slaughterhouses is considered a particularly relevant risk within the production cycle (Yang et al., 2025; Kedkovid et al., 2020). This study evaluated the effectiveness of cleaning and disinfection (C&D) of transport vehicles at slaughterhouses using moistened sock swabs and total bacterial counts as a practical monitoring approach.

Materials and Methods

The study was conducted at the two pig slaughterhouses located in the district where the project was implemented; no additional pig slaughterhouses exist in the cooperating neighboring district. During a defined sampling period, pig transport trucks scheduled for C&D were randomly selected. Thirty sock swab samples were collected from 15 pig transport trucks before and after C&D. Sampling was performed using moistened sock swabs by systematically walking the loading area following a standardized pattern. Samples were immediately transported to the laboratory and analyzed in duplicate using serial dilution and plate count methods to determine total microbial load, expressed as colony-forming units per milliliter (CFU/ml). The sock swab method was adapted from poultry transport hygiene protocols.

Results and Discussion

A reduction in microbial load was observed in all paired samples. Across all trucks, median microbial load decreased from 4.49 x 10^4 CFU/ml before C&D to 7.72 x 10^1 CFU/ml after, corresponding to an overall reduction of approximately 10^3. According to literature, C&D is considered effective when reductions exceed 10^6 (Böhm et al., 2002); however, this threshold was not consistently achieved, partly due to low initial contamination levels. In five trucks, no reduction of 10^3 was achieved. These trucks showed a median initial load of 8.47 x 10^4 CFU/ml and a median post-C&D load of 1.02 x 10^3 CFU/ml.

Conclusion

Total microbial count monitoring using sock swabs provides a practical, reproducible method to assess C&D efficacy in pig transport vehicles. The observed variability highlights the need for evidence-based hygiene benchmarks. Further studies should evaluate applicability to viral agents or specific bacterial pathogens and assess feasibility as a routine monitoring tool at slaughterhouses.

Keywords: Disinfection, Microbial load, Pig transport trucks, Sock swabs, Transmissible swine diseases.

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TRANSCRIPTOME STUDY IN PIGLETS WITH THYMUS ATROPHY DUE TO PERIWEANING FAILURE TO THRIVE SYNDROME

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Introduction and Objectives

Previous studies have suggested that Periweaning Failure to Thrive Syndrome (PFTS) may have a polygenic genetic component, but to date there is no clear etiology (Bertolini et al., 2018). Thymic atrophy is one of the most frequently observed lesions in animals with PFTS (Rodríguez-Ruiz et al., 2025). The objective of this study was to evaluate gene expression by studying the transcriptome based on the degree of thymus atrophy in healthy and PFTS-affected animals.

Materials and Methods

The animals studied were post-weaning piglets: 12 healthy animals without thymic atrophy; 3 sick animals with mild thymic atrophy; and 10 sick animals with severe thymic atrophy. Thymic samples were taken in duplicate: they were embedded in 10% formalin for histopathology and in RNAlater for total RNA extraction. The mRNA was purified and after fragmentation, cDNA was synthesized. Qubit and real-time PCR were used, transcriptome sequencing was performed on Illumina platforms, and bioinformatics analysis was carried out using the NCBI reference genome of Sus scrofa.

Results and Discussion

When comparing healthy animals against sick animals with mild thymus atrophy, were studied 32,293 genes and we observed a large number of genes with differential expression, padj < 0.05 (1,071 up/614 down) with 22.8% of the variance explained in PC2 ($P = 0.006$) and a trend with 33.2% in PC1 in ANOVA. Thymic atrophy progresses from mild to severe bilateral as the disease progresses (Rodríguez-Ruiz et al., 2025), therefore when comparing with sick animals with severe thymus atrophy, the differences in expression were even greater; of the 32,669 genes analyzed, 3,647 up and 2,353 down were obtained, with 40.2% of the variance explained in PC1 ($P = 7.83 \times 10^{-7}$). The most overexpressed genes between groups are ADIPOQ and APOD (lipid metabolism and meat quality), PDK4 (glucose and fatty acid metabolism affecting skeletal muscle and intramuscular fat), and MMP2 (muscle development and immune response), which is consistent with what was previously observed in mice (Bertolini et al., 2018).

Conclusion

Animals with PFTS and severe thymus atrophy exhibit statistically differentiated gene expression in 6,000 genes, affecting different metabolic pathways of lipids, glucose, and intramuscular fat.

Keywords: Atrophy, Genetics, Piglets, PFTS, Thymus.

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ACTIVE SURVEILLANCE OF CLASSICAL SWINE FEVER DURING GRADUAL VACCINATION CESSATION IN TAIWAN'S DOMESTIC PIG FARMS TOWARD CSF-FREE STATUS

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Introduction and Objectives

Classical swine fever (CSF) is a WOAH-listed notifiable disease that causes substantial economic losses. Taiwan launched a three-phase elimination program in 2021 and obtained official WOAH CSF-free certification in May 2025. After successful sentinel and environmental surveillance during Phase 1 (2021 - 2022), Phase 2 focused on the gradual cessation of CSF vaccination from 2023 to June 2024. Vaccination was first discontinued in non-breeding pigs from January to June 2023, followed by complete cessation in all pigs from July 2023 onward. Accordingly, this study summarizes active CSF surveillance conducted on domestic pig farms during Phase 2.

Materials and Methods

The active surveillance in domestic pig farms incorporated both virological and serological testing. Blood and oral swabs were collected from 12,705 pigs (16 - 20 weeks of age) across 886 farms and tested for CSFV RNA by real-time RT-PCR (RRT-PCR). In parallel, CSFV-specific antibodies were measured by virus neutralization tests (VNT). A traceback system was applied when serological findings suggested possible field exposure: follow-up clinical inspections and virological and serological testing were conducted if a farm's geometric mean titer was ≥ 1:8 in 2023 in the absence of a vaccination record, or if at least one pig had a neutralizing antibody (NA) titer ≥ 1:32 in 2024.

Results and Discussion

Virological surveillance confirmed no detection of wild-type CSFV strains in domestic pigs by RRT-PCR. Serological monitoring revealed a significant decline in CSFV seropositivity, dropping from 93.3% in January 2023 to 6.7% by June 2024. The traceback system was implemented in 83 farms in 2023 and in 36 farms during the first half of 2024. Based on RRT-PCR, VNT results, and clinical inspections, wild-type CSFV infection was ruled out in all retested pigs.

Conclusion

In conclusion, CSFV NA titers in domestic pig farms declined steadily following vaccination cessation. Although sporadic seropositivity was detected, traceback investigations consistently ruled out wild-type CSFV infection, with residual titers most likely attributable to maternal antibodies or unauthorized vaccination. Together, these surveillance results indicate a negligible risk of wild-type CSFV circulation and provide scientific evidence supporting Taiwan's official CSF-free status.

Keywords: Classical swine fever, Elimination, Neutralizing antibodies, Surveillance.

A METHOD FOR PREPARING A PEDV TRVLP VACCINE

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Introduction and Objectives

Coronaviruses cause significant respiratory and gastrointestinal diseases. Porcine Epidemic Diarrhea Virus (PEDV), an alpha-coronavirus, is a major global threat to swine. Its nucleocapsid (N) protein is essential for replication and assembly. This study aimed to develop a safer, replication-competent PEDV virus-like particle (trVLP) system for research and vaccine development.

Materials and Methods

We constructed a recombinant PEDV trVLP (PEDV EGFP/ΔN) by replacing the N gene with an enhanced green fluorescent protein (EGFP) reporter. This design restricts complete viral replication to cells that externally supply the PEDV N protein. The system was assessed for transcription, replication, and particle formation.

Results and Discussion

The PEDV EGFP/ΔN trVLPs maintained transcriptional and replicative functionality, as shown by EGFP expression and RNA synthesis, while virion assembly was strictly dependent on the provided N protein. This system offers superior safety compared to conventional vaccines, as it cannot produce infectious virus in normal cells. It thus provides a versatile and controllable platform for studying PEDV biology and developing novel vaccines.

Conclusion

We successfully established a replication-restricted PEDV trVLP system that balances key viral functions with enhanced biosafety. This platform is valuable for fundamental coronavirus research and represents a promising strategy for developing next-generation vaccines against PEDV and related pathogens.

Keywords: PEDV, trVLP, Vaccine development.

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PATHOGENICITY OF *CLOSTRIDIUM PERFRINGENS* TYPE A ALPHA-TOXIN AND IMMUNOPROTECTION ANALYSIS OF A NON-TOXIC MUTANT

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Introduction and Objectives

Clostridium perfringens (*C. perfringens*) is a zoonotic opportunistic anaerobic spore-forming bacterium with seven genotypes (A - G) (Rood et al., 2018). *C. perfringens* type A and type C can cause necrotic enteritis in piglets, and can also infect humans, livestock and companion animals. The investigation into *C. perfringens* and exploration of its pathogenicity and countermeasures are warranted.

Materials and Methods

A total of 110 piglet fecal samples were collected from three pig farms in Hainan Province, China. *C. perfringens* was isolated and identified by physiological test, 16S rRNA sequencing, and toxin genotyping PCR. The hemolytic activity, phospholipase activity, and toxicity of recombinant α-toxin were verified, followed by pathogenicity tests. A non-toxic mutant was constructed by site-directed mutagenesis, and its immune protective efficacy against the strain with the highest hemolytic activity was verified in BALB/c mice.

Results and Discussion

C. perfringens was detected in 65 out of 110 samples (59.09%), which were type A and showed > 99% 16S rRNA sequence homology. Intraperitoneal injection of 6×10^8 CFU resulted in 100% mortality in mice (n = 10) within 3 days. Necropsy showed hemorrhagic effusion in the thoracic and abdominal cavities, bleeding in multiple organs (especially extensive intestinal bleeding), and obvious gastric distension. Pathological examination revealed necrosis and sloughing of intestinal villi. Intraperitoneal injection of 0.5 mg of recombinant α-toxin (100% mortality) produced similar lesions. This confirms that α-toxin is the major virulence factor of *C. perfringens* type A. Conversely, the mutant lacked phospholipase and hemolytic activities, had no cytotoxicity or pathogenicity in mice (0.5 mg). Mice were immunized with the mutant emulsified in an adjuvant via multiple subcutaneous injections. Following challenge with α-toxin, no deaths were observed within 7 days, resulting in 100% protection, and thus holding promised preventive potential.

Conclusion

C. perfringens type A was predominant on the sampled farms, which produces α-toxin only and induces severe pathology. The favorable protective efficacy of the mutants offers valuable insights for preventing and controlling *C. perfringens* infections.

Keywords: Clostridium perfringens, α-toxin; Non-toxic mutant, Immune protection.

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ANALYSIS OF ANTIGEN AND ANTIBODY OF PORCINE CIRCOVIRUS TYPE 3 COMBINED DETECTION RESULTS IN PORCINE SERUM SAMPLES

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Introduction and Objectives

Porcine circovirus type 3 (PCV3) was first identified in 2016. It is associated with reproductive disorders in sows and growth retardation in piglets, exerting a severe impact on swine production (Reséndiz-Sandoval et al., 2023). This study investigated the prevalence of PCV3 antigen and antibodies in large-scale pig farms across China and systematically analyzed its infection dynamics.

Materials and Methods

A total of 321 serum samples were randomly collected from healthy and diseased pigs across three farms in China. PCV3 antigen and antibody detection of the samples was performed using the double-antibody sandwich ELISA and indirect ELISA established in our laboratory. The detection results were statistically analyzed according to different farms and feeding stages, with a combined statistical analysis performed simultaneously.

Results and Discussion

Statistical analysis revealed a high prevalence of PCV3 across swine farms, affecting all production stages. The average antigen and antibody positive rates were 89.78 and 66.98%, respectively. Among sows and piglets, antigen positivity was 78.7% (133/169) and 66.67% (40/60), while antibody positivity was 92.46% and 95% respectively. Nursery pigs exhibited the lowest antigen and antibody positive rates across all stages, at 20.51% (8/39) and 69.23% (27/39). Concurrent antigen and antibody positivity was observed in 64.5% (207/321) of samples, suggesting a middle-to-late or persistent infection stage within the herd. Additionally, 28.0% (90/321) of samples were antigen-negative but antibody-positive, reflecting prior widespread exposure or a substantial immune background in the population.

Conclusion

This study revealed that PCV3 infection was prevalent across all farms and all feeding stages. Specifically, the infection rates were high in sows and piglets, while nursery pigs exhibited the lowest infection rate. The antigen and antibody detection results can provide a reference for targeted prevention and control strategies in pig farms.

Keywords: Antigen and antibody detection, ELISA, Porcine circovirus type 3.

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WHOLE GENOME SEQUENCE ANALYSIS OF AFRICAN SWINE FEVER VIRUS IDENTIFIED DURING OUTBREAKS FROM 2022-2024 IN NEPAL

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Introduction and Objectives

African Swine Fever is a highly contagious viral disease of pigs caused by African Swine Fever Virus (ASFV), leading to substantial economic losses due to its high mortality and trade restrictions. Based on the partial sequence of the ASFV p72 major capsid protein gene (B646L), 24 distinct ASFV genotypes identified are found in Africa. (Achenbach et al., 2017; Quembo et al., 2018). However, only genotypes I and II have spread beyond the continent. (Njau et al., 2021; Simulundu et al., 2017). ASF was first confirmed in Nepal in May 2022 and has since spread across the country. This study aims to molecularly characterize the ASFV strains responsible for outbreaks throughout the country since 2022.

Materials and Methods

Between 2022 and 2024, a total of 19 blood samples were collected from ASFV-infected pig farms in Lamjung, Dhulikhel, Kavresthali and Tikabhairav. Viral DNA was extracted, confirmed positive by PCR. All the positive samples were sent to the Animal and Plant Health Agency (APHA), UK for whole genome sequence analysis. Since all the samples reveal the same nucleotide sequences based on P72 and P54 genes, only two samples were subjected to whole genome sequencing (WGS).

Results and Discussion

The Nepal isolate has a genome length of 190,584 bp, with a GC content of 38.89%, encoding 195 coding sequences spanning 171,012 bp. Comparative analysis with the ASFV Georgia 2007/1 reference revealed 18 coding sequence variants, including 9 synonymous, 8 missense, and 1 stop-gained mutation, as well as upstream, downstream, and intergenic changes. Amino acid substitutions were detected in key proteins including p72, EP402R, B602L, CP204L, K145R, MGF360-12L, EP153R, DP71L and A238L. Phylogenetic analysis of whole genome sequences classified the Nepal isolate as genotype II, closely related to isolates from Malaysia, China, India, Russia, Poland, and Germany. Gene-level analysis using the p72 sequence further showed clustering near sequences from China, India, Russia and Vietnam, suggesting potential routes of introduction into Nepal.

Conclusion

This is the first complete ASFV genome sequences from Nepal, and the results provide essential baseline genomic data for ASFV in Nepal, supporting surveillance, epidemiological tracing and disease control strategies.

Keywords: African swine fever virus, Genome sequencing, P72.

Acknowledgements: The authors thank the Nepal Agricultural Research Council (NARC), Nepal and Animal and Plant Health Agency (APHA), UK for the support with providing testing facilities.

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DNA METHYLATION STUDY IN PIGLETS WITH PERIWEANING FAILURE TO THRIVE SYNDROME

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Introduction and Objectives

DNA methylation is an epigenetic modification process in which methyl groups are added to the C5 position of DNA, mediated by DNA methyltransferase (DNMT) (Goldberg et al., 2007). The study of DNA methylation plays a fundamental role in understanding gene expression, individual development, and the mechanisms of disease onset and progression. The aim of this study was to evaluate DNA methylation by assessing the function of affected genes in weaned piglets with Periweaning Failure to Thrive Syndrome (PFTS).

Materials and Methods

DNA extracted from blood samples of 27 weaned piglets in Spain was studied; 13 were healthy and 14 had PFTS. Bisulfite sequencing of the Sus scrofa genomic DNA was performed. The reads were aligned to the reference genome using Bismark software and analyzed to quantify CpG methylation levels. Differentially methylated regions were identified using bioinformatics analysis, and functional annotation was performed using Gene Ontology (GO).

Results and Discussion

The analyzed DNA showed genomic methylation on all chromosomes. The percentages of methylated cytosines were similar between healthy and diseased piglets in the different sequence contexts: CpG (73.73% healthy and 73.53% diseased), CHH (0.12% healthy and diseased), and CHG (0.12% healthy and 0.13% diseased). CpG islands are the main methylation sites in mammals and can be associated with gene silencing (Goldberg et al., 2007) and higher levels of oxidative stress (Mungala et al., 2020). In our case, we found no differences between healthy and diseased piglets, possibly due to a small sample size and the multifactorial nature of the disease. Genetic enrichment analysis of GO in significantly hypermethylated regions ($P < 0.01$) for piglets with PFTS showed affected genes encoding proteins related to molecular and plasma membrane binding capacity, which could be related to cellular homeostasis, immune response, stress, or pathogen-host interaction.

Conclusion

No differences in CpG methylation levels were detected between healthy and diseased piglets. Piglets with PFTS showed hypermethylated genes encoding proteins related to cell adhesion and the plasma membrane.

Keywords: DNA, methylation, piglets, PFTS.

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PIG MOVEMENTS IN THE PROVINCE OF QUEBEC, CANADA: A DESCRIPTIVE STUDY

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Introduction and Objectives

Pig movements are a major risk factor for introducing diseases into herds and represent an effective pathway for pathogen spread at larger spatial scales. The objective of this study was to describe live pig movements involving sites in the province of Quebec, Canada, over a three-year period (2022-2024).

Materials and Methods

A retrospective study was conducted using movement declarations registered by Quebec stakeholders in the mandatory Canadian traceability system between January 1st, 2022, and December 31st, 2024. A pig movement was defined as ≥ 1 live pig(s) transported within a day 1) between two facilities located in Quebec, 2) from another country or province to a facility located in Quebec, or 3) from a facility in Quebec to another country or province. For facilities within Quebec, the type of facility (i.e., pig site, backyard farm, slaughterhouse, wild boar farm, pet pig owner or others) was provided by the Éleveurs de porcs du Québec. Others were further classified as research, diagnostic and educational, or exhibition facility. Movement frequencies were described according to the type of facilities involved and directions.

Results and Discussion

A total of 205,169 movements were observed over the 3-year period, associated mostly with swine production sites (n = 205,032), and rarely with wild boar (n = 105) or pet pig (n = 32) facilities. Overall, 183,994 (89.7%) movements occurred between two Quebec facilities, 215 (0.1%) involved another country and 20,960 (10.2%) involved another Canadian province. For movements involving two facilities within Quebec, 115,900 (63.0%) were directed to slaughterhouses, 67,182 (36.5%) involved two farms (pig sites, backyard farms) and 912 (0.5%) involved research, veterinary diagnostic or exhibition facilities. The 59 imports originated from the United States and pigs were delivered to pig sites (n = 22) or research facilities (n = 37), whereas the 156 exports were transported to the United States (n = 149) or Mexico (n = 7). From the 15,302 entries from other Canadian provinces, 12,998 (84.9%) were destinated to Quebec slaughterhouses, 2,300 (15.0%) to pig sites and only 4 (< 0.1%) to other types of facilities.

Conclusion

A better knowledge of pig movements is a key feature for understanding how pathogens can be dispersed at the provincial level.

Keywords: Movement, Pig, Traceability.

Acknowledgements: This project was funded by the Agri-Food Innovation Partnership Program under the Canadian Agricultural Partnership Agreement between the governments of Canada and Quebec and by Les Éleveurs de porcs du Quebec.

COINFECTION OF PCV2, PCV3, PCV4 AND PRRSV IN FARMS IN JALISCO, MEXICO

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Introduction and Objectives

Porcine circovirus (PCV) is a ubiquitous viral agent in pigs, belonging to the genus Circovirus. Currently, the genus Circovirus comprises four species: PCV1-4. Problems associated with the presence of new Circovirus types have recently been described on farms, so the objective of this study was to identify coinfection with PCV2, PCV3, PCV4, and PRRSV in pig farms in the state of Jalisco.

Materials and Methods

In Jalisco, 80 commercial farms participated in the study, distributed across four regions according to pig density. A total of 4,207 serum samples were taken from clinically healthy pigs. An average of 35 samples were obtained per farm, distributed by production stage: unweaned piglet, weaned, growing, fattening, finishing, and pregnant sows (71/80 farms vaccinated against PCV2 and 53/80 farms vaccinated against PRRSV). The samples were pooled into groups of 5 serum samples (n = 844). DNA and RNA were extracted from each pool using commercial kits (QIAGEN). The DNA was analyzed by qPCR to detect ORF2 for PCV2 and PCV4, ORF1 for PCV3, and ORF7 for PRRSV, in order to identify positive samples, defined as those with a Ct < 35.

Results and Discussion

The most frequently detected virus was PRRSV with 305/844 pools (36.1%), followed by PCV2 with 235/844 (27.2%), PCV3 with 205/844 (24.2%) and PCV4 3/844. Coinfections involving PCV2 and PCV3 were present in 55/844 pools analyzed. Dual detection of PCV2/PRRSV was identified in 9.4% (80/844 pools), while identification of PCV3/PRRSV occurred in 81 pools (9.5%). The triple detection (PCV2-PCV3-PRRSV) occurred in 2.72% (23/844). The highest proportion of positive pools was found in the weaning stage for PRRSV (61.07%), the fattening stage for PCV2 (39.47%), and the growing stage for PCV3 (32.91%). The three positive samples for PCV4 were found in each of the aforementioned stages.

Conclusion

This study represents the first regional survey involving PCV4 in Mexican swine farms PCV4 was detected in three pool serum samples from clinically healthy pigs. Genetic characterization of PCV4 detected in this and other regions of the country will continue. PCV2-PCV3-PRRS coinfection is an event identified in low percentages, but present in pigs without clinical signs.

Keywords: Co-infection, Porcine circovirus, PRRSV.

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THE ROLE OF *MYCOPLASMA SUIS* AND CO-INFECTION WITH PORCINE CIRCOVIRUS TYPE 3 IN REPRODUCTIVE FAILURE AT A LARGE BREEDING PIG FARM

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Introduction and Objectives

Reproductive failure is still a major problem in the swine industry, causing huge economic losses worldwide. In this study, we investigated the reproductive failure associated pathogen in a breeding farm showing raising stillborn, mummified fetuses, and weak-born piglets, increasing the pre-wean and post-wean mortality.

Materials and Methods

A total of 1,000 sows were monitored, of which 85 exhibited clinical manifestations, these sow samples and their fetuses were selected for sample collection. PCR and RT-PCR assays were performed to detect PRRSV, CSFV, PRV, PCV2, PCV4, and PPV. In addition, quantitative real-time PCR was used to quantify the viral loads of ASFV, *M. suis*, and PCV3. Visceral tissues collected from mummified and stillborn fetuses were fixed and processed for histopathological evaluation using staining techniques, including RNAscope and in situ hybridization (ISH). Furthermore, the complete genome of PCV3 and the partial 16S rRNA gene of M. suis were sequenced for genetic characterization.

Results and Discussion

No evidence of ASFV, PRV, PPV, PRRSV, CSFV, or PCV4 infection was detected. Conversely, *Mycoplasma suis* and PCV3 were identified, while PCV2 was only sporadically detected. In sow blood samples, detection rates reached 42.4% for PCV3 and 30.6% for *M. suis*. Among stillborn and mummified fetuses, *M. suis* was detected in 37.5 and 29.2% of samples, respectively, whereas PCV3 was detected in 14.3% of both groups. Importantly, PCV3 prevalence was significantly higher than that of *M. suis* in reproductive failure cases (62.5 vs. 18.8%, $P < 0.01$). Histopathological examination consistently revealed necrotizing myocarditis, pulmonary congestion and hemorrhage, hepatic degeneration and necrosis, and lymphoid depletion associated with periarteritis. Phylogenetic analysis placed the PCV3 strain within the PCV3b subgroup, closely related to Vietnamese isolates, and *M. suis* infection was confirmed through 16S rRNA gene sequencing.

Conclusion

Collectively, these findings indicate that *M. suis*, particularly in co-infection with PCV3, plays a significant role in porcine reproductive failure in Vietnam and provides valuable evidence to support improved disease prevention and control measures.

Keywords: Breeding pig farms, *M. suis,* PCV3, Reproductive failure.

Acknowledgements: The authors thank the Animal Biomedical Research Laboratories, Nong Lam University HCMC, Vietnam, for the support in providing testing facilities.

Posters

Topic 5: Advancements in Immunology and Vaccination (AIV)

THOROUGH VACCINE PREPARATION BEFORE VACCINATION TO PREVENT UNDESIRABLE SIDE EFFECTS: A CASE REPORT

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* are pathogens commonly found in large-scale pig herds having a detrimental economic impact. Vaccination against both pathogens is a common control strategy widely used worldwide. A Ready-To-Use bivalent PCV2 and *M. hyopneumoniae* vaccine has been recently registered in China. It contains a recombinant baculovirus-expressed PCV2 ORF antigen and a *M. hyopneumoniae* inactivated strain, combined with an oil-in-water adjuvant. Compliant handling of oil-in-water formulations before vaccination is required and manufacturer guidelines must be followed to ensure optimal protection. This case report investigates the impact of incorrect vaccine preparation compared to vaccine preparation following the manufacturer recommendations in a Chinese pig farm.

Materials and Methods

On April 1st, 2025, a batch of commercial piglets (n = 1,500) was vaccinated at 21 days of age (Porcilis® PCV M Hyo). Systemic reactions were observed in 115 piglets, including vomits, depression and apathy, within the first 4 hours post-vaccination, resulting in 12 dead piglets. Thorough anamnesis and investigations revealed insufficient warming up and shaking of the vials prior to use. On next batch (April 22nd), a new group of 1,500 piglets were vaccinated. This time the vaccine was tempered to 28C in a warm bath and shaken vigorously before administration. If present, mild (collapse, trembling, vomiting, and reddening of the skin) and serious (death) adverse reactions were recorded. Percentage of pigs with mild reactions and Mortality (%) from both groups [Insufficient (I) vs Thorough (T) vaccine preparation] was analyzed by using Fisher's exact test.

Results and Discussion

Within 4h post-vaccination, 12 pigs exhibited mild side reactions (vomiting and/or apathy), and no fatalities occurred. Significant differences were described between groups for both parameters. Percentage of mild reactions (I: 7.7%; T: 0.8%) ($P < 0.05$) and Mortality (I: 0.8%; T: 0.0%) ($P < 0.05$) were significantly lower in the Group T compared to Group I. The same vaccine batch was used in both groups (D315A02). The casualties in Group I suggested an anaphylactic reaction.

Conclusion

This case report confirms that shaking and warming up the investigated vaccine before use significantly reduces the incidence of side effects and prevents serious reactions after vaccination.

Keywords: *Mycoplasma hyopneumoniae,* PCV2, Safety, Vaccination, Vaccine compliance.
Acknowledgements: The authors thank the producer for the field support during the trial.

IMPACT OF PORCINE CIRCOVIRUS 2 (PCV2) VACCINE CHOICE ON PROPORTION OF SLOW-GROWING PIGS AND PROFITABILITY

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Introduction and Objectives

PCV2 is found in most pig herds in Australia. Pigs typically show signs of weight loss and emaciation. PCV2 vaccines aid in the control of diseases associated with PCV2. As new vaccines and methods of delivery become commercially available, they should be assessed under farm conditions against existing, effective vaccines. The objective of this trial was to compare the proportion of slow-growing pigs and the profitability of two commercial PCV2 vaccine systems.

Materials and Methods

The study was conducted at a 2,700 sows facility positive for PCV2 and negative for *Mycoplasma hyopneumoniae*. Pigs (n = 6,608) were vaccinated at 21 days of age with either vaccine A (Ingelvac CircoFLEX®, Boehringer Ingelheim) administered intramuscularly using a needle and injection device or vaccine B (Porcilis® PCV IDAL, MSD), administered by intradermal injection using the needle-free IDAL® device. At 22.5 weeks of age, the proportion of slow-growing pigs (pigs marketed after batch closure) was recorded and analysed using the Yates Corrected Chi-Square statistic. Sale value was assessed by using individual slaughter data and an Australian payment grid to adjust prices under normal, poor, and favourable market conditions (feed and pork prices2). Costs were calculated using a typical Australian ration budget and calculated consumption curves3. Non-feed costs were estimated at a fixed daily rate. Profit per head performance was compared using an independent samples t-test.

Results and Discussion

The proportion of slow-growing pigs was significantly different ($P < 0.0001$) between groups (vaccine A 14.2%; vaccine B 22.9%). The average profit per head was significantly higher for vaccine A under all three sets of market conditions. Under normal market conditions, the average profit per head was $29.82 for vaccine A vs $27.79 for vaccine B ($P = 0.011$). The results show an 8.7% reduction in slow-growing pigs and $2.04 increase in average profit per head in favour of Ingelvac CircoFLEX under normal market conditions.

Conclusion

This study demonstrated that the impact of PCV2 vaccine choice on the proportion of slow-growing pigs and profitability can differ significantly. Decreasing the number of slow-growing pigs can increase the number of annual production cycles, improve asset efficiency, and increase farm profitability.

Keywords: PCV2, Profitability, Production, Performance, Vaccine.

HETEROLOGOUS VACCINE IMMUNOGENICITY AND EFFICACY OF THE PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS MODIFIED LIVE VACCINE - PREVACENT PRRS®

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSv) vaccines need to provide cross-protection against the highly diverse PRRSv strains. Cross protection, or heterologous vaccine efficacy, relies on a vaccine's ability to induce a strong immune response against various strains. Cross-protection is difficult to assess and to generate with MLV vaccines. This study combined Prevacent vaccination followed by in vivo challenge with four heterologous PRRSV type 2 (PRRSV-2) strains: NC174 (lineage L1C.unclassified), NADC30 (lineage L1C.4), VR2332 (lineage L5A.5), or NADC20 (lineage L9E.3)) with ex vivo and in vitro lung pathology analysis, tissue viral loads, and the humoral and adaptive immune response to investigate vaccine efficacy and immunogenicity.

Materials and Methods

Sixty (60) weaned pigs, half of which were Prevacent PRRS® vaccinated, and half were Mock (PBS/media) vaccinated, were divided into five challenge groups of ten pigs (5 Mock and 5 Vaccinates) four weeks after vaccination and placed in separate challenge rooms. The challenge was performed intranasally with 106 TCID50/ml of the designated variant. Pre-vaccination (day -28), pre-challenge (day 0), and 7 days post-challenge samples were collected to assess viral loads, anti-PRRSV IgA/G, neutralizing antibodies, and the PRRSV2 strain-specific T-cell response. At day 14 post-challenge (necropsy), lung (gross and histological) lesions and IgA levels in bronchoalveolar lavage were evaluated.

Results and Discussion

Prevacent PRRS® reduced viremia of NADC 20, NADC 30, and VR2332 infections, showing significantly less interstitial pneumonia in NADC 20 and NADC 30 challenges. Prevacent PRRS® induced strain-specific neutralizing antibody titers in more animals in the NADC20, NADC30, and VR2332 groups than their mock-vaccinated counterparts. Prevacent is primed for a larger IFN-γ response post challenge for NC174, NADC20, and NADC30.

Conclusion

Prevacent induced a strong T-cell response that is cross-reactive against the different type-2 PRRSV lineages, especially for the CD4 T-cell response. Prevacent induced a pre-challenge differentiation of CD4 T-cells into IFNγ-producing memory/effector cells and primed them for a significantly stronger post-challenge IFNγ against NC174, NADC20, and NADC30. The study showed that the MLV vaccine Prevacent elicited various degrees of both heterologous vaccine efficacy and immunogenicity.

Keywords: Cross-protection, Efficacy, Heterologous challenge, Porcine Reproductive and Respiratory virus, Vaccine.

EFFICACY AND SAFETY ASSESSMENT OF A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE IN CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* are primary pathogens causing respiratory disease in pigs and having a detrimental impact on the swine industry. In China, both pathogens are still in a high proportion of farms (Fan et al., 2023; Zhang et al., 2021) representing a concern for both Chinese producers and authorities (3). Recently, a Ready-to-Use (RTU) bivalent PCV2 and *M. hyopneumoniae* vaccine has been registered in China. This trial aims to evaluate the efficacy and safety of this vaccine under field conditions in China.

Materials and Methods

This randomized, side-by-side trial was conducted in a wean-to-finish herd (Guangxi province) with documented subclinical PCV2 and *M. hyopneumoniae* (10% PCR-positive at weaning) infections. In total, 938 piglets were allocated to three groups and vaccinated using different schemes: A (test vaccine, n = 320; Porcilis® PCV M Hyo at 21 days of age); B (n = 309; Ingelvac® MycoFlex & Ingelvac® CircoFlex at 21d); C (n=309; Ingelvac® CircoFlex at 21d & Suvaxyn® M Hyo at 21 and 42d). No control group was included due to ethical reasons. Average Daily Gain (ADG), prevalence and severity of mycoplasma-like lesions (Madec score) at slaughter were investigated. Sera (n = 25) and tracheo-bronchial swabs (n = 25) were collected (7, 11, 15, 19, 23, 25 wk), PCV2 and *M. hyopneumoniae* quantified (qPCR) and the AUC calculated. Mortality was recorded. Vaccine safety was assessed by recording adverse reactions. Data on ADG, severity and prevalence of lung lesions/mortality were analyzed by AN(C)OVA, Wilcoxon-rank sum and Fisher's tests, respectively.

Results and Discussion

ADG was significantly higher in group A (911.1 ± 5.0) compared to Group B (885.1 ± 5.0) and C (890.7 ± 5.0) ($P < 0.05$). Both Prevalence (A: 36.5%; B: 92.5%; C:58.5%; $P < 0.05$) and Severity (A: 0.9 ± 1.6; B:5.9 ± 4.1; C:1.4 ± 2.1; $P < 0.05$) of pneumonia were significantly lower in group A compared to other groups. PCV2 and *M. hyopneumoniae* were detected during the trial, but there were no significant differences among groups, nor for mortality. Mild reactions were observed (A: 0.62%; B: 0.65%; C: 0%), and pigs recovered within 15 minutes.

Conclusion

The RTU tested vaccine was safe and efficacious under these field conditions in China, conferring protection against field infections against both PCV2 and *M. hyopneumoniae* by increasing ADG and reducing pneumonia at slaughter.

Keywords: *Mycoplasma hyopneumoniae*, Lung lesions, PCV2, Performance, Vaccination.

Acknowledgements: The authors thank the producer for the field support during the trial and Qi Cao for the statistical analysis.

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EFFICACY EVALUATION OF A BIVALENT VACCINE CONTAINING PORCINE CIRCOVIRUS TYPE 2B AND *MYCOPLASMA HYOPNEUMONIAE* AGAINST AN EXPERIMENTAL DAUL CHALLENGE

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Introduction and Objectives

The purpose of this study was to evaluate the efficacy of a new, single-dose bivalent vaccine (Circo/MycoGard, Pharmgate Animal Health) containing type 2b (PCV2b) and *Mycoplasma hyopneumoniae* against a dual PCV2b and *M. hyopneumoniae* challenge. Since co-infection with these two pathogens commonly contributes to porcine respiratory disease (1) and worsens clinical and production outcomes, this study investigated whether the vaccine could reduce clinical signs, pathogen load, and lesions under an experimental dual challenge model.

Materials and Methods

A total of 24 pigs were divided into three groups: vaccinated/challenged, unvaccinated/challenged, and unvaccinated/unchallenged controls. The vaccine was administered once at 10 days of age. At 35 days of age, pigs were experimentally challenged with PCV2b and then *M. hyopneumoniae*. Clinical signs, weight gain, pathogen load (PCR), antibody responses, IFN-γ secreting cells (IFN-γ-SC), and lung/lymphoid lesions were measured.

Results and Discussion

Pigs in vaccinated/challenged group induced significantly higher ($P < 0.05$) levels of neutralizing antibodies against PCV2b from 14 to 21 days post challenge (dpc) and significantly higher ($P < 0.05$) numbers of PCV2b and *M. hyopneumoniae* specific IFN-γ-SC in PBMC from -14, 0, 14, and 21 dpc when compared with pigs in unvaccinated/challenged group. The vaccinated/challenged group showed significantly less PCV2b genomic copies in the blood and significantly less *M. hyopneumoniae* genomic copies in nasal swabs from 7 to 21 dpc compared to the unvaccinated/challenge group. The vaccinated/challenge group had significantly lower macroscopic (17.4 ± 5.3) and microscopic (0.9 ± 0.34) lung lesion scores for *M. hyopneumoniae* and significantly lower microscopic lymphoid lesion scores (0.7 ± 02.) for PCV2b infection at 21 dpc compared to the unvaccinated/challenge group (45.8 ± 3.2, 3.5 ± 0.4, and 3.5 ± 0.5, respectively).

Conclusion

The single-dose bivalent PCV2b and *M. hyopneumoniae* vaccine effectively protected pigs against experimental dual challenge, reducing clinical signs, pathogen levels, and tissue lesions while improving growth performance. The results indicate that the evaluated bivalent vaccine was effective in protecting pigs against PCV2b and *M. hyopneumoniae* infection.

Keywords: Bivalent vaccine, Experimental challenge, *Mycoplasma hyopneumoniae*, Porcine circovirus type 2, Porcine respiratory disease complex.

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EVALUATION OF A BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE IN A COMMERCIAL CHINESE PIG FARM IN HUNAN PROVINCE

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Introduction and Objectives

Porcine Circovirus Type 2 (PCV2) and *Mycoplasma hyopneumoniae* both cause respiratory disease in pigs, having a significant impact on performance. The aim of this clinical trial was to evaluate different PCV2 and *M. hyopneumoniae* vaccination schemes in a Chinese commercial pig farm.

Materials and Methods

A controlled, side-by-side trial was conducted in a farm with a history of PCV2 and *M. hyopneumoniae* infections in the province of Hunan. A total of 6240 piglets were housed in a four-story wean-to-finish barn (1560 piglets/floor). At weaning, each floor served as a replicate, and piglets were randomized and evenly allocated within each replicate, with pens assigned one-to-one (one Control pen, one Experimental pen). Control pigs (C; n = 3120; n = 780/replicate) were vaccinated against PCV2 and *M. hyopneumoniae* at 21 days of age (bivalent; 金圆支) and PCV2 at 56d (monovalent; 圆立优). Experimental group (E; n = 3120; n = 780/replicate) was vaccinated only once (bivalent; Porcilis® PCV M Hyo) at 21d. Sera were collected (n = 20; 5/replicate) at 3, 7, 11, 15, 19 and 23wk of age and tested for PCV2 viremia (qPCR). Survival rate, ADG and Pneumonia lesions (Madec score) at slaughter (n = 150) were recorded. Pneumonia Score was analyzed by Fisher's exact test; survival rate by Wilcoxon-rank sum test.

Results and Discussion

All blood samples were PCR-negative at 3, 7 and 23wk. At 11, 15 and 19wk, 3 pigs tested PCR-positive from E, C and E groups, respectively. The viral load was very low (1.46 - 178 GE copies/µL) in all cases. However, this small sample size may have led to low power and failure to detect true positives. Severity of pneumonia lesions was significantly lower in Group E (4.1 ± 2.8) than in Controls (6.3 ± 3.3) ($P < 0.05$). Survival rate was similar between groups (E: 97.9%; C: 97.0%; $P > 0.05$). Pigs from Group E reached slaughter weight 3 days earlier (E: 146.4; C: 150.1). ADG was numerically higher in Group E (805.6 g/pig/d) compared to Group C (794.4 g/pig/d).

Conclusion

Under the conditions of this study, the single-dose vaccination scheme from the experimental group reduced the severity of Mycoplasma-like pneumonia lesions and numerically improved ADG.

Keywords: Lung lesions, Mycoplasma hyopneumoniae, PCV2, Performance, Vaccination.

Acknowledgements: The authors thank the producer for the field support during the trial.

INCREASED GROWTH PERFORMANCE AND CLINICAL PROTECTION CONFERRED BY A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* IN A CHINESE COMMERCIAL FARM IN ZHEJIANG PROVINCE

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* play a primary role in Porcine Respiratory Disease Complex, a respiratory condition impacting pig performance. This study investigates the clinical protection conferred by a RTU PCV2 and *M. hyopneumoniae* vaccine newly registered in China.

Materials and Methods

A controlled, side-by-side trial was conducted in a farrow-to-finish farm in Zhejiang province (China). At weaning, a total of 641 weaned piglets were divided into two groups and housed in the same compartment: experimental (E; n = 387) and control group (C; n = 254). Group E was vaccinated with a bivalent RTU PCV2 and *M. hyopneumoniae* vaccine (Porcilis® PCV *M Hyo*) at 26 days of age, while Group C received a two-dose *M. hyopneumoniae* vaccine at 7 and 21 days of age (Suvaxyn M Hyo®) and a PCV2 vaccine at 37 days of age (CircoFlex®). A longitudinal sampling was performed and sera collected at 3, 15, 18, 20, 23 and 30wk of age (n = 10/group). PCV2 qPCR was performed to quantify viral load in blood. Pneumonia was scored at slaughter (Madec score). Average Daily Gain (ADG) was calculated at group level during the fattening period. Pneumonia lesions were analyzed by Fisher's (Prevalence) and Wilcoxon-rank sum (Severity) tests.

Results and Discussion

PCV2 was detected sporadically in pigs from both groups, but viral load was unquantifiable or very low (< 2.1 copies/µL). The rest of pigs were PCR-negative during the trial. Both Prevalence (E: 2.5%; C: 18.2%; $P < 0.05$) and Severity (E: 0.04 ± 0.25; C: 0.35 ± 0.84; $P < 0.05$) of pneumonia lesions were significantly lower in group E compared to group C. Pigs from group E reached slaughter weight 6 days earlier (E:198; C:204). ADG was numerically higher in group E (932.2 g/pig/d) compared to Group C (910.6 g/pig/d).

Conclusion

Under the conditions of this trial, the RTU vaccine significantly reduced the prevalence and severity of pneumonia lesions. Both vaccination schemes reduced PCV2 viremia to insignificant loads. These findings confirm the excellent clinical protection against both PCV2 and *M. hyopneumoniae* conferred by the RTU vaccine validating the increased growth performance observed (+21 grams/pig/day) compared to the control group. Future studies should use larger samples when PCV2 incidence is low.

Keywords: Lung lesions, *Mycoplasma hyopneumoniae*, PCV2, Performance, Vaccination.

Acknowledgements: The authors thank the producer for the field support during the trial.

GILTS PROTECTED AGAINST PCV2 AFTER VACCINATION WITH A BIVALENT COMBO PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE IN A GILT DEVELOPMENT UNIT IN HEBEI PROVINCE, CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) is responsible for causing PCV2-Reproductive Disease. A measure to control this clinical manifestation is to vaccinate gilts against PCV2. This case report aims to investigate the protection conferred by a Ready-To-Use (RTU) combined PCV2 and *Mycoplasma hyopneumoniae* vaccine in gilts infected with PCV2 under field conditions in China.

Materials and Methods

A controlled, side-by-side clinical trial was performed in a gilt development unit in Hebei province. The herd was not vaccinated against PCV2 and had a history of PCV2 infection. This was confirmed by a preliminary screening (100% gilts tested positive by both ELISA and PCR at 82, 110 and 140 days of age). In total, 200 gilts were included in the study and divided in 2 groups: Control (C; n = 100) vaccinated against *M. hyopneumoniae* at 7 and 21 days of age; and Experimental group (E; n = 100) vaccinated against PCV2 and *M. hyopneumoniae* (Porcilis® PCV M Hyo) at 21 days of age. Blood samples were randomly collected (10 pigs/group) at 8, 12, 16, 20 and 24 weeks of age. Sera was investigated to determine infection dynamics by calculating antibody seroprevalence and quantifying viral load in blood by ELISA and qPCR, respectively.

Results and Discussion

In the Control group, antibody seroprevalence increased from 67 to 100% from 12 to 20 weeks, respectively, suggesting an active PCV2 circulation in this group. PCV2 viremia was detected in pigs from the Control group at 12, 16 and 24 weeks, ct-values ranging between 26.12 and 36.19, which confirmed the previous finding. In the Experimental group, antibody seroprevalence decreased immediately after vaccination (20%) and remained low until 20 weeks of age, where a sudden seroconversion was described. However, viremia remained undetectable during most of the study, except at 24 weeks when a very low viral load was found (Ct-value = 38.20). No PCV2-associated mortality or clinical signs were reported.

Conclusion

Under the conditions of this field trial, the tested vaccine shortened PCV2 viremia and reduced it to insignificant or undetectable levels. These results confirmed that the RTU combined PCV2 and *M. hyopneumoniae* vaccine protected gilts infected with PCV2.

Keywords: PCV2, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

PERFORMANCE ASSESSMENT OF A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE IN A LARGE-SCALE HERD IN HENAN PROVINCE, CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* cause important economic losses to pig industry in China. This field trial investigates the performance of a Ready-To-Use (RTU) combined PCV2 and *Mycoplasma hyopneumoniae* vaccine in a large-scale herd in China.

Materials and Methods

A controlled, side-by-side clinical trial was performed in a two-site large-scale herd (10.000 sows) in Henan province. The herd had a history of *M. hyopneumoniae* infection and severe bronchopneumonia reported at the slaughterhouse. Circulation of PCV2 (10-18 weeks of age) was confirmed by qPCR, suggesting PCV2-subclinical infection. The breeding herd was PRRSV-stable and Aujeszky's Disease Virus free. In total, 789 piglets were housed in the same compartment and divided in 2 groups: Control (C; n = 514) and Experimental group (E; n = 254). Prior to weaning (21 days of age) pigs were vaccinated against PCV2 and *M. hyopneumoniae* (C: Cirbloc® M Hyo; E: Porcilis® PCV M Hyo). Blood samples were randomly collected (10 pigs/group) at 12, 17, 23 and 27 weeks of age to quantify viral load (qPCR). Average daily gain (ADG) was calculated by weighing piglets at group level at weaning and prior to slaughter. And at the slaughterhouse, pneumonia prevalence and severity assessed (110 lungs/group; Madec score). Lung lesions were analyzed by using Fisher's (Prevalence) and Wilcoxon-rank sum (Severity) tests.

Results and Discussion

No PCV2 viremia was detected in either group. Prevalence of pneumonia was significantly lower in group E (71%) compared to group C (85%) ($P < 0.05$). The severity of those lesions was significantly reduced in group E (2.17 ± 2.9) when compared to controls (3.58 ± 4.01) ($P < 0.05$). Live weight prior slaughter was 4.0 kg higher in group E (128.1 kg) than in controls (124.1 kg). ADG was also improved in the experimental group (739.23 g/pig/day) compared to control group (718.98 g/pig/day). No PCV2-Disease was observed, and survival rate was similar between groups (E: 95.94%; C: 95.92%).

Conclusion

Under the conditions of this field trial, the tested vaccine significantly reduced the severity and prevalence of pneumonia lesions and numerically improved performance. PCV-Disease was kept control in both groups. Future studies should use larger samples when PCV2 incidence is low.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Pneumonia, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

FIELD CASE REPORT: READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE ACHIEVES PORCINE RESPIRATORY DISEASE COMPLEX CONTROL AND LOWERS LABOR

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* play a role in Porcine Respiratory Disease Complex (PRDC). Both cause severe respiratory disease and poor performance leading to economic losses. This case report describes a control approach to PRDC by using a recently registered Ready-To-Use bivalent PCV2 and *M. hyopneumoniae* vaccine in China.

Materials and Methods

This study was performed in a farrow-to-finish herd (600 sows) working on a weekly system and located in the province of Heilongjiang. During December 2024, PRDC in growers/fatteners was reported, involving PRRSV circulation and subclinical PCV2 infection. On January 18th, 2025, a batch of pigs (n = 1465) was vaccinated against *M. hyopneumoniae* (7 and 21 days of age; M+PAC®) and PCV2 (14 days of age; Circovac®). The subsequent batch (n = 1387) was vaccinated with a single-shot RTU bivalent vaccine at 21 days of age (Porcilis® PCV M Hyo). From weaning onwards, both batches were housed in adjacent rooms with identical climate, housing and similar entry weight and health status. The first batch was considered as an historical Control group (C), whereas the second one as the Experimental group (E). Ten pigs/group were bled at 11, 15, 19 and 23 weeks of age. All pigs were weighed at group level at weaning and prior to slaughter. Comparison between both groups was done based on PCV2 viremia (qPCR) and performance (Average Daily Gain, ADG; mortality). Average time to slaughter was calculated for each group.

Results and Discussion

No PCV2 viremic pigs were detected in either group during the study. Live weight at slaughter (kg) was 135.88 in Controls and 136.78 in the Experimental group. ADG (g/pig/day) was 768 g and 776 g in Control and Experimental groups, respectively. Days to slaughter were similar between both groups (C:176.9; E: 176.3). Mortality was low in both groups (C: 2.87%; E: 2.24%). Workload and labor were reduced from handling pigs 3 times (Control) to once (Experimental).

Conclusion

In this case report, both vaccination schemes successfully controlled the described PRDC case. The tested vaccine demonstrated a similar performance outcome and better convenience, reducing labor during vaccination.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Performance, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

EFFICACY AND SAFETY ASSESSMENT OF A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE IN A PIG HERD IN HEILONGJIANG PROVINCE, CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* have an important economic impact in the swine industry. This trial investigates the efficacy and the safety of a Ready-To-Use bivalent PCV2 and *M. hyopneumoniae* vaccine under field conditions in China.

Materials and Methods

A controlled, randomized, side-by-side clinical trial was performed in a two-site herd (2.000 sows) in Heilongjiang province. The breeding herd was Pseudorabies Virus-free and PRRSV-stable. After weaning (25 days of age), 1000 piglets were enrolled in the study, divided into 2 groups and vaccinated against PCV2 and *M. hyopneumoniae*: Control (C; n = 500; C: Cirbloc® M Hyo) and Experimental group (E; n = 500; Porcilis® PCV M Hyo). Groups were allocated to separate adjacent wean-to-finish barns that were matched for weight at entry (litter level randomization), feed, climate, and all management conditions. Sera were collected (10 pigs/group) at 11, 15, 19 and 23 weeks of age and tested for PCV2 viral load (qPCR). Average Daily Gain (ADG) was calculated by weighing pigs at group level at weaning and prior to slaughter. Feed Conversion Ratio was computed for the same period, at barn/group level. Mortality was recorded individually during the study. Adverse reactions, when present, were recorded during the first 24 hours after vaccination. Mortality rate was analyzed by using Fisher's test.

Results and Discussion

No PCV2 viremia was detected in either group during the study. Weight at weaning was similar between groups. Live weight at slaughter was 129.6 kg and 122.6 kg in group E and C, respectively. ADG was 669.5 (E) and 661.6 (C) g/pig/day. Days to slaughter weight were 185 in both groups. FCR was reduced in the experimental group (2.72) compared to control group (2.91). Only 3 pigs (E: 1/500; C: 2/500) showed mild adverse reactions and all recovered within 4h post-vaccination. Mortality rate was lower in the Experimental group (2.0%) compared to controls (4.0%) ($P < 0.05$).

Conclusion

The tested vaccine demonstrated efficacy and safety under the conditions of this trial. Viremia was no detected in either group, a larger sample size would have increased the power of detection. Performance outcomes were numerically improved in the experimental group.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Performance, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

CONTROL OF PCV2 SUBCLINICAL INFECTION WITH A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE: EFFICACY, SAFETY, AND LABOR REDUCTION

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Introduction and Objectives

The most common manifestation of Porcine circovirus type 2 (PCV2) is the subclinical infection, which is linked to impaired performance and economic losses (Segales et al., 2022). This case report describes the use of a recently registered, ready-to-use bivalent PCV2 and *M. hyopneumoniae* vaccine to control PCV2 subclinical infection in China.

Materials and Methods

This case was conducted in a farrow-to-finish herd (360 sows; 5-week system) located in the province of Heilongjiang. In November 2024, PRRSV circulation and subclinical PCV2 infection were detected in growers/fatteners. On December 14th, a batch of pigs (C: historical Control; n = 1000) was vaccinated against *M. hyopneumoniae* (7 and 21 days of age) and PCV2 (14 days of age). The subsequent batch (E: Experimental group; n = 1000) was vaccinated with a single-shot RTU bivalent vaccine at 21 days (Porcilis® PCV M Hyo). After weaning, both batches entered the wean-to-finish unit, each batch housed under identical housing conditions with similar entry weight and health. From weaning, both vaccination schemes (C: n = 462; E: n = 457) were compared for efficacy and safety. Sera (n = 10) were collected at 11, 15 and 19 weeks and PCV2 load quantified (qPCR). Pigs were weighed at group level at weaning and prior to slaughter, then Average Daily Gain (ADG) calculated. Adverse reactions were recorded for 24 hours post-vaccination.

Results and Discussion

PCV2 viral load was very low in either group (103-104 copies/mL). Live weight at slaughter (kg) was higher in Group E (140.42) than group C (136.66). ADG (g/pig/day) was 747.5 and 730.8g in Experimental and Control groups, respectively. Days to slaughter were similar between both groups (187 days). Only 3 (E:1; C:2) pigs presented mild reactions post-vaccination (decreased activity), but all recovered within 12h. The experimental group was handled once during vaccination, whereas the controls three times.

Conclusion

In this case report, both vaccination schemes effectively controlled PCV2, lowering viremia to negligible levels. The tested vaccine delivered superior performance outcomes and greater convenience, reducing vaccination labor. No safety concerns were observed with either scheme. Given low incidence/subclinical infection, larger sample size is recommended to investigate PCV2 infections.

Keywords: Labor, *Mycoplasma hyopneumoniae*, PCV2, Performance, Viremia.
Acknowledgements: The authors thank the producer for the field support during the trial.

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EVALUATION OF INTRADERMAL VACCINATION IN PIGLETS TO IMPROVE WELFARE

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Introduction and Objectives

Needle-free intradermal (ID) vaccination of pigs is a growing practice, but uptake has been slow in North America. This study aimed to prove some of its proposed benefits in a realistic research environment, to increase interest and demonstrate how it can counter labour shortages while promoting animal welfare.

Material and Methods

1123 weaner piglets were randomly assigned into treatment groups: an ID group, an IM group, and a control group. Piglets were vaccinated in a random order with an injector device (with a capped or uncapped needle) or MSD's IDAL device. Time, audio, and video were recorded. 190 piglets were bled one-hour post-vaccination. Then six groups were recorded for thirty minutes with a novel object. The rest of the pens' behaviours were recorded via scan observations two- and three-hours post-vaccination.

Results and Discussion

ID piglets had lower cortisol levels (ID mean = 94.37 nmol/L, IM mean = 185.16 nmol/L, $P < 0.001$), less vocalizations >1000 Hz (ID mean screams per pen = 2.36, IM mean = 16.64), and less intense vocalizations (ID mean intensity = 61.14 dB, IM mean = 68.20 dB). ID vaccination was faster (ID mean time per pen = 01:30.26 min, IM mean = 01:54.51 min), resulted in no adverse reactions (IM = 11), and no human injuries (IM = 2). More ID piglets interacted with the ball (ID mean = 2.02 pigs per minute, IM mean = 0.24) and for longer (ID mean = 23:29.67 min, IM mean = 07:51.68 min), while also moving it farther (ID mean = 139.33 ft, IM mean = 6.67 ft).

Conclusion

Our results suggest that intradermal vaccination can be an effective and safe method of protecting swine, while enhancing animal welfare and promoting higher worker safety with better time management. It can also help to relieve some stresses caused by nationwide labour shortages.

Keywords: Animal welfare, Animal behaviour, Intradermal vaccination, Intramuscular vaccination, Producer welfare.

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ALGAE EXTRACT SUPPLEMENTATION BOOSTS HUMORAL IMMUNITY INDUCED BY ATTENUATED PRRSV-1 VACCINATION

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Introduction and Objectives

Some studies have shown an inhibitory effect of algae on PRRSV replication in vitro (Guo et al., 2019). Hervet et al., 2022 have demonstrated that Ulva spp extract induces transcriptomic upregulation of pro-inflammatory genes (IL-8, IL-6, IFN-β) in immune cells and inhibits PRRSV replication upon short-term in vitro treatments. This study investigates the use of Searup® supplementation composed of an Ulva spp (green algae) extract to modulate the immune response to PRRS vaccination with a MLV vaccine.

Materials and Methods

The study used 58 PRRSV-negative pigs (~25kg) on a commercial farm, divided into six experimental groups to test an oral algae supplement (3 ml/dose) with the Ingelvac® PRRSFLEX EU (MLV) vaccine: Group 1 & 2 (No Algae): Vaccinated (n = 10) vs. non-vaccinated (n = 7). Group 3 & 4 (VacSwPost): Algae on days 1–5 post-vaccination; Vaccinated (n = 11) vs. non-vaccinated (n = 10). Group 5 & 6 (VacSwPre): Algae 1 day before and 2 post-vaccination (excluding day 0); Vaccinated (n = 10) vs. non-vaccinated (n = 10). Blood samples were collected at days -2, 0, 2, 4, 8, and 12 post-vaccination (dpv). Analysis included viral titration of the vaccine strain (MLV) via RT-qPCR targeting the ORF7 gene, anti-PRRSV IgG ELISA, and a multiplex Luminex assay for 10 cytokines. Data were analyzed using Kruskal-Wallis tests, with Principal Component Analysis (PCA) to identify variability drivers.

Results and Discussion

The VacSwPre group (pre-vaccination supplementation) showed the most significant benefits: Increased Humoral Response: Anti-PRRSV IgG levels were significantly higher than the standard vaccine group by 12 dpv (days post vaccination). Vaccine Viral Load: Interestingly, the vaccine virus (not wild-type) titers were significantly higher in the VacSwPre group at 4 dpv, suggesting the seaweed aided initial vaccine processing. Cytokine Modulation: This group showed a significant downregulation of pro-inflammatory cytokines (IL-1α, IL-6, and IL-10) at 2 and 6 dpv, indicating a more controlled immune reaction.

Conclusion

This study shows that oral algae supplement around vaccination (VacSwPre) modulates the immune response to a commercial MLV PRRSV vaccine. These results pave the way for future research into neutralizing antibodies, cellular immunity, and clinical protection against wild virus strains for this and other types of PRRSv vaccines.

Keywords: Algae extract, PRRSV, Oral supplementation, Vaccine.

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EFFECTS ON ACUTE PHASE PROTEINS IN PIGLETS OF TWO DIFFERENT PCV-2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINATION PROTOCOLS

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Introduction and Objectives

The aim of this study was to evaluate the response of weaned piglets to vaccination with two different PCV-2 and *Mycoplasma hyopneumoniae* vaccine combinations based on Hp (Haptoglobin), CRP (Protein-C reactive) and rectal temperature. HP and CRP are two biomarkers that have been used in published studies to assess vaccine safety in piglets.

Materials and Methods

In total, 40 commercial piglets from the same flow were divided into two groups and vaccinated intramuscularly at 28 days of age. Both groups were equally distributed by sex and weight and stayed in the same airspace and caregiver during all the trial duration. The first group (A, n = 20) received a fresh mixture of CircoFLEX® and MycoFLEX® in a single injection of 2 ml (FLEXcombo®; Boehringer Ingelheim). The second group (B, n = 20) was vaccinated with 2 ml of a ready-to-use (RTU) product, Cirbloc Mhyo® (Ceva Santé Animale). Blood samples were taken just before vaccination and at 24h and 48h after vaccination. Rectal temperatures were taken just before vaccination and at 6 h after vaccination.

Results and Discussion

Both protocols increased CRP and HP serum concentration in comparison to the basal level of the respective group. This increase was significantly higher ($P < 0.05$) in group B at 24 hours post-vaccination. Hp and CRP concentrations were significantly higher in group B compared to group A. The average rectal temperature in pigs vaccinated with treatment A increased slightly but not significantly (+0.4 ºC). The average rectal temperature of group B presented a significant increase ($P < 0.05$) in the next 6 hours after vaccination (+1.3ºC above basal levels). The rectal temperature of piglets from group B was significantly higher ($P < 0.05$) than those from group A.

Conclusion

The release of APPs was significantly higher in piglets vaccinated with protocol B (Cirbloc Mhyo®). Furthermore, a significant increase in rectal temperature was observed in group B pigs. As described in other studies, vaccination with FLEXcombo® has a minor negative effect on well-being parameters and induces less stress, compared to other vaccines such as RTUs, which is important for intestinal integrity and growth performance during the nursery period.

Keywords: Acute phase proteins, PCV-2 and *Mycoplasma hyopneumoniae*, Vaccine safety.

EXPERIMENTAL EFFICACY OF A NOVEL COMBINED VACCINE (XENOVAX PCM4) OF PCV2A/D, *MYCOPLASMA HYOPNEUMONIAE* AND *M. HYORHINIS*

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Introduction and Objectives

A new commercial combined vaccine containing two PCV2 genotypes (PCV2a and PCV2d), *Mycoplasma hyopneumoniae*, and *M. hyorhinis* was introduced into the Korean market, where PCV2d is the most prevalent PCV2 genotype, and polyserositis caused by *M. hyorhinis* is increasing. The efficacy of a new combined vaccine of porcine circovirus types 2a/d (PCV2a/d), *Mycoplasma hyopneumoniae*, and *M. hyorhinis* was evaluated (Suh et al., 2025).

Materials and Methods

A total of 45 pigs were randomly divided into 9 groups (5 pigs per group). The pigs in vaccinated groups were immunized intramuscularly with 2.0 mL of the combined vaccine (XENOVAX PCM4, Careside Co. Ltd) and then challenged against single PCV2a, single PCV2d, single *M. hyopneumoniae*, and co-PCV2d and *M. hyorhinis* challenges. The number of genomic DNA copies for PCV2a, PCV2d, *M. hyopneumoniae* and *M. hyorhinis* was then quantified by real-time PCR. The antibody responses against PCV2, *M. hyopneumoniae*, and *M. hyorhinis* were measured by ELISA. Neutralizing antibody responses against PCV2a and PCV2d was also measured.

Results and Discussion

Vaccinated pigs exhibited enhanced growth performance. The vaccine successfully induced systemic adaptive immunity, including humoral and cellular responses against PCV2a, PCV2d, *M. hyopneumoniae*, and *M. hyorhinis*. The vaccination reduced viral loads in blood, and mycoplasmal loads in larynx and nasal shedding, and lesion (mycoplasmal pneumonia, lymphoid lesion and fibrinous hepatitis) severity related to these pathogens. Vaccination of pigs with a combined vaccine resulted in the induction of cellular immune response to *M. hyopneumoniae* and demonstrated protection by significantly lowering mycoplasmal laryngeal loads while reducing lung lesions. Vaccination has proven to induce systemic humoral and cellular responses to *M. hyorhinis* and reduce *M. hyorhinis* nasal loads while reducing the severity of polyserositis.

Conclusion

The results of the present experimental challenge study demonstrate that a new combined vaccine is efficacious in protecting pigs against PCV2a, PCV2d, *M. hyopneumoniae*, and *M. hyorhinis* challenge. This combined vaccine is optimal for improving growth performance and controlling complicated co-infections by these four pathogens.

Keywords: *Mycoplasma hyopneumoniae, M. hyorhinis*, Porcine circovirus type 2, Vaccine.

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FIELD EVALUATION OF A NOVEL COMBINED VACCINE (XENOVAX PCM4) OF PCV2A/D, *MYCOPLASMA HYOPNEUMONIAE* AND *M. HYORHINIS* WITH AN EMPHASIS ON GROWTH PERFORMANCE

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Introduction and Objectives

A new combined vaccine containing PCV2a/d, *Mycoplasma hyopneumoniae*, and *M. hyorhinis* was introduced into the Korean market. A field efficacy trial was conducted on three farms to evaluate a novel combined vaccine containing porcine circovirus types 2a/d (PCV2a/d), *M. hyopneumoniae*, and *M. hyorhinis* (Suh et al., 2025).

Materials and Methods

Three farms with a history of subclinical PCV2 infection, enzootic pneumonia, and polyserositis were enrolled. Each farm included 40 piglets (18 days old), which were randomly allocated to vaccinated or unvaccinated groups. Pigs in the vaccinated group received a single 2.0 mL intramuscular dose of the combined vaccine (XENOVAX PCM4, Careside Co. Ltd) at 21 days of age, while unvaccinated pigs received phosphate-buffered saline. The number of genomic DNA copies for PCV2a, PCV2d, *M. hyopneumoniae* and *M. hyorhinis* was then quantified by real-time PCR. The antibody responses against PCV2, *M. hyopneumoniae*, and *M. hyorhinis* were measured by ELISA. Neutralizing antibody responses against PCV2a and PCV2d was also measured

Results and Discussion

Vaccination significantly improved ($P < 0.05$) body weight and average daily weight gain on all three farms compared with unvaccinated pigs. Vaccinated pigs mounted protective humoral (IgG and neutralizing antibody) and cellular (interferon-gamma secreting cells) immune responses against PCV2, *M. hyopneumoniae*, and *M. hyorhinis*. Furthermore, vaccination reduced viral (PCV2a and PCV2d) loads in serum, laryngeal (*M. hyopneumoniae*), and nasal (*M. hyorhinis*) samples, and decreased the severity of associated lesions (mycoplasma pneumonia, lymphoid lesion, fibrinous hepatitis). These field trials demonstrated that the combined vaccine conferred efficient protection against PCV2d, *M. hyopneumoniae*, and *M. hyorhinis* infection in swine herds.

Conclusion

The combined vaccine demonstrated strong efficacy under field conditions, providing protection against subclinical PCV2 infection, enzootic pneumonia caused by *M. hyopneumoniae*, and polyserositis caused by *M. hyorhinis*. The vaccine elicited robust humoral and cellular immune responses, resulting in reduced viremia, decreased mycoplasmal loads in the larynx and nasal cavities, and mitigation of lesion severity. These findings support its potential as an effective intervention for improving both health and productivity in swine herds.

Keywords: *Mycoplasma hyopneumoniae, M. hyorhinis,* Porcine circovirus type 2, Vaccine.

References

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EXPERIMENTAL EFFICACY OF A NOVEL MODIFIED-LIVE PRRSV-1 VACCINE (XENOVAX EU-PRRS) AGAINST PRRSV-1 CHALLENGE IN SOWS AND GROWING PIGS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) is still the most economically important viral disease yhreatening pig production worldwide. As the name suggests two clinical presentations are associated with PRRS; reproductive failure in sows and respiratory disease in pigs of any age (Zimmerman et al., 2019). The objective of this study was to determine the efficacy of a modified live PRRSV-1 vaccine against a heterologous PRRSV-1 strain challenge in pregnant sows and growing pigs.

Materials and Methods

Twelve pregnant sows and twenty four pigs from PRRSV-free farms were randomly assigned to three groups (four sows and eight pigs per group); vaccinated-challenged, unvaccinated-challenged, and unvaccinated-unchallenged groups. Sows in the vaccinated-challenged group received a 1.0 mL intramuscular dose of modified-live PRRSV-1 vaccine (XENOVAX EU-PRRS) at 28 days of age days before breeding and were subsequently challenged intranasally with a heterologous PRRSV-1 strain at 93 days of gestation. The sequence homology of ORF5 between vaccine and challenge strain is 93.23%. Pigs in the vaccinated-challenged group received a 1.0 mL intramuscular dose of modified-live PRRSV-1 vaccine (XENOVAX EU-PRRS) at 21 days of age and were subsequently challenged intranasally with a heterologous PRRSV-1 strain at 56 days of gestation.

Results and Discussion

Vaccinated-challenged sows improved reproductive performance, including a higher number of live-born piglets (11.33 ± 0.58) and fewer stillbirths (2.5 ± 1.29) compared with live-born piglets (4.5 ± 1.29) and fewer stillbirths (7.75 ± 1.2.22) of unvaccinated-challenged sows. Viral genomic loads were lower in vaccinated-challenged sows and their offspring as well. Vaccinated-challenged sows also elicited a significantly higher frequency of PRRSV-1 specific interferon-γ secreting cells. Vaccinated challenged pigs exhibited significantly lower respiratory scores, viremia, macroscopic and microscopic lung lesion scores, and PRRSV-antigen with interstitial pneumonia than unvaccinated challenged pigs. Lower neutralizing antibody titers (1:8) were observed after vaccination. The induction of PRRSV-specific IFN-γ-SCs by the new modified- live PRRSV-1 vaccine produced a protective immune response, leading to the reduction of PRRSV viremia.

Conclusion

Vaccination of modified live PRRSV-1 vaccine provided protection of pregnant sows and growing pigs against heterologous PRRSV-1 challenge based on clinical, virological, and immunological pathological outcomes under experimental conditions.

Keywords: Modified-live vaccine, Porcine reproductive and respiratory syndrome virus-1.

References

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FIELD EFFICACY OF A NOVEL MODIFIED-LIVE PRRSV-1 VACCINE (XENOVAX EU-PRRS) IN SOWS AND GROWING PIGS WITH AN EMPHASIS ON REPRODUCTIVE AND GROWTH PERFORMANCE

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) remains the most economically important viral disease continuously threatening the pig industry worldwide. The disease is characterized by reproductive failures in sows and by respiratory disease in growing pigs. The objective of this study was to determine the efficacy of a modified live PRRSV-1 vaccine in pregnant sows and growing pigs with an emphasis on reproductive and growth performance under field conditions.

Materials and Methods

Three PRRS endemic farms were selected based on their history of PRRS-associated reproductive and respiratory failures. Three farms did not use PRRS MLV. On each farm, a total of 10 sows and 40 pigs were randomly allocated to two treatment groups (5 sows and 20 pigs per group). Vaccinated sows and pigs received a 1.0 mL intramuscular dose of modified-live PRRSV-1 vaccine (XENOVAX EU-PRRS) at 28 days of age days before breeding and 21 days of age, respectively. Unvaccinated sows and pigs received a 1.0 mL intramuscular dose of PBS at the same age.

Results and Discussion

Clinical data showed a significant improvement in reproductive performance in vaccinated sows. Sows in the vaccinated groups had significantly reduced numbers of stillborn piglets (n = 0.71) in farm compared to those (n = 1.51) from unvaccinated sows. Sows in the vaccinated groups had significantly increased number of live-born piglets (n = 12.6) in farm. Sows in the vaccinated groups had significantly increased number of weaned piglets in farms compared to those (n = 7.8) from unvaccinated sows. No adverse systemic or local side effects relative to vaccination were observed during the entire gestation. The overall growth performance (from 3 weeks of age to the date of the first group of pigs was shipped to slaughter) of the vaccinated animals was significantly higher body weight (109.79 kg) than that (106.26 kg) of the control animals at the 3 farms.

Conclusion

Vaccination of sows with this modified-live PRRSV-1 vaccine was effective to improve reproductive performance in endemic PRRS farms. The new modified-live PRRSV-1 vaccine improved growth performance, and decreased the mortality and lung lesions when evaluated under field conditions.

Keywords: Field trial, Modified-live vaccine, Porcine reproductive and respiratory syndrome virus-1.

References

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SAFETY AND IMMUNOGENICITY ESSAY WITH A NOVEL LIVE PED RECOMBINANT VACCINE IN A COMMERCIAL PIG FARM

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Introduction and Objectives

Porcine epidemic diarrhea (PED) is a viral disease that can cause up to 100% mortality in piglets, making the development of effective vaccines essential. This field study evaluated the safety and immunogenicity of a novel live recombinant vaccine based on a Newcastle disease virus (Paramyxovirus-1) vector carrying the PEDV Spike gene (AVX/PED-S1S2).

Materials and Methods

Two groups were formed on the same farm using a double-blind design: Group A, 52 unvaccinated pigs; Group B, 52 vaccinated pigs that received two intramuscular doses of AVX/PED-S1S2 (2.0 mL per dose) at 17 and 19 weeks of age. Due to field trial limitations, safety and immunogenicity were defined and measured as follows. Safety was assessed by observing animals for 4 hours after each vaccination for signs of adverse reactions (anaphylaxis, fever, vomiting, shock), monitoring productive performance, and checking for local injection-site reactions during the first week. Immunogenicity was evaluated by detecting specific antibodies by indirect ELISA at weeks 17, 19, and 22, using a kit for antibodies against the PEDV nucleocapsid (ID Screen PED Indirect, ID.Vet) and another for antibodies against the PEDV Spike (INgesim, Gold Standard Diagnostics). Using both kits allows differentiation between antibodies from natural infection (nucleocapsid) and those induced by the vaccine (Spike). Rectal swabs and blood samples were also collected from both groups for qPCR to rule out natural field exposure to PEDV.

Results and Discussion

Vaccination did not cause systemic or local adverse reactions nor affect productive performance. Nucleocapsid ELISAs were negative in both groups, indicating absence of whole-virus infection; Spike ELISAs were 100% positive only in vaccinated pigs three weeks after the second dose, demonstrating induction of Spike-specific antibodies. qPCR of rectal swabs ruled out PEDV infection.

Conclusion

Despite limitations of conducting a safety and immunogenicity trial in the field, the AVX/PED-S1S2 vaccine proved safe and immunogenic in pigs, inducing a specific immune response against the PEDV Spike protein. Results from the two ELISA kits indicate the vaccine also has potential as a DIVA tool to differentiate vaccinated animals from those exposed in the field.

Keywords: AVX/PED-S1S2 vaccine, DIVA, Nucleocapsid, Spike, Porcine Epidemic Diarrhea.

FIELD OBSERVATION TO ASSESS GROWTH PERFORMANCE AFTER VACCINATION WITH A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE RECENTLY REGISTERED IN CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* cause severe respiratory disease and poor performance. Both play a role in the Porcine Respiratory Disease Complex (PRDC) and inflict significant economic losses on the pig industry. Vaccination is one of the most common tools used to control these pathogens. This field observation aimed to evaluate growth performance after vaccination with a Ready-to-Use (RTU) bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China.

Materials and Methods

A farrow-to-finish herd (500 sows; 5-week system) with a history of PCV2 subclinical infection and located in Shanxi province (China) was selected for this trial controlled, randomized, side-by-side trial. In total, 1221 piglets from the same batch were enrolled in the study and divided into two groups. Pigs in the Control group (C; n = 606) were vaccinated with a combo PCV2-*M. hyopneumoniae* vaccine (金圆支) at 14 days of age; whereas pigs in the Experimental group (E; n = 615) received the RTU vaccine (Porcilis® PCV M Hyo) at 21 days. Sera was collected from 10 pigs/group at 11,15,19 and 22 weeks of age. Then PCV2 viral load quantified using qPCR testing. Pigs were weighed (at group level) at weaning (26 days), at transfer to fattening (54 days) and prior to market. Average Daily Gain (ADG) calculated for these periods.

Results and Discussion

PCV2 viremia remained undetectable during the study in both groups. Average entry weight (C: 7.90 kg; E: 7.85 kg) and live weight at market (C: 143 kg; E: 142 kg) were similar between groups, but average time to market was 5 days shorter in group E (206 days) than in controls (211 days). ADG during the fattening period was 814.7 g for Controls and 846.0g for Experimental group. ADG during the overall period was 730.3 and 745.3 g for Group C and E, respectively.

Conclusion

Under the conditions of this field case, both vaccines lead to an absence of PCV2 viremia. The RTU vaccine improved growth and performance. The absence of an unvaccinated control group did not allow us to demonstrate PCV2 and *M. hyopneumoniae* circulation.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Performance, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

PERFORMANCE ASSESSMENT AFTER VACCINATION WITH A BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE RECENTLY REGISTERED IN CHINA – A CASE REPORT

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* have a significant impact on the pig industry. This case report assesses the performance of a bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China.

Materials and Methods

The case was reported on a single-site farrow-to-finish farm (1500 sows) in Fujiang Province with a history of PCV2-systemic disease confirmed by clinical signs and lab diagnosis. At weaning, two consecutive batches were selected and compared to each other. Weaned piglets from one batch served as the historical Control group (C; n = 1128), while piglets from the subsequent batch were selected as the Experimental group (E; n = 1960). Weaners from Group C were vaccinated against PCV2 and *M. hyopneumoniae* at 21 days of age (Fostera PCV MH; historical vaccine used in the farm), while Group E was vaccinated at 26 days of age (Porcilis® PCV M Hyo). Sera were collected (10 pigs/group) at 4, 9, 14, 17 and 20 weeks of age and PCV2 viral load quantified (qPCR). Each group was housed in adjacent rooms under identical conditions. Pigs were weighed at group level at the beginning of fattening (10 weeks of age) and prior to slaughter, then Average Daily Gain (ADG) calculated for this period. Mortality was recorded during the fattening period. At the slaughterhouse, pneumonia lesions were evaluated (Madec score). Severity of pneumonia was analyzed by Wilcoxon test, prevalence of pneumonia and mortality by Fisher's exact test.

Results and Discussion

ADG was numerically higher in group E (910.5g/p/d) compared to Group C (877.7g/p/d). Mortality was significantly lower in group E (0.8%) compared to group C (1.9%) ($P < 0.05$). Both severity (E: 0.23 ± 0.57; C: 0.42 ± 0.76) and prevalence of pneumonia (E: 16.7%; C: 25.8%; $P < 0.1$) were numerically lower in Group E. PCV2 remained undetectable during the study, likely due to a limited sample size.

Conclusion

Under the conditions of this case, the tested vaccine significantly reduced mortality, and a numerical diminished the severity and prevalence of pneumonia, leading to a notable performance outcome. The lack of negative control did not allow us to demonstrate the circulation of both PCV2 and *M. hyopneumoniae.*

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Performance, Vaccination.

Acknowledgements: The authors thank the producer for the field support during the trial.

SAFETY AND EFFICACY EVALUATION OF A SINGLE-DOSE READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE RECENTLY REGISTERED IN CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* cause significant losses to the pig industry. This controlled, parallel trial investigates the safety and efficacy of a single-dose ready-to-use bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China by evaluating PCV2 viremia, growth performance and pneumonia lesions at slaughter.

Materials and Methods

A wean-to-finish unit in Shandong province was selected. Previous reports confirmed PCV2 circulation and severe pneumonia. In total, 1500 piglets were enrolled in two groups. Control group (C; n = 764) received a PCV2-*M. hyopneumoniae* vaccine (local Chinese brand) at 40 days of age, followed by an additional PCV2 dose (local Chinese brand) at 60 days. Experimental group (E; n = 736) received a single-dose bivalent vaccine (Porcilis®PCV M Hyo) at 40 days. Post-vaccination adverse reactions were recorded. Sera (15 pigs/group) were collected at 5, 15, 21 and 27 weeks, and PCV2 viral load was quantified using qPCR. All pigs were weighed at weaning (30 days) and before slaughter at pen level. Average Daily Gain (ADG) was calculated. Percentage of pigs reaching slaughter (survival %) was recorded. At slaughter, pneumonia lesions were scored (Madec) (n = 400 lungs/group). Slaughter weight was analyzed using Anova, survival % and pneumonia prevalence by Fisher's exact test, and severity of pneumonia by Wilcoxon test.

Results and Discussion

Adverse reactions were observed only in controls 1h post-vaccination (vomiting, convulsions). Before vaccination (5 weeks), mean viral load was similar between groups ($< 10^4$ copies/mL). It subsequently decreased in both groups to negligible levels, with no differences between groups. At 27 weeks, PCV2 still circulated only in controls. Live weight at slaughter was significantly higher in Group E (128.22 ± 6.06; CV: 4.72%) than in controls (125.85 ± 7.06; CV: 5.61%) ($P < 0.05$). ADG was higher in group E (750.9 grams/day) compared with C (737.6 grams/day). Survival % was numerically higher in group E (97.15%) than in controls (96.34%) ($P > 0.05$). Both severity (E: 4.18 ± 4.00; C: 6.30 ± 3.75; $P < 0.05$) and pneumonia prevalence (E: 80.26%; C:96.02%; $P < 0.05$) were significantly lower in the Experimental group.

Conclusion

Under these conditions, the single-dose protocol was safe and efficacious, significantly reducing pneumonia severity and prevalence, and a significantly improving growth performance and weight uniformity.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Pneumonia, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

FIELD EVALUATION OF A READY-TO-USE SINGLE-DOSE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE IN CHINA: SAFETY AND PERFORMANCE

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* still cause significant losses to the pig industry in China. This controlled, side-by-side trial aimed to investigate the safety and efficacy of a single-dose Ready-to-Use (RTU) bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China.

Materials and Methods

A wean-to-finish unit in Shandong province (China) was selected for this trial. PCV2 and *M. hyopneumoniae* were present on the farm but only causing subclinical problems. A total of 2829 piglets were enrolled in the study at weaning (21 days of age) and divided into two groups. Control group (C; n = 1670) was vaccinated with a two-dose RTU PCV2-*M. hyopneumoniae* vaccine (圆支) at 21 and 60 days of age. Experimental group (E; n = 1159) received a single-dose RTU bivalent vaccine (Porcilis® PCV M Hyo) at 21 days. Longitudinal blood sampling (n = 20 pigs/group) was performed at 3, 15, 19 and 25 weeks of age, and sera were analyzed to determine PCV2 viral load using qPCR. All pigs were weighed (at group level) at weaning and before slaughter. Average Daily Gain (ADG) was calculated for this period. Percentage of pigs reaching slaughter (survival %) was recorded. Pneumonia lesions were recorded at slaughter (Madec) (n = 750 lungs/group). Survival % and pneumonia prevalence were analyzed using Fisher's exact test, severity of pneumonia using Wilcoxon test.

Results and Discussion

No adverse reactions were observed in either group. All sera samples tested PCV2-negative by PCR. Live weight at slaughter was 135.68 kg and 134.50 kg in Group E and C, respectively. ADG was higher in Group E (831.3 grams/day) compared to C (823.2 grams/day). Survival % was numerically higher in Group E (98.62%) than in Controls (97.66%) ($P = 0.07$). Severity of pneumonia lesions was significantly reduced in Group E (0.56 ± 1.47) when compared to Controls (0.96 ± 1.36) ($P < 0.05$). Prevalence of pneumonia was significantly lower in the Experimental group (E: 28.2%; C: 55.9%; $P < 0.05$).

Conclusion

In this large wean-to-finish unit, the single-dose RTU vaccine was safe and associated with improved respiratory outcomes compared with a two-dose regime, including significantly lower pneumonia prevalence and severity, and numerically higher ADG, slaughter weight, and survival.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Pneumonia, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

NEW RANGE OF VACCINE ADJUVANTS, ICTYOLANE, CAN PROMOTE IFNΓ PRODUCING CELLS IN AN OPTIMIZED SAFETY PROFILE

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Introduction and Objectives

Swine vaccines development is challenging to obtain effective cellular immune response. Water-in-Oil (W/O) emulsions based on mineral oil can be used to obtain strong antibody response and proliferation of IFNγ producing cells, but local reactions at the injection site such as inflammation, fibrosis or abscesses are limiting their use. Here we present the development of two vaccine adjuvants rendering Oil-in-Water (O/W) emulsion, intended to induce strong immune response in an optimized safety profile; Ictyolane 15, based on mineral oil and Ictyolane 23D based on biodegradable oil and amphiphilic immunostimulant.

Material and Methods

Vaccines with a Influenza wild type NP recombinant protein were prepared and administrated to 4 groups of 5 week-old piglets in a two shots vaccination scheme 28 days apart, including one group with each O/W test items, a W/O vaccine formulation positive control and antigen (Ag) alone group. Total antibody response was assessed after the primo-vaccination, the booster dose and at sacrifice of the animals at day 56. The spleen of half groups were harvested 10 days after the boost and the IFN-γ producing cells were numerated. General safety has been followed up after each vaccination and local reactions at injection site have been evaluated after the sacrifice of the piglets

Results and Discussion

All adjuvanted vaccines groups induced a significantly higher response compared to Ag group for total IgG and IFN-γ. W/O formulation induced a higher response than O/W formulations. A strong booster effect has been noticed at day 56 with O/W vaccines. Grade 2 local reactions (on a scale of 4) were noticed at the injection site with W/O formulation, no reaction was observed with O/W vaccines

Conclusion

Two new vaccine O/W adjuvants, Ictyolane 15 and Ictyolane 23D, have shown a significant immune response as compared to antigen alone, and a very high safety profile. They are promising adjuvants to obtain safe and efficient commercial vaccines for swine.

Keywords: Adjuvants, Cellular immune response, IFN-γ, Vaccine.

EFFECTIVENESS OF A COMMERCIAL *GLÄSSERELLA PARASUIS* VACCINE UNDER FIELD CONDITIONS IN CHINA

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Introduction and Objectives

Glässer's disease, caused by *Glässerella parasuis*, is a common bacterial disease in the swine industry with a significant impact on animal health and productivity (Tianning et al., 2025). Control has traditionally relied on antibiotics; however, antimicrobial resistance (Huang et al., 2025), intensive production systems, and increasing restrictions on antibiotic use have driven the need for alternative preventive strategies such as vaccination (Wentao et al, 2025). This study evaluated the effectiveness of vaccination for the prevention and control of Glässer's disease under field conditions.

Materials and Methods

In June 2025, an industrial farm (4,800 sows) reported clinical problems, where 50-day-old piglets showed wasting and fibrinous polyserositis. Antibiotic treatments with doxycycline and amoxicillin administered via drinking water showed limited efficacy, and nursery mortality remained above 6%. In July 2025, a vaccination program against Glässer's disease was implemented in the farrowing unit. Three consecutive batches (25,243 piglets) were vaccinated with a commercial vaccine (HIPRASUIS® GLASSER). Mortality was compared with three previous unvaccinated batches totaling 32,319 piglets. Antibiotic use before and after vaccination was assessed, and a logistic regression model was applied to evaluate differences in mortality between groups.

Results and Discussion

Vaccination led to a significant reduction in nursery pig mortality, decreasing from 9% before vaccination to 4% after vaccination ($P = 0.0199$). Additionally, amoxicillin use during the nursery period was reduced by 58%, with monthly costs declining from 29,790 to 12,329 RMB. Nursery pigs are particularly susceptible to infectious diseases due to declining maternal immunity and stressors such as weaning and mixing. *G. parasuis* infection represents a frequent challenge during this stage (Angen et al., 2007), especially in the context of antibiotic reduction. Non-vaccinated pigs showed a 3.1- fold higher odds of mortality compared with vaccinated pigs, highlighting the benefits of preventive immunization.

Conclusion

Vaccination with HIPRASUIS® GLASSER proved to be an effective tool for the prevention and control of Glässer's disease under field conditions, reducing nursery mortality and antibiotic use while supporting sustainable pig production and antimicrobial reduction strategies.

Keywords: Antibiotic reduction, Glasser disease, Vaccination.

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DEVELOPMENT OF A MARKER RECOMBINANT VACCINE AGAINST CLASSICAL SWINE FEVER

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Introduction and Objectives

Classical swine fever (CSF) is a highly contagious multisystem viral disease affecting pigs. In the Russian Federation, CSF control is effectively achieved through mass vaccination of pigs with live attenuated vaccines. However, the use of live vaccines is bound up with a risk of recombination between vaccine strains and field viruses and often causes difficulties due to international trade regulations. The objective of the present study was to develop a recombinant marker vaccine against CSF suitable for implementation of a DIVA (Differentiating Infected from Vaccinated Animals) strategy aimed at disease eradication.

Materials and Methods

To generate an efficacious vaccine, a recombinant baculovirus co-expressing the ectodomains of the CSFV E2 glycoproteins from the Shi-Min and Alfort-Tübingen strains was constructed. Apart from the antigens, the final expression product comprised secretion signal peptides, a 14-histidine tag, and HA and MYC marker epitopes. Coding sequences were codon-optimized for expression in insect cells. Antigenicity and immunogenicity of the vaccine were evaluated in pigs of different age and sex groups. Serum antibody levels against CSFV E2 and ERNS glycoproteins were measured using ELISA. Animals were challenged with a virulent CSFV Shi-Min strain at doses ranging from 1,02 to 105 lg LD50/cm³.

Results and Discussion

The optimal immunizing dose of recombinant E2 glycoprotein was determined to be 60 μg. The vaccine induced high levels of post-vaccination serum antibodies to the E2 glycoprotein after the second immunization, while antibodies against CSFV ERNS were absent. Vaccinated animals also developed high titers of virus-neutralizing antibodies, with group geometric mean titers of 1:111 on day 21 after the first vaccination and 1:256 and 1:111 on days 21 and 96 (time of slaughter) after the second vaccination, respectively ($P < 0.05$). The vaccine provided 100% protection of immunized pigs against challenge with the virulent Shi-Min strain. Vaccinated pigs exhibited significantly milder clinical signs and shorter viremia periods following challenge.

Conclusion

The vaccine designed in the present study effectively protects pigs against CSFV infection and enables reliable serological differentiation between infected and vaccinated animals

Keywords: Classical swine fever, DIVA, Glycoprotein E2, Marker vaccine.

DEVELOPMENT OF A RECOMBINANT VACCINE AGAINST EDEMA DISEASE IN SWINE

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Introduction and Objectives

Edema disease (ED) is a Shiga toxin (Stx2e) toxemia that results in severe edema at specific sites in pigs that have absorbed Stx2e from the intestine following colonization by a Shiga-toxin-producing *E. coli* (STEC). ED mostly occurs in recently weaned piglets; the disease may be sporadic or may affect an entire herd and may first manifest as sudden death without prior signs of sickness (Zimmerman et.al., 2012). Vaccines against ED based on recombinant Shiga toxin were proven to be effective in disease prevention. The objective of the present study was to develop a subunit vaccine against STEC-associated disease and to test it under field conditions on a farm.

Materials and Methods

Recombinant Stx2e subunits A and B were produced in *E. coli* BL-21 strain and then purified by metal affinity chromatography; antigens were characterized using anti-sera to commercial edema vaccines via ELISA and immunoblotting. Vaccine compositions were evaluated in laboratory animals and pigs. Two industrial pig farms participated in field trials where experimental vaccine was compared to Ecoporc-Shiga (CEVA) commercial vaccine, 160774 piglets were assigned for the trial.

Results and Discussion

Recombinant Stx2e subunits (rStxA, rStxB) reacted specifically with rabbit antisera to Vepured vaccine (Hipra) in immunoblot and ELISA. The vaccine composition based on the Carbopol971P adjuvant, 10 µg rStxA and 40 µg rStxB demonstrated no adverse effects on guinea pigs, rabbits and 2-5 days old piglets: local reaction in inoculation spot, rectal temperature, general condition of animals remained normal. In a course of the field trial, 90404 piglets received Ecoporc-Shiga while 76370 piglets received experimental vaccine. At the day of slaughter, livability and daily weight gains where 96,56% and 966,1 g for the control Ecoporc Shiga cohort and 96,74% and 966,9 g for the experimental cohort.

Conclusion

A subunit vaccine based on recombinant Stx2e subunits StxA and StxB was developed, both specific components of it reacted with an antisera to commercially available vaccine. The vaccine was proven to be safe and in comparative field trial it demonstrated efficacy on par with commercially available analogue. The vaccine developed may be recommended for use to prevent STEC-associated disease on farms.

Keywords Edema, *E. Coli*, STEC, Stx2e, vaccine.

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IMPROVEMENT OF PRODUCTION PARAMETERS AFTER PIGLET VACCINATION WITH VEPURED® IN A VEROTOXIN POSITIVE FARM IN JAPAN

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Introduction and Objectives

Edema disease (ED) is caused by systemic vascular damage due to Verotoxin 2e (VT2e) and presents a variety of symptoms collectively known as Verotoxigenic Associated Syndrome (VAS). However, many of these symptoms are difficult to detect on farms. Over 80% of Japanese farms test positive for VT2e, and infected farms are often unaware of it. The objective of this study was to determine whether the VT2e vaccine VEPURED® improves production parameters on farms that show no clear clinical signs of ED.

Materials and Methods

This study was conducted on a farm with 3,000 sows. Although the farm did not exhibit clear clinical signs of ED, PCR testing (VEROCHECK®) confirmed the presence of VT2e-producing E. coli. The farm began administering VEPURED® (ED vaccine, HIPRA, 1 ml, at 1 week of age) to piglets in January 2024. A total of 94,989 piglets born from January to December 2023 were designated as the control group, and 63,845 piglets born from January to December 2024 were designated as the VEPURED® group. Productivity parameters were calculated from aggregated weekly lot-level production data. Statistical analysis was performed using linear regression and post-hoc testing to evaluate differences in production parameters between the two groups.

Results and Discussion

The average body weight and carcass weight at slaughter were 100.53 kg and 66.46 kg in the control group, compared with 103.80 kg and 69.33 kg in the VEPURED® group. Both measures were significantly higher in the VEPURED® group ($P < 0.05$ and $P < 0.001$, respectively). Consequently, the feed conversion ratio (FCR), calculated based on slaughter weight and carcass weight, was 2.25 and 3.41 in the control group, and 2.19 and 3.28 in the VEPURED® group, respectively, both significantly lower in the VEPURED® group ($P < 0.01$). Furthermore, mortality from weaning to slaughter decreased from 12.34% in the control group to 9.06% in the VEPURED® group, representing a significant reduction ($P < 0.001$).

Conclusion

The results of this study show that VT2e can reduce productivity in pig farms, even when the animals do not show obvious clinical symptoms.

Keywords: Edema disease (ED), Less growth, Production Parameters, Verotoxin.

EVALUATION OF THE HETEROLOGOUS PROTECTION OF A PRRSV1 MLV ON PRRSV2-POSITIVE SWINE FARMS IN JAPAN

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) virus causes economic losses in the global swine industry. PRRS virus type 2 (PRRSV2) is predominant in Japan. however, there are field reports of heterologous protection of PRRS virus type 1 (PRRSV1) MLV vaccines against PRRSV2 field virus in Japan. This study was conducted to evaluate the heterologous protection of PRRSV1 MLV vaccine against PRRSV2 under field conditions.

Materials and Methods

This study was conducted on a farm with 1,500 sows operating on two farms (farm A and farm B). PCR testing was performed using blood samples collected from 3 piglets per farm at each sampling point. Samples were collected at 30 days of age and subsequently at 30-day intervals up to 150 days of age for pre-trial monitoring, and then every three months after trial initiation. Mortality was compared between two periods. Non-vaccination period: the farm was positive for PRRSV2 field strain and no vaccination was applied (March 2024 - October 2024; n = 24,218) and Vaccination period: piglets were vaccinated at 3 weeks of age with the PRRSV1 MLV vaccine UNISTRAIN® PRRS (HIPRA) (November 2024–October 2025; n = 36,389). Sows were PRRS-negative and showed no evidence of vertical transmission during the study and therefore were not vaccinated. Mortality data were analyzed using logistic regression.

Results and Discussion

At farm A, the PRRSV2 field strain was detected in the fattening phase until January 2025, but was not detected thereafter. At farm B, detection of PRRSV2 field strain shifted from nursery to fattening phase. However, PRRSV2 field strain positivity was still observed at 30 days of age in October 2025. Mortality in the fattening phase decreased from 3.41% in the Non-vaccination period to 2.63% during the Vaccination period ($P < 0.001$). Mortality from weaning to slaughter age also declined significantly, from 5.78% to 4.96% ($P < 0.001$). These findings indicate that UNISTRAIN® PRRS provided heterologous protection against the circulating PRRSV2, and that delayed onset of field infection likely contributed to the improved mortality rates.

Conclusion

UNISTRAIN® PRRS induced effective heterologous protection against the Japanese field PRRSV2, contributing to improved productivity under field conditions.

Keywords: Cross-protection, Mortality rate, Porcine Reproductive and Respiratory Syndrome (PRRS).

COMPARISON OF MORTALITY AFTER NEEDLE-FREE AND INTRAMUSCULAR ADMINISTRATION OF A PORCINE CIRCOVIRUS TYPE 2-*MYCOPLASMA HYOPNEUMONIAE* COMBINATION VACCINE IN JAPAN

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* (M. hyo) are among the most widespread respiratory pathogens in pig production and are known to reduce performance by increasing respiratory symptoms, decreasing growth, and elevating mortality (Chae et al., 2006). Intradermal (ID) vaccination using needle-free devices has gained attention due to potential advantages over traditional intramuscular (IM) injection, including reduced risk of pathogen transmission (Nitullo et al., 2022), improved immune stimulation, and benefits for animal welfare. However, evidence regarding the effectiveness of needle-free ID administration of PCV2 + M. hyo combination vaccines in Japan is limited. The objective of this study was to compare mortality outcomes between needle-free ID vaccination with MHYOSPHERE® PCV ID and IM administration of another commercial PCV2 + M. hyo vaccine (Vaccine A).

Materials and Methods

The study was conducted on a farrow-to-finish farm with 1,500 sows between August and October 2025. Piglets were assigned to two groups: the MHYOSPHERE® PCV ID group vaccinated intradermally using the HIPRADERMIC® UX device (n = 3,297), and the Vaccine A group receiving a commercial intramuscular PCV2 + M. hyo vaccine (n = 3,258). The farm operated under a weekly production system; therefore, groups were allocated by week of birth, alternating the two vaccines. Each vaccine was administered once at 3 weeks of age. Mortality was analyzed using logistic regression.

Results and Discussion

Nursery mortality was 1.26% in the Vaccine A group and 0.76% in the MHYOSPHERE® group, demonstrating a significant reduction in mortality ($P < 0.05$). Reduced mortality during the nursery stage - when immunological and environmental stress is high, may contribute to overall productivity improvements.

Conclusion

Needle-free intradermal MHYOSPHERE® PCV ID reduced nursery mortality compared with Vaccine A. These results support this one-shot approach as an effective option to improve herd health.

Keywords: Intradermal needle-free vaccination, Mortality rate, *Mycoplasma hyopneumoniae*, Porcine circovirus type 2.

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EVALUATION OF IMMUNE PROTECTION EFFICACY OF PORCINE EPIDEMIC DIARRHEA VIRUS S TRIMER PROTEIN VACCINE

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Introduction and Objectives

Porcine epidemic diarrhea virus (PEDV) is a major enteric pathogen threatening the global swine industry. Its Spike protein (S protein) serves as the core antigen for inducing effective immunity. This study aimed to evaluate the immune protection efficacy of the PEDV S-Trimer protein against clinically prevalent PEDV.

Materials and Methods

Fifteen PEDV-experienced sows at 70 days of gestation were randomized into three groups (n = 5 each): S-Trimer vaccine group, commercial TGEV + PEDV inactivated vaccine group, and non-immunized control group, with immunization at 91 and 105 days of gestation. Colostral PEDV sIgA (IDEXX kit) and neutralizing antibodies (microtiter method) were detected; the serum neutralization (SN) test adopted PEDV MJ strain and Vero cells. Five days post-lactation, piglets were challenged with PEDV wild-type MJ strain (10^5 $TCID_{50}$/piglet), which was cultured in Vero cells without virulence alteration. Diarrhea and mortality of piglets were monitored until weaning.

Results

Trimer group had significantly higher colostral sIgA positive rate (100 vs. 80%) and mean S/P ratio (2.35 vs. 1.18) than the inactivated vaccine group. Both vaccine groups had 100% neutralizing antibody positivity, but the S-Trimer group had a higher mean titer (1:400 vs. 1:238). Post-challenge, the S-Trimer group's piglets had lower diarrhea (24 vs. 90%) and mortality (15 vs. 41.5%) rates.

Discussion and Conclusion

Correspondingly, the enhanced maternal antibody levels were associated with improved protection of piglets against virulent challenges. Our results demonstrated that immunization of sows with the PEDV S-Trimer vaccine can induce higher levels of maternal antibodies. After the challenge, the piglets in this group exhibited lower diarrhea and mortality rates. In conclusion, the PEDV S-Trimer protein confers robust immune protection, thereby offering a reliable technical basis for the precise prevention and control of PEDV in swine herds.

Keywords: Immune Protection , PEDV, S-trimer protein.

FIELD EVALUATION OF SOW VACCINATION AGAINST PORCINE CIRCOVIRUS 2 (PCV2): EFFECTS ON REPRODUCTIVE PERFORMANCE AND REDUCTION OF VIRAL CIRCULATION

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Introduction and Objectives

PCV2 can vertically transmit during gestation via the placenta, resulting in reproductive disorders, such as fetal mortality and abortion. Although sow vaccination has been suggested to reduce vertical transmission from sows to piglets and improve reproductive performance (Pejsak et al., 2012), field validation remains insufficient. This study assessed the effect of sow vaccination with Ingelvac CircoFLEX (Boehringer Ingelheim Animal Health Japan, Japan) on reproductive outcomes and PCV2 infection under commercial farm conditions.

Materials and Methods

This study was conducted on a 750-sow farrow-to-finish farm in Miyagi prefecture, Japan. Piglets received routine PCV2 vaccination with Ingelvac CircoFLEX at 21 days of age. In June 2024, mass vaccination of sows and gilts with Ingelvac CircoFLEX was performed, followed by vaccination at gilt introduction and sow weaning. Annual comparisons of reproductive parameters and weaning performance were conducted between the pre-vaccination (June 2023–May 2024) and post-vaccination (June 2024 - May 2025) periods using unpaired Student's T-test, with significance set at $P < 0.05$. PCV2 infection was monitored by PCR on blood and testicular processing fluid (PF) samples.

Results and Discussion

Sow and gilt vaccination resulted in a significant increase in total born piglets (+0.36 piglets/litter) and birth weight (+72.5 g/piglet), while conception and farrowing rates showed no significant difference. Weaned piglets per litter and weaning rate were significantly improved by +0.36 piglets/litter and +1.82%, respectively. PCR analysis revealed PCV2 positivity in blood samples of finishing pigs before vaccination at 60, 90, 120, and 150 days of age; all samples were negative after October 2024. PCV2 positivity in PF samples declined progressively: initially detected in piglets from parity 1, 2 - 3, and 4 - 5 sows, then limited to parity 2 - 3 by March 2025, and completely negative after August 2025.

Conclusion

Sow vaccination is considered to enhance and stabilize maternal immune status and limit transplacental transmission of PCV2, which could significantly improve reproductive performance. Furthermore, PCR results suggested that reducing vertical transmission from sows to piglets may decrease virus circulation within the herd. These findings indicated that, in addition to routine piglet vaccination, sow vaccination could improve reproductive outcomes and reduce PCV2 detection rates under field conditions.

Keywords: Porcine circovirus type2, Reproductive disorder, Sow vaccination, Vertical transmission.

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COMPARATIVE ANALYSIS OF SLAUGHTER LUNG SCORES AND FIELD DATA OF TWO COMMERCIAL *MYCOPLASMA HYOPNEUMONIAE* & PCV2 VACCINES IN A CHINESE COMPANY

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Introduction and Objectives

Mycoplasma hyopneumoniae (Mhyo), the causative agent of enzootic pneumonia (EP) and porcine circovirus type 2 (PCV2) infections are of major concern in most farms. Typically, vaccination is practiced to control these pathogens, and reduce economic losses. The objective of this study was to compare the EP-like lung lesions and field data from pig herds vaccinated with two different Mhyo & PCV2 vaccines in a Chinese company.

Materials and Methods

From Nov 2023 to Nov 2025, piglet batches in a Western China group company were randomly assigned to receive either CIRBLOC® M Hyo (PCV2 & M.hyo RTU vaccine) or PCV2 vaccine A & Mhyo vaccine B separately at 19 days of age. Lung scoring was performed via the Ceva Lung Program to evaluate: % of lungs with EP-like lesions; % average affected lung area; Batches impacted by non-vaccine factors (e.g., severe diarrhea, extreme temperatures) were excluded. Survival rate and ADG (adjusted to 170 days) were analyzed as key performance indicators.

Results and Discussion

Over a two-year period, 30 batches underwent lung scoring. The 14 batches (571 lungs) vaccinated with CIRBLOC® M Hyo showed a broncho-pneumonic lesions rate of 52.19% and an average affected area of 1.58%. In comparison, 11 batches (415 lungs) vaccinated separately with PCV2 vaccine A and Mhyo vaccine B exhibited a lesion-rate of 62.41% and an average affected area of 2.64%. Field performance was analyzed for 165 qualifying batches. The 108 batches (319,689 pigs) vaccinated with CIRBLOC® M Hyo achieved a survival rate of 96.32% and an ADG of 756 g. The 26 batches (78,893 pigs) vaccinated separately with vaccines A and B showed a survival rate of 96.23% and an ADG of 741 g.

Conclusion

This study demonstrated that combo vaccine CIRBLOC® M Hyo provided better efficacy compared to PCV2 and Mhyo vaccination separately in terms of both lung lesion scoring and production performance. In the field, combo vaccine (single dose) presents less stress to the animals, less labor requirements and lower operational costs to farm staff. Furthermore, a single-dose regimen simplifies the vaccination process, increasing the likelihood of full herd coverage.

Keywords: Combo Vaccine, Lung Scoring, *Mycoplasma hyopneumoniae*, Porcine Circovirus type 2.

COMPARATIVE FIELD EFFICACY TRIAL OF ENTERISOL® ILEITIS AND REGULAR PROGRAM IN A FARM IN THE SOUTH OF VIETNAM

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Introduction and Objectives

Lawsonia intracellularis (L. intracellularis) is the causative agent of ileitis, a common enteric disease in growing pigs that negatively affects growth performance and farm profitability. A serological survey conducted from 2020 to 2022 across 40 pig farms in the North, Central, and South regions revealed that all farms (100%) had infected pigs, confirming that L. intracellularis is widely circulating in Vietnam (Nguyen et al., 2023). Enterisol® Ileitis is an oral vaccine that offers a practical and less stressful method of immunization to prevent ileitis (Boehringer Ingelheim Animal Health). This study aimed to evaluate the field efficacy of Enterisol® Ileitis under Vietnamese farm conditions, focusing on productivity and economic outcomes.

Materials and Methods

A controlled trial was conducted from May to September 2023 on a nursery-to-finisher farm in Southern Vietnam, sourcing piglets from a 2,400-sow farrow-to-wean unit. A total of 1,293 pigs were randomized into two groups: Vaccinated group (n = 649): vaccinated orally with Enterisol® Ileitis at 3 weeks of age. Control group (n = 644): no vaccination. Parameters recorded included mortality rate, average daily gain (ADG), feed conversion ratio (FCR), and return on investment (ROI).

Results and Discussion

Vaccinated pigs outperformed controls: mortality decreased from 2.64 to 1.54%, ADG improved (713 vs 704 g), and FCR was lower (2.68 vs 2.74). ROI reached 3.99, indicating that every VND invested in vaccination returned nearly fourfold. The estimated annual profit increase was approximately 542 million VND (20,600 USD) for this farm with this improvement.

Conclusion

Enterisol® Ileitis improved growth performance, reduced mortality, and delivered strong economic benefits under commercial conditions in Vietnam. Oral vaccination represents an effective and cost-efficient strategy for controlling ileitis and improving swine production profitability.

Keywords: ADG, Enterisol® Ileitis, FCR, *Lawsonia intracellularis*, ROI.

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TEMPERATURE MONITORING IN VACCINE REFRIGERATORS FOR SWINE FARMS IN SOUTHERN BRAZIL

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Introduction and Objectives

Achieving effective vaccination outcomes requires regular auditing of all factors that influence efficacy, with proper storage being a particularly critical point. Most vaccines have low thermostability and must be kept between 2 and 8°C throughout the cold chain (Dumpa et al., 2019). Farms utilize a wide range of refrigerators with varying efficiency and maintenance standards, resulting in uncertainty and failures during the final storage stage. This study presents temperature-monitoring data from vaccine refrigerators used by swine producers in southern Brazil in 2024.

Materials and Methods

Temperature monitoring was performed using 286 temperature data loggers' readings collected from refrigerators located on farms, at distributors, integrators, and cooperatives in southern Brazil in 2024. Two models of data loggers (TESTO 174T® and ELITECH RC-5+®) were utilized. Each reading covered a mean of 60 days (ranging from a minimum of 7 to a maximum of 120 days) of continuous measurement at 30-minute intervals. Conformity rate of the temperature to store vaccines was defined as the percentage of temperature readings within the recommended 2°C to 8°C range.

Results and Discussion

The 286 temperature data loggers' readings generated 871,248 temperature records, corresponding to 18,151 days of monitoring. Seventeen readings (5.94%) showed conformity rates below 50% (i.e., more than half of the registered temperatures out of the recommended range), with extreme temperatures ranging from -7.90°C to 34.1°C. Low conformity was primarily reported at temperatures below 2°C, which may denature protein antigens or disrupt antigen–adjuvant complexes, thereby reducing vaccine immunogenicity (Frandoloso et al., 2022). A total of 144 readings (50.34%) had conformity between 51% and 99%, still representing a significant risk to vaccine quality. Only 125 readings (43.7%) achieved a conformity of more than 99%, the threshold considered fully adequate for vaccine preservation. Small deviations (≤ 1%) likely reflected rapid door openings or restocking, with minimal expected impact.

Conclusion

Most monitored refrigerators showed temperature deviations that could compromise vaccine integrity. Continuous auditing and corrective actions are crucial for ensuring proper storage conditions and maintaining vaccine efficacy in swine production systems.

Keywords: Vaccine storage, Temperature monitoring, Swine production.

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EFFECT OF A LIVE ATTENUATED ORAL VACCINE FOR *LAWSONIA INTRACELLULARIS* ON INTESTINAL QUALITY OF SWINE IN BRAZIL

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Introduction and Objectives

Porcine proliferative enteropathy can present clinically as bloody diarrhea and high mortality, or subclinically mainly causing losses in productivity, weight gain, and feed conversion (Vanucci et al., 2025). Vaccination is a tool to prevent severe disease, improve intestinal health, and reduce field performance losses (Gómez-Osorio et al., 2025). The objective of this study was to demonstrate improvements in intestinal quality in animals vaccinated with a live attenuated vaccine.

Materials and Methods

A batch of 1945 weaned piglets (~29 days old) (D0) in a commercial nursery in Brazil was divided into two groups: a vaccinated Group (GV) and a control group, that were unvaccinated (GC). On D0, each piglet was identified. GV animals received 2 mL of a live attenuated vaccine (Enterisol Ileitis, Boehringer Ingelheim). At 65 days of age (D36), the piglets were transferred to the same finishing farm, maintaining the distribution of the two groups in the same pens. A group of 430 pigs from each group was evaluated at the slaughterhouse at 170 (GC) and 171 (GV) days of age. At the slaughterhouse, the percentage of condemned intestines, intestinal length, and yield for Tuscan sausage were evaluated.

Results and Discussion

At the slaughterhouse, vaccination with live attenuated vaccine resulted in 20% lower percentage of condemnations in the intestinal evaluation line in the vaccinated group (V: 28 and NV: 35), which yielded 97 cm more intestine (V: 17.40 m and NV: 16.43 m), representing 3.5 kg more of encased Tuscan sausage. Oral vaccination promotes local and systemic protection, reducing intestinal lesions and excretion of intracellular fluid. (Nogueira et al., 2013), which improves intestinal integrity, enabling better nutrient utilization and increased gut resistance (Karuppannan & Opriessnig, 2018). The results of this evaluation reinforce the importance of vaccination for protection against porcine proliferative ileitis, a measure that contributes to improved productive performance, enhances intestinal quality, and enhances the industrial utilization of by-products, thereby adding economic value to the production system.

Conclusion

Vaccination with a live attenuated oral vaccine during the nursery phase improved intestinal quality, as reflected in greater intestinal length, and increased Tuscan sausage production.

Keywords: Vaccination, Ileitis, Sausage.

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SEROPREVALENCE AND SHEDDING OF *LAWSONIA INTRACELLULARIS* BY PIGS IN 13 COMMERCIAL FARMS IN MINAS GERAIS STATE - BRAZIL

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Introduction and objectives:

Lawsonia intracellularis (LI) is a bacterium that causes ileitis, which can lead to economic losses and, especially in a subclinical form, may not result in evident symptoms but cause losses in zootechnical performance (McOrist, 2005). The aim of this study was to evaluate the dynamics of Li infection by detecting antibodies in serum and by detecting shedding of this agent in pig feces from different commercial farms.

Material and methods:

In 2024, monitoring was carried out on 13 farms in the Minas Gerais and São Paulo provinces and the Federal District, involving pigs in the growing and finishing phases (9 - 23 weeks of age). These farms asked the study to verify the circulation of LI because of the intensive use of antibiotics and zootechnical indices below reference values. Between 15 and 30 blood samples were collected individually from 3 different ages on each farm. Feces were collected in pools (3 animals per pen comprised of 1 sample). Serum was analyzed for the detection of antibodies (IgG) to LI (ELISA - Svanovir®L. intracellularis). The feces were analyzed for LI quantification by qPCR. The animals evaluated had not been vaccinated against LI.

Results and discussion:

It was evident that in 100% of the farms (60.8% of the pigs) evaluated, pigs tested positively in the ELISA test. In seven of these farms, 50% or more of the pigs were seropositive, an average of 58% (23.3 to 100%). In 12 farms (92.3%), pigs excreted LI. The results showed that LI was present on these farms, infecting animals even in the absence of the classic clinical presentation (bloody diarrhea).

Conclusion:

Infection with LI was detected in all sampled growing and finishing farms, even in the absence of classic clinical manifestations of the infection and awareness of LI circulation is important because subclinical presentation can cause zootechnical and economic losses.

Keywords: Vaccine, Subclinical, Ileitis.

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EVALUATION OF RECTAL TEMPERATURE IN PIGLETS WITH DIFFERENT VACCINATION PROTOCOLS FOR CIRCOVIRUS TYPE 2, *MYCOPLASMA HYOPNEUMONIAE* AND *LAWSONIA INTRACELLULARIS*

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Introduction and Objectives

At weaning, piglets experience stress from environmental changes, social mixing, and the abrupt end of milk feeding, often combined with vaccination. Vaccination at weaning is widely used to control several pathogens, but commercial vaccines can cause adverse effects. Thus, this study aimed to evaluate the side effects of different vaccine protocols against porcine Circovirus type 2 (PCV2), *Mycoplasma hyopneumoniae* (Mhp), and *Lawsonia intracellularis*.

Material and Methods

A total of 216 piglets (male and female), averaging 20 days of age, from two Brazilian farms (Farm 1: n = 135; Farm 2: n = 81) were assigned to two vaccination protocols: T1: FLEXcombo® (Ingelvac®CircoFLEX + Ingelvac®MycoFLEX) + Enterisol Ileitis® (Boehringer Ingelheim Vetmedica Inc.) and T2: Circumvent® CML (MSD Animal Health). Rectal temperature was recorded individually at 0 hours (pre-vaccination) and 8 hours post-vaccination to assess systemic reactions.

Results and Discussion

As expected, pre-vaccination temperatures did not differ between treatments ($P = 1$) (Farm 1: T1 = 39.8°C vs. T2 = 39.7°C; Farm 2: T1 = 39.7°C vs. T2 = 39.6°C). However, 8 hours after vaccination T2 treatment had higher rectal temperature ($P > 0.001$) than T1 treatment in both farms (Farm 1: T1 = 40,1°C vs T2 = 41.1ºC; Farm 2: T1= 40,0°C vs T2 = 41,3°C. Hyperthermia following vaccination can lead to behavioral changes such as depression, inactivity, somnolence, and anorexia (Hart, 2010). Evidence suggests that vaccines inducing hyperthermic responses increase metabolic energy expenditure, resulting in a severe inflammatory reaction and worsened physiological adaptation (Hernández-Caravaca et al., 2017). Even that, T2 treatment in Farm 2 had a significant number of piglets experiencing transient swelling at the injection site (mild: 93%, moderate: 3,6% and severe: 3,2%), with immediate systemic reactions having been observed in 1,2 % of those animals. There are no adverse effects observed in T1 treatment.

Conclusion

The T1 protocol (FLEXcombo® + Enterisol Ileitis®) demonstrated no hyperthermia or adverse reactions, confirming its low reactivity and potential welfare benefits. Conversely, the T2 protocol was associated with hyperthermia and local/systemic side effects, which may compromise animal welfare.

Keywords: Vaccination, Piglets, Welfare, Hyperthermia.

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EFFECT OF ENTERISOL SALMONELLA T/C® VACCINATION ON THE REDUCTION OF SALMONELLA IN PIGS AT SLAUGHTER

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Introduction and Objective

Salmonella is a highly relevant pathogen as it is a zoonotic disease (Bearson et al., 2025). Thus, the objective of this study was to compare pigs vaccinated with a bivalent S. Typhimurium and S. Choleraesuis vaccine to non-vaccinated pigs, evaluating the excretion of Salmonella spp in feces (pre- and post-slaughter) and the colonization of lymph nodes at the time of slaughter.

Material and Methods

Eighty litters (14 days of life in average), in a farm in Brazil, were allocated: 40 in the vaccinated group (VG) and 40 in the control group (CG). The VG received 2 mL of Enterisol Salmonella T/C® vaccine (Boehringer Ingelheim Vetmedica, Inc.) orally via drench. The CG received 2 mL saline solution orally via drench. Piglets were co-mingled in the same farm during both the nursery and finishing phases. In the finishing phase, fecal samples of 40 piglets/group were collected for evaluating Salmonella excretion on the day before loading for slaughter. Ileocecal lymph node and feaces were also collected post-slaughter.

Results and Discussion

A significant increase ($P \leq 0.05$) of 112% was observed in the excretion of Salmonella spp. isolated in fecal samples from unvaccinated animals at the slaughterhouse, compared to samples collected before loading from the farm. Vaccinated animals maintained similar excretion levels at both time points, suggesting that the vaccine can avoid the increase in Salmonella spp. excretion due to this stress factor. VG had 85,7% less pigs colonized by Salmonella in ileocecal lymph nodes than CG (17.5 vs 2.5%, $P < 0.05$).

Conclusion

These results demonstrate that Enterisol Salmonella T/C® vaccine is an effective tool in helping reduce the prevalence of pigs excreting in feaces and carrying in ileocecal lymph nodes Salmonella at the slaughterhouse, thus reducing the possibility of pork contamination. This study further shows in field conditions and after transport that this vaccine can reduce Salmonella colonization and shedding in pigs (Leite et al., 2025).

Keywords: Vaccine, Salmonella, Prevalence.

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EFFECT OF A LIVE ATTENUATED ORAL VACCINE FOR *LAWSONIA INTRACELLULARIS* ON ZOOTECHNICAL PERFORMANCE IN BRAZIL

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Introduction and Objective

Ileitis is a highly prevalent disease in pig farms, which can present clinically as bloody diarrhea and high mortality, or subclinical and chronic forms, causing losses in weight gain and feed conversion (Lawson and Gebhart, 2000). Vaccination is a tool to prevent severe disease and reduce performance losses. The objective of this study was to demonstrate the improvement in zootechnical performance of pigs vaccinated with a live attenuated vaccine.

Materials and Methods

A batch of 1945 weaned piglets (~29 days old) (D0) in a commercial nursery farm in Brazil was divided into a vaccinated Group (VG) and a control group (CG). They were weighed individually and mixed in the same pens. On D0, they were individually tagged and weighed to obtain the average daily weight gain (ADWG). The VG received 2 mL of a live attenuated oral vaccine (Enterisol Ileitis, Boehringer Ingelheim Vetmedica Inc). At 65 days of age, they were transferred to the same finishing farm, maintaining the same distribution in the pens. After 126 days from the first weighing (D126), the final individual weighing of the pigs was carried out.

Results and Discussion

Bloody diarrhea was not observed in any animal during the experiment. There was no significant difference ($P > 0.05$) in mortality between VG (1.75%) and CG (1.95%). Oral vaccination with live attenuated vaccine against Lawsonia intracellularis resulted in improved final weight ($P = 0.02$), with an increase of 2.05 kg (VG: 129.76 kg and CG: 127.71 kg) and ADWG in 16 grams more per day (VG: 968 g and CG: 952 g) than the CG, over 126 days of evaluation. The results of this study reinforce the importance of vaccination for protection against ileitis, a tool that contributes to improved productive performance and adds economic value to the production system.

Conclusion

Vaccination with a live attenuated oral vaccine during the nursery phase improved productive performance during the nursery and finishing phases.

Keywords: Vaccination, *Lawsonia intracelullaris*, Weight gain.

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HETEROLOGOUS GENOGROUP 1 LIVE PRIME AND GENOGROUP 2B INACTIVATED BOOST ENHANCES NEUTRALIZATION AGAINST GENOGROUP 2 PORCINE EPIDEMIC DIARRHEA VIRUS IN PIGS

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Introduction and Objectives

Genogroup 1 (G1) and genogroup 2 (G2) porcine epidemic diarrhea virus (PEDV) strains show partial antigenic cross-neutralization. In Japan, only a G1 live attenuated vaccine has been used since the late 1990s, and PED outbreaks in 2013 have since declined while this vaccine remains in use. In contrast, other Asian countries often employ a heterologous live-prime/inactivated-boost (LK) regimen to induce protection against G2 strains, but immunological data supporting such strategies remain limited. This study compared neutralizing antibody titers to quantify G1-G2 cross-reactivity and evaluated whether a G2b inactivated booster after G1 live priming increases G2-specific titers versus G1 live vaccination alone.

Materials and Methods

Two strains were used: the G1 vaccine strain P-5V and a Japanese G2b field isolate (2014). Strain-specific antisera were examined in cross-neutralization assays. Pigs received two intramuscular doses 4 weeks apart: a homologous live–live (LL) group (n = 6; G1 live twice) or a heterologous live–killed (LK) group (n = 3; G1 live then G2b inactivated). Sera collected 2 weeks after dose 2 were tested for virus neutralization against G1 vaccine strain P-5V and the G2b isolate. Only G2b titers are shown.

Results and Discussion

Sera from G1 live-immunized pigs showed neutralizing titers of 1:16 to ≥ 1:64 against homologous G1 but only 1:2 to 1:4 against heterologous G2b, indicating weaker cross-neutralization; the geometric mean titer (GMT) against G2b was 14-fold lower than that against G1. A G2b strain-specific reference antiserum showed similar titers against both G1 and G2b. In the vaccination trial, G2b-neutralizing titers were 1:2 to 1:8 in the LL group and 1:32 to ≥ 1:64 in the LK group; despite small group sizes, the GMT against G2b was 14-fold higher in the LK group than in the LL group (Mann-Whitney U test, $P < 0.05$). Thus, boosting with a G2b inactivated vaccine after G1 live priming enhanced the G2b-neutralizing response compared with repeated G1 live vaccination.

Conclusion

These findings demonstrate that a parenteral (intramuscular) G1-live/G2b-inactivated regimen induces G2b-specific immunity. This strategy offers a safe, evidence-based option for controlling circulating PEDV strains.

Keywords: Heterologous prime-boost, Neutralizing antibody, Porcine epidemic diarrhea virus.

THE EFFICACY OF AN ORAL LIVE ATTENUATED ILEITIS VACCINE IN A SUBCLINICALLY INFECTED COMMERCIAL SOW-TO-FINISHING FARM IN VIETNAM

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Introduction and Objectives

Lawsonia intracellularis (LI) is the causative agent of Porcine Proliferative Enteropathy (PPE), a globally significant swine disease impacting growth performance. Previous studies in Vietnam reported LI seroprevalence up to 90% in gilts and sows (Tran et al., 2023). Subclinical infection (SI) caused by LI significantly reduces growth rate and feed efficiency (Paradis et al., 2012). Understanding age-related prevalence and vaccine efficacy in SI farms is essential for control. This trial assessed the efficacy of Enterisol Ileitis in a commercial sow-to-finishing farm with SI.

Materials and Methods

Eighty blood samples were collected from pigs at 4, 8, 12, 16, 20, and 24 weeks of age, as well as primiparous (Parity ≤ 1) and multiparous sows (Parity > 1). LI prevalence was determined by ELISA. A total of 1,779 weaned piglets (25 days old) from an LI-positive sow farm were randomly assigned to two groups: control group (CON, n = 889) without vaccination and vaccinated group (VAC; n = 890) with Enterisol® Ileitis by oral drench at three weeks. Pigs were weighed at entry and at market age (24 weeks). Feed intake was monitored daily to calculate FCR. All pigs were housed under identical conditions and fed the same diet. Performance metrics (ADG, FCR) were compared between groups.

Results and Discussion

LI prevalence was 0% at 4-8 weeks but increased sharply: 30, 80, and 90% at 12, 16, and 20 weeks, peaking at 100% in pigs from 24 weeks to sows. This indicates a strong age-related susceptibility. Vaccinated pigs showed ADG improvement of 25g/day (VAC 758 g vs CON 733 g) and better FCR (VAC 2.36 vs CON 2.41) reflecting improved feed efficiency of 0.043kg/feed/kg weight gain in vaccinated animals. ROI was 1:4.6 under current market conditions (piglet 1,800,000 VND; live pig 67,000 VND/kg; feed 13,000 VND/kg, vaccine 40,000 VND). These results confirm that Enterisol® Ileitis provides significant economic and health benefits in LI-SI herd.

Conclusion

LI prevalence rises dramatically from 12 weeks onwards, reaching maximum levels in finishers and sows. The use of Enterisol Ileitis effectively improves ADG and FCR, delivering substantial economic gains in subclinically infected farms.

Keywords: ADG, Enterisol Ileitis, FCR, *Lawsonia intracellularis*, Subclinical infection.

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ORAL LIVE ILEITIS VACCINATION REDUCES *LAWSONIA INTRACELLULARIS* COLONISATION OF THE ILEUM AT SLAUGHTER WHEN COMPARED TO AN INJECTABLE VACCINE

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Introduction and Objectives

Porcine Proliferative Enteropathy, caused by *Lawsonia intracellularis* is one of the most prevalent enteric diseases in European countries (Arnold et al., 2019). Pigs are usually infected sub-clinically and therefore it is often difficult for producers to assess the impact of the disease and the economic return of control programs. Sampling at slaughterhouses for qPCR testing has been proposed as a good method for diagnosing the disease (Jansen et al., 2018). The aim of this study is to investigate whether there are different results in ileum slaughterhouse sampling by qPCR in animals immunized against L.I. using different vaccines.

Materials and Methods

This study was conducted in a 3,000-place finishing unit housing two consecutive groups of pigs raised under the same conditions. Pigs at finishing were suffering from clinical ileitis confirmed by qPCR in fecal samples. The first group was intramuscularly vaccinated at 3 weeks of age with an inactivated intramuscular L.I. vaccine, Porcilis Lawsonia and the second group was vaccinated with an attenuated live L.I. vaccine, Enterisol Ileitis, by drinking water at 8 weeks of age, in both cases. A total of 50 ilea were collected per group at slaughter and sent to the lab for PCR testing Growth parameters and feed efficiency were compared between the two groups. Fisher's exact test was used to compare the results.

Results

None of the ileums from pigs in oral vaccinated group were positive, while 16% ($P < 0,05$) of the ileums from pigs of killed IM vaccine were positive with ct values between 26.05 and 38.22. Regarding the production parameters, the average daily gain was 10 grams more per day with an adjusted 18 - 100 feed conversion ratio of 0,054 kg less in the group vaccinated with the oral vaccine, which results in 5.0 kg of feed saved per pig marketed and a €1.45 higher return on investment for the group vaccinated with the oral vaccine.

Discussions and Conclusions

Under the conditions of this study oral vaccination resulted in a higher average of daily gain a better FCR and a significant reduction of *Lawsonia intracellularis* positive ilea when compared to the IM vaccinated group.

Keywords: Ileum colonization, *Lawsonia intracellularis*, Oral vaccinartion, Production parameters.

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PROTECTIVE EFFICACY OF A REDUCED-DOSE (1 ML) MONOVALENT FMD VACCINE ASSESSED BY HETEROLOGOUS CHALLENGE IN PIGS

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Introduction and Objectives

Foot-and-mouth disease (FMD) is one of the most economically important viral diseases affecting swine and is mainly controlled through vaccination. Reduced injection volumes are increasingly considered to improve injection-site safety while maintaining protective efficacy. This study evaluated the protective efficacy of a newly developed reduced-dose (1 mL) monovalent FMD vaccine formulated with O1 Campos vaccine strain against heterologous challenge in pigs.

Materials and Methods

Two groups of FMD-naïve piglets (G1 and G2; n = 10 animals each) were vaccinated intramuscularly with Bioaftogen ONE (Biogénesis Bagó, Argentina) at 0 days post-vaccination (dpv) for G1 and at 0 and 28 dpv for G2, respectively. A non-vaccinated control group (G3, n = 2) was included. The challenge test was conducted at SENASA, WOAH FMD Reference Laboratory in Argentina. Animals were challenged intramuscularly with 100,000 ID_{50}/mL/pig of a heterologous FMD virus strain (O/SEA/mya-98/VTN/24FS02/24) at 28 dpv for G1 and 28 days post-revaccination (dprv) for G2. Clinical protection was assessed post-challenge. Virus neutralization (VN) antibody titers against homologous and heterologous strains were measured at 26 dpv (G1) or 26 dprv (G2) and at 8 days post-infection (dpi) at SENASA (WOAH, 2022).

Results and Discussion

All pigs vaccinated with Bioaftogen ONE were clinically protected following heterologous challenge, with no evidence of generalized vesicular disease, while control animals developed typical clinical signs, confirming the robustness of the challenge model. Neutralizing antibody responses against both the homologous (O1 Campos) (26 dpv: 2.45 log_{10}; 26 dprv: 2.56 log_{10}) and heterologous (O/SEA/mya-98/VTN/24FS02/24) (26 dpv: 1.88 log_{10}; 26 dprv: 2.13 log_{10}) strains were consistently high in vaccinated pigs and remained above cut-off levels of 1.5 log_{10} throughout the study period (Gubbins et al., 2022).

Conclusion

The reduced-dose (1 mL) monovalent FMD vaccine Bioaftogen ONE conferred complete clinical protection against O/SEA/mya-98/VTN/24FS02/24 heterologous viral challenge in pigs and elicited strong virus-neutralizing antibody responses against both homologous and heterologous strains. These findings confirm the protective efficacy of Bioaftogen ONE as a 1 mL vaccine formulation.

Keywords: Foot-and-mouth disease, Heterologous challenge, Oil-adjuvanted vaccine, Pigs, Protective efficacy.

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EARLY PROTECTION AND DURABLE IMMUNITY INDUCED BY A 1 ML–DOSE FMD VACCINE IN SWINE

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Introduction and Objectives

Foot-and-mouth disease (FMD) is a highly contagious transboundary disease with major economic impact. A newly developed 1 mL - dose FMD vaccine containing O1 Campos strain has demonstrated high potency in homologous challenge tests in pigs. This study aimed to evaluate both the onset of protection and the duration of immunity induced by this vaccine in swine.

Materials and Methods

A monovalent O1 Campos inactivated vaccine was produced by Biogénesis Bagó as a 1ml-dose water-in-oil single emulsion. A homologous challenge test was conducted at SENASA1. Ten FMD-naïve pigs were vaccinated intramuscularly with 1 mL dose. Two pigs remained unvaccinated as controls. At 7 days post-vaccination (dpv), animals were challenged with 100,000 ID_{50} of O1 Campos virus. Clinical evaluations were performed daily with the final assessment conducted at 8 days post-infection (dpi). The trial was valid if both controls developed FMD lesions on more than one foot. Vaccinated animals with lesions on at least one foot were considered non-protected. Virus neutralization (VN) antibody titers were determined at 0 and 5 dpv and at 8 dpi at SENASA. To assess the duration of immunity, two groups of ten seronegative pigs were vaccinated intramuscularly with one or two doses (0 and 30 dpv). Animals were bled on day 0, 14 and monthly up to 180 dpv; antibodies were measured by Liquid Phase ELISA.

Results and Discussion

The challenge trial met validity criteria, as controls developed typical FMD lesions. Four vaccinated animal showed FMD-compatible lesions resulting in 60% protection at 7 dpv. VN titers at 5 dpv were low (mean 0.79 $\log_{10}$) even in protected animals but increased significantly by 8 dpi (1.91 $\log_{10}$), suggesting effective immune priming. Additionally, the vaccine induced high ELISA antibody titers by 14 dpv in both vaccinated groups (2.17 and 2.56 $\log_{10}$), which increased and remained above the protective cut-off (2.11 $\log_{10}$)2 for up to 180 days in single-vaccinated animals (above 3 $\log_{10}$).

Conclusions

The 1 mL-dose FMD vaccine containing O1 Campos strain induced rapid onset of protection by 7 dpv. It also elicited robust and long-lasting antibody responses detectable for up to 180 days.

Keywords: 1mL-dose vaccine, Duration of immunity, Foot-and-mouth disease, Onset of protection, Swine.

HIGH POTENCY OF A 1 ML FOOT-AND-MOUTH DISEASE VACCINE CONFIRMED BY HOMOLOGOUS CHALLENGE IN PIGS

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Introduction and Objectives

When swine are included in foot-and-mouth disease (FMD) vaccination programs, the most common practice is the intramuscular administration of 2 mL of an oil-adjuvanted vaccine. Reducing vaccine volume while maintaining high potency may be a practical approach to improve vaccine safety and vaccination practices. This study evaluated the potency of a newly developed 1 mL-dose FMD vaccine containing the O1 Campos strain through a homologous challenge test (PD_{50}) in pigs.

Materials and Methods

A monovalent O1 Campos vaccine was produced by Biogénesis Bagó as a 1ml-dose water-in-oil single emulsion (Bioaftogen ONE). The homologous challenge test was conducted at SENASA, WOAH FMD Reference Laboratory in Argentina. Three groups of five seronegative, FMD-naïve pigs each were vaccinated intramuscularly with 1 mL (full dose), 0.25 mL (1:4 dose), or 0.0625 mL (1:16 dose), respectively. Two pigs remained unvaccinated as controls. At 28 days post-vaccination (dpv), animals were challenged with 100,000 ID_{50} of O1 Campos virus. Clinical evaluation was performed at 8 days post-infection (dpi). The trial was considered valid if both controls developed lesions on more than one foot. Vaccinated animals with lesions on at least one foot were considered non-protected. Vaccine potency was calculated using Spearman-Kärber and expressed as PD_{50}. Virus neutralization (VN) antibody titers were determined at 0 and 26 dpv and at 8 dpi at SENASA.

Results and Discussion

The PD_{50} trial met validity criteria, as both control pigs developed typical FMD lesions. Only one vaccinated animal showed FMD-compatible lesions and was classified as non-protected. Unexpectedly, this animal belonged to the full-dose group, whereas all animals in the reduced-dose groups remained protected. The calculated potency was 25.40 PD_{50}. High mean VN antibody titers were observed across all vaccinated groups at 26 dpv (1.95, 1.63, and 1.51 log_{10} for the 1, 0.25, and 0.0625 mL doses, respectively).

Conclusions

The Bioaftogen ONE vaccine demonstrated high potency in pigs, with a PD_{50} value exceeding the minimum potency requirements. These findings support the use of a newly developed 1 ml dose FMD vaccine, offering a practical solution for vaccination programs in swine and ensuring effective protection against FMD.

Keywords: 1mL-dose vaccine, FMD, High Potency, PD50, Swine.

CONTROL OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME BY A NON-TRADITIONAL APPROACH

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) continues to pose a major challenge for swine producers around the world, causing economic losses of $4 - 7 USD per marketed pig (Holtkamp et al., 2024). These losses are due to failed reproduction, respiratory issues, higher death rates, poor growth, and increased medical costs. This study aimed to develop a stabilization strategy for a swine herd with ongoing PRRS infection over two years.

Materials and Methods

The study was conducted on a Spanish swine herd comprising 750 sows. Assessments were conducted regarding a digital biosecurity system to track farm staff movements within the farm (Biorisk Internal®), management practices, productivity outcomes, and vaccination protocol. Additionally, PRRS PCR assays conducted on tongue tips, family fluids, and oral fluids yielded positive results, signifying instability in herd immunity. Consequently, an integral control strategy was formulated. An inoculum containing 102 live PRRS virus particles obtained from nursery pigs within the herd and prepared in a high-tech diagnostic laboratory was administered on the same day, 2 ml once intramuscularly to all sows and gilts in the population. Personnel movement protocols were modified to restrict access between production areas. Rigorous McRebel® procedures were implemented, MLV PRRS vaccination was discontinued, and sanitation standards were elevated and subject to regular inspection in all areas.

Results and Discussion

After inoculation, PRRS PCR tests were performed on tongue tips and family fluid samples at ten and fourteen weeks, respectively. So far, all results have remained negative. As a result, nursery depopulation is planned, and auto-replacement gilts will continue to be inoculated to maintain herd stability. Production parameters improved, with preweaning mortality decreasing from 20.13 to 12.56% and nursery mortality declining from 30.56 to 1.5%. The annual return on investment was 12:1.

Conclusion

These results show that the nontraditional intervention enhanced herd health and has prevented PRRS outbreaks for nine months. Regular monitoring and stronger biosecurity can help stabilize immunity and minimize the risk of virus introduction and spreading within the population, ensuring that long-term disease control strategies remain effective and sustainable.

Keywords: Biosecurity, Live virus inoculation, PRRSv.

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EFFECTS OF IMMUNOCASTRATION ON ESTRUS SUPPRESSION AND REPRODUCTIVE TRACT CHARACTERISTICS IN GILTS

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Introduction and Objectives

Immunocastration, achieved via immunization against gonadotropin-releasing factor (GnRF), is increasingly used in female finishing pig production to manage reproductive function. The objective of this study was to evaluate the efficacy of immunocastration in suppressing estrus and altering reproductive tract characteristics in gilts.

Materials and Methods

A total of 200 Danish gilts aged 30 weeks were enrolled in a randomized complete block design trial conducted at a commercial sow farm in southern China. Blocking was based on initial body weight, and gilts were randomly allocated to two groups with similar body weights: treated gilts (n = 100; two 2 mL Improvac® injections at 30 and 34 weeks) and non-treated controls (n = 100). Each group was kept in four pens in the same room. Heat detection was performed weekly starting from 32 weeks by observing gilts for signs of estrus, including mounting behavior, vulvar swelling, restlessness, and a standing reflex in response to back-pressure. The ear tag number of each gilt displaying estrus was recorded by a designated observer. At 38 weeks, 90 gilts from each group were euthanized for measurement of uterine and ovarian parameters. The remaining 10 gilts from each group were euthanized and assessed at 48 weeks. Estrus data were analyzed using the chi-square test, and uterine and ovarian data using analysis of variance (ANOVA).

Results and Discussion

There was no significant difference in estrus rates between groups from 32 to 34 weeks (51%, $P > 0.05$). During weeks 36 to 38, estrus was detected in 55% of the controls but was completely suppressed in the treated gilts. At 38 weeks, the treated group showed marked reduction in ovarian and uterine weights by 72 and 71%, respectively (both $P < 0.001$), as well as significant decreases in uterine length (-32%), width (-37%), and ovarian size (-44%) (all $P < 0.001$). By 48 weeks, estrus resumed in some treated gilts, with 70% showing recovery of ovarian and uterine characteristics, no significant differences compared to the controls ($P > 0.05$).

Conclusion

Immunocastration effectively and reversibly suppresses estrus and causes reproductive organ atrophy in gilts.

Keywords: Estrus, Gilt, Immunocastration, Reproductive tract characteristics.

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EFFECTS OF IMMUNOCASTRATION ON TESTICULAR TRAITS SPERM QUALITY, AND BOAR TAINT IN DANISH DUROC BOARS

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Introduction and Objectives

Immunocastration vaccine induces antibody production against gonadotropin-releasing factor (GnRF), offering a non-surgical approach to suppress testicular function and mitigate boar taint. This study evaluated the effects of immunocastration on testicular traits, sperm quality, and boar taint in adult Danish Duroc boars.

Materials and Methods

Twenty-one Danish Duroc boars (mean age 1.18 ± 0.37 years) were used in a randomized complete block design at a boar stud in southern China. Boars were allocated to two groups: an immunocastration group (IC; n = 17; two 2 mL Improvac® injections on Day 1, Day 28) and a control group (EM; n = 4; untreated). Semen samples were collected at four time points (Days 0, 27, 42, and 56) to assess sperm quality. On Day 63, 14 boars (10 IC, 4 EM) were euthanized for testicular measurements. At the slaughter line, neck fat samples were collected from all boars and scored for boar taint on a 5-point scale by a blinded, trained panel of 5 experts using the hot iron method1(1 = no boar taint; 5 = strong boar taint). Semen data (group, age, boar ID, collection time, and their interaction as fixed effects), testicular data (group, age, boar ID, and testicular side), and boar taint data (group, age, boar ID, and panelist) were analyzed by mixed-effects models.

Results and Discussion

Sperm quality parameters in the EM group remained stable. No significant differences in sperm motility or abnormal spermatozoa were observed between groups at D0 and D27. By Day 56, IC boars showed substantial declines in total motility, progressive motility, and increased abnormal spermatozoa compared to D0 and D27 ($P < 0.05$). Additionally, significantly higher percentages of spermatozoa with proximal droplets ($P < 0.001$), distal droplets, and bent tails ($P < 0.01$) were observed, with proximal droplets displaying the greatest increase. By Day 63, IC boars showed significant reductions in testicular length (-19.39%), width (-20.12%), and weight (-46.67%) relative to the EM boars (all $P < 0.05$). Mean boar taint scores were lower in the IC group (2.26) versus the EM group (3.17) ($P < 0.05$).

Conclusion

Immunocastration in Danish Duroc boars under the conditions of this study significantly reduced testicular size and weight, impaired sperm quality, and prevented boar taint.

Keywords: Adult boar, Boar taint, Sperm quality, Testicular traits.

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A NEW GENERATION GLYCOCONJUGATE VACCINE AGAINST *STREPTOCOCCUS SUIS*

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Introduction and Objectives

Streptococcus suis causes significant economic losses to the swine industry and raises concerns about animal welfare. This organism is also an emerging zoonotic pathogen. In the absence of effective commercial vaccines, the incidence of disease in pigs is controlled by extensive antimicrobial prophylaxis. *S. suis* is covered by a capsular polysaccharide (CPS), which is the major virulence factor. Of the 29 described serotypes based on the CPS antigenicity, serotype 2 is the most clinically prevalent. Studies have proven the protective capacity of CPS-specific antibodies. CPS is thus an attractive antigen but its poor immunogenicity limits its use as vaccine. However, when conjugated to protein carriers to produce glycoconjugate vaccines, carbohydrates acquire the required immunochemical ability.

Methodology and Results

Recent advances in chemical synthesis have spawned a new generation of carbohydrate-based vaccines. These developments overcome many of the limitations associated with traditional glycoconjugate vaccines. In this study, we designed the first chemically synthesized glycoconjugate vaccine against *S. suis* and provided proof-of-concept of its protective capacity. Eight fragments of the CPS from *S. suis* serotype 2, ranging in size from a monosaccharide to a heptasaccharide were selected for synthesis. These compounds were prepared bearing a linker to facilitate their conjugation to the carrier protein CRM197 (a non-toxic mutant of diphtheria toxin), using a maleimide–thiol coupling reaction. Mouse immunization pre-trials were performed for preliminary target selection based on the capacity of conjugated-CPS fragments to induce a high antibody response, a diversity of IgG sub-classes and functional ability of antibodies to eliminate *S. suis* by opsonophagocytosis. In the swine immunization and challenge model, the levels of antibodies induced by the different pre-selected conjugated-CPS fragments vary but the IgG isotype pattern was similar. However, not all conjugated-CPS fragments were efficient in inducing protection. The conjugate prepared with the heptasaccharide showed strong clinical protection and is thus promising target for a swine vaccine.

Conclusion

Our findings demonstrate the importance of not only chemically designing the right epitope but also that clinical evaluation in pigs is required to predict the real value of a chemically synthesized fragment as a vaccine candidate.

Keywords: Capsular polysaccharide, Glycoconjugate, *Streptococcus suis*, Vaccine.

EVALUATION OF CROSS-PROTECTIVE HUMORAL IMMUNITY AMONG PCV2A, PCV2B, AND PCV2D USING MULTIVALENT CAPSID IMMUNIZATION

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) remains one of the most economically important viral pathogens in the global swine industry. In recent decades, the circulating PCV2 population has undergone a shift in genotype from PCV2a to PCV2b, and more recently, to PCV2d. This ongoing replacement has raised concerns regarding vaccine effectiveness and the breadth of cross-protective immunity. Although most commercial PCV2 vaccines are based on the PCV2a genotype, their ability to protect against heterologous genotypes remains unclear (Malwade et al., 2025). Therefore, this study aims to evaluate cross-protective immune responses elicited by the three major PCV2 genotypes, PCV2a, PCV2b, and PCV2d, using a mouse immunization model.

Materials and Methods

Capsid proteins from PCV2a, PCV2b, and PCV2d were produced using a baculovirus expression system and purified by His-tag affinity chromatography. Mice were immunized twice with the purified proteins formulated as bivalent or trivalent genotype combinations, with a booster administered at 14 days post-vaccination. Serum samples were collected 14 days after each immunization for analysis and screened using genotype-specific PCV2 antigen-coated plates. Neutralizing antibody responses were subsequently assessed by virus neutralization assays against PCV2a, PCV2b, and PCV2d.

Results and Discussion

Following immunization, IFA seropositivity was detected against all PCV2 genotypes, and strong antibody reactivity persisted after the booster, with most groups remaining positive at high serum dilutions. Neutralizing antibodies were detectable as early as two weeks post-immunization, and both bivalent and trivalent formulations elicited cross-neutralizing activity against all three PCV2 genotypes. Notably, a single dose was sufficient to induce measurable neutralization. Collectively, these findings support the potential of this multivalent PCV2 vaccine to provide improved protection against currently circulating field strains in pigs.

Conclusion

This study demonstrates that multivalent immunization with PCV2 capsid proteins elicits strong humoral responses with broad cross-neutralizing activity against PCV2a, PCV2b, and PCV2d. Sustained IFA reactivity and boosted neutralizing antibody titers further support multivalent PCV2 vaccine strategies as a promising approach to enhance cross-protective immunity against the major circulating genotypes.

Keywords: Capsid protein, Cross-protection, Multivalent vaccine, Porcine circovirus type 2.

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COMPULSORY VACCINATION AGAINST PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME (PRRS): EVALUATION OF COST, COVERAGE AND COMPLIANCE IN LIAONING PROVINCE, NORTHEASTERN CHINA

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Introduction and Objectives

Mandatory immunization often comes with controversy. The study aimed to investigate the vaccination rate of the community, individual vaccination rate, support rate for mandatory immunization policies, total social expenditure and service situation of vaccination, and describe the spatial distribution. Analyze the immune effects of Compulsory inoculation vaccines and self purchased vaccines, and analyze the apparent and actual factors that affect the immune decision-making of PRRS. Establish a mathematical model for effectively inferring whether a scale field has received Compulsory inoculation vaccines through easily accessible epigenetic information. Conduct a quantitative epidemiological evaluation of the clinical immune efficacy of the PRRS vaccine.

Materials and Methods

Field investigation and questionnaire were conducted across 737 farms selected randomly. The questionnaire comprised 22 closed, semi-closed and open-ended questions. Univariable and multivariable logistic regression analyses were employed to identify significant associations between compulsory vaccination and farmer's perceptions. Prediction model for vaccine willingness has been established. Vaccine evaluation model was established and all vaccines available on the market were evaluated.

Results and Discussion

By August 2015, the herd-level vaccination coverage in Liaoning province stood at 96.49% (95%CI, 94.49 - 98.49%). The primary reasons for opting for self-funded vaccination were perceived higher quality (51.47%), brand preference (23.53%) and specific vaccine strain (16.18%). However, vaccine price did not significantly influence the farmer's decision. The findings showed that self-funded vaccines did not outperform government vaccines in terms of antibody level, immunity failure, or post-immunization growth. Farms with annual slaughter numbers ranging from 400 - 2,500 heads, non-breeding, and single species were more likely to use compulsory PRRS vaccines. An identification model for farms not adhering to compulsory vaccinations was developed, achieving an area under the ROC curve of 87.7%. Strategies aimed at addressing social factors could prove effective in bolstering the uptake of compulsory vaccinations. These interventions include disseminating vaccine evaluation information to the public, enhancing confidence in domestic brands, and offering compulsory vaccine selections with various strains.

Conclusion

The findings underscore the importance of addressing social factors and providing diverse vaccine options to further enhance acceptance and adherence to compulsory vaccination programs in the swine farming industry.

Keywords: Compulsory Vaccination, China, Porcine Reproductive and Respiratory Syndrome (PRRS), Social factors, Vaccination.

COMPARING THE SEROLOGIC RESPONSE OF A NEEDLE-FREE INTRADERMAL VACCINATION DEVICE TO A NEEDLE-FREE INTRAMUSCULAR VACCINATION SYSTEM AGAINST PCV2 AND *L. INTRACELLULARIS* IN A SUBSET OF PIGS IN CANADA

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Introduction and Objectives

Needle-free vaccination systems are increasingly adopted in swine production due to improvements in worker safety, animal welfare, and operational efficiency. The intradermal IDAL® device administers vaccines using a two-phase mechanism (high-pressure skin penetration followed by low-pressure deposition), whereas the Pulse250 uses a high-pressure liquid jet for intramuscular delivery. Differences in the route of administration may influence the kinetics and magnitude of the humoral response. This study compared serologic responses to PCV2 and *Lawsonia intracellularis* vaccines administered intradermally versus intramuscularly across the nursery, grower, and finishing phases, as well as PCV2 viremia and *L. intracellularis* fecal shedding.

Material and Methods

From a high-health herd, cross-bred source farm, three-week-old pigs (n = 224) were enrolled in cohorts of 56 pigs per week over four weeks. Rooms were randomized to receive vaccination with either IDAL® (Tx1) or Pulse250 (Tx2). Blood was collected for PCV2 PCR and indirect immunofluorescence assay (IFA), and for *L. intracellularis* IFA at pre-vaccination (weaning) and at three-, six-, and 18-week post-vaccination. Fecal rectal swabs for *L. intracellularis* PCR were obtained at 6 and 18 weeks.

Results and Discussion

Pre-vaccination serology indicated comparable elevated baseline antibody levels between treatment groups: PCV2 IFA titers, Tx1 = 725.8 and Tx2 = 583.5; *L. intracellularis* IFA titers, Tx1 = 140 and Tx2 = 116.2. For PCV2, the levels for Tx1 continued to increase over time post-vaccination (738, 1058, 2889), whereas for Tx2, they peaked at 18 weeks, following a decrease at 6 weeks (1382, 1071, 1443). For *L. intracellularis*, Tx1 levels decreased after weaning and peaked at 18 weeks (117, 70, 136), while Tx2 levels continued to increase until 18 weeks (91, 118, 124). Both groups had comparable PCV2 and *L. intracellularis* CTs, as well as the number of positive animals over time.

Conclusion

The data indicate a different serologic response between delivery methods, with comparable antibody levels at later time points, and similar PCV2 and *L. intracellularis* PCR levels. These findings demonstrate that the intradermal IDAL device is an effective alternative to intramuscular needle-free delivery, offering operational and welfare advantages.

Keywords: Intradermal, immunogenicity, Ileitis, PCVAD, Serology.

EVALUATION OF EARLY PRRS VACCINATION IN A SWINE FARM EXPERIENCING EARLY PRRS OUTBREAKS IN PIGLETS IN WESTERN THAILAND

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS), caused by PRRS virus (PRRSV), remains a major constraint to swine production globally, resulting in significant economic losses (Thanawongnuwech et al., 2013). In PRRSV-positive farrowing units, early infection of piglets frequently associated with vertical transmission, can impair piglet viability and elevate pre-weaning mortality (Bøtner et al., 1994). This study aimed to evaluate whether advancing the age of PRRSV vaccination improves piglet health and production performance in a commercial farrowing unit experiencing early PRRS outbreaks in Western Thailand.

Materials and Methods

A controlled, six-month field trial was conducted on a farrowing-to-finishing farm with 4,000 sows. The study used a pre-post design with two consecutive three-month phases (May-July and August-October). In the first phase, piglets received the conventional PRRS vaccination. In the second phase, piglets were vaccinated at one week of age with Fostera® PRRS, a live vaccine registered for use in piglets from one day of age. Each phase involved four farrowing units under standard farm management. Primary outcomes measured were average daily litter weight gain (ADLWG), pre-weaning mortality, the percentage of sows nursing off, and nursery mortality. PRRSV viremia was assessed using real-time PCR on blood samples from four-week-old piglets. Production parameters were analyzed using mixed-effects models, with statistical significance at $P < 0.05$.

Results and Discussion

Early vaccinated piglets demonstrated significantly improved production performance compared with the conventional protocol. ADLWG increased 1,440 to 1,800 grams/day, while pre-weaning mortality and the proportion of sows nursing off were reduced. PRRSV viremia was not detected at weaning in piglets vaccinated at one week of age. Nursery mortality decreased from 16.08% under the conventional protocol to 5.64% following early vaccination ($P < 0.05$). These findings indicate that early PRRS vaccination can mitigate the impact of early PRRSV infection and improve piglet health and productivity.

Conclusion

Early administration of the Fostera® PRRS at one week of age significantly reduced pre-weaning and nursery mortality and improved overall production efficiency. Early PRRS vaccination represents an effective intervention for farrowing unit experiencing early PRRS outbreaks.

Keywords: Early vaccination, Early infection, Porcine Reproductive and Respiratory Syndrome.

Acknowledgements: The authors thank SPR Farm, Ratchaburi province and farm consultant for farm access and support in data collection, and Zoetis (Thailand) Limited for technical and scientific support.

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DISEASE STABILIZATION THROUGH BLANKET PRRSV VACCINATION USING INGELVAC® PRRS MLV IN A PRRSV-POSITIVE SWINE FARM IN MALAYSIA: A CASE REPORT

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) remains a major challenge for commercial pig production, especially in PRRSV-positive herds where recurrent clinical instability can occur. A commercial pig farm in Malaysia experienced increasing reproductive and post-weaning losses in April 2025, characterized by a rise in the abortion rate, elevated mortality among weaner pigs and gestation sows off feed across mixed parity. This case report describes the implementation and outcome of a blanket PRRSV vaccination program using Ingelvac® PRRS MLV in a PRRSV-positive commercial pig farm in Malaysia and characterizes the circulating PRRSV strains through ORF5-based phylogenetic analysis.

Materials and Methods

To stabalise the herd, the farm implemented a disease stabilization strategy centered on blanket vaccination using a modified live PRRSV vaccine (Ingelvac® PRRS MLV). The vaccination program was applied in April and May, followed by routine PRRSV mass vaccination every 3 months apart across breeder units. Concurrently, molecular surveillance was conducted through routine sampling of one-week-old piglets and breeder-unit oral fluid samples. PRRSV-positive samples were analyzed by ORF5 gene sequencing to determine the genotype classification of the circulating PRRSV strains in the farm.

Results and Discussion

PRRSV Type-2 was detected in multiple production units, including one-week-old piglets, and 8- and 12-week-old porkers, which indicates ongoing viral circulation within the farm. ORF5-based phylogenetic analysis revealed that the detected strains were genetically closely related to Lineage 1H when compared to other reference genes. The sequenced isolates demonstrated close genetic similarity to PRRSV strains originating from the United States, suggesting a common ancestral lineage and persistent within-farm circulation. Following the implementation of the blanket vaccination program, the farm achieved clinical stabilization with reduced reproductive losses, improved weaner survival and farrowing rate, despite continued low-level viral detection.

Conclusion

This case report demonstrates that blanket PRRSV vaccination using Ingelvac® PRRS MLV can be an effective strategy for achieving disease stabilization in PRRSV-positive commercial pig farms. Continuous molecular surveillance remains essential to support long-term PRRS management in endemic settings.

Keywords: Blanket vaccination, Commercial pig farms, Modified live virus vaccine, ORF5, PRRSV-2.

Acknowledgements: The authors thank Boehringer Ingelheim Malaysia Sdn Bhd for providing support for conducting this research.

IMPACT OF A 5-STEP PRRS CONTROL STRATEGY ON PRRSV DYNAMICS IN SOWS AND PIGLETS: CASE REPORT

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is a leading cause of economic losses in pig production worldwide, primarily due to reproductive failures in sows and respiratory illness in growing pigs (Poul et al., 2017). Effective control of PRRSV is essential for improving pig health and productivity, yet remains challenging, especially in large-scale operations. This study evaluated the impact of Boehringer Ingelheim's 5-step process for PRRS control in a 4800-sow farrow-to-finish commercial farm in Vietnam.

Materials and Methods

After a period of respiratory instability and elevated mortality rates among weaners due to PRRS and Porcine Respiratory Disease Complex, the farm adopted a new vaccination protocol in August 2022. This protocol involved administering IngelvacPRRSMLV in combination with FLEXcombo vaccines (MycoFLEX and CircoFLEX) as a single injection. The vaccination strategy was integrated into a comprehensive 5-step PRRS control program, which included strengthened biosecurity measures, enhanced management practices, and optimized pig flow, supported by regular farm audits. To evaluate the program's effectiveness, PRRSV circulation was monitored through quarterly PCR sampling from 2022-Q1 to 2025-Q3, including samples from sows (fetuses, stillborns), piglets (weaners/growers), and gilts. Sample types included gilts and growers' oral fluids, stillbornes tongue tip fluids, family oral fluids (18-day-old piglets), processing fluids (one-week-old piglets), and lung samples from nursery mortalities. PCR data were analyzed using JMP18 statistical software.

Results and Discussion

A total of 240 samples were analyzed, with 26.67% PCR positive. Processing fluids from one-week-old piglets and gilts' oral fluids had the highest negative rates (100 and 96.7%, respectively), while fetus and lung samples from weaned pigs had the lowest Ct values. Longitudinal analysis of nursery piglets and growers showed a change in the trend toward more stable but low Ct values starting in 2023-Q3 for nursery piglets and 2023-Q1 for finishers.

Conclusion

The integration of IngelvacPRRSMLV and FLEXcombo within a comprehensive 5-step program supported overall PRRS control, as evidenced by significantly improved production performance (study accepted). However, persistent low Ct values in nursery piglets highlight the need for additional interventions (i.e.,partial nursery depopulation, breeding herd closing). Consistent and more frequent PRRS status monitoring is recommended to improve decision-making and risk identification.

Keywords: 5-step process, FLEXcombo, IngelvacPRRS MLV, PRRSV, PCR.

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PRODUCTION AND CLINICAL VALUE OF AN INACTIVATED *LAWSONIA INTRACELLULARIS* VACCINE UNDER ENDEMIC COMMERCIAL CONDITIONS

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Introduction and Objectives

In enzootic *Lawsonia intracellularis* systems, the practical question is whether an inactivated vaccine delivers measurable field value in outcomes that matter to production decisions. This study evaluated an inactivated *L. intracellularis* vaccine using growth performance, enteric clinical scores, and mortality as primary endpoints under routine commercial conditions.

Materials and Methods

A pragmatic field comparison was conducted in a commercial grow-finish farm with recurrent proliferative enteropathy. At weaning, piglets were assigned to an inactivated L. intracellularis vaccination group or an unvaccinated control group, then commingled and managed under standard practices. Vaccination was administered at 3-6 weeks or at 7 weeks of age depending on batch. Average daily weight gain (ADWG), standardized diarrhea/clinical scores, and mortality were recorded through marketing. Serology was used to characterize exposure and vaccine-associated immune responses. Fecal qPCR confirmed endemic exposure pressure but was not treated as a primary efficacy endpoint.

Results and Discussion

Across batches (vaccinated n = 103; control n = 60), vaccinated pigs achieved higher ADWG than controls (0.707 vs 0.677 kg/day; +0.031 kg/day, +31 g/day), with batch-level advantages ranging from +0.012 to +0.071 kg/day. Vaccination was also associated with lower enteric clinical scores compared with controls. Mortality was numerically reduced in vaccinated pigs (2% vs 7%), although the magnitude varied by batch. Serology supported widespread exposure and vaccine-associated immune responses consistent with ongoing field challenge.

Conclusion

Under endemic commercial conditions, an inactivated *L. intracellularis* vaccine provided tangible production and clinical benefits and showed a favorable mortality trend, supporting its inclusion as a practical component of herd health programs, particularly when early-life vaccination can be implemented.

Keywords: Diarrhea, Growth performance, Inactivated vaccine, *Lawsonia intracellularis*, Mortality.

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VACCINE VIRUS SHED AND SPREAD PROPERTIES FOLLOWING ADMINISTRATION OF PRRSGARD®, A NOVEL CHIMERIC PRRSV VACCINE

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Introduction and Objectives

Choices between PRRSV modified live virus (MLV) vaccines may be influenced by efficacy, ability of vaccine virus spread to non-target populations or decreased performance following vaccination (drag). PRRSGard® is a unique vaccine with a chimeric lineage 1 virus (Chamba et al., 2018). The objective of this report is to compare trials evaluating the shedding profile, performance drag, and immunological response of PRRSGard to determine repeatability.

Materials and Methods

Trial inclusion criteria included different pig ownership, genetics, and geographical location. Similar source farm PRRSV status, vaccination protocols, and the involvement of a negative control were required. Two studies fit the criteria. Trial 1 consisted of 672 wean pigs in 28 pens sharing the same air space (Smith et al., 2020). Fourteen pens were vaccinated with PRRSGard, and 14 pens were vaccinated with saline. Twenty-five pigs were sampled weekly and tested by PRRSV rRT-PCR and ELISA. Performance differences of the entire population were captured 48 days post-vaccination (dpv). Trial 2 consisted of 1,800 wean pigs divided into two rooms (Kettelkamp, E. et al., 2023). Room 1 was vaccinated with PRRSGard and the other with saline. Additionally, 10 pigs in room 1 were not vaccinated with PRRSGard to assess transmission in the same air space. Sixty pigs were sampled weekly up to 49 dpv and performance differences captured on 119 dpv.

Results and Discussion

Trial 1 results showed no PRRSGard vaccine virus spread to non-vaccinated pens. Additionally, there were no differences in average daily weight gain or livability. Viremia was detected at the first sampling event following vaccination and began dropping 35 dpv. Seroconversion occurred between 14-28 dpv. Trial 2 results indicate viremia in vaccinated pigs by 3 dpv, which began dropping off at 35 dpv and seroconversion within 14–28 dpv. No vaccine virus spread to non-vaccinated pigs until ~91 dpv, confounded by a clinical influenza A virus infection at this time. There were no differences in performance.

Conclusion

PRRSGard appears to elicit an appropriate immune response with limited performance drag and shedding to non-target populations, though more trials need to be conducted for full statistical analysis.

Keywords: PRRSGard, Porcine Reproductive and Respiratory Syndrome virus, Shed, Spread, Vaccine.

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REPEATABILITY OF CIRCO/MYCOGARD® CROSS PROTECTION TO PORCINE CIRCOVIRUS TYPE 2D

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Introduction and Objectives

Porcine Circovirus Type 2 (PCV2) is pathogenic and considered ubiquitous in swine populations. While PCV2 vaccines have been very successful, efficacy is often questioned in commercial situations as PCV2 adapts/evolves through viral mutations. Currently, PCV2d is the predominant genotype circulating in the United States (Madson, 2019). Circo/MycoGard® (CMG) is a PCV2b/*Mycoplasma hyopneumoniae* combination vaccine previously proven to offer cross-protection to PCV2d challenges (Chamba et al., 2020). The objective of this trial was to prove repeatability of cross-protection in a different environment.

Materials and Methods

Thirty commercial gilts were selected at approximately 21 days of age and placed into two groups, vaccinated and control. No Porcine Reproductive and Respiratory Syndrome virus (PRRSv) vaccine was administered. The vaccinated group received CMG per label instructions, and the control groups received saline (day 0). All pigs were challenged on day 42 with a lineage 1, PRRSv genotype 2, RFLP 1-8-4 and on day 49 with PCV2d. Individual pig weights were captured on day 0, 42, and 70. All pigs were euthanized on day 70 with gross lung lesion scoring and lung, superficial inguinal and tracheobronchial lymph nodes collected for histopathology and immunohistochemistry scoring.

Results and Discussion

There were no significant differences in average weight on D0 or D42. The vaccinated group weighed 4.6 kg more than the control group on D70 ($P = 0.04$) with 0% mortality after challenge vs. 10.3% mortality in the control group. The lung lesion scores for the vaccinated group were 0.33 vs. 19.62 in control pigs ($P < 0.0001$) with significantly less lung inflammation and PCV2 lymph node colonization found in the vaccinated group.

Conclusion

Circo/MycoGard is effective in eliciting cross-protection to PCV2d challenge and results are repeatable in different environmental conditions and challenge models.

Keywords: Circo/MycoGard, PCV2d, Cross-protection, PCVAD, Vaccine.

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VACCINE EFFICACY OF A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE RECENTLY REGISTERED IN CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* cause significant losses to the pig industry. This controlled, randomized, parallel trial assesses the efficacy of a Ready-to-Use (RTU) bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China.

Materials and Methods

A two-site herd in Anhui province (China) was selected. Site 1 (800 sows; breeding/nursery) was PRRSV-stable. Site 2 (fattening) had a history of PCV2 systemic disease and severe pneumonia at slaughter. In total, 2297 piglets from the same batch were enrolled in two groups. Control group (C; n = 1200) was vaccinated twice against PCV2 and *M. hyopneumoniae* (Fostera®PCV MH) at 7 and 21 days of age; whereas the Experimental group (E; n = 1097) received a single-dose RTU vaccine (Porcilis® PCV M Hyo) at 21 days. Sera were collected at 3, 8, 15 and 22 weeks of age, and PCV2 viral load quantified (qPCR; AUC). At 8 weeks of age, pigs were transferred to site 2 and each group was housed in adjacent identical rooms. Pigs were weighed at arrival and before slaughter, and Average Daily Gain (ADG) calculated for this period. Feed Conversion ratio (FCR) was measured at room level. Percentage of pigs reaching slaughter (survival %) was recorded. At slaughter, pneumonia lesions were scored (Madec). Survival % and prevalence of pneumonia were analyzed by Fisher's exact test, severity of pneumonia by Wilcoxon test.

Results and Discussion

PCV2 viremia was detected in both groups (4 - 7 Log_{10} copies/mL), but viral load was not significantly different. Entry weight and days weaning-to-slaughter (198) were similar between groups. Live weight at slaughter was 173.96 kg in Group E and 171.77 kg in Controls. ADG was 825 grams/day in Group E and 813 grams/day in Group C. FCR was 2.67 and 2.81 for Group E and C, respectively. Survival % was significantly different between groups (E:97.8%; C:95.3%; $P < 0.05$). Both severity (E:1.58 ± 1.68; C:4.45 ± 4.09; $P < 0.05$) and prevalence of pneumonia (E:56.2%; C:85.7%; $P < 0.05$) were significantly different between groups.

Conclusion

Under these conditions, both vaccines demonstrated a successful control of PCV2 viremia. The single-dose vaccination scheme (Group E) significantly improved survival % and reduced prevalence and severity of pneumonia.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Pneumonia, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

EFFECTS OF IMPROVAC® ON GROWTH PERFORMANCE AND CARCASS TRAITS IN FEMALE FINISHING PIGS FROM A LARGE-SCALE INTEGRATED PORK PRODUCTION SYSTEM IN CHINA

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Introduction and Objectives

Immunocastration with Improvac®, an immunological alternative to physical castration, has been shown to temporarily suppress ovarian function in female pigs, with potential benefits for growth performance. While controlled studies and meta-analysis results (Poulsen et al., 2020) suggest positive effects in gilts, evidence from large-scale commercial production systems remains limited. The objective of this study was to evaluate the effects of Improvac® on growth performance and carcass traits in female finishing pigs under commercial field conditions in China.

Material and Methods

A total of 2,600 female finishing pigs were randomly allocated into either an Improvac®-treated group or a non-treated control group. Following weaning, both groups were managed under identical housing, nutrition, and health protocols in adjacent barns. Improvac®-treated pigs received two 2 mL injections at 13 and 18 weeks of age. Body weights were recorded at 3 and 24 weeks of age and feed consumption was monitored throughout the wean-to-finish period to calculate average daily gain (ADG) and feed efficiency. At 24 weeks of age, 30 pigs per group were randomly selected for carcass evaluation, including hot carcass weight, dressing percentage, and backfat thickness.

Results

Improvac-treated females achieved a significantly higher final body weight compared with non-treated controls (123.69 vs. 121.45 kg; + 2.24 kg; $P = 0.05$). ADG increased by 1.93% (763.21 vs. 748.75 g/d) and wean-to-finish feed efficiency improved by 2.36% (2.48 vs. 2.54). No significant differences were observed in hot carcass weight (95.14 ± 8.95 vs. 94.77 ± 8.39 kg), dressing percentage (77.18 vs. 76.90%), or backfat thickness (29.61 vs. 28.25 mm).

Conclusion

Under large-scale commercial conditions, Improvac® administration in female finishing pigs improved growth performance and feed efficiency without adversely affecting carcass traits. These results support immunocastration as a practical management tool to enhance production efficiency in female finishing pigs within large-scale integrated pork production systems.

Keywords: Carcass trait, Gilts, Growth performance, Immunocastration.

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EFFECTS OF IMPROVAC® ON GROWTH PERFORMANCE AND CARCASS TRAITS IN MALE FINISHING PIGS FROM A LARGE-SCALE INTEGRATED PORK PRODUCTION SYSTEM IN CHINA

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Introduction and Objectives

In China, physical castration is still commonly practiced to control boar taint in male pigs, despite growing concerns related to animal welfare and production efficiency. Immunocastration using an anti-gonadotropin-releasing factor (GnRF) vaccine has been widely adopted in other regions and has demonstrated improvements in growth performance and carcass composition1. This study aimed to evaluate the effects of immunocastration with Improvac® on growth and carcass traits in a large-scale integrated pork production system in southern China.

Material and Methods

A total of 2,600 male piglets were randomly allocated at 3 days of age to either immunocastration (IC; n = 1,300) or physical castration (PC; n = 1,300). Following weaning, both groups were housed separately in adjacent barns (26 pens per group, 50 pigs per pen). IC pigs received two 2 mL doses of Improvac® injections at 14 and 18 weeks of age. Body weights were recorded at 3 and 24 weeks, and feed intake was monitored throughout the wean-to-finish period. At 24 weeks, 30 pigs per group were randomly selected for carcass evaluation. Performance and carcass parameters were statistically compared between treatments.

Results

Immunocastrated pigs had a significantly higher market weight compared with physically castrated pigs (130.19 vs. 122.90 kg; + 7.29 kg, $P = 0.018$). Average daily gain was 6.45% greater in the IC group (806.30 vs. 757.44 g/d; $P < 0.001$) and wean-to-finish feed efficiency improved by 2.78% (2.45 vs. 2.52). Hot carcass weight was significantly higher in the IC group (99.12 ± 8.95 vs. 94.77 ± 8.39 kg; $P < 0.001$), while dressing percentage was numerically lower but not statistically different between groups (75.63 vs. 76.02%; $P = 0.130$). When adjusted to the same carcass weight, backfat thickness was reduced by 1.21 mm in IC pigs compared to the PC pigs (29.09 vs. 30.30 mm; $P = 0.004$). These results are consistent with published evidence supporting improved lean growth efficiency following immunocastration.

Conclusion

Under commercial production conditions in China, immunocastration with Improvac® significantly improved growth performance, feed efficiency, and carcass weight, while reducing backfat thickness compared to physically castrated counterparts. These findings suggest that immunocastration represents an effective and welfare-friendly alternative for enhancing productivity and carcass quality in a large-scale integrated pork production system.

Keywords: Carcass traits, Growth performance, Immunocastration, Male pigs.

References

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EVALUATION OF THE LOCAL IMMUNE RESPONSE IN THE SMALL INTESTINE OF WEANED PIGLETS EXPOSED TO DIFFERENT FEED ADDITIVES

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Introduction and Objectives

Immunoglobulin A (IgA) plays a fundamental role in the intestinal mucosa as the first line in the colonization of pathogens, thus generating protection against different diseases in the post-weaning phase (Miralles et al., 2024). The objective of this study is to evaluate the immune response in the intestinal mucosa by counting IgA-producing cells (IgA+) in weaned piglets subjected to diets with different food additives.

Materials and Methods

Three groups of 20 animals each were established according to their diet: feed without additives (Control), feed with a mixture of fatty acids and Saccharomyces cerevisiae yeast (Ad1), and feed with beta-glucans derived from algae (Ad2). Necropsies were performed at 10 weeks post-weaning, and jejunal and ileal samples were taken and fixed in 10% formalin, were dehydrated and embedded in paraffin blocks. After cutting 5 µm sections, immunohistochemistry was used to detect IgA+. The slides were scanned, and the immunolabeled cells were counted using QuPath software in 10 consecutive, non-overlapping fields. ANOVA and Kruskal-Wallis statistical analyses were performed using the Jamovi 2.3.24 statistical program.

Results and Discussion

The average number of IgA+ cells in the ileum remained stable among the different groups Ad1 (151.51 ± 6.14), Ad2 (151.2 ± 5.67), and Control (148.41 ± 5.39). In the jejunum, however, similar to findings in previous studies of animals vaccinated against *E. coli* (Miralles et al., 2024), we observed a lower number of IgA+ cells in the Control group (141.69 ± 6.60), which increased significantly in the Ad1 (151.17 ± 5.39) and even more so in the Ad2 (153.49 ± 4.93). Expressed as a percentage, in the jejunum we observed a statistical trend ($P = 0.07$) between the Control group (52% ± 2.43) and both additives (57.2% ± 1.35). Our results, like other previous studies with feed additives (Che et al., 2024), suggest that local and continuous stimulation in the feed promotes greater IgA production and mucosal protection in weaned piglets.

Conclusion

Weaned piglets fed a diet supplemented with beta-glucans develop a greater local immune response in the intestinal mucosa with more IgA+ cells than those fed feed without additives.

Keywords: Beta-glucans, Fatty acids, IgA, Piglets, Saccharomyces cerevisiae boulardii.

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EVALUATION OF THE EFFICACY OF AN OIL-IN-WATER ADJUVANT IN A FOOT-AND-MOUTH MINERALIZED VIRUS-LIKE PARTICLES VACCINE IN PIGS

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Introduction and Objectives

Foot-and-mouth disease (FMD), caused by the FMD virus, is a highly contagious infection characterized by vesicular lesions in cloven-hoofed animals, posing a severe economic threat to the global livestock industry. VLP vaccines streamline FMD management by enabling safer, low-containment production while inherently supporting DIVA strategies through the total absence of non-structural proteins. This study aimed to evaluate the efficacy of a single-dose, bivalent mineralized VLP vaccine (serotypes O and A) formulated with the oil-in-water (O/W) adjuvant Montanide™ ISA 15A VG. The evaluation criteria targeted an immunity duration of at least six months and a challenge protection rate of at least 80%.

Materials and Methods

Twenty healthy pigs were vaccinated intramuscularly with a single 2 mL dose of the bivalent O/W adjuvanted VLP vaccine; four pigs served as a negative control group. Safety was assessed by monitoring adverse and local reactions at the injection site. Immunogenicity was quantified by measuring specific anti-FMDV antibodies via ELISA weekly for the first month and monthly thereafter. Six months post-vaccination, the pigs were divided for viral challenge: 10 vaccinated and 2 control pigs were challenged with 1000 ID50 O type/MYA98 strain, while the remaining 10 vaccinated and 2 control pigs were challenged with 1000 ID50 A type/GDMM strain. Protection was assessed over a 10-day observation period, where the appearance of any clinical FMD symptoms was classified as non-protection.

Results and Discussion

The vaccine demonstrated an excellent safety profile, with no adverse reactions or local inflammation observed at the injection site. Regarding immunogenicity, the vaccinated group developed significant antibody titers by day 14. These levels continued to rise, peaking at three months post-immunisation and remaining elevated through the six-month period. Upon challenge, all control pigs developed clinical disease. In contrast, the vaccinated group achieved a 100% protection rate against both serotypes.

Conclusion

These results confirm that the oil-in-water adjuvant Montanide™ ISA 15A VG is highly effective for formulating high-performance FMD VLP vaccines. The bivalent formulation provided a robust safety profile and full clinical protection six months after a single-dose immunization, meeting and exceeding the study's efficacy requirements.

Keywords: Foot-and-mouth disease virus (FMDV), Emulsion adjuvant, Virus-like particle vaccine.

COMPARATIVE EVALUATION OF GROWTH OUTCOMES FROM NEEDLE-FREE VACCINATION WITH BIVALENT VACCINES AGAINST PORCINE CIRCOVIRUS TYPE2 AND *MYCOPLASMA HYOPNEUMONIAE* IN A JAPANESE SWINE FARM

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Introduction and Objectives

Vaccination against Porcine Circovirus type2 (PCV2) and *Mycoplasma hyopneumoniae* (Mhyo) has been established to encounter the economic losses associated with these pathogens. Needle-free vaccination has become popular recently with having devices for intradermal or intramuscular administration. The purpose of this study was to compare needle-free intramuscular and intradermal PCV2/Mhyo vaccinations in an endemically infected herd in Japan.

Materials and Methods

This study was conducted on a PRRSV-positive farm with 250 sows where food waste was fed to pigs during the finishing period. On the weaning day at 3 weeks of age, piglets born from 22 sows were equally divided into two groups based on body weight. Group IM (n = 102) received 2ml of mix-on-use PCV2/Mhyo vaccine (FLEXcombo®; Boehringer Ingelheim Animal Health Japan Co., Ltd.) intramuscularly by using a battery-powered needle-free intramuscular injector (Henke-Sass, Wolf GmbH). Group ID (n = 102) were vaccinated with a single, simultaneous dose of 0.2 ml of each PCV2/Mhyo vaccine (Porcilis® PCV IDAL, Porcilis® M Hyo IDAL; MSD Animal Health Co., Ltd.) intradermally. Both vaccines were administered according to the manufacturer's instructions. After co-housing the two groups of piglets until 20 weeks of age, the body weight of each piglet was measured individually. Body weight was analyzed by Student's t-test and post-weaning mortality by chi-square test using JMP 18.2.2.

Results and Discussion

There was a significant difference in body weight at week 20 with having a mean body weight of 57.65 kg for the IM group and 54.03 kg for the ID group ($P \leq 0.05$). The number of deaths during the study was 8 in the IM group (Mortality: 7.843%) and 11 in the ID group (10.784%).

Conclusion

Needle-free intramuscular administration of the PCV2/Mhyo vaccine resulted in a 3.62 kg increase in body weight and a 2.941% reduction in mortality at 20 weeks of age compared to the needle-free intradermal administration of another PCV2/Mhyo vaccine. This superiority seems to be a combination of the vaccine efficacy with a device that ensures the correct and full delivery of a vaccine dose intramuscularly.

Keywords: Needle-free vaccination, *Mycoplasma hyopneumoniae*, Porcine Circovirus type 2.

REDUCTION OF PCV2 VIREMIA AFTER VACCINATION WITH A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE RECENTLY REGISTERED IN CHINA

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Introduction and Objectives

Porcine Circovirus type 2 (PCV2) and *Mycoplasma hyopneumoniae* cause severe respiratory disease and poor performance in pigs. Both pathogens are key players in the Porcine Respiratory Disease Complex and lead to significant economic losses. Vaccination is one of the most common tools used to control both pathogens. This controlled, randomized, side-by-side trial aimed to evaluate the efficacy of a Ready-to-Use (RTU) bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China.

Materials and Methods

For this trial, a farrow-to-finish herd (600 sows; 2-week system) with a history of PCV2 disease in fatteners and located in Shaanxi province (China) was selected. The herd was Aujeszky's Disease virus free and PRRSV positive, but stable. A batch of 717 piglets was enrolled in the study and divided into two groups: Control (C; n = 367) and Experimental (E; n = 350). Pigs in the Control group were vaccinated with a combo PCV2-*M. hyopneumoniae* vaccine (local vaccine) at 21 days of age and received a second dose of PCV2 at 16 weeks of age. On the other hand, pigs in the Experimental group were vaccinated only once at 21 days with a RTU bivalent vaccine (Porcilis® PCV M Hyo). Ten pigs per group were bled at 18, 22 and 26 weeks of age, and sera were tested by qPCR to quantify PCV2 viral load. All pigs were weighed at group level at weaning (21 days) and prior to slaughter (185 days). Average Daily Gain (ADG) was calculated for this period.

Results and Discussion

PCV2 viral load remained < 5.0 Log_{10} copies/mL in group C and undetectable or at insignificant levels (< 3.5 Log_{10} copies/mL) in Group E. Average entry weight (C: 7.30 kg; E: 7.30 kg) and Average live weight at slaughter (C: 143.8 kg; E: 144,5 kg) were similar between groups. ADG from weaning to slaughter was 832.3 and 836.6 grams/pig/day in the control and experimental group, respectively.

Conclusion

Under the conditions of this trial, both vaccination strategies showed a comparable performance regarding growth and PCV2 control. The RTU vaccine achieved a reduction in PCV2 viremia and was associated with a slight improvement in growth compared to the control group.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Performance, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

SAFETY AND PERFORMANCE OF A READY-TO-USE BIVALENT PCV2 AND *MYCOPLASMA HYOPNEUMONIAE* VACCINE UNDER SUBCLINICAL PCV2 INFECTION IN CHINA

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Introduction and Objectives

Subclinical infections caused by Porcine Circovirus type 2 (PCV2), together with *Mycoplasma hyopneumoniae,* significantly affect productivity in the Chinese swine industry. This trial investigates the safety and efficacy of a Ready-to-Use (RTU) bivalent PCV2 and *M. hyopneumoniae* vaccine recently registered in China in a herd with PCV2 subclinical infection.

Materials and Methods

A controlled, parallel trial was performed in a wean-to-finish unit in Shandong province (China) with PCV2 and *M. hyopneumoniae* infections confirmed by laboratory analysis. At weaning (21 days of age), 4632 piglets were enrolled and divided into two groups: the Control group (C; n = 2320), vaccinated with a PCV2-*M. hyopneumoniae* vaccine (local Chinese brand); and the Experimental group (E; n = 2312) which received an RTU bivalent vaccine (Porcilis® PCV M Hyo). Adverse reactions post-vaccination were recorded. Longitudinal blood sampling (n = 15 pigs/group) was performed (3, 7, 11, 15, 19, 23 and 26 weeks of age), and PCV2 viral load in serum measured (qPCR; AUC). Average group weight at weaning and before slaughter was used to calculate Average Daily Gain (ADG). Mortality and proportion of lightweight finishers (< 90 kg; runt percentage) were recorded. Pneumonia lesions were assessed at slaughter (Madec; n = 120 lungs/group). Mortality, runt percentage and pneumonia prevalence were analyzed using Fisher's exact test, pneumonia severity and PCV2 AUC by Wilcoxon test.

Results and Discussion

No systemic or local adverse reactions were observed in either group. From 7 weeks onward, PCV2 was detected in both groups. Median AUC were significantly different between groups (C: 1.39×10^7; E: 1.68×10^6 copies/mL; $P < 0.05$; difference C-E:1.09×10^7; CI [4.01×10^5 - 4.26×10^6]). Live weight at slaughter was 126.42kg and 121.01kg in Group E and C, respectively. ADG was 697g/day in Group E and 665g/day in Controls. Mortality % (E: 2.2%; C: 4.8%; $P < 0.05$) and runt percentage (E: 0.1%; C: 1.3%; $P < 0.05$) were significantly lower in Group E. Pneumonia severity was significantly reduced in Group E (4.7 ± 3.8) compared with Controls (7.9 ± 4.4) ($P < 0.05$) and pneumonia prevalence was also significantly lower (E: 86.4%; C: 97.4%; $P < 0.05$).

Conclusion

In this study, the new RTU vaccine was found safe and efficacious for controlling PCV2 infection by significantly reducing viremia, mortality and runt percentage. Pneumonia severity and prevalence were also significantly reduced.

Keywords: *Mycoplasma hyopneumoniae*, PCV2, Pneumonia, Vaccination, Viremia.

Acknowledgements: The authors thank the producer for the field support during the trial.

IMPACT OF MATERNALLY DERIVED ANTIBODIES ON THE IMMUNE RESPONSE TO NEEDLE-FREE INTRADERMAL AND INTRAMUSCULAR MODIFIED LIVE CLASSICAL SWINE FEVER VACCINATION IN FOUR-WEEK-OLD PIGS

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Introduction and Objectives

In Thailand, both sows and piglets are vaccinated against classical swine fever (CSF). Maternally derived antibodies (MDA) specific to CSF virus can interfere with vaccine-induced immune responses (Guo et al., 2020). Needle-free intradermal (nf-ID) vaccination has been reported to elicit robust immune responses (Shuai et al., 2026) and therefore may help to overcome MDA interference. The objective of this study was to compare immune responses induced by needle-free intradermal and conventional intramuscular (IM) vaccination with a modified live CSF vaccine in MDA-negative and MDA-positive four-week-old pigs.

Materials and Methods

A total of 10 pigs derived from two sows, comprising four MDA-negative and six MDA-positive animals, were allocated to either the nf-ID (n = 5) or IM (n = 5) vaccination groups. All pigs were vaccinated once with a modified live CSF vaccine (LOM strain). For nf-ID vaccination, pigs received 0.5 mL of vaccine at two separate intradermal injection sites using a needle-free device, resulting in a total dose of 1.0 mL, equivalent to that administered via the IM route. Serum neutralizing (SN) antibody titers against the ALD strain-CSF virus were compared on days 0 (D0), 1 (D1), 14 (D14), and 28 (D28) post-vaccination using Mann-Whitney U test for vaccination routes and MDA status, and Wilcoxon signed-rank test for changes of titers from D1 to D28.

Results and Discussion

Vaccination routes were not significantly different, geometric mean titers (GMTs) of SN antibodies were comparable between the nf-ID and IM groups, with values of 9.2/9.2, 12.1/12.1, and 21.1/18.4 on D1, D14, and D28, respectively. In MDA-negative pigs, GMTs were markedly increased from D1 to D28; 1.0, 9.5, and 38.1, respectively ($P < 0.05$). In contrast, MDA-positive pigs exhibited reduced SN titers following vaccination. The MDA-positive pigs' titers were 40.3 on D1 and reduced to 14.3, and 12.7 on D14 and D28 post-vaccination ($P > 0.05$).

Conclusion

MDA markedly interfered with immune responses to modified live CSF vaccination in four-week-old pigs via both intradermal and intramuscular routes.

Keywords: Hog cholera, Intradermal, Intramuscular, Maternal antibodies, Needle-free vaccination.

Acknowledgements: The authors acknowledge Dodram Pig Research Center for research grant and Reborn Agency for the needle-free-intradermal device.

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PRODUCTION OF RECOMBINANT PORCINE CIRCOVIRUS TYPE 4 VIRUS-LIKE PARTICLES USING THE BACULOVIRUS EXPRESSION SYSTEM

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Introduction and Objectives

Porcine circovirus type 4 (PCV4) is an emerging pathogen firstly identified in 2019, reported predominantly in Asia, and associated with postweaning multisystemic wasting syndrome and reproductive failure in pigs. Current porcine circovirus type 2 vaccines are not expected to provide effective cross-protection against PCV4, indicating the need for PCV4-specific antigen development. PCV4 contains two major open reading frames; notably, ORF2 encodes the capsid (Cap) protein, the primary structural and immunogenic antigen. This study aimed to produce recombinant PCV4 virus-like particles (VLPs) using a baculovirus expression system as antigens for vaccine and diagnostic development. This platform was selected for its advantages in ensuring correct protein folding, post-translational modification.

Materials and Methods

The ORF2 gene (PCV4b genotype) was codon-optimized, synthesized, and fused at its C-terminus to a GGGGS linker and a hexahistidine (6xHis) tag for purification and detection. The construct was cloned into a pFastBac Dual transfer vector to generate a recombinant bacmid capable of co-expressing the Cap protein and a Green Fluorescent Protein (GFP) reporter. This recombinant bacmid was then transfected into Sf9 insect cells. Recombinant baculovirus stocks were amplified and used to infect Sf9 cells at a multiplicity of infection (MOI) of 5. Infected cells, monitored via co-expressed GFP, were harvested at 4 dpi. Ni-NTA-purified Cap was analyzed by SDS-PAGE and anti-His Western blot, and VLP assembly validated by transmission electron microscopy (TEM).

Results and Discussion

SDS-PAGE analysis revealed a prominent band at approximately 28 kDa, consistent with the predicted molecular weight of the PCV4 Cap monomer. Western blotting using an anti-His-tag antibody confirmed a single specific band, supporting successful expression and correct identity of the His-tagged protein. TEM examination demonstrated well-formed, spherical virus-like particles with diameters of approximately 20 nm, consistent with circovirus morphology, confirming that the recombinant Cap protein successfully self-assembled into VLPs within the insect cell system.

Conclusion

Recombinant PCV4b VLPs were successfully produced with authentic morphology and expected molecular characteristics. These VLPs have potential utility as an antigen platform for developing ELISA-based serodiagnosis of PCV4. Future studies will evaluate their immunogenicity in animal models to support PCV4 vaccine development.

Keywords: Baculovirus expression system, Porcine circovirus type 4, Recombinant capsid antigen, Virus-like particles.

Acknowledgements: The authors thank the National Institute of Animal Health, Thailand, for providing the testing facilities and support for this study.

EFFICACY OF A NOVEL PORCINE CIRCO VIRUS VACCINE TETRAVALENTS ON VIRUS CLEARANCE IN FATTENNING PIG FARM: USING IDEXX REALPCR PCV2/PCV3 MULTIPLEX DNA TEST

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Introduction and Objectives

PCV2 causes clinical signs including PMWS and PDNS, which negatively affect pig health and growth performance. In Thailand, studies have revealed the presence of PCV2 and PCV3 infections, as well as its co-infection. Previously, we developed adenovirus-based-tetravalent-vaccine (PCV2a/2b/2d/PCV3), and infection status which determined by the PCV2 specific IgG/IgM by using ELISA (INgezim®, Ingenasa, Madrid, Spain), showed a higher number of uninfected pigs in tetravalent-group (60%) than commercial-group (20%). We further evaluated vaccine efficacy by comparing viral clearance of nursery pigs vaccinated with either commercial-vaccine (PCV2a) or adenovirus-based-tetravalent-vaccine.

Materials and Method

A total-of-60-nursery-pigs (4-week) were divided into 2 groups, intramuscularly vaccinated with commercial-vaccine (a single dose) and tetravalent-vaccine. The 1st-dose was administered at 4-week-of-age, followed by 2nd-dose at 7-wk-of-age. Blood samples were collected from jugular vein before the 1st-dose and 3-weeks after the 2nd-doses. Samples were performed DNA extraction using Genomic DNA MiniKit (Geneaid Biotech Ltd., Taiwan). Duplex real-time-PCR was carried out using RealPCR-PCV2/PCV3-DNA-Mix to detect PCV2/PCV3. The standard curves of PCV2/PCV3 were performed for quantification following the manufacturer's protocol (IDEXX Laboratories, Inc., USA).

Results and Discussion

The PCV2/3 viral load in serum at 4-week in both groups was not found. This indicated that there was no infection/no viremia in weaned pigs. However, at 3-week and 6-week post-vaccination, a higher proportion of serum positive (Ct < 40) with PCV2/3 viral load in commercial-vaccine is higher than in tetravalent-group (7/30, 11/30 vs 2/30, 1/30; 12/30, 16/30 vs 3/30, 5/30, respectively) which is relevant to the infection status determined by ELISA. This viral load and infection status corresponded with higher feed intake and ADG (810 vs 730 g/day) in tetravalent-group than commercial-group. Subsequently, pigs in tetravalent-group showed a higher market-weight at 24 weeks than those in commercial-group (108 and 96.81 kg). A more effective vaccine could mitigate the impact of subclinical infections by reducing the PCV2/3 viral load, allowing for better energy utilization, and consequently, increased feed intake led to a higher growth rate.

Conclusion

Tetravalent-vaccine with its ability to provide protection against multiple-strains-of-PCV, demonstrated advantages over commercial-vaccine in term of viral clearance as validated by using RealPCR-PCV2/3-Multiplex-DNA-test.

Keywords: Antibody levels, Growth rate, Pigs, Porcine circovirus, Vaccine.

Acknowledgements: The authors thank IDEXX Laboratories Co., Ltd., for supporting the RealPCR PCV2/PCV3 Multiplex DNA test for this study.

GENOME-WIDE CHARACTERIZATION OF PROTEASE AND PROTEASE INHIBITOR REPERTOIRES IN *BRACHYSPIRA HYODYSENTERIAE*

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Introduction and Objectives

Our laboratory recently demonstrated that a curcumin-derived metalloprotease inhibitor (CMC2.24) mitigates *Brachyspira spp.* induced swine dysentery, including mitigated clinical disease and reduced fecal metalloprotease activity during peak colitis1. Building on this therapeutic rationale, we identified and classified protease and protease inhibitor loci in *B. hyodysenteriae* from 117 North American isolates.

Materials and Methods

A total of 117 *B. hyodysenteriae* isolates were retrieved from NCBI BioProject PRJNA12281382. Paired-end Illumina reads were quality filtered, assembled de novo, and annotated. Genome quality was assessed using CheckM, and high-completeness, low-contamination assemblies were retained for downstream analyses. Predicted protein-coding sequences were screened against the MEROPS protease database using BLASTp, and protease loci were classified by catalytic class and family.

Results and Discussion

After quality filtering, 97 genomes were retained, exhibiting high completeness (> 99%) and minimal contamination (< 2%). Across this curated dataset, 8,964 high-confidence protease-coding loci were identified, corresponding to an average of 90.4 ± 1 proteases per genome. Metalloproteases constituted the dominant catalytic class, followed by serine and cysteine proteases, while threonine proteases and asparagine peptide lyases were consistently present at lower frequencies. Aspartic, glutamic, and protease inhibitor classes were rare. Protease repertoire size and class composition were highly conserved across isolates, with limited inter-genome variability.

Conclusion

This genome-wide analysis provides a reference framework for protease and protease inhibitor genes in *B. hyodysenteriae* and identifies metalloproteases as potential virulence factors in swine dysentery. Their predominance and conservation support their role in host–pathogen protease interactions and highlight metalloprotease pathways as potential therapeutic targets.

Keywords: Bacterial genomics, CMC2.24, Metalloproteases, Swine dysentery.

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EFFICACY OF ORAL VACCINATION AGAINST ENTEROTOXIGENIC *ESCHERICHIA COLI* ON GROWTH PERFORMANCE AND MORTALITY RATES IN NURSERY PIGLETS

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Introduction and Objectives

Enterotoxigenic *Escherichia coli* (ETEC) expressing F4 and F18 fimbriae are primary causes of post-weaning diarrhea (PWD) and edema disease (ED), leading to significant industry losses (Laird et al., 2021). Given an 80% F18 prevalence on the study farm, this trial evaluated the efficacy of a live non-pathogenic oral vaccine on bacterial shedding, growth, and mortality.

Materials and Methods

Diagnostic screening was conducted at 2 weeks of age (WOA) via fecal PCR for fimbrial antigens (F4, F18) and toxins (Stx2e, LT, STa, STb). Piglets were allocated to two cohorts: Group C (Control; managed with therapeutic Halquinol during clinical outbreaks) and Group T (Vaccinated with Suigen Coli F18 at 3 WOA). Longitudinal fecal shedding was monitored at 4, 6, and 8 WOA. Productive performance, specifically ADG and mortality, was tracked from weaning through 8 WOA.

Results and Discussion

Baseline screening at 2 WOA confirmed the presence of F4, F18 antigens, and LT toxins. By 6 WOA, Group C suffered clinical diarrhea outbreaks requiring Halquinol intervention, which correlated with a temporary suppression of bacterial detection. In contrast, Group T maintained consistent detection of F4 and F18 antigens alongside LT/ST toxins but remained free of clinical symptoms. This indicates successful colonization by the vaccine strain and the establishment of robust clinical immunity despite the presence of wild-type markers. Group T exhibited significantly superior performance compared to Group C, achieving a higher ADG (310.16 vs 242.52 g/day) and reduced mortality (1.12 vs 4.00%).

Conclusion

Oral F18+ *E. coli* vaccination effectively minimized mortality and prevented growth retardation during the high-risk nursery period. These findings support oral immunization as a robust alternative to antimicrobials in ETEC-endemic herds.

Keywords: Enterotoxigenic *Escherichia coli* (ETEC), F18 fimbriae, Nursery piglets, Oral bacteria vaccination.

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COMPARISON OF EP-LIKE LUNG LESIONS ACCORDING TO *MYCOPLASMA HYOPNEUMONIAE* VACCINATION STRATEGIES IN SOUTH KOREAN PIG FARMS

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Introductions and Objectives

Mycoplasma hyopneumoniae (Mh) is a major cause of enzootic pneumonia (EP) and production losses in pig farms. Vaccination is widely used for EP control, but field outcomes may vary by vaccination strategy and field program. This study compared EP-like lung lesions at slaughter among different Mh vaccination strategies in South Korean pig farms using the Ceva Lung Program (CLP).

Materials and Methods

From January 2020 to December 2025, 1,284 batches (43,778 lungs) from South Korean pig farms were evaluated at multiple slaughterhouses using CLP with a modified Madec grid (0 - 4 scale). Batch-level indicators included EP index, mean affected area of all lungs, mean affected area of pneumonic lungs, and cranial pleurisy scoring. Vaccination strategies were classified into four groups: Other monovalent (89 farms, 11,065 lungs; n = 328 batches), RTM (ready-to-mix combination; 129 farms, 20,636 lungs; n=611 batches), RTU (ready-to-use combination; 58 farms, 10,405 lungs; n = 300 batches), and Vaccine H (Hyogen) (18 farms, 1,672 lungs; n = 45 batches). Non-Hyogen commercial products were anonymized (Vaccine_1 - Vaccine_7). Vaccination protocols were implemented according to the manufacturer's instructions. Group comparisons were performed using the Mann-Whitney test.

Results

Vaccine H was associated with lower EP-like lesion severity than the other vaccine groups. Vaccine H had a lower EP index (1.04 ± 1.16) than RTU (1.96 ± 1.49), Other monovalent (2.24 ± 1.60), and RTM (2.22 ± 1.73). Vaccine H also showed a lower mean affected area of all lungs (1.61 ± 1.97%) and a lower mean affected area of pneumonic lungs (4.30 ± 3.64%) than the other vaccine groups.

Discussion and Conclusion

These findings indicate that field-based grouping of vaccination strategies can reveal meaningful differences in EP-like lung lesion outcomes at slaughter. Slaughterhouse lung lesion monitoring using CLP may provide practical swine herd health indicators for veterinarians and producers when evaluating respiratory control programs.

Keywords: Ceva Lung Program, Enzootic Pneumonia, *Mycoplasma hyopneumoniae*.

Acknowledgements: The authors thank the animal hospital in Dodram Cooperative, for the support with providing assessing the lung lesions.

FEED ADDITIVE SUPPLEMENTATION INFLUENCES IMMUNE RESPONSES FOLLOWING *MYCOPLASMA HYOPNEUMONIAE* VACCINATION IN COMMERCIAL NURSERY PIGS

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Introduction and Objectives

Nutritional strategies that support immune competence of piglets during the critical post-weaning phase may improve piglet robustness against disease and potentially enhance responses to vaccination. This study evaluated the effects of a feed additive containing specific phytogenic compounds and glycerol monolaurate (Innovad Group, Belgium) on vaccine-induced immune responses in nursery pigs.

Materials and Methods

In total, 436 piglets were randomly allocated to a control (standard diet) or a treated group (diet supplemented with the feed additive). The supplement was provided at 0.5 kg/T from day 19 until weaning (day 28), and at 1 kg/T from weaning until 10 weeks of age. All pigs were vaccinated intramuscularly against *M. hyopneumoniae* at 5 (Suvaxyn® Mhyo, Zoetis) and against *M. hyopneumoniae* and porcine circovirus type 5 (PCV2) at 26 days of age (Circomax®, Zoetis). Rectal temperature before and 8 hours post-vaccination, serum antibody responses against *M. hyopneumoniae* (ELISA) and PCV2 (IPMA), and the neutrophil-to-lymphocyte ratio in blood, were evaluated at D26, D30, 6 weeks and 10 weeks of age. Statistical models included sampling day and pen effects. Data were analyzed using Welch's t-test for body temperature and linear mixed-effects models for longitudinal serological and hematological variables.

Results and Discussion

Although antibody levels of *M. hyopneumoniae* did not differ significantly between groups, S/P values were numerically higher in treated pigs at D26, D30 and 6 weeks of age (+0.10 S/P units on average). PCV2 antibody levels were similar between the groups. Rectal temperature post-vaccination was 42°C higher in pigs of the supplemented group ($P < 0.01$). The neutrophil-to-lymphocyte ratio in pigs from the supplemented group was higher (0.98 vs 1.45) at 6 weeks of age ($P < 0.05$).

Conclusion

Supplementation with a phytogenic and glycerol monolaurate feed additive modulated immune indicators in vaccinated nursery pigs, indicating its potential to enhance immune responses upon vaccination of piglets under field conditions.

Keywords: Feed Additives, Immunomodulation, *Mycoplasma hyopneumoniae* Vaccination, Nursery Pigs, Phytogenic Compounds.

Acknowledgements: The authors acknowledge the colleagues from the pig team, the faculty of Veterinary Medicine of Ghent University.

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CLINICAL SAFETY AND IMMUNOGENICITY OF THE SAFESUI GLASSER ONE VACCINE IN PREGNANT SOWS

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Introduction and Objectives

Glässer's disease (GD), caused by *Glaesserella parasuis* (Gps), is widely distributed in commercial swine herds and is primarily transmitted from sows to piglets in the farrowing unit. Vaccination of sows and piglets is a key preventive strategy. This study evaluated the clinical safety and immunogenicity of the Safesui Glasser ONE (SGO) vaccine administered to pregnant sows. SGO is the first single-dose, broad-spectrum vaccine against GD (Frandoloso et al., 2024).

Materials and Methods

Pregnant sows (n = 12/group) were allocated into three groups following VICH GL44 principles: G1 received one vaccine dose at gestation day (D) 65; G2 received two doses at D65 and D86; and G3 received placebo. Safety was assessed immediately (up to 4 hours) and for 14 days after vaccination or revaccination. Local tolerance at the injection site was evaluated. Sow serum samples were collected at D65, D86, D100, and D114, and colostrum samples were collected prior to completion of farrowing. Anti-Gps serovar 5 (SV5) IgG titers were determined by indirect ELISA. The study was approved by the Animal Ethics Committee of AFK Imunotech (protocol no. 03/23 and 12/24).

Results and Discussion

After the first vaccination (D65+2 h), tachypnea was the most frequently observed finding (G1: 1/12, 8.3%; G2: 3/12, 25%), while dyspnea was observed in 1/12 sows in both vaccinated groups. After revaccination (D86+2 h), dyspnea was recorded in 1/12 sows in G2 only. Mean rectal temperatures showed mild and transient increases that remained within physiological limits. Injection-site edema was observed after the first vaccination at D65+ 4 h (G1: 2/12; G2: 5/12) and D66 (G1: 1/12; G2: 6/12), and after revaccination at D86+4 h in 4/12 sows in G2; all local reactions were transient. No other clinically relevant findings were observed. Baseline anti-Gps SV5 IgG titers (D65) were comparable among groups, whereas at D86 sows receiving two vaccine doses (G2) showed significantly higher serum SV5 IgG titers than G1 and placebo ($P < 0.05$).

Conclusion

Safesui Glasser ONE demonstrated an acceptable clinical and local safety profile in pregnant sows and induced significantly higher anti-*Glaesserella parasuis* SV5 IgG titers following a two-dose gestational regimen.

Keywords: *Glaesserella parasuis*, Immunogenicity, Sows, Safesui Glasser ONE, Vaccine.

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DURATION OF MATERNALLY DERIVED ANTIBODIES AND THEIR IMPACT ON PIGLET VACCINATION WITH SAFESUI GLASSER ONE

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Introduction and Objectives

Early control of Glässer's disease is strongly influenced by maternally derived antibodies transferred from vaccinated sows (Frandoloso and Schryvers, 2020). This study evaluated the persistence of maternally derived anti-*Glaesserella parasuis* (Gps) antibodies in piglets born to sows vaccinated with Safesui Glasser ONE (SGO) and their impact on the serological response of piglets vaccinated at 21 days of age.

Materials and Methods

A total of 48 neonatal piglets born to sows vaccinated with one dose of SGO at 65 days of gestation, two doses of SGO at 65 and 86 days of gestation, or to non-vaccinated sows were allocated into six experimental groups. At 21 days of age, piglets from groups G1 (offspring of sows vaccinated with one dose), G3 (offspring of sows vaccinated with two doses), and G5 (offspring of non-vaccinated sows) were vaccinated intramuscularly with 2 mL of SGO. Piglets from groups G2, G4, and G6, originating from the same respective sow groups, received sterile saline solution at weaning. Blood samples were collected from all piglets at 7, 14, 21, 28, 35, and 42 days of age for determination of anti-Gps serovar 5 (SV5) IgG titers by Indirect ELISA. The study was approved by the Animal Ethics Committee of AFK (protocol no. 12/24).

Results and Discussion

At 7 days of age, mean anti-Gps IgG titers were significantly higher ($p < 0.05$) in piglets from vaccinated sows (G1/G2 ≥ 2,752; G3/G4 ≥ 6,427) compared with those from non-vaccinated sows (G5/G6 ≤ 1,200). At vaccination (D21), IgG titers were comparable between vaccinated and control piglets within the same maternal groups. At D35, control groups showed IgG titers < 800, whereas vaccinated piglets maintained significantly higher titers (≥ 800 and ≤ 3,200). At D42, vaccinated groups remained significantly higher ($p < 0.05$) than their respective controls, with no further increase compared to D35.

Conclusion

Piglets born from vaccinated sows maintained higher anti-*Glaesserella parasuis* IgG titers up to 35 or 42 days of age following one- or two-dose sow vaccination, respectively. Importantly, maternally derived antibodies did not interfere with the serological response of piglets vaccinated with SGO.

Keywords: *Glaesserella parasuis*, Passive Immunity, Safesui Glasser ONE, Vaccine.

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CHARACTERIZATION AND IMMUNOGENICITY ASSESSMENT OF A SELF-AMPLIFYING MRNA ENCODING FOOT-AND-MOUTH DISEASE VIRUS STRUCTURAL PROTEINS

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Introduction and Objectives

Foot-and-mouth disease (FMD) is a highly contagious viral disease affecting cloven-hoofed livestock. While conventional inactivated vaccines are effective, they are limited by biosafety risks, the need for high-containment facilities, and DIVA compatibility issues. Therefore, we evaluated a self-amplifying mRNA (saRNA) platform derived from Venezuelan equine encephalitis virus (VEEV) encoding FMDV antigens.

Materials and Methods

Three saRNA constructs (2BT, scFv-2BT, and capsid precursor [CP]) based on the FMDV O/Boeun/SKR/2017 strain were synthesized and formulated using either lipid nanoparticles (LNPs) or lipid-RNA lipoplexes (LPXs). FMDV antigen expression was validated via western blotting and immunofluorescence assay (IFA). saRNA replication kinetics were monitored using quantitative real-time PCR (qRT-PCR) up to 120 hours post-transfection. Immune responses were first screened in mice following inoculation with LNP- or LPX-formulated saRNAs using ELISA and virus neutralization tests (VNT). Subsequently, the humoral and cellular immune responses, as well as the protective efficacy against FMDV challenge, were evaluated in pigs.

Results and Discussion

In vitro analysis confirmed the successful expression of FMDV antigens from all three saRNA constructs. qRT-PCR revealed that while non-replicating mCherry mRNA was detectable only up to 48 hours, the saRNA persisted for up to 120 hours, confirming its self-amplifying capability. A comparison of the two delivery platforms showed that LPX exhibited higher gene delivery efficiency than LNP, although protein expression levels remained comparable. In the mouse model, only the LPX-formulated CP saRNA elicited FMDV-specific and neutralizing antibody responses comparable to those of a commercial vaccine. Similarly, in pigs, the LPX-formulated CP saRNA induced humoral immune responses equivalent to the commercial vaccine (PI: 88.67 vs. 80.83; neutralizing titers: 378 vs. 296). Notably, the saRNA platform successfully elicited cellular immune responses, which were absent in the commercial vaccine group. Following FMDV challenge, the LPX-formulated CP saRNA provided clinical protection comparable to the commercial vaccine and effectively suppressed both viremia and viral shedding.

Conclusion

These findings demonstrate that LPX-formulated CP saRNA induces potent protective humoral and cellular immunity in swine. This study highlights the potential of saRNA-based strategies as an effective and biosafety-compliant alternative for the control of foot-and-mouth disease.

Keywords: Capsid precursor, FMDV, Multi-epitope, Self-amplifying mRNA, vaccine.

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EFFICACY OF A PORCINE BIVALENT MYCOPLASMA SUBUNIT VACCINE AGAINST *MYCOPLASMA HYORHINIS* AND *M. HYOPNEUMONIAE*

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Introduction and Objectives

Mycoplasma hyopneumoniae (Mhp) is the causative agent of swine enzootic pneumonia (SEP) and *Mycoplasma hyorhinis* (Mhr) is a pathogen causing polyserositis and arthritis in afflicted pigs. Both contribute to retarded growth and low feed efficiency. Since vaccination with a Mhr subunit vaccine was previously shown to reduce lung lesions in Mhp challenged pigs, a Mhp antigen was therefore included in the Mhr subunit vaccine to generate a Mhr/Mhp bivalent subunit vaccine. In this study, the efficacy of this bivalent vaccine against Mhr and Mhp was evaluated.

Materials and Methods

Specific pathogen free pigs were immunized with one dose of Mhr/Mhp bivalent subunit vaccine or normal saline at 3 weeks old and challenged with either *Mycoplasma hyopneumoniae* or *Mycoplasma hyorhinis* at 7 weeks old. After Mhr challenge, clinical symptoms were observed and recorded daily, and pigs were sacrificed at 21 days post challenge and examined for polyserositis (peritonitis, pleurisy, pericarditis) and arthritis. For Mhp challenge, pigs were sacrificed at 28 days post challenge and lung tissues were examined. Serum samples were collected for Mhr and Mhp antibody analysis.

Results and Discussion

Both Mhr and Mhp antibody levels were significantly higher in vaccinated pigs than in control pigs immediately prior to challenge (Mhr: 0.17 ± 0.02 vs 0.02 ± 0.01; Mhp: 1.27 ± 0.05 vs 0.01 ± 0.01, in S/P ratio). The clinical score associated with Mhr was lower in vaccination group starting on day 9 after challenge and the vaccinated pigs had significantly lower average lesion scores for polyserositis (3.25 ± 0.82 vs 6.25 ± 1.11) and arthritis (4.00 ± 0.92 vs 8.75 ± 1.21) than control pigs after Mhr challenge. Pathological examination of the lung tissue in Mhp challenged pigs showed that the vaccinated pigs had lower lung lesion scores than control pigs (14.0 ± 1.1 vs 20.4 ± 0.8). These results demonstrated that vaccinating pigs with one dose of bivalent subunit Mhp/Mhr vaccine at 3 weeks old can reduce clinical symptoms associated with Mhr and Mhp.

Conclusion

To our knowledge, this is the first bivalent porcine mycoplasma subunit vaccine. The results from present study demonstrate that this bivalent vaccine is efficacious against *Mycoplasma hyorhinis* and *Mycoplasma hyopneumoniae* infections in pigs.

Keywords: Bi-valent, *Mycoplasma hyorhinis, Mycoplasma hyopneumoniae*, Subunit vaccine.

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CHARACTERIZATION OF THE AVIRULENT VACCINE STRAINS WITH VP1/3C POINT MUTATIONS AND PROTECTION IN THE PIGS AGAINST FOOT-AND-MOUTH DISEASE

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Introduction and Objectives

Foot-and-mouth disease (FMD) is a highly contagious viral disease of cloven-hoofed animals that causes substantial economic losses and disrupts international trade. In endemic regions, routine vaccination with inactivated vaccines remains the primary control strategy; however, these vaccines have notable limitations. Consequently, this study aims to develop a live-attenuated vaccine (LAV) as a strategic approach to effectively control FMDV and overcome the limitations of existing vaccination strategies.

Materials and Methods

Live-attenuated vaccine candidates were generated by site-directed mutagenesis of the IRES, VP1, and 3C regions of Foot-and-mouth disease virus (FMDV). In vitro viral replication and innate immune responses were assessed by virus titration, ELISA, and qRT-PCR. Vaccine safety, immunogenicity, and protective efficacy were evaluated in mouse and swine models using serological assays and wild-type virus challenge.

Results and Discussion

Single and double mutations effectively restored the attenuated interferon (IFN) responses of the parental virus in vitro. All vaccine candidates were well-tolerated and demonstrated a favorable safety profile in mice with double- and triple-mutated LAVs, providing 100% safety in suckling mice. Notably, the single 3C(C142T) mutant and the VP1(E83K)/3C(C142T) double-mutant LAVs conferred 100% protection against homologous challenge, as evidenced by high SP-ELISA inhibition (> 50%) and elevated virus neutralization titers (> 2). In swine, primary immunization with the LAVs induced no detectable clinical signs or viremia (n = 12). Following homologous challenge one-week post-immunization, intradermal administration of the VP1/3C double-mutant LAV provided 100% protection (n = 4), accompanied by strong serological responses including high SP-ELISA inhibition (> 50%), and virus neutralization titers (>2).

Conclusion

Collectively, these results demonstrate that the engineered VP1/3C double-mutant LAV is safe and elicits robust protective immune responses in both murine and swine models, highlighting its potential as a promising vaccine candidate for controlling FMDV.

Keywords: 3C (C142T), Foot-and-mouth disease, Immunity, LAV, VP1(E83K).

Acknowledgements: This work was supported by the National Research Foundation (RS-2021-NR060136).

CHARACTERIZATION OF THE AVIRULENT VACCINE STRAINS WITH LBPRO REPLACEMENT AND 3C MUTATION FOR PROTECTION AGAINST FOOT-AND-MOUTH DISEASE IN THE PIGS

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Introduction and Objectives

Foot-and-mouth disease virus (FMDV) causes a highly contagious livestock disease with major economic consequences. Bovine rhinitis virus (BRV) shares conserved motifs and sequence similarity with FMDV but exhibits substantially lower virulence. This study evaluated whether replacing the FMDV leader proteinase with the BRV leader proteinase, together with a 3C (C142T) mutation, could attenuate FMDV and generate an effective live-attenuated vaccine (LAV) candidate.

Materials and Methods

The study designed three types of live attenuated vaccine (LAV) by substituting the leader proteinase (Lpro) of the FMD virus (FMDV) with Lbpro from bovine rhinitis B virus (BRBV) serotypes EC11, B10, and BRAV SD1, and by introducing a 3C(C142T) point mutation into the FMDV 3C proteinase. Initially, the effects were confirmed in vitro. Vaccine safety, immunogenicity, and protective efficacy were evaluated in mice and swine models using serological assays and wild-type virus challenge.

Results and Discussion

BRBV/BRAV Lbpro induces a higher innate immune response than FMDV Lbpro under a virus challenge in vitro. Initial in vivo results in a mouse model showed that the LAVs induced a safe and positive immune response, characterized by the development of specific neutralizing antibody titers (> 2) and high SP-ELISA inhibition (> 50%). All LAVs except the BRAV-SD1 Lbpro-replaced vaccine (n = 5), which provided 80% protection, provided 100% protection against homologous challenge in the mouse model (n = 10). Subsequent porcine model experiments yielded mixed results. Immunization did not induce detectable virus-neutralizing titers or a significant SP-ELISA response at the time of the challenge. However, the single intramuscular dose of the BRBV-EC11 Lbpro-replaced vaccine (n = 3) elicited a comparatively higher protective response than the other 3 LAVs tested (n = 10)

Conclusion

Collectively, these results demonstrate that engineered LAVs are safe and elicit robust protective immune responses in the murine model but show mixed results in the swine model. The results of the current study demonstrate the need to maintain a finely tuned balance between attenuation and replicative fitness in the design of LAVs.

Keywords: 3C, BRBV, Foot-and-mouth disease, LAV, Lbpro.

Acknowledgements: This work was supported by the National Research Foundation (RS-2021-NR060136).

FIELD REPORT ON "KAICO POWDER" IN VIETNAM: INNOVATION IN SWINE PRODUCTION VIA NOVEL SILKWORM TECHNOLOGY

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Introduction and Objective

KAICO Ltd., a Japanese biotech startup from Kyushu University, has developed a recombinant protein production platform utilizing the silkworm-baculovirus expression system. Leveraging this technology, we prepared an orally administered silkworm pupae-derived recombinant protein-containing preparation for pigs. This study aimed to evaluate the field performance and economic impact of this oral preparation in comparison with a conventional PCV2 injectable vaccine program in a commercial environment.

Materials and Methods

Two large-scale field trials were conducted at the Lac Ve farm of Dabaco, a leading Vietnamese livestock company, involving a total of 5,008 weaned piglets. To ensure scientific objectivity and comparability, piglets were allocated by pens, with pens randomly assigned to one of two study groups and managed under comparable environmental and husbandry conditions. Trial 1 compared 850 pigs administered the oral powder preparation at a dose of 0.1 g/head/day for 5 consecutive days mixed with feed (Powder group) against 850 pigs receiving the farm's routine injectable PCV2 control program (Control group). Trial 2 expanded the scale to 2,200 pigs in the Powder group and 1,108 pigs in the Control group. We monitored production performance indicators (ADG, Mortality Rate, FCR, etc.) and analyzed the economic impact based on field data.

Results and Discussion

In both trials, the Powder group demonstrated production performance comparable to, or numerically better than, the injectable vaccine group. In Trial 2, specifically, the Powder group achieved a better FCR and lower mortality rate. Economically, these improvements resulted in a total calculated benefit of USD 3.3 per head, primarily driven by feed cost savings of USD 2.2 per head due to improved FCR. Furthermore, operational analysis confirmed that oral administration reduced labor time by approximately 99% compared to conventional injections (reducing labor from 1 hour for 7 workers down to 5 minutes for 1 worker per ~1,200 pigs).

Conclusion

These findings from over 5,000 pigs demonstrate that this orally administered silkworm pupae-derived recombinant protein-containing preparation is an effective "edible" solution that maintains high productivity. By generating a clear economic benefit and drastically reducing labor costs, this technology offers a sustainable tool for maximizing farm profitability and improving animal welfare.

Keywords: Economic efficiency, Immunoenhancement, Labor saving, Oral administration, Porcine circovirus type 2 (PCV2).

Acknowledgements: We would like to express our gratitude to Dabaco Group for their cooperation in conducting the large-scale field trials, and to Sojitz Corporation and GreenVet for their strategic support in the development and distribution of this project.

EFFICACY OF AN ATTENUATED RM48 STRAIN VACCINE AGAINST *MYCOPLASMA PNEUMONIA* OF SWINE VIA INTRAPLEURAL INJECTION

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Introduction and Objectives

Vaccination is key for controlling enzootic pneumonia caused by *Mycoplasma hyopneumoniae* (Mhp). The attenuated RM48 strain, developed through 790 passages in suckling rabbits ($\geq 5 \times 10^7$ CCU/dose) (Shen et al., 2014), was evaluated for clinical safety, pathogen blocking, growth performance, and lung protection via intrapleural injection.

Materials and Methods

Two hundred thirty-nine 3 - 5-day-old Mhp-negative piglets from 20 litters were randomly allocated to RM48 group (10 litters, 119 piglets) or control (10 litters, 121 piglets). The RM48 group received single intrapleural vaccination; controls received sterile PBS. Parameters included: (1) clinical safety (7-day monitoring) (Silva et al., 2024); (2) pathogen surveillance (qPCR of pharyngeal swabs at 14 - 154 days post-vaccination); (3) growth performance (ADG, FCR); (4) lung lesions (28-point scoring at 160 days to calculate lung lesion reduction rate, or LLR) (Garcia-Morante et al., 2016).

Results and Discussion

[Clinical Safety] Immunized piglets showed normal temperature (38.5 - 39.2°C) without swelling, pain, or respiratory symptoms, superior to oil-adjuvanted vaccines causing inflammation (Silva, CA, et al., 2024). Stable attenuation through 790 passages (Shen et al., 2014) avoided mineral oil irritation.

[Pathogen Blocking] All qPCR results were negative in immunized pigs versus 30 - 90% detection in controls. This suggests effective wild-type Mhp blocking (Suh et al., 2025), though challenge studies are needed.

[Growth Performance] ADG improved 4.6% (701 ± 19 g vs 670 ± 52 g, $P < 0.05$); FCR was 2.38 versus 2.56. ADG increase correlated with LLR ($r = -0.78$, $P < 0.01$), confirming Mhp impairs growth via chronic pneumonia.

[Lung Protection] Mean lesion scores were 0.58 ± 0.16 (RM48) versus 3.89 ± 1.24 (control), with 85.1% LLR; 80% of immunized pigs had no visible lesions.

Conclusion

Single intrapleural immunization with *M. hyopneumoniae* live vaccine (RM48 strain) at 3-5 days of age demonstrated excellent safety, effective Mhp blocking, significant lung lesion reduction (85.1%), and improved daily weight gain (4.6%), representing a control tool with both good immunological efficacy and economic benefits.

Keywords: Attenuated RM48 strain vaccine, Intrapleural injection, Mycoplasma pneumonia of swine.

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EVALUATION OF SWINE INFLUENZA VACCINATION ON LUNG LESIONS IN A SWINE INFLUENZA–*STREPTOCOCCUS SUIS* CO-INFECTION MODEL

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Introduction and Objectives

Swine influenza virus (SIV) is a contagious respiratory pathogen causing acute febrile disease in pigs. By disrupting respiratory defenses, SIV predisposes to secondary bacterial infections, including *Streptococcus suis*, contributing to the porcine respiratory disease complex. The pathophysiological impact of SIV-*S. suis* co-infection and the protective potential of early-life SIV vaccination remain poorly defined. This study evaluated their interaction and the efficacy of SIV vaccination in weaned piglets.

Materials and Methods

Eighteen piglets from six litters were allocated at 5 days of age to three experimental groups (n = 6/group): T01, non-vaccinated and challenged post-weaning with pandemic H1N1 SIV (pH1N1); T02, non-vaccinated and co-challenged with pH1N1 and *S. suis* serotype 2; and T03, vaccinated with an inactivated pH1N1 vaccine at 5 and 19 days of age and subsequently challenged with pH1N1 and *S. suis* serotype 2. Piglets were weaned at 28 days and housed in separate pens per treatment. After a 5-day acclimation period (day 0, D0), all piglets were sedated and intratracheally challenged with pH1N1 (3mL; 7.5$\log_{10}$ $TCID_{50}$). On D2, all animals received intranasal challenge with *S. suis* serotype 2 (5×10^8 CFU/mL) for T02 and T03. Animals were euthanized on D6 for lung collection. Gross lesions were scored using a weighted system from Halbur et al. (1995), estimating the percentage of lungs affected, while histopathological lesions were evaluated on H&E-stained sections (1 - 5 scale), assessing epithelial damage, inflammatory infiltration, and broncho-interstitial pneumonia.

Results and Discussion

Non-vaccinated piglets challenged with pH1N1 (T01) or co-challenged with *S. suis* (T02) exhibited extensive and comparable lesions (mean ± range: 12.2 [4.5 - 20.1] and 11.2 [0.5 - 20.3], respectively; $P > 0.05$). Vaccinated piglets (T03) had markedly lower gross lesion scores (2.1 [0 - 6.35]; $P < 0.05$ vs T01/T02). Histopathology mirrored these results: T01 and T02 showed similar degrees of epithelial damage, peribronchiolar cuffing, and interstitial inflammation, while T03 had consistently reduced scores across all parameters.

Conclusion

Under these experimental conditions, co-infection with S. suis did not exacerbate lung lesions beyond those caused by pH1N1. In contrast, early-life SIV vaccination substantially mitigated gross and microscopic pulmonary pathology, demonstrating its efficacy in protecting weaned piglets against virus-associated lung damage.

Keywords: Disease model, Experimental challenge, Porcine respiratory disease complex, Piglets vaccination.

Acknowledgements: The authors thank all the animal caretakers who participated in the project.

POSTERS

TOPIC 6: HERD HEALTH MANAGEMENT (HHM)

NON-INVASIVE INDICATORS OF UDDER INVOLUTION IN SOWS AFTER WEANING

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Background and Objectives
Genetic progress has enabled sows to wean an increasing number of piglets for the same lactation duration. This improvement requires high colostrum and milk production, followed by an abrupt cessation of lactation at weaning. This dry-off phase occurs just after peak milk production and is often accompanied by visible udder signs such as swelling, redness, and milk leakage. However, little information is available about how dry-off influences early udder involution in sows. A previous trial has described udder skin temperature patterns linked to engorgement scores and weaning-to-estrus intervals. This study aimed to explore non-invasive indicators on udder and their interaction during the first days after weaning.

Material and Methods
74 highly-prolific sows, in France, were included in the study. Udder Engorgement (UE, a visual score from 0 to 3), Udder Skin Temperature (UST) and Udder Pressure (UP) were collected once daily: the day of weaning (D0) and the two following days (D1, D2). UST was recorded using an infrared thermometer and UP using an algometer. A linear mixed-effects model was run to study UST and UP overtime.

Results and Discussion
UST and UP are independent parameters with distinct temporal patterns. Statistical modeling shows a bell-shaped curve. UST decreased from D0 to D1 (-1.38°C) and sharply increased from D1 to D2 (+1.40°C). In contrast, UP rose sharply from D0 to D1 (+14 N) and reached a plateau from D1 to D2. Parity rank, litter weight at weaning had no effect on these dynamic. UE score is highly significant ($P < 0.01$) on UP pattern.

Conclusion
Dry-off in sows is characterized by an initial drop in udder temperature followed by a rapid rise around 48 hours post-weaning, suggesting an inflammatory response. Udder pressure, peaking within 24 hours and remaining elevated afterward, differs from the pattern observed in dairy cows. Extending the monitoring period could provide further insight into mammary involution. The strong relationship between visual engorgement and udder pressure indicates that this parameter may serve as a useful, non-invasive welfare indicator, helping to assess sow comfort and potential consequences on subsequent reproduction and maternal capacities.

Keywords: Dry-off, Sow, Udder temperature, Udder pressure, Weaning.

EFFECT OF ORAL ADMINISTRATION OF AN ENERGY BOOSTER AT BIRTH ON PIGLET VITALITY PARAMETERS AND PREWEANING PERFORMANCE

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Introductions and Objectives

Piglets from highly prolific sows face intense competition for colostrum, particularly lighter or less vigorous ones. A delay in colostrum intake can impair survival and development, contributing to preweaning mortality rates as high as 20% and poor uniformity at weaning (Farmer et Edwards, 2022). Providing a nutritional energy supplement immediately after birth is a common practice to support weaker piglets. This trial aimed to identify easily detectable parameters within the first 24 hours of life on preweaning performances and the effects of an energy booster on vitality traits and performances.

Material and Methods

The trial was conducted on a commercial pig farm in France on 323 piglets followed from birth to weaning coming from 31 highly prolific sows. During farrowing, one out of two piglets per sow received the oral nutritional supplement (2 ml/piglet, a mix of glucose, MCFA, B vitamins, and a caffeine source). Once the newborn piglets were standing and their umbilical cords had detached. Piglets were weighed at birth, 24h, 7 days and at weaning (21 days). Time for birth, stand up and for the first colostrum intake was collected. Ear temperature at 24h was measured, as an indicator of successful adaptation after birth.

Results and Discussion

The trial showed that piglet vitality criteria within the first 24 hours have effects lasting until weaning. Thus, higher ear temperature at 24 hours was associated with lower mortality and a shorter interval to first colostrum intake optimized average daily gain from birth to weaning. Among the lightest piglets (<1 kg), those that received the energy booster performed a lower interval from first stand up to the first colostrum intake (-45 minutes, $P < 0.05$) and mortality was reduced in the test group.

Conclusion

Piglets care provided during the first 24 hours of life plays a crucial role in optimizing survival and performance, particularly for low-birth-weight piglets. The administration of an oral energy booster shortly after birth enhances early vitality by promoting faster colostrum intake and reduces mortality.

Keywords: Colostrum intake, Early mortality, Newborn piglet, Nutraceutical, Vitality.

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EFFECT OF ORAL ADMINISTRATION OF A NUTRACEUTICAL AT BIRTH ON PIGLETS PERFORMANCES AND OXIDATIVE STATUS AT WEANING

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Introduction and Objectives

Highly prolific genetics have led to larger litters but also to reduced uniformity at birth, lower piglet vitality, and insufficient colostrum intake in newborns. This inadequate passive immune transfer can negatively affect survival, growth, and resistance to disease. It may also result in an altered oxidative status at weaning, a known indicator of piglet health (Buchet et al., 2017). Nutraceuticals, such as energy boosters, are increasingly used during this vulnerable period. This case study aimed to evaluate the administration of an oral nutraceutical at birth on piglets' performance and oxidative status at weaning.

Material and Methods

6 litters from LW × Landrace sows farrowing simultaneously in the same facility in France were monitored. 3 litters received an oral nutraceutical (2 mL/piglet) administered as soon as the newborns were standing. 30 piglets were included in the trial (15 treated and 15 controls) selected among the last 8 borns per litter, with similar average birth weights and no cross-fostering. Data collected included birth and weaning weights (day 21), as well as plasma biomarkers: hydroperoxides (dROMS), antioxidant capacity (BAP), Oxidative Stress Index (ISO), and Haptoglobin concentrations.

Results and Discussion

Average daily gain (ADG) from birth to 21 days was significantly higher in the treated group (196 g/day) compared to controls (146 g/day; $P < 0.01$). dROMS were also significantly lower in treated piglets (306 µmol/L) than in controls (348 µmol/L; $P < 0.01$), indicating reduced oxidative stress. A negative correlation was observed between dROMS and ADG ($P < 0.05$). Other oxidative stress markers (BAP, ISO) showed no treatment effect. Haptoglobin concentrations tended to be higher in controls ($P < 0.10$), with the highest values (> 0.80 mg/mL) found in the control group (4 out of 5 piglets).

Conclusion

Thanks to the nutraceutical, growth was better, which can be explained by a better ability to take quickly the colostrum. The study suggests that limited colostrum uptake increases susceptibility to oxidative stress and inflammation, as reflected in higher dROMS and haptoglobin levels. Further studies are needed to confirm the relationship between immune transfer and oxidative stress biomarkers in preweaning piglets.

Keywords: Haptoglobin, Nutraceutical, Oxidative stress, Preweaned piglets.

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ASSESSING SWINE DISEASE CO-INFECTIONS BY AGGREGATING DISEASE DIAGNOSTIC CODE DATA FROM DIAGNOSTIC LABORATORIES IN THE UNITED STATES OF AMERICA

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Introduction and Objective

Swine producers frequently encounter polymicrobial disease challenges, with pathogen co-infections complicating disease expression and affecting management strategies. Additionally, there is a lack of information regarding the primary swine co-infections that occur in swine barns. This study aimed to characterize co-diagnosis patterns in swine from samples submitted to the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL) and expand the capability to integrate confirmed disease diagnoses from a second laboratory, the Ohio Animal Disease Diagnostic Laboratory (OH-ADDL), utilizing a standardized disease coding system (Dx code) (Derscheid et al., 2021).

Material and Methods

Confirmed porcine disease diagnoses from the ISU-VDL and OH-ADDL were collated using Dx code data that was anonymized, cleaned, and stored in a secure SQL database with automated daily updates via API. Cases were classified by season, age, and type of production. ISU-VDL co-diagnosis cases, from 2020 to 2025, were defined as the presence of two or more distinct etiologies within a single case, and their trends were analyzed by anatomic system (i.e., respiratory, digestive, etc.) and insult type (e.g., bacterial, viral, etc.) by creating binary outcomes in the database for each affected system and insult type.

Results and Discussion

The final collated database was developed to harmonize and analyze 45,310 confirmed tissue diagnosis cases. Among all cases, 52.62% were co-diagnosed cases, affecting 42 U.S. states, with a seasonal variation showing reduced co-diagnosis rates during the summer. The wean-to-market production phase accounted for 86.45% of co-diagnosed cases. The co-diagnosis cases were more abundant in respiratory and systemic anatomic systems, with PRRSV and *Streptococcus suis* being the most predominant co-diagnosed pathogens. Age-specific trends revealed respiratory co-diagnoses peaking in nursery and grow-finish pigs, while digestive co-diagnoses were common in suckling piglets. The predominant co-diagnosed digestive pathogens were *E. coli* and rotavirus. Interlaboratory data integration in 2025 enabled increased representativeness, capturing disease occurrence in states that were not initially in the database.

Conclusion

The study demonstrated the value of standardized Dx code data for epidemiological surveillance, highlighting the complexity of co-infections in swine. Additionally, the findings underscore the importance of collaborative data sharing in enhancing swine health management strategies.

Keywords: Co-diagnosis, Diagnostic codes, Respiratory, and Enteric, Surveillance.

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EXPLORING PRODUCER'S EXPERIENCES, OPINIONS, AND EXPECTATIONS FOR NEEDLE-FREE INTRADERMAL VACCINATION – HOW CAN WE IMPROVE OUR WELFARE ALONG WITH THE PIGS?

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Introduction and Objectives

Needle-free intradermal (ID) vaccination has been shown to have welfare and safety benefits. Despite its general acceptance, intramuscular (IM) vaccination is still the predominant method in North America. Notably, many farms using ID devices have been using the same one for years, creating interest in where this technology may go in the future. The aim of our study was to determine what reservations producers may have about ID vaccination, if they are satisfied with their current equipment, and what their expectations are for future ID devices.

Material and Methods

Three vaccination teams participated with fourteen member's total. Teams were given the same needle-free ID device (NFID; IDAL applicator MSD Animal Health) and vaccines to compare to their current equipment (either IM vaccination with a needle or a different NFID device). All vaccinators filled out a pre-study and post-study survey.

Results and Discussion

Pre-Study Survey (n = 14): 93% of participants agreed that vaccination is stressful for pigs, with 100% being open to trying new methods. The most disliked aspects of their old equipment were vaccine wastage, dry firing, and changing needles. All but two participants had used different ID devices in the past (not IDAL), with 75% strongly disagreeing that the device saved them time, and 83% disagreeing that ID vaccination reduced pigs' stress. 92% agreed that they would use ID devices again, if it were a different device than what they have already tried. Post-Study Survey (n = 19): 100% agreed that the pigs' stress was reduced, and 90% reported feeling less tired after vaccinating. 100% agreed that vaccinating with the trial device was safer. While 95% preferred the trial device to their current technology, 100% said "yes" to using it again in the future. 68% agreed that vaccinating with the trial device saved them time.

Conclusion

Our results reflect the need to advocate for producer-focused products. There is a large gap in the market for convenient ID devices that allows needle vaccination to predominate, but the IDAL can improve the welfare of both the animals and producers during vaccination.

Keywords: Animal welfare, Intradermal vaccination, Intramuscular vaccination, Producer welfare, Survey.

Acknowledgements: The authors would like to thank the participants and Merck Animal Health for their support.

OPTIMIZING PCV2 VACCINATION TIMING IN SOW HERDS: IMPLICATIONS FOR PIGLET GROWTH AND HEALTH

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) is a globally prevalent virus that negatively affects swine health. It can infect piglets during fetal development via placental transmission. Piglet vaccination around weaning is a common practice in swine herds, and it has proven effective in reducing viral load and improving productivity. Recent studies suggest that vaccinating sows may also decrease vertical transmission (Figueres, 2024; Lopez-Moreno, 2025). This study aimed to evaluate piglet performance based on different intervals between sow vaccination and farrowing, to identify an optimal vaccination protocol.

Materials and Methods

A multi-site Hungarian farm with 1,600 sows and a 3-week batch farrowing system was selected. The farm transitioned from biannual mass vaccination with Ingelvac CircoFLEX® to per-cycle sow vaccination at weaning. PCV2 circulation had previously been confirmed via PCR in fetal tongue tips and piglet serum. Production batches were grouped by the interval between sow vaccination and farrowing: long (24 - 27 weeks), medium (12 - 21 weeks), and short (3 - 9 weeks). Key performance indicators were statistically analyzed during the nursery phase.

Results

A total of 86 nursery batches and 60 fattener batches were evaluated. In the nursery phase, piglets from the medium interval group showed a trend toward lower nursery mortality (2.2%; 95% CI 1.78-2.65) compared to the long (2.48%; 95% CI 1.83-3.1) and short (2.8%; 95% CI 2.21-3.4) groups ($P = 0.1$). Average daily weight gain was numerically different in the medium-interval group (400 g/day), compared to the short (374 g/day) and long (394 g/day) intervals. In the fattener phase, there were no statistically significant differences found among groups with respect to mortality, average daily weight gain, or feed conversion.

Discussion & Conclusion

Maintaining high immunity in sows during gestation is crucial to minimizing vertical transmission of PCV2 to piglets. While piglet vaccination is standard, sow vaccination adds protection by reducing in utero exposure. The medium interval group (12 - 21 weeks) showed trends toward improved nursery performance, suggesting this timing may optimize maternal antibody transfer and piglet resilience. Shorter intervals may not allow full immune response, while longer intervals risk waning immunity. A per-cycle sow vaccination protocol (every 21 weeks) appears practical and effective. These findings support refining sow vaccination timing.

Keywords: PCV2, Vaccination protocol, Whole-herd.

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CIRCUMVENT CML PLUS ANTIMICROBIALS IMPROVES ILEITIS CONTROL AND GROWTH DURING PRRSV OUTBREAK: RANDOMIZED FIELD TRIAL

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Introduction and Objectives

Subclinical *Lawsonia intracellularis* infection impairs growth and feed efficiency in finishing pigs and can be exacerbated during concurrent viral challenges such as porcine reproductive and respiratory syndrome virus (PRRSv). This trial evaluated whether vaccination with Circumvent® CML combined with standard antibiotic protocols provided superior control of subclinical ileitis and improved growth performance compared with antibiotics alone during a PRRSv outbreak.

Materials and Methods

On a 1,350-sow commercial farm experiencing an active PRRSv outbreak, pigs were allocated by barn to one of two interventions applied during the production cycle: Circumvent® CML vaccination at 24 days of age plus antibiotics (treatment) or antibiotics alone (control). Performance metrics and statistical analysis (ANOVA of body weights), and pathogen detection (*Lawsonia intracellularis* shedding by PCR) were monitored. Intestinal lesion scoring at slaughter and treatment records were reviewed to assess clinical and subclinical disease impact. The operational context included typical commercial antibiotic protocols implemented in both groups.

Results and Discussion

Vaccinated cohorts receiving Circumvent® CML in addition to antibiotics exhibited significantly reduced *L. intracellularis* shedding compared with cohorts treated with antibiotics alone (lower proportion of PCR-positive samples and/or reduced bacterial load as reported in source data). Growth performance favored the vaccination-plus-antibiotics group: higher body weights at finishing and increased average daily gain were observed, translating to improved production outputs under outbreak conditions. Slaughter lesion assessments showed fewer and less severe intestinal lesions consistent with *Lawsonia* infection among vaccinated pigs. Operationally, the combined intervention correlated with enhanced herd-level resilience during the concurrent PRRSv challenge. In this commercial field setting challenged by PRRSv, addition of Circumvent® CML vaccination to routine antibiotic management was associated with better control of subclinical *Lawsonia intracellularis* (reduced shedding and lesion severity) and improved growth performance compared with antibiotics alone.

Conclusion

These findings suggest that targeted vaccination against *L. intracellularis* can help mitigate production losses attributable to subclinical ileitis, particularly when herds face concurrent immunosuppressive viral disease. While the trial design reflects pragmatic farm conditions and barn-level allocation, results support inclusion of Circumvent® CML in integrated health programs; randomized controlled trials across multiple sites would further validate efficacy and economic benefit.

Keywords: Circumvent CML, Circovirus, Ileitis, *Mycoplasma*.

ELIMINATION OF *MYCOPLASMA HYOPNEUMONIAE* FROM BREED-TO-FINISH SWINE FARM: A CASE STUDY

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Introduction and Objectives

The elimination of *Mycoplasma hyopneumoniae* (*M. h.*) is a proven strategy offering substantial sanitary and productive benefits (Silva et al., 2019). The purpose of the study was to implement a *M. h.* eradication program in a Brazilian breed-to-finish herd and to evaluate the resulting zootechnical and economic outcomes.

Materials and Methods

The *M. h.* eradication program was conducted at a Brazilian 1,620-sow breed-to-finish farm. The strategy implemented was herd closure; during this period, no animals were introduced to the facility. The protocol included sequential sow vaccination, herd medication, and cleaning and disinfection protocols. Sanitary monitoring assessed *M. h.* prevalence by collecting tracheal swabs from 10% of the sow population every 21 days for PCR diagnosis. Key zootechnical indicators were evaluated and compared between the *M. h.* positive status period and the *M. h.* negative status period. Costs, including vaccination, medication, structural changes, and opportunity costs - were estimated using a partial budget model (Yeske, 2020). The economic analysis will compare zootechnical performance and cost reduction metrics between the positive status period and the negative status period.

Results and Discussion

The economic analysis showed that the total cost of the *M. h.* eradication program was US$ 453.00 per sow, with opportunity costs representing the largest expense. Subsequent costs included structural modifications, laboratory testing, medication, cleaning, and immunization. Crucially, the program generated a significant annual economic benefit estimated at US$ 741.00 per sow. This major benefit stemmed primarily from enhanced zootechnical performance, specifically an improved feed conversion ratio (-0.310 kg) and increased average daily gain (+0.038 kg) in the finishing phase. A reduction in the mortality rate of 0.88 percentage points also contributed substantially to the positive financial outcome. Furthermore, the farm saw sustainable benefits through reduced antimicrobial use and the discontinuation of *M. h.* piglet vaccination. Ultimately, the *M. hyo*-free herd's improved efficiency resulted in a Return on Investment (ROI) of just 7.33 months.

Conclusion

The successful *M. h.* eradication protocol achieved sustained pathogen freedom at 54 weeks, leading to significant zootechnical improvements in the finishing phase and reduced mortality. The return on investment was in 7.33 months.

Keywords: Cost of sanitary intervention, Medication, Respiratory diseases, Swine health, Vaccination.

Acknowledgements: The authors thank DanBred Brasil for their support in providing the testing facilities and funding for this study.

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METHODS FOR DIAGNOSING UMBILICAL INFECTION IN PIGLETS

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Introduction and Objectives

Umbilical bacterial infection (UI) may predispose pigs to umbilical outpouchings (UO). UI are usually diagnosed by culturing swabs (S) from an incised umbilicus in euthanised piglets (Blirup-Plum et al., 2025). This study evaluates whether bacterial culture from umbilical fine needle aspirates (FNASP) is a useful alternative for detecting UI.

Materials and Methods

A total of 602 and 325 piglets from two Danish herds were examined for clinical signs of UI (hard and swollen umbilicus). In herd A, 22 (10 days old) symptomatic piglets were selected. In herd B, 15 (7 days old) symptomatic piglets were selected, along with 15 asymptomatic. Piglets were euthanised, and the umbilicus was cleaned with wet wipes and disinfected with 70% alcohol before sample collection using FNASP and then incision/ swabbing. Both sample types were plated on calf blood agar followed by overnight incubation at 37°C under aerobic and anaerobic conditions. Any bacterial growth was considered indicative of infection.

Results and Discussion

Clinical signs of UI were observed in 5.5 and 4.6% of piglets in herds A and B, respectively. In herd A, 100% of S samples and 95.4% of FNASP samples were culture-positive, whereas in herd B the corresponding proportions were 93 and 77%. In asymptomatic piglets in herd B, 20% S and 0% FNASP had plate growth. Paired data for FNASP and S were available for 45 pigs. The sensitivity for FNASP was 0.82 [0.66 - 0.98], and the specificity was 1 [0.59-1] using swab culture as the gold standard. None of the cultures exhibited pure growth; however, further analyses are required to confirm and characterise the results. At present, the clinical relevance of culture-positive swabs remains unclear, as no previous studies have directly assessed their association with disease outcomes. The positive swabs in some of the asymptomatic piglets indicate possible contamination, and therefore an overestimation of the UI prevalence based on swabbing.

Conclusion

FNASP is a useful method for detecting UI in live pigs and can provide valuable information when assessing long-term risks associated with UI. Early identification and treatment of UI are important, given the potential link between UI and umbilical complications later.

Keywords: Fine needle aspirate, Piglets, Umbilical infection.

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COMPARISON OF TWO IRON PROTOCOLS FOR CONTROLLING ANEMIA IN PIGLETS AT WEANING ON FARMS IN ARGENTINA

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Introduction and Objectives

Iron deficiency anemia (IDA) is one of the most frequent hematological disorders in suckling piglets, significantly affecting their growth, feed efficiency, and immune status. The aim of this study was to compare hemoglobin (Hb) levels in piglets treated with iron dextran or gleptoferron, its effect on frequency of IDA at weaning and the relationship between body weight and hemoglobin concentration, under field conditions.

Material and Methods

Between December 2024 and September 2025, 998 piglets were sampled from 23 farms (ranging from 250 to 7,000 sows) in different provinces of Argentina. All farms used iron dextran and 770 piglets were sampled. In 9 of these farms, a second evaluation was subsequently carried out using Gleptoferron as a replacement alternative (n = 228). In each farm, 10% of the pre-weaning litters (16 to 23 days old) were sampled. The Hemocue® Hb 201+ device was used, and the piglets were classified according to their hemoglobin levels (Anemic: < 9 g/dL / Subanemic: 9 - 11 g/dL / Optimal: > 11 g/dL). Individual weights of three piglets (small, medium, and large) per litter were determined. ANOVA and simple linear regression models were used.

Results and Discussion

In the 23 farms sampled, the average Hb level was: 10.16 g/dL: 25% anemic, 43% subanemic, and 32% optimal. Under iron dextran supplementation, Hb levels averaged 10.00 g/dL and showed a marked negative correlation with body weight (-0.49 g/dL per kg; $R^2 = 0.1791$). Piglets supplemented with gleptoferron achieved a higher average hemoglobin level (11.48 g/dL), with less variability and a much weaker weight-hemoglobin association (-0.20 g/dL per kg; $R^2 = 0.0615$).

Conclusion

In all components of the study, iron dextran supplementation presented consistent limitations: a high prevalence of anemia, marked variability, and an inverse relationship between growth and hemoglobin. The fastest-growing piglets, those with the highest iron requirements, were the most affected. In contrast, piglets treated with Gleptoferron showed higher and more stable hemoglobin levels, less weight variability, and a lower percentage of anemia.

Keywords: Anemia, Gleptoferron, Iron Dextran.

IMPLEMENTATION OF BIOSECURITY MEASURES ON PRRS ON A SELECTION OF FARMS IN THE NETHERLANDS

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) remains a challenging disease in swine herds. While Modified Live Virus (MLV) vaccination is commonly used, sustainable control requires a holistic approach. This study was done to systematically evaluate biosecurity practices and their effectiveness on different farms and investigate common practices and possible risk factors for PRRSv circulation on those farms. For this, the COMBAT biosecurity tool from Boehringer Ingelheim was utilized.

Materials and Methods

The COMBAT audit examines risk factors for PRRSV introduction and spreads through up to 98 questions across five categories: General, External Biosecurity, Transport, Internal Biosecurity, and Management. Between 2022 and 2025, audits were conducted on 43 sow herds in the Netherlands, with two herds audited twice. Seventeen herds were part of farrow-to-finish operations, while 23 did not finish pigs. Two experienced field veterinarians conducted on-site interviews for a thorough assessment

Results and Discussion

Among the farms, 5 housed fewer than 500 sows, 29 had 500 - 2,000, and 7 exceeded 2,000 sows. Notably, 72% of farms were located within 500 meters of another pig farm, yet in 81% of cases, the PRRS status of neighboring herds was unknown. Regarding external biosecurity, 49% purchased gilts from outside sources, with most doing so every 1 - 3 months; only 23% tested these animals before introduction, and 27% provided no quarantine for replacements. Quarantine durations varied, with only 29% isolating gilts for 12 weeks or more. About half of the farms allowed truck drivers into clean areas, increasing the risk of disease introduction. Internal biosecurity measures showed that 88% of farms had MLV PRRSv vaccination protocols; however, only 58% always vaccinated piglets, and 23% did not vaccinate piglets at all. Management practices revealed that 63% cross-fostered piglets within the same batch, often even after three days, and 49% mixed piglets from different week groups at weaning.

Conclusion

In summary, the audited farms reflect average sow herds in the Netherlands. Although biosecurity audits were consistently performed, results indicate that several key measures - such as gilt quarantine, pre-introduction testing, limiting driver access, and age-group separation - were insufficiently applied, suggesting significant opportunities for improvement in preventing PRRSV circulation

Keywords: Biosecurity, PRRSv.

COMPARISON OF TWO DIFFERENT COMMERCIAL PCV2/MHYO RTU VACCINES IN BRAZIL AND ITS IMPACT ON LUNG HEALTH

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Introduction and Objectives

Mycoplasma hyopneumoniae (*M.hyo*) and Porcine Circovirus type 2 (PCV2) are important pathogens of PRDC. Vaccination has been one of the main tools to control both agents (Sibila et al., 2021). Lung lesions are a strong indicator of the prevalence of enzootic pneumonia, in that sense the evaluation of bronchopneumonia-like lung lesions at slaughterhouse is a recognized method to assess the effectiveness of vaccines. This study aimed to examine the possible association of lung lesions at slaughterhouses with two different commercial RTU against M.hyo and PCV2

Material and Methods

A randomized, comparative field trial was conducted at a farm affected by PCV2 and M.hyo, the animals underwent two different protocols at weaning. Animals in Group 1: single dose 2 mL of Subunit PCV2d/Mhyo RTU (CIRBLOC® M hyo - Ceva Animal Health), 320 lungs. Group 2: two-dose vaccination of Mhyo + PCV2a/b RTU, 2 mL IM, 307 lungs. Average values were calculated for Ep like lesions, using T-test

Results and Discussion

The lungs evaluated from the animals in Group 1 showed a bronchopneumonia (BP) frequency of 24.61% and Group 2 was 35.56%. The percentage of the affected areas was 1.8 and 2.25% for Groups 1 and 2, respectively. The incidence of dorsal-caudal pleurisy was 5.0% for Group 1 and 6.1% for Group 2. When comparing the scar lesions Group 2 had a 23.2% prevalence and Group 1 at 27.9%. These data show lower challenge levels when compared to prevalence studies conducted in the country. (Calveyra et al., 2021; Filsner et al., 2024). Standardized assessment of lung lesions is a valuable tool for monitoring respiratory health in the herd and supporting more accurate decision-making when defining control protocols.

Conclusion

The results showed that the vaccination with CIRBLOC® M hyo, was more effective, reducing the prevalence and severity of bronchopneumonia lesions compared to the protocol of Group 2.

Keywords: Porcine Circovirus, Vaccine.

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SCALING UP AN ELISA FOR MONITORING SEROCONVERSION AFTER EDEMA DISEASE VACCINATION

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Introduction and Objectives

Edema disease (ED) caused by verotoxin 2e (VTx2e) -producing E. coli strains, typically affects piglets 1-2 weeks post-weaning, and ranges from peracute to subclinical. Vaccination is the preferred method for ED control, considering antibiotic use reduction and ZnOx bans in some countries. Despite effective vaccines and ED's economic impact, no commercial test exists to monitor ED seroconversion after vaccination. The aim of this work is to scale up and improve a bench-scale (BS) indirect ELISA to industrial production (Ready to use "RTU") to monitor ED post-vaccination seroconversion state of vaccinated piglets.

Materials and Methods

For comparison purposes, an in-house reference set of sera with high, medium and low neutralizing titers against recombinant VTx2e, along with negative and internal control sera, were tested using the BS assay and a pilot batch of the test produced under industrial conditions (RTU). During the industrial scaling process, changes were introduced in the washing, the volume of blocking solution, the coating method and the working volume of the ELISA. The detection antibody (commercial IgG) and coating antigen (recombinant fraction of VTx2e) were the same in the two assays (BS and RTU). A second experiment series compared the performance of two different detection antibodies (commercial IgG in BS assay vs a proprietary IgA anti-IgG in the RTU) using two pilot kits, one for each antibody class. Sensitivity and specificity were assessed by analyzing 440 sera belonging to ED naïve piglets and piglets 21 and 28 days after vaccination.

Results and Discussion

Both the BS and the RTU assays showed similar sensitivity (72.8 vs 74.4%) and specificity (95.8 vs 95.9%). Secondary antibody substitution in the RTU assay improved both parameters, especially sensitivity (95.1% sensitivity and 97.8% specificity), with a more robust performance showed by fewer false positive.

Conclusion

Altogether, these results indicate that the RTU ELISA assay can be effectively used in post-vaccination seroconversion assessment in vaccinated piglets between 21- and 28-days post-immunization.

Keywords: Edema disease, ELISA, Vaccination monitoring, Verotoxin 2e.

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MONITORING PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS IN NEONATAL PIGLETS IN THE NETHERLANDS: THREE YEARS OF PCR SURVEILLANCE AND TRENDS

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Introduction and Objectives

Effective control of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in swine production relies on ensuring piglets are born free of infection. Monitoring PRRSV in neonatal piglets provides an early indication of sow herd status. The Dutch National PRRS Plan, initiated in 2021, aims to improve PRRSV control. This study evaluates the impact of the plan on PRRSV status in neonatal piglets over a three-year period.

Materials and Methods

From July 2022 to October 2025, samples were collected from neonatal piglets in a representative selection of Dutch sow herds. Each quarter, an average of 30.6 farms submitted 271 pooled samples, including processing fluids (Vilalta et al., 2019), tongue fluids (Baliellas et al., 2021), and umbilical cord fluids (Martin-Valls et al., 2018). Samples were tested by PCR in one of three Dutch commercial laboratories. A batch or farm was classified as positive if at least one sample had a Ct value below 40.

Results and Discussion

PRRSV was consistently detected in approximately 55% of farms per quarter. Over the three-year period, the ratio of positive batches to positive farms decreased, indicating gradual improvement in PRRSV control. Seasonal variation was observed, with higher positivity rates in the first half of the year. Specifically, the percentage of positive farms ranged from 55 to 65% across years, while the ratio of positive batches to positive farms declined from 0.55 to 0.35. Quarterly analysis showed the highest farm positivity in the first quarter, with a gradual decrease in subsequent quarters.

Conclusion

Despite limitations related to field conditions and sample handling, PRRSV remains endemic in the Netherlands. However, control measures are gradually improving herd status, as evidenced by declining positivity ratios and seasonal trends.

Keywords: Monitoring, Neonatal piglets, Netherlands, PRRSV, PCR surveillance.

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IMPACT OF SOW AND PIGLET VACCINATION STRATEGIES ON NEONATAL PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS PREVALENCE IN DUTCH HERDS: A DESCRIPTIVE FIELD STUDY

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) continues to pose a major challenge to swine production in the Netherlands. Despite widespread vaccination, with over 90% of sow herds vaccinated, monitoring reveals that approximately 55% of sow herds have at least one farrowing batch per quarter testing positive for PRRSV by PCR (internal data). This descriptive field study aimed to investigate the relationship between vaccination protocols in sows and piglets and the prevalence of PRRSV in neonatal piglets.

Materials and Methods

PCR testing was performed at three accredited laboratories, with results considered comparable. From July 2022 to October 2025, samples were collected from neonatal piglets in 27 representative Dutch sow herds (average 1,165 sows/herd). Included farms submitted at least six sample batches within a three-month period during the application of their farm specific PRRSV vaccination protocols. PCR testing was performed at one of three accredited Dutch laboratories, with results considered comparable.

Results and Discussion

Batch vaccination is vaccination at specific moments in the sow cycle. Mass vaccination is whole herd vaccination 3 or more times a year. 37% of farms had zero PRRSV-positive neonatal batches. Sow vaccination scheme; Batch vaccination (52% of farms) had 29% average PRRSV-positive batches versus Mass vaccination (41%): 25% average. Sow vaccination type; Killed vaccine (KV, 11% of farms): 51% average PRRSV-positive batches versus Modified live vaccine (MLV, 59%): 22% average versus MLV+KV (26%): 33% average. Piglet vaccination scheme (MLV vaccination only); No piglet vaccination (33% of farms): 23% average PRRSV-positive batches versus Vaccination in 1st week of life (15%): 61% average (all these farms used KV or MLV+KV in sows) versus Vaccination in 3rd week of life (48%): 18% average. Causal relationships between vaccination protocols and neonatal PRRSV prevalence cannot be established from this dataset. Notably, in sows all mass-vaccinated herds used MLV, KV was only applied in batch protocols. Early piglet vaccination correlated with higher neonatal PRRSV prevalence, suggesting that timely immunity may not be achieved when neonatal prevalence is high.

Conclusion

Stabilizing sow herds should be prioritized before piglet vaccination strategies to control PRRSV effectively.

Keywords: Field study, Herd stabilization, Neonatal piglets, PRRSV, Vaccination protocols.

IDENTIFYING SOURCES OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS INSTABILITY IN SOW HERDS THROUGH PARITY-BASED NEONATAL MONITORING

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Introduction and Objectives

In sow herds affected by Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), pinpointing the source of (re)infection is crucial for reducing virus prevalence in neonatal piglets. This study evaluated a monitoring approach that compares PRRSV Polymerase Chain Reaction (PCR) results between first parity (P1) and older parity (P2+) sows to identify instability sources.

Materials and Methods

A prospective cohort study was conducted in 41 farms representative for the Netherlands, from 2023 to 2025, focusing on periods of PRRSV instability. Per farrowing batch neonatal samples (processing fluids, tongue fluids, or umbilical cords) were collected by farm staff, pooled by parity group (P1 and P2+), and tested for PRRSV by PCR (Kylt, Indical) at one of two commercial laboratories (Laboratories). The results are regarded positive when the Ct value was below 40. Inclusion required at least 12 samples per case and a minimum of ≥ 25% PCR positivity. Thirteen cases from nine farms fulfilled all inclusion criteria. The analysis compared positivity rates and cycle threshold (Ct) values between P1 and P2+ groups using matched herd-week pairs (111 pairs met criteria).

Results and Discussion

In 4/ 13 cases, P1 samples had ≥ 20% higher PCR positivity than P2+; in 1/ 13 average Ct values were ≥ 20% lower in P1; in 3/ 13 minimum Ct values were ≥ 20% lower in P1. Conversely, in 9/ 13 cases, P2+ samples had ≥ 20% higher PCR positivity; Ct values were never ≥ 20% lower than P1. Statistical analysis showed P2+ litters had 1.54 times higher odds of testing positive than P1 litters, though this was not statistically significant (mixed logistic regression, $p = 0.18$). Estimated positivity was 37% for P1 and 48% for P2+, with substantial variation between pairs. No significant difference in Ct values was observed (Wilcoxon signed-rank test, $P = 0.87$).

Conclusion

In conclusion, parity-based PCR monitoring can potentially help identify instability sources and inform vaccination and biosecurity strategies. While not scientifically validated, this approach proved useful enough for guiding field interventions. We expect that more continuous monitoring and stricter sampling protocols will minimize cross-contamination and improve accuracy.

Keywords: PRRSV, Parity, PCR monitoring, Sow herd stability.

EFFICACY OF IRON DEXTRAN ADMINISTERED VIA NEEDLE-FREE INJECTION VERSUS NEEDLE-AND-SYRINGE INJECTION IN NURSING PIGLETS

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Introduction and Objectives

Nursing piglets are susceptible to iron deficiency anemia (IDA) due to multifactorial factors, including species-specific physiology, high iron requirements for high-yield productivity, and husbandry practices (Szudzik et al., 2018). To prevent IDA, the swine industry routinely provides parenteral iron during the first week of life, usually delivered by needle and syringe (NS). Meanwhile, a recent study reported that needle-free injection device (NFID) showed the potential to deliver parenteral iron to piglets (Tobias et al., 2023). This study aimed to compare hemoglobin (HGB) concentration in piglets at weaning when administered iron dextran via NFID vs NS; and to determine the efficacy of iron dextran administered via NFID on preventing IDA at weaning by using HGB as an indicator of iron status.

Materials and Methods

Seventy-six commercial piglets (3.6 days old, 2.1 kg) were randomly assigned to one of two treatment groups and administered 1 mL of 200 mg iron dextran (ID). Piglets in NFID treatment group were administered ID using a commercial air-powered needle-free injector device while those in NS treatment were administered intramuscularly by a 20G × 1/2" needle and a 3 mL syringe. Blood samples were collected before iron administration and at weaning (19.3 days old). Hematology was performed by a national veterinary health laboratory. Neither creep feed nor milk replacer was provided throughout the trial. Student's *T*-test was performed to compare treatment groups.

Results and Discussion

Preliminary results illustrate that HGB ± SD (g/L) at weaning of NFID group (114.1 ± 8.9) was lower than that of NS group (120.7 ± 8.0) ($P = 0.001$). However, HGB at weaning in NFID group was above published cut-off values of IDA (90 g/L, $P < 0.001$) and iron deficiency (110 g/L, $P = 0.004$). The difference of HGB between groups may be considered biologically relevant. Other factors associated with HGB at weaning will be explored by mixed linear regression.

Conclusion

The difference of HGB concentration at weaning between two modes of administration was significant. However, HGB of NFID group demonstrated the potential to reach biological relevance to those of NS group.

Keywords: Animal welfare, Drug delivery, Iron dextran, Needle-free injection, Piglet processing.

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CONTROL STRATEGIES FOR *ASCARIS SUUM* IN PIG FARMS IN XUEJIA DISTRICT, TAINAN, AND ANALYSIS OF LIVER REJECTION RATES AT THE TAINAN MEAT MARKET

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Introduction and Objectives

Ascaris suum is a common parasite in pigs in Taiwan. In addition to impairing pig growth, migrating larvae cause mechanical damage to organs, particularly the liver, leading to fibrosis and lesions. These liver abnormalities often result in rejection during carcass inspection, causing economic losses. In 2009, Typhoon Morakot severely impacted southern Taiwan, leading to flooding in many pig farms. The resulting environmental imbalance contributed to an increase in *Ascaris suum* infections. This study focused on a vertically integrated pig farm in Xuejia, Tainan, with 20,000 pigs. Retrospective analysis of liver rejection reports from the meat market in August 2010 revealed a liver rejection rate of 31%. The parasite detection rates were between 30% and 10% in different age groups.

Materials and Methods

Due to the economic losses caused by liver rejection rates, the farm owner sought assistance on August 10, 2010. Our team provided guidance, revising and shifting the farm's deworming program. To evaluate the effectiveness of the program, monthly fecal sample screenings and liver rejection rate analyses were conducted. Before and after treatment, fecal samples were collected from 10 randomly selected pigs per category and examined using the flotation method for parasite egg detection. Liver rejection rates were analyzed based on daily reports from the Taichung Daan Meat Market.

Results and Discussion

The results, covering 2010 - 2011, showed a significant decrease in both parasite egg detection rates and liver rejection rates ($P < 0.05$). It shows that a well-structured deworming program, coupled with regular monitoring, can significantly reduce *Ascaris suum* infections. The infection rate dropped from 31% to below 5%, increasing farm profitability.

Conclusion

However, because *Ascaris suum* is transmitted faecal-orally, infection as well as reinfection remains at higher risks after flooding, as eggs may have prolonged survival rate in moist bedding and soil. Continuous monitoring is essential. Additionally, from 2012 to 2013, we analyzed liver rejection rate from Tainan's meat markets, identifying the top 5 pig farms with the highest rejection rates. These farms underwent retrospective investigations and corrective measures focusing on deworming protocols and husbandry management. After a two-years intervention, liver rejection rates significantly declined.

Keywords: *Ascaris suum*, Meat market, Route of transmission.

COUNTERACTING FUMONISINS THROUGH ENZYMATIC DETOXIFICATION IN PIGLETS

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Introduction and Objectives

Fumonisins (FUM) are secondary metabolites produced by various Fusarium species on corn and rank among the most widespread mycotoxins globally. In swine nutrition, corn is the main source of elevated FUM levels in feed. Beyond their acute, chronic, and subclinical effects, FUM disrupts sphingolipid metabolism by inhibiting ceramide synthase. This inhibition leads to an accumulation of sphinganine and sphingosine and a depletion of complex sphingolipids. Such disruption interferes with cell signaling in the lungs, heart, liver, and immune cells, driving the associated clinical outcomes. The sphinganine-to-sphingosine (Sa:So) ratio in serum serves as a biomarker for FUM exposure. Fumonisin esterase is an enzyme designed to degrade FUM. It acts in the gastrointestinal tract by cazalyzing the hydrolysis of FUM into partially and fully hydrolyzed derivatives that are non-toxic or significantly less toxic.

Materials and Methods

Seventy-two mixed-sex pigs with an initial body weight of approximately 10.7 kg were randomly allocated to three dietary groups: (1) a negative control (NC) receiving an uncontaminated diet, (2) a positive control (PC) fed a diet containing 5 ppm FUM, and (3) a treatment group (TG) receiving 5 ppm FUM supplemented with 15 U fumonisin esterase/kg. All animals were fed ad libitum for 42 days. Sa:So was measured in serum at day 29 and 42.

Results and Discussion

On day 29, the Sa:So ratio was 0.214 in the NC, 0.456 in the PC, and 0.299 in the TG. The difference between PC and TG was significant ($P < 0.001$), indicating that fumonisin esterase substantially reduced the FUM-induced increase in Sa:So ratio. On day 42, the ratios were 0.216 (NC), 0.407 (PC), and 0.311 (TG), with a significant difference ($P = 0.003$) between PC and TG.

Conclusion

FUM exposure markedly elevated the Sa:So ratio compared to the control, confirming its disruption of sphingolipid metabolism. Supplementation with fumonisin esterase consistently lowered the ratio compared to the PC, demonstrating its efficacy in mitigating FUM effects.

Keywords: Enzymatic detoxification, Fumonisins, Piglets.

COUNTERACTING ZEARALENONE THROUGH ENZYMATIC DETOXIFICATION IN PIGLETS

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Introduction and Objectives

Zearalenone (ZEN) is a mycoestrogen produced by Fusarium species such as *F. graminearum* and *F. culmorum*. By binding to estrogen receptors, ZEN disrupts endocrine function and causes reproductive disorders in animals and humans. Pigs are particularly sensitive, making effective mitigation strategies essential. Our group developed ZenA, a zearalenone hydrolase that degrades ZEN in the gastrointestinal tract. ZenA acts as a lactonase, converting ZEN into hydrolyzed zearalenone (HZEN), a non-estrogenic metabolite and the main ZEN derivative in swine. This study evaluated ZenA's ability to degrade ZEN in weaning piglets.

Materials and Methods

Thirty-six pigs (≈ 9.2 kg) were randomly assigned to three diets: (1) negative control (NC), uncontaminated; (2) positive control (PC), 200 ppb ZEN; (3) treatment group (TG), 200 ppb ZEN + 10 U ZenA/kg. Animals were fed ad libitum for 42 days. Fecal ZEN and HZEN concentrations were analyzed on days 1, 21, and 42.

Results and Discussion

On day 1, fecal ZEN concentrations were 25.3 ng/g in the positive control (PC) group and 9.2 ng/g in the treatment group (TG), showing a significant reduction with ZenA supplementation (P = 0.023). HZEN levels were 7.0 ng/g in both groups, with no detectable difference (values were constant and below the limit of quantification). By day 21, ZEN levels increased in both groups but remained markedly lower in the TG (127.2 ng/g) compared with the PC (347.6 ng/g), representing a significant reduction (P = 0.025). In contrast, HZEN concentrations rose substantially in the TG (63.9 ng/g) relative to the PC (7.0 ng/g), confirming significant biotransformation of ZEN to HZEN (P = 0.018). On day 42, the same pattern persisted. Fecal ZEN concentrations were significantly higher in the PC (354.6 ng/g) than in the TG (200.7 ng/g) (P = 0.025). Meanwhile, HZEN levels continued to be elevated in the TG (105.7 ng/g) compared with the PC (7.0 ng/g) (P = 0.018).

Conclusion

ZenA supplementation effectively degraded ZEN in pigs, as shown by reduced fecal ZEN and increased HZEN. ZenA offers a safe, efficient solution to mitigate ZEN contamination in swine production.

Keywords: Enzymatic detoxification, Piglets, Zearalenone.

ACCUMULATION OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS IN MIXED-AGE GROUPS OF NURSERY PIGLETS IN DUTCH FARROW-TO-FEEDER HERDS

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) type 1 is endemic in the Netherlands, with over 90% of sow herds vaccinated and 40% of nurseries testing positive by PCR (Beek, 2024). Standard practice when transporting piglets to the finishing barn at 8 - 10 weeks of age, involves moving underweight piglets to younger batches, resulting in mixed-age groups. This study aimed to compare PRRSV dynamics in mixed versus intact groups of piglets at the end of the nursery phase in endemic herds.

Materials and Methods

Oral fluid samples were collected every four weeks at the end of nursery in two farrow-to-feeder herds (average 1100 sows) over 15 and 4 consecutive periods, respectively. 'Intact' rooms housed piglets of a single age, while 'mix' rooms included piglets of multiple ages due to selection for underweight. Oral fluids from three non-adjacent pens per room were pooled and tested for PRRSV by PCR at a commercial laboratory (VLG, Epe, Netherlands). Data were analyzed using Chi-square and Mann-Whitney U tests.

Results and Discussion

PRRSV PCR positivity was observed in 10/19 intact group samplings and 15/ 19 mixed group samplings (Chi-square, $P = 0.087$). The average PCR cycle threshold (Ct) value was higher in intact groups (35.81) than in mixed groups (33.33), indicating a higher viral load in mixed groups (Mann-Whitney U, $P < 0.00001$). The boxplot analysis showed that mixed groups consistently had lower median and average Ct values, confirming greater PRRSV accumulation. One farm showed a clear trend toward increased positivity in mixed groups, while the other did not, likely due to fewer samples. These findings suggest that mixing piglets of different ages at the end of nursery increases PRRSV accumulation, posing a risk for viral recirculation within the herd.

Conclusion

To control PRRSV in farrow-to-feeder herds, it is crucial to prevent accumulation in specific groups, as these can facilitate horizontal transmission and recirculation within the population. Both farms adapted their protocols based on these findings by first loading from the intact (low risk) groups and last loading the mixed (high risk) groups, followed by cleaning-disinfection of the alley and loading bay.

Keywords: Mixed-age groups, Nursery piglets, PRRSV, Viral load.

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A PAN-EUROPEAN ASSESSMENT OF SLAUGHTERHOUSE LUNG LESIONS IN PIGS: 2025 SURVEY FINDINGS

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Introduction and Objectives

Lung lesion scoring at slaughter remains a practical and informative tool for evaluating respiratory health in commercial pig herds. Characteristic patterns associated with enzootic pneumonia and pleuropneumonia - particularly lesions linked to *Mycoplasma hyopneumoniae* and *Actinobacillus pleuropneumoniae* - enable structured monitoring of herd-level disease pressure. This survey aimed to consolidate updated lung-scoring data generated across major swine-producing regions of Europe during 2025, providing an overview of the current respiratory health status.

Materials and Methods

Data were collected through the Ceva Lung Program over a 12-month period (mid-December 2024 to mid-November 2025) in multiple EU countries. Bronchopneumonia-like lesions were scored using a modified Madec grid, while APP-like pleurisy was assessed using a modified SPES system, generating the APP Index (APPI). Scoring was performed at slaughterhouses by trained veterinarians or qualified slaughterhouse technicians following standardized procedures. Slaughter checks were carried out for routine diagnostic or monitoring purposes, without predefined herd selection. All recorded data were automatically transferred to a centralized database. Median values were calculated for: proportion of lungs exhibiting bronchopneumonia (% BP), percentage of affected parenchyma among diseased lungs, prevalence of dorso-caudal pleurisy (% DP), and APPI.

Results and Discussion

In total, 384,190 lungs from 3,755 scoring sessions were evaluated. Most data originated from Spain, France, Germany, and the Netherlands. The median %BP was 31.76%, median affected parenchyma 4.35%, median %DP 8.7%, and median APPI 0.24. As data derived from routine field activities rather than a designed epidemiological study, potential confounders include unequal country participation, variability in slaughterhouse throughput, differences in herd management, and unmeasured factors such as vaccination or antimicrobial use. These limitations restrict data interpretation but are inherent to large-scale surveillance datasets.

Conclusion

At the European level, the burden of enzootic pneumonia and pleuropneumonia in 2024 - 2025 remains comparable to previous years assessed using the same system. These findings underscore the value of routine slaughterhouse monitoring for tracking respiratory disease dynamics in swine populations.

Keywords: *Actinobacillus pleuropneumoniae*, lung lesion scoring, *Mycoplasma hyopneumoniae*, monitoring, respiratory disease.

UPDATED REGIONAL ASSESSMENT IN FOUR EUROPEAN COUNTRIES OF PRDC PATHOGENS USING LUNG LESION SCORING AND SCREENING PCR

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Introduction and Objectives

To effectively tackle Porcine Respiratory Disease Complex (PRDC), it is often essential to assess lung lesions at slaughter and identify causative pathogens. This study combines pathoanatomical lung examination with PCR to detect key PRDC agents in slaughter pigs from Germany, the Netherlands, Belgium, and Austria. It serves as an update to regional findings from 2024.

Materials and Methods

In total, 459 farms with low to high respiratory problems were included. Lungs were scored according to a standardized lung scoring methodology [1]. Within each batch, the investigator selected up to five lungs and sampled the transition area between healthy and affected parenchyma. Pooled samples were then analyzed by a screening-PCR for following pathogens: *Actinobacillus pleuropneumoniae* (App), *Mesomycoplasma hyopneumoniae (M. hyo),* Betaarterivirus suid 1 + 2 (PRRSV 1+2), Swine influenza A virus (swIAV) and Porcine circovirus type 2 (PCV2). The latter pathogen was genotyped at Ct-values ≤ 32.

Results and Discussion

M. hyo was found on average in 354 (77.1%) farms, followed by PCV2 (223; 48.6%), PRRSV1 (167; 36.4%), App (42; 9.2%), PRRSV2 (18; 3.9%) and swIAV (22; 4.8%). In total, 91 farms (19.8%) were sequenced for PCV2. Most prominent genotype was PCV2d (80.2%), followed by PCV2a (14.3%) and PCV2b (5.5%).

Conclusion

Compared to our previous evaluation, this study included 7.5 times more farms and revealed a lower prevalence for *M. hyo* (77.1% vs. 90.2%) and PRRSV1 (36.4% vs. 47.5%). App, PRRSV2, and swIAV remained the least prevalent agents. Interestingly, PCV2 was found more frequently (48.6% vs. 45.9%), with a notable increase in the identification of the PCV2d genotype (80.2% vs. 69.2%). These changes may be attributed to the larger number of farms included, differences in their geographic distribution, and a potential shift in pathogen epidemiology. Taken together, these findings suggest that PCV2, particularly the PCV2d genotype, is still on the rise, warranting close monitoring and potentially adapted control strategies.

Keywords: Lung lesion scoring, PCV2, Porcine Respiratory Disease Complex, Screening-PCR.

SWINE PNEUMONIA. HISTOPATHOLOGY AND VIRUS DETECTION FROM LUNG LESIONS FROM DIFFERENT PIG CATEGORIES IN ARGENTINA

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Introduction and Objectives

Swine pneumonia (SP) represents a major cause of global economic losses. Key associated pathogens include viruses (PCV-2, PCV-3, SIV, SHV-1, and PRRS) and bacteria (*M. hyopneumoniae, P. multocida, and A. pleuropneumoniae*). While Argentina is PRRS-free, SHV-1 remains endemic on outdoor farms. Previous research at slaughter identified *P. multocida* and *M. hyopneumoniae* as the primary agents of catarrhal and suppurative bronchopneumonia (Cappuccio et al., 2018). The present study aimed to detect DNA/RNA of PCV-2, PCV-3, and SIV using molecular techniques (qPCR/RT-qPCR) and to correlate these findings with histopathological lesions in lungs and lymph nodes from 15 farms.

Material and Methods

A total of 94 lung and 34 lymph node samples were collected from nursery (N), growing/finishing (GF), and slaughter pigs (SP) across 15 indoor farms between 2021 and 2023. Samples underwent histopathological classification following Caswell and Williams (2016). For molecular detection, genetic material was extracted using commercial kits. PCV-2 was detected by qPCR (Olvera et al., 2004) and PCV-3 by qPCR (Palinski et al., 2016), with Ct values > 35 considered negative. For SIV detection, RT-qPCR was used to identify the IAV M gene (Spackman et al., 2002).

Results and Discussion

PCV-2 Ct values ranged from 20.56 to 34.55, while PCV-3 values ranged from 25.99 to 32.8. At least one viral agent was detected in 38.46% of samples in Nursery (N) and 25% in both GF and SP. PCV-3 was detected exclusively in lymph nodes, with PCV-2/PCV-3 coinfection found in only one GF sample. Histopathological correlations included: SIV was associated with suppurative bronchopneumonia and necrotic bronchiolitis (N), as well as BALT hyperplasia and granuloma formation (GF/SP). PCV-2 was linked to suppurative bronchopneumonia, BALT hyperplasia, and bronchiolar necrosis (N); fibrinous bronchopneumonia and reactive lymph node hyperplasia (GF); and bronchiolosclerosis (SP). PCV-3 was associated only with lymph node depletion (N) and lymphoid hyperplasia (GF).

Conclusions

This study confirms the circulation of PCV-2, PCV-3, and SIV across the surveyed farms. The prevalence of catarrhal or suppurative bronchopneumonia rather than the interstitial pneumonia typically of viral infections suggests the presence of mixed infections with bacteria.

Keywords: Histopathology, Influenza A virus, Porcine circoviruses 2 and 3, Swine pneumonia.

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DYNAMIC EVALUATION OF *MYCOPLASMA HYOPNEUMONIAE* VACCINE EFFICACY AND ITS IMPACT ON PRODUCTION METRICS

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Introduction and Objectives

Mycoplasma hyopneumoniae (Mhp) is a major respiratory pathogen in swine, significantly reducing production efficiency. While vaccination is a key measure to control enzootic pneumonia, large-scale studies evaluating its effects on herd health, performance, and economic outcomes are limited. This study aimed to assess the practical value of Mhp vaccination in commercial swine operations by integrating oropharyngeal swab qPCR for Mhp outcomes with production metrics.

Materials and Methods

A controlled trial was conducted on a large swine farm in Fujian, using a two-site, three-week batch system. Nursing piglets were randomized to either treatment (n = 1,066; vaccinated with *Mycoplasma hyopneumoniae* inactivated vaccine at 7 days of age, boosted at 25 days of age; and co-administered tulathromycin injection at weaning at 0.2 mL per head to provide effective control of respiratory pathogens during this high-risk transition period) or the control group (n = 1,055; neither Mhp vaccination nor antibiotic injection). Both groups were weaned at 25 days and transported off-site to the finishing farm, raised under identical management in separate units. Oropharyngeal swab samples (n = 10 per group) were collected at 45, 60, 90, 120, 140, and 150 days of age for Mhp detection by qPCR. Production metrics including average weaning weight, lactation and nursery-to-finish survival rates, number of pigs marketed, market weight, age at market, average daily gain (ADG), feed conversion ratio (FCR), and average medication cost per head were recorded.

Results and Discussion

The vaccinated group outperformed the control group in nursery-finish survival rate (97.20 vs 95.80%), overall ADG (746.9 vs 712.5 g), FCR (2.54 vs 2.60), medication cost per head (¥33.80 vs 39.80), and age at market (177 vs 183 days). Oropharyngeal qPCR detected 0% Mhp positivity in the vaccinated group at all time points, whereas the control group exhibited increasing positivity rates, reaching 100% from 120 days onward. These results indicate that the combined intervention of vaccination and weaning antibiotic administration effectively reduced Mhp detection rates and improved key production metrics.

Conclusions

In large-scale swine farms, the combined intervention of Mhp vaccination and weaning antibiotic injection showed a trend to reduce herd infection rates and enhance production efficiency.

Keywords: *Mycoplasma hyopneumoniae,* Production metrics, Vaccination.

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ANTIBACTERIAL ACTIVITY OF THE CULTURE SUPERNATANT OF *LACTOBACILLUS PLANTARUM* K9 AGAINST VARIOUS PATHOGENS ISOLATED FROM SWINE IN KOREA

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Introduction and Objectives

Lactobacillus plantarum K9 holds strong potential for industrial application, as the strain has been validated for various functionalities, including the production of antimicrobial peptides (AMPs), antiviral activity, and lactic acid production. In this study, the antibacterial activity of the culture supernatant of *L. plantarum* K9 was evaluated against various pathogens isolated from swine in Korea.

Materials and Methods

The culture supernatant of *L. plantarum* K9 was concentrated tenfold. *Clostridium perfringens*, F18+ *E. coli*, Salmonella *Typhimurium*, and *Streptococcus suis* strains were isolated from pigs. Three strains of each pathogen were tested. The minimum inhibitory concentrations (MICs) of the culture supernatant were determined using the microtiter plate method, following the recommendations of the National Committee for Clinical Laboratory Standards (NCCLS). The supernatant was serially diluted twofold, ranging from 1:1 to 1:1,024.

Results and Discussion

The MICs of the culture supernatant of *L. plantarum* K9 were 1:128 for *C. perfringens*, approximately 1:85 for F18+ *E. coli*, 1:64 for S. *Typhimurium*, and 1:256 for *Strep. suis*.

Conclusion

These findings suggest that further research on the potential use of the culture supernatant of *L. plantarum* K9 as a feed additive to reduce diseases caused by these pathogens in pigs is warranted.

Keywords: Antimicrobial peptides, *Clostridium perfringens*, *Lactobacillus plantarum, Streptococcus suis,* The minimum inhibitory concentrations.

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FIELD PRACTICES IN ORAL FLUID SAMPLING ACROSS U.S. SWINE SYSTEMS: FINDINGS FROM A NATIONAL SURVEY ON ADOPTION, PRACTICES, AND OPPORTUNITIES FOR STANDARDIZATION

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Introduction and Objectives

Oral fluids are collected by allowing pigs to chew on suspended cotton ropes, after which the fluids are extracted and submitted for pathogen or antibody testing. This non-invasive, cost-effective approach has been widely adopted for monitoring endemic and emerging diseases in swine. However, information regarding oral fluid sampling practices, sample management, and whether oral fluid is used for active or passive surveillance programs in practice remains unknown. This study characterizes oral fluid sampling practices across U.S. pig production systems and the diversity of current approaches.

Materials and Methods

An online questionnaire was developed to assess oral fluid usage in U.S. swine systems by covering four components: respondent demographics, oral fluid implementation and primary use, sampling protocols, and sample handling/processing. After a pilot with three production systems, the refined 26-question survey was distributed from June to October 2023 through the Morrison Swine Health Monitoring Project and the American Association of Swine Veterinarian weekly e-newsletter. Responses underwent a two-stage cleaning process to remove ineligible or fraudulent entries, and descriptive statistics were generated for quantitative and categorical data, with open-ended responses summarized qualitatively.

Results and Discussion

A total of 67 valid responses were received, representing an estimated 58M growing pigs and 3.9M sows. Nearly all respondents (99%) reported being familiar with or using oral fluid sampling for diagnostic purposes. The median of ropes hung per barn was 2 (Interquartile range [IQR]: 1; 4), with 68% using one rope per two pens. The median of pens sampled per barn was 6 (IQR: 4; 10). Pigs typically accessed the rope for a median of 20 minutes (IQR: 17.5; 30). Sampling frequency varied by farm types. Half of gilt-development-unit (GDU) respondents collected samples monthly. When submitting samples to the veterinary diagnostic laboratories, pig age (91%) was the most frequently included information.

Conclusion

This study reveals the widespread and varied adoption of oral fluid sampling, highlighting the need for standardized collection procedures to support consistent interpretation and improve reliability for detecting emerging pathogens.

Keywords: Disease surveillance, Oral fluid, Sampling procedure, Sampling.

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GLOBAL MYCOTOXIN OCCURRENCE IN KEY RAW MATERIALS AND SWINE FINISHED FEEDS IN 2025

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Introduction and Objectives

Effective mycotoxin risk management starts with testing feedstuffs and assessing risks to implement mitigation strategies to ensure animal health and productivity. This study aimed to determine the incidence and contamination levels of six major mycotoxins in key feed ingredients and complete pig feeds globally in 2025.

Materials and Methods

From January to December 2025, a total of 25,006 samples from 92 countries were analyzed for Aflatoxins (Afla), Zearalenone (ZEN), Alpha Trichothecenes (A-Tricho), Beta Trichothecenes (B-Tricho), Fumonisins (FUM), and Ochratoxin A (OTA). Samples included common feed ingredients and complete feeds. Analyses used ELISA and LC-MS/MS methods.

Results and Discussion

In general, mycotoxin profile would vary depending on geographic location and weather conditions which largely influence the prevailing fungi type and the mycotoxin they produce. The 2025 Report showed the following mycotoxin profiles of the most common raw materials: Corn: most prevalent were FUM (77%), B-Tricho (71%), and ZEN (66%) with average levels of 2,041 ppb, 1,191 ppb, and 202 ppb, respectively. Wheat: B-Tricho (59%), ZEN (30%), and A-Tricho (19%) dominated, averaging 430 ppb, 70 ppb, and 42 ppb. Soybean Meal: ZEN (71%), B-Tricho (40%), Afla (35%), and A-Tricho (29%) averaged 128 ppb, 166 ppb, 4 ppb, and 42 ppb. Alarmingly, 96% of all samples showed co-contamination, increasing risk through additive and synergistic effects. For the Swine Feeds Report covering the same period: Among 1,454 samples, B-Tricho (84%), ZEN (77%), and FUM (45%) were most common, with averages of 332 ppb, 53 ppb, and 372 ppb. Co-contamination reached 98%, posing significant health challenges due to synergy and additivity of mycotoxins.

Conclusion

This global survey underscores widespread mycotoxin contamination and frequent co-contamination in feedstuffs and pig feeds. Mycotoxin risk management requires: routine testing and monitoring; risk-based assessment; and effective mitigation strategies to safeguard animal health and productivity.

Keywords: Co-contamination, Mycotoxins, Risk management, Synergy.

IMPROVEMENT OF BOAR STUDS PRRSV SURVEILLANCE: COMPARISON OF A IIPCR VS TWO RT-PCR USING POOLED BLOOD SWABS

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Introduction and Objectives

Surveillance of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is critical for boar studs, where routine surveillance is mainly based on blood swabs (BS, Reicks1) from subgroups of boars, tested on RT-PCR. Further, boar studs are far away from VDLs, and the long time-to-results compromise the semen quality. Therefore, producing innocuous semen requires extensive surveillance protocols and faster diagnostic results. The aim of this study was to evaluate two VDLs RT-PCR (PCR1: VetMAX™, PCR2: RealPCR™), versus an in-site iiPCR (PCR3: POCKIT Central™), using field BS and pooling strategies (1:5, 1:10, 1:15).

Materials and Methods

Paired serum samples (SS, n = 13) and BS (n = 158) were collected from PRRSV negative boar studs and positive farms. PRRSV status of SS was confirmed by RT-PCR1 and three positives SS categories (CtLow < 29.9, CtMed 30.0-34.9, CtHigh > 35.0) and their corresponding BS were selected. Then, one BS from each Ct group was diluted using negative BS accordingly to create the Pools (1:5, 1:10, 1:15). All resultant samples and negative control were triplicated and then tested on the three PCRs.

Results and Discussion

Qualitative results (neg-pos) showed negative controls (3/3) correctly classified by all PCRs (DxSP = 100%) and a high detection rate (24/24, DxSe = 100%) when testing in Pool 1:5 and 1:10; However, for Pool 1:15 the DxSe was 100% (12/12), 92% (11/12), and 75% (9/12) for PCR1, PCR2, and PCR3, respectively. The false negatives from PCR2 and PCR3 corresponded to samples (Ct High x Pool 1:15). Quantitative results (Ct values) showed that false negatives on PCR3 were Ct: 37, 41 and 40, on PCR2, and all were highest diluted samples (Pool 1:15). Repeatability was satisfactory among all PCRs. Kruskal-Wallis and Tukey analyses showed no statistically significant differences between Pool 1:5 and 1:10, however very diluted samples 1:15 were different ($P < 0.05$).

Conclusion

This study supports improvements on PRRSV surveillance by using an iiPCR in-site to get faster results and affordably testing of 100% boars using Pool 1:10 instead of current 1:5. That is higher "sampling sensitivity" while similar "diagnostic sensitivity". Dilutions higher than 1:10 are not recommended neither for RT-PCR nor iiPCR testing BS.

Keywords: Boar stud, iiPCR, PRRSV, RT-PCR, Surveillance.

PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS ORF5 VARIANT DETECTION DYNAMICS IN THE U.S.

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Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a major challenge for U.S. swine production due to its genetic diversity and rapid evolution. Monitoring PRRSV diversity through ORF5 sequencing helps track the emergence, persistence, and disappearance of variants. Using sequence data shared with the Swine Disease Reporting System (SDRS) from 2006 - 2025, this study describes the dynamics of PRRSV variants circulating in the U.S.

Materials and Methods

PRRSV ORF5 Sanger sequencing data from six veterinary diagnostic laboratories, representing over 98% of U.S. swine samples tested at National Animal Health Laboratory Network labs, were compiled. A centralized SQL database organized 124,901 unique ORF5 variants with metadata, and the dataset was visualized in Power BI®. Variants were classified by detection patterns from 2020 to 2025: accelerating (≥ 2-fold increase in 2025 compared to 2024), decelerating (≥ 50% reduction), stable incidence (consistent detections across 2024 and 2025), and rare/extinct (< 5 detections across 2024 - 2025). Active variants were those detected in a given year. New variants were first detected in that year, dropped variants were absent after appearing the previous year, and reappeared variants had been detected in earlier years but not the year prior.

Results and Discussion

A total of 202 PRRSV variants were evaluated. Active variants increased slightly from 2020 to 2023 (103 to 111), but declined to 93 in 2024 and 80 in 2025, indicating a reduction in circulating diversity. Nine variants were accelerating (1A.5, 1A.46, 1A.48, 1A.50, 1A.55, 1A.13.49, 1C.2.39, 1C.5.32, and 1H.18), with the variant 1C.5.32 expanding from 72 detections in 2023 to 2,757 in 2025. In contrast, 28 variants were decelerating, while 42 showed stable detections. Another 123 were classified as rare or extinct. Turnover was evident, with new variants declining from 18 in 2020 to 3 in 2025. There were 14 in 2023, 28 in 2024, and 21 in 2025, dropping variants. Finally, reappeared variants showed fluctuating patterns with 7 in 2023, 1 in 2024, and 5 in 2025.

Conclusion

Quantifying the emergence, decline, disappearance, and re-emergence of PRRSV variants provides producers and veterinarians with timely information on PRRSV dynamics, supporting more informed monitoring, control, and prevention strategies.

Keywords: Genetic diversity, PRRSV, ORF5 sequencing, Variant dynamics, Viral evolution.

EFFECTS OF INJECTABLE COMBINED GLEPTOFERRON AND TOLTRAZURIL ON ENHANCING THE QUALITY OF WEANED PIGLETS

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Introduction and Objectives

Traditional prevention of iron deficiency anemia (IDA) and coccidiosis in piglets involves iron injection during the first 1 - 3 days of life and oral toltrazuril on days 3 - 5. A combined injectable product containing toltrazuril and gleptoferron (Forceris®) has recently been developed. This study aimed to compare weaned piglet quality, specifically weaning weight and weight distribution, after switching from iron dextran plus oral toltrazuril to injectable combining gleptoferron and toltrazuril.

Materials and Methods

Retrospective data from 2024 were collected from a single farm with a history of coccidiosis, including 89,000 weaned piglets. Piglets weaned from January to June received iron dextran and oral toltrazuril (46,941 piglets), while those weaned from August to December received injectable combined gleptoferron and toltrazuril (42,059 piglets). Piglets weaned in July were considered transitional. Weaning weights were measured at 21 days of age. A two-sample T-test was used to analyze weight differences between the two groups.

Results and Discussion

Piglets treated with injectable combined gleptoferron and toltrazuril had significantly higher weaning weights than those treated with iron dextran and oral toltrazuril (5.70 vs. 5.25 kg; $P < 0.01$). A clear upward trend in average weaning weight was observed starting in August, coinciding with the introduction of the injectable protocol. Moreover, the proportion of piglets exceeding the 5.0 kg optimal target weight increased substantially when the injectable combination was used (82.7 vs. 59.7%). The enhanced performance is likely associated with superior pharmacokinetics of toltrazuril and its metabolite in intestinal tissues, improved treatment compliance via injection (Karembe et al., 2021), and the expected higher efficacy of gleptoferron compared with iron dextran in preventing IDA (Sperling et al., 2018).

Conclusion

Forceris® improved both weaning weight and the proportion of heavier piglets. Improved control of coccidiosis and iron deficiency anemia contributed to better growth performance during the farrowing period.

Keywords: Coccidiosis, Gleptoferron, Injectable toltrazuril, Iron deficiency anemia, Piglets.

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EVALUATION OF LONG-ACTING CEFTIOFUR FOR THE PREVENTION AND TREATMENT OF POSTPARTUM DISORDERS IN SOWS

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Introduction and Objectives

Postpartum disorders, including Metritis-Mastitis-Agalactiae (MMA), remain a significant challenge in commercial sow herds, especially during the periparturient period, negatively affecting sow welfare and piglet growth performance (Kemper, 2020). Strategic antimicrobial interventions around farrowing may reduce the incidence and severity of postpartum infections (Tang et al., 2010). This study evaluated the effectiveness of a long-acting ceftiofur formulation administered pre-farrowing for the prevention of postpartum disorders and for clinical recovery in sows showing signs of MMA during lactation under commercial farm conditions.

Materials and Methods

A total of 170 sows from a commercial sow herd were allocated to either a Prevention or Treatment program. In the Prevention program, sows were assigned to two groups: a control group receiving the farm's standard postpartum antibiotic (penicillin-streptomycin administered on days 1 and 3 after farrowing) and a ceftiofur group receiving a single dose pre-farrowing injection of long-acting ceftiofur administered two days before farrowing. In the Treatment program, sows showing clinical signs consistent with MMA during lactation were treated according to group assignment. Clinical parameters, including metritis, purulent vaginal discharge, and mastitis were recorded. Piglet performance indicators, including birth weight and weaning weights were measured. Recovery rates and production parameters were compared between groups using appropriate statistical tests, with significance defined as $P < 0.05$.

Results and Discussion

No clinical cases of MMA were observed in either prevention group during the first postpartum week. Among sows that developed clinical signs later in lactation, the treatment sows with long acting ceftiofur demonstrated a significantly higher recovery rate compared to controls (100 vs 57.1%; $P < 0.05$). Piglets born to sows received long acting ceftiofur had significantly higher weaning weights compared with the control group (5.92 vs. 4.82 kg; $P < 0.001$), indicating improved lactational performance and piglet growth.

Conclusion

Pre-farrowing administration of long-acting ceftiofur was associated with improved clinical recovery in sows affected by postpartum disorders and improved piglet growth performance. These findings support the strategic use of long-acting ceftiofur as part of an integrated herd health management program to mitigate postpartum disorders in commercial sow herds.

Keywords: Ceftiofur, Sow, Farrowing, Herd Health Management.

Acknowledgements: The authors thank C.P. Cambodia Co., LTD. for farm access and support in data collection, and Zoetis (Thailand) Limited for technical and scientific support.

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GUANIDINOACETIC ACID ALLEVIATES GROWTH RETARDATION OF LOW-BIRTH WEIGHT PIGLETS BY IMPROVING AMINO ACID UTILIZATION: INSIGHTS FROM MULTI-OMICS ANALYSES

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Introduction and Objectives

Higher proportions of low-birth weight (LBW) in large litters often exhibit a lifelong poor growth performance, representing a major challenge in practice (Trevisi et al., 2023). Impaired energy and nutrient transport in LBW piglets suggest that guanidinoacetic acid (GAA), a precursor of creatine, may serve as a promising nutritional intervention. Using multi-omics analyses, this study investigated whether dietary GAA supplementation could mitigate LBW-associated growth retardation and explored the underlying mechanism.

Materials and Methods

Thirty Yorkshire sows (parity 3.67 ± 1.20) with similar litter size (13 ± 2) were selected. Within each litter, high-birth weight (HBW, 1.94 ± 0.14 kg) piglets were defined as two with birth weights above the litter mean, whereas LBW piglets (1.17 ± 0.12 kg) were 2.0 SD below the mean (n = 60). After weaning, HBW and LBW piglets were each assigned to receive either control diet or diet supplemented with 1g/kg GAA. Growth performance was monitored for 28 days post-weaning; piglets were then euthanized to collect longissimus dorsi muscle and plasma for transcriptomic and metabolomic analyses.

Results and Discussion

By day 28 post-weaning, LBW piglets exhibited lower growth rates and body weight (about - 3.0 kg, $P < 0.05$) than HBW piglets. Within LBW piglets, however, GAA supplementation increased ADG during the last three weeks post-weaning ($P < 0.05$) to 250 g/d, even comparable to HBW piglets fed the control diet ($P > 0.05$). Transcriptomic analysis revealed that the top birth-weight-related differentially expressed genes were enriched in protein autophosphorylation pathways (GO: 0046777), accompanied by distinct plasma metabolites involved in glutathione, glycine, serine, and threonine metabolism. Notably, GAA-induced metabolic alterations were mainly enriched in glycine, serine, and threonine metabolism, while genes involved in 1-deoxycerimides biosynthesis (WP5194) were downregulated, suggesting enhanced amino acids (AAs) uptake in muscle, as further supported by lower circulating AAs concentrations in GAA-supplemented piglets.

Conclusion

Low birth weight is a key determinant of growth retardation in post-weaning piglets, potentially associated with lower protein turnover, as indicated by elevated plasma AAs levels. Intriguingly, GAA supplementation mitigated LBW-associated growth retardation and promoted muscle amino acid utilization, potentially via modulating the 1-deoxycerimides synthesis.

Keywords: Amino acids, Birth weight, Guanidinoacetic acid, Pigs.

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LAMP PCR TESTS TO DETECT SALMONELLA IN PIGS AT THE ARRIVAL AT SLAUGHTERHOUSE OR TO DETECT BATCH OF PIGS WITH HIGH LEVEL OF SALMONELLA SHEDDING

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Introduction and Objectives

Salmonella spp contamination is a major concern in pig farms and slaughterhouse. Detection of high-Salmonella-shedding pig batches at the arrival at slaughterhouse is essential to guarantee a low level of carcasses contamination. However, conventional microbiological detection methods take two days to give a result. LAMP PCR technology, realized without a pre-culture step, can detect DNA from Salmonella in only 35 min allowing to introduce pre-slaughter corrective interventions.

Materials and Methods

LAMP PCR test was compared to a standard quantitative PCR test to verify the possibility to detect four Salmonella strains at different concentrations (10^7 to 10^0 CFU/g) isolated from the pig and pork sector to verify the limit of detection of the test. LAMP PCR test was further compared to microbiological Salmonella enumeration according to ISO/TS 65779-2:2012 standard, to detect the level of Salmonella shedding of pig batches (20 analysis of two pools of six pig feces).

Results and Discussion

LAMP PCR and PCR tests are both able to detect genomic DNA of different concentrations of Salmonella strains with a similar limit of detection (10^3 or 10^2 CFU/g depending of the strain). LAMP PCR can detect the highest concentration of Salmonella (> 440,000 NPP/g). No false positive detection was observed. For concentrations below 440,000 NPP/g, sensitivity decreases in function of the load.

Conclusion

LAMP PCR is able to detect DNA from Salmonella in pig feces in only 35 min. The method is able to detect highly contaminated pig batches at arrival at the slaughterhouse by analyzing two pools of six pig feces. LAMP PCR is a promising tool to detect the pig batches at high level of risk and to introduce rapid pre slaughter corrective interventions.

Keywords: Lamp PCR, Quantification, Salmonella.

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IMPACT OF PRE-FARROW CEFTIFUR SODIUM ON TREATMENT AND MORTALITY RATE IN PIGLETS

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Introduction and Objectives

Initial piglet colonization primarily occurs during birth via vaginal secretions for bacterial organisms, particularly *Streptococcus suis (S. suis*). Previous studies suggest that pre-farrow ceftiofur sodium (Naxcel®) treatment of dams may reduce colonization in piglets and improve progeny performance (Gottschalk et al., 1999; Amass et al., 1996). The objectives of this study were to assess the impact of pre-farrow ceftiofur administration to dams and piglets (Gascho et al., 2016).

Materials and Methods

A 2,500-head commercial sow farm that was negative for porcine reproductive and respiratory syndrome virus, *Mycoplasma hyopneumoniae, Actinobacillus pleuropneumoniae*, and porcine epidemic diarrhea virus was used. Twenty-six farrowing rooms were allocated to either a "Treated" or "Control". The room was the experimental unit. All dams received Naxcel® at the label dose of 5 mg/kg IM on day 114 for the treatment and control of S. suis. Key production parameters were recorded at the room level, including pre-weaning mortality and timing and frequency of treatments. Mixed-effects linear regression was used to assess production and treatment outcomes, and Poisson regression evaluated treatment incidence rates with pig days as an offset. Statistical significance was defined as $P < 0.05$.

Results

Pre-weaning mortality was similar across treatment groups ($P = 0.298$), with an average of 11.9%. The average number of piglet treatments was lower in Treated rooms than in Control rooms ($P = 0.026$). Treatment incident rates were 0.009 and 0.006 per pig-day for control and treated groups, respectively. Poisson regression showed a significant 32.9% reduction in treatment incidence in treated rooms (rate ratio: 0.671; 95% CI: 0.49 - 0.92; $P = 0.013$). Most treatments occurred between days 1 - 6 (50%) and 7 - 12 (36%) of piglet age.

Discussion and Conclusion

Results of this study indicate that pre-farrow Naxcel® administration to dams can reduce the number of piglet treatments and clinical signs associated with S. suis prior to weaning, which, in turn, may decrease labor demands and overall antibiotic use. Pre-weaning mortality and the timing of piglet treatments were not impacted, with most individual piglet treatments occurring within the first 6 days of age, regardless of dam treatment. This could potentially minimize mortality-related losses and improve animal welfare by reducing disease prevalence and minimizing animal handling.

Keywords: Ceftiofur, Naxcel, Pre-farrowing treatment, Treatments.

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PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS-2 (PRRSV-2) SURVEILLANCE, PREVALENCE, PRODUCTION OUTCOMES, AND INTERVENTION STRATEGIES IN ONTARIO, CANADA

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) is a production-limiting disease with global impact. Although regional differences exist, monitoring disease dynamics and management approaches is important in understanding PRRS changes over time, and ultimately, optimal control strategies. A surveillance program was established at a swine-focused veterinary practice (servicing 185,000 sows across independently managed sites) in Ontario, Canada to monitor and evaluate PRRS outbreaks and their intervention strategies.

Materials and Methods

Sow herds are enrolled in the program upon exhibiting clinical signs of PRRS infection, with subsequent sequencing. Dedicated staff conduct surveys with veterinarians to gather information on demographics, clinical severity, genetic sequencing classifications, co-infections, outbreak history, biosecurity, farrowing schedule, suspected infection route, and mitigation strategies (e.g. elimination/stabilization, vaccination/serum inoculation). Production and diagnostic information are also collected and databased to compare metrics across herds. Timelines are created, establishing dates and procedures to be implemented on-farm, reviewed quarterly with veterinarians and producers.

Results and Discussion

Since 2022, 85% (n = 190) of sow herd outbreaks have been monitored using this surveillance model. Annual trends can be observed related to strategies used (PRRS season defined as Oct - Sept), with similar proportions of herds eliminating in 2024 - 2025 (52.4%, n = 22) versus 2023 - 2024 (46.8%, n = 29), due to increased severity of production impacts. A combination of MLV and serum inoculation was used by a majority of herds in 2023 - 2024 (50%, n = 11) and 2024-2025 (51.7%, n = 15). The remaining herds in 2024 - 2025 that chose stabilization or to 'remain positive' were located in a pig-dense region (35%, n = 7) or the impact on production was tolerable (25%, n = 5). Suspected reason for outbreak was consistently aerosol or 'unknown' for a majority of herds surveyed, across all PRRS seasons.

Conclusion

Implementing a surveillance program facilitates continuous learning and understanding of endemic disease trends and identifying effective mitigation strategies within a clinical practice. The ongoing evaluation of production outcomes by strain or intervention has become vital as PRRS virus continues to evolve and strategies change. This program demonstrates that veterinary practices can successfully implement surveillance systems, often providing detailed and specific data not possible to obtain through broader initiatives.

Keywords: Monitoring, Production, PRRSV, Surveillance.

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ACUTE PHASE PROTEINS AND CLINICAL SIGNS DO NOT PREDICT ODDS OF RECOVERY IN MODERATE TO CRITICAL LAMENESS

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Introduction and Objectives

Lameness is a painful condition which alters behavior and is a main contributor to early culling and euthanasia (Heinonen et al., 2013). Lameness is multifactorial (Engiles et al., 2022) and establishing a diagnosis antemortem is difficult (Engblom et al., 2008); hence, lameness can contribute to non-prudent antibiotic use and long stays in sick pens due to ineffective treatment. The objective was to investigate if acute phase proteins and clinical signs could be used to predict odds of recovery in lame gestating sows.

Materials and Methods

The study included lame sows from three conventional herds. The sows were included from the gestation unit. The sows had to be moderately to critically lame. To assess recovery all sows were included, treated and evaluated using identical protocols. Treatment consisted of 7 days in a sick pen combined with 5 days of antibiotics and NSAIDs. All sows were evaluated weekly (clinical examination). Re-treatment occurred until recovery (no lameness apparent at inspection) or until day 28. Blood samples were collected from V. Jugularis to measure C-reactive protein (CRP) and pig major acute phase protein (Pig-MAP) levels using ELISA. Information on parity, herd, signs of other diseases than lameness, lameness score, signs of inflammation on affected leg(s), CRP and Pig-MAP level were collected for each sow at inclusion. The ability to predict odds of recovery was evaluated using a logistic multivariate analysis.

Results and Discussion

The CRP level at inclusion was 240.5 µg/mL in the recovery group (n = 63 sows) and 327.4 µg/mL in the non-recovery group (n = 53 sows) for Pig-MAP the level at inclusion was 2.03 µg/mL in the recovery group and 2.29 µg/mL in the non-recovery group. The multivariate analysis revealed that herd ($P < 0.05$) had a significant effect on the odds of recovery but neither the clinical signs, nor acute phase protein levels at inclusion significantly changed the odds-ratios of recovery.

Conclusion

The clinical signs and acute phase protein levels measured at inclusion could not be used to predict odds of recovery and the only significant effect on the odds of recovery was herd.

Keywords: Acute phase proteins, Diagnostics, Gestating sows, Lameness, Recovery.

Acknowledgements: The authors thank the herd owners for allowing us to conduct this study and The Technical University of Denmark for the ELISA analysis.

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ASSESSMENT OF THE IMPACT OF 2 DRYING PRODUCTS ON NEWBORN PIGLET THERMAL REGULATION AND EARLY BEHAVIOUR

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Introduction and Objectives
Piglet hypothermia at birth is a major risk factor for piglet mortality. Desiccants are commonly used to help warm piglets at birth, and the addition of essential oils may enhance their benefits. This study evaluated the effects of different desiccants on piglet hypothermia at birth and early-life behaviour.
Materials and Methods
Three treatments were assigned to 255 piglets from 25 litters across two batches: 27% received no desiccant, 35% received a drying product based on absorption and without essential oils, and 38% received Mistral®, a desiccant containing natural eucalyptus essential oils. Piglets were randomly assigned to treatments within each litter based on their birth order prior to the trial. Rectal temperatures were measured at 0, 15, 30, 45, 60, 90 and 120 minutes of life, and the farrowing crates were video recorded from the farrowing until 10 hours post-birth.
Results and Discussion
Rectal temperature decreased during the first 30 minutes of life, regardless of the treatment. For all groups, piglets did not recover their initial temperature by the end of the 120 minutes of measurements. Results showed that piglets with higher birth weights had significantly higher rectal temperature ($P < 0.001$). Piglets treated with the eucalyptus natural essential oils-based desiccant tended to have higher rectal temperatures than undried piglets in the 2-hour period post-birth ($P = 0.06$). The analysis of video recordings revealed that the treatment influenced the area occupied by the piglets.
Conclusion
This study suggested that the use of a desiccant influenced both the thermal regulation of newborn piglets and their behaviour, leading to different space occupation patterns according to the treatment. As the trial was conducted in a highly prolific herd and considering the increase in litter size along with the confirmed risks of hypothermia for lightweight piglets, these results are promising. Further studies are needed to confirm these results under various conditions, including different herds, animals, management practises and environments.
Keywords: Desiccant, Hypothermia, Piglet behaviour, Thermoregulation.

SINGLE SPLIT-SUCKLING IMPROVES COLOSTRUM INTAKE AND PREWEANING PERFORMANCE IN PIGLETS

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Introduction and Objectives

Colostrum intake is closely associated with growth and survivorship of piglets, as it is the primary source of nutrients and immune factors (Muns et al., 2016). In hyperprolific sows, an imbalance between the number of functional teats and piglets results in inadequate colostrum intake. This study evaluated the effects of a single split-suckling practice on piglet colostrum intake, growth performance, and preweaning mortality.

Materials and Methods

A total of 693 live-born piglets from 44 litters were randomly assigned to a control (C; n = 423) or a split-suckling (S; n = 270) groups after farrowing. The split-suckling involved removing the six heaviest piglets for 1 h followed by smaller for 30 min at 4 h after the onset of farrowing, and was applied once. All piglets were weighed at birth and at 24 h to estimate colostrum intake (Theil et al., 2014), and again on days 3 and 21 of lactation. Preweaning mortality was recorded with date and cause. Continuous and categorical variables were analyzed using general linear mixed models and generalized linear mixed models.

Results and Discussion

On average, litter size, number of piglets born alive, and birthweight were 17.7 ± 4.1, 16.2 ± 3.4, and 1366 ± 348 g, respectively. At 24 h after farrowing onset, split-suckled piglets consumed more colostrum (+132 g, $P < 0.001$). Average-daily-gain during the first 3 day-of-lactation was higher in split-suckled piglets (+30 g/d, $P = 0.002$). Total preweaning mortality was lower in split-suckled piglets (-8.2%, $P < 0.001$). Among dead piglets, a greater proportion of control piglets died due to crushing (+21.0%, $P = 0.003$) and weakness (+42.1%, $P = 0.005$). The higher colostrum intake observed in split-suckled piglets indicated that this practice effectively enhanced access to colostrum. Adequate colostrum intake is critical for piglet survival, particularly during the first week of life (Adi et al., 2025). In addition, improved early growth enhanced piglet vitality, as piglets with low body weight are more susceptible to crushing by the sow (Muns et al., 2016).

Conclusion

The implementation of a single split-suckling practice at 4 h after the onset of farrowing improves piglet colostrum intake and early-lactation growth, thereby reducing preweaning mortality associated with crushing and weakness in hyperprolific litters.

Keywords: Average daily growth, Colostrum consumption, Piglet birthweight, Piglet separation.

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ERRADICATION OF *GLAESSERELLA PARASUIS* SEROTYPE 7 ST454 THROUGH DEPOPULATION AND REPOPULATION ON A FARM IN PERU

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Introduction and Objectives

The objective of this project was to eradicate serotype 7 by depopulation-repopulation of a high health farrow to finish 1500 sow farm, due to the high impact on mortality, health costs (USD.2.0/pig sold) and feed conversion (> 0.10 point).

Materials and Methods

The project began in December 2024 with the importation of gilts from a serotype 7-free herd. An off-site breeding facility was used to house the gilts until the farm was completely depopulated, cleaned, and disinfected. The gilts were artificially inseminated at the off-site breeding facility starting in week 6 of 2025. The depopulation process (week 0) began in week 16 of 2025 with the weekly culling of sows. All piglets were weaned off-site from week 20 of 2025 until the weaning-finishing facility was empty. All surfaces of the facility were power washed to remove 100% of organic material using industrial detergent and then thoroughly rinsed. Then the quality of the process was assessed by Adenosine triphosphate based luminometry prior to disinfection. Disinfection was achieved by torching all surfaces and applying glutaraldehyde and quaternary ammonium. Then the farm was kept empty for 2 weeks prior to repopulating it. We estimate that the cost of the project was USD$1368 per installed female, which includes the cost of importing negative gilts, inter-site movement, off-site rental, cleaning and disinfection, and indirect expenses.

Results

The farm was monitored for one year using syndromic surveillance (sampling of suspected pigs for isolation and PCR serotyping) with no growth of serotype7. After thorough cleaning and disinfection of the farm, pregnant females and the production line were introduced until fully populated. The production line showed no clinical signs and had a wean to finish mortality rate of < 1.5%. A stratified sampling of 60 samples per month was implemented at age of 6, 9, 12, and 15 weeks using the Biochek OppA ELISA, with antibody titers < 250 which are considered negative.

Conclusion

Depopulation and repopulation are effective methods for disease elimination. The success of the process depends on the rigorous planning and execution. Biosecurity maintenance is also needed to sustain the health status of the farm after repopulation.

Keywords: *Glaesserella parasuis* serotype7 St454.

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PORKCOLOMBIA'S PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME CONTROL PROGRAM WITHOUT VACCINE INTERVENTION

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Introduction and Objectives

Porcine Reproductive and Respiratory Syndrome (PRRS) causes substantial reproductive, respiratory, and economic losses in swine production worldwide. This study aimed to develop a safe and effective method to induce PRRS virus (PRRSV) immunity in Colombian sow herds in the absence of commercially available vaccines.

Materials and Methods

Between 2021 and 2025, thirty-eight commercial swine farms participated in the Porkcolombia–FNP PRRS Control Program. Herd status was determined using PCR and ELISA testing, following the classification proposed by Holtkamp et al. (2021). Sows and replacement gilts were inoculated intramuscularly with 2 mL of inoculum containing 10^2 live PRRS virus particles (PLVI), based on the RT-qPCR-to-virus particle correlation described by Ma et al. (2018). The inoculum was produced using PCR-positive nursery pig serum diluted in saline with antibiotics. It was prepared two days prior to administration, stored at -70 °C, transported under controlled conditions, thawed under refrigeration, and administered immediately.

Results and Discussion

Inoculation efficacy was confirmed when serum samples collected at 5 and 15 days post-inoculation tested PCR-positive and ELISA-positive. Herds were classified as stable when gilts aged 180 - 200 days tested PCR-negative and ELISA-positive 15 - 30 days before herd entry, tongue-tip and family fluid samples were PCR-negative, and no clinical signs were observed for at least 34 weeks following PLVI. Program outcomes included five PRRS-negative farms, ten stable herds, ten nearly stable herds, and eleven herds with other classifications. Two lateral introductions were attributed to biosecurity failures or incomplete nursery depopulation. No confections were reported.

Conclusion

Implementation of the PLVI protocol, combined with routine diagnostics, gilt acclimation, McRebel® management practices, effective sanitation, and staff training, can support PRRS control and reduce the risk of future outbreaks where vaccination is not available.

Keywords: Live Virus Inoculation, Porcine Reproductive and Respiratory Syndrome.

Acknowledgements: The authors thank Porkcolombia–FNP leadership, the Swine Board, participating producers, and farm personnel for their support and collaboration.

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THE 3D CONCEPT: THE RELATIONSHIP BETWEEN CONDEMNATIONS, PERFORMANCE AND RESPIRATORY AGENTS USING MULTIVARIATE ANALYSIS WITH HIERARCHIC AGGLOMERATIVE CLUSTER

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Introduction and Objectives

Respiratory diseases are leading causes of economic loss in swine production, driving reductions in growth, efficiency, and carcass value. To address the need for a structured, data-driven approach to quantify and prioritize losses, we developed the '3D' methodology, integrating field information, performance, diagnostics, and slaughterhouse outcomes. This study aimed to correlate condemnations, performance, and pathogenic infections through multivariate analysis using hierarchical agglomerative clustering.

Materials and Methods

Between January and July 2024, 856 flocks (1,036,983 pigs) from a cooperative in western Paraná, Brazil, were analyzed using laboratory diagnostics, performance, and respiratory condemnations according to flocks. Hierarchic agglomerative cluster was used to identify groups of variables. Clusters are generated internally by homogeneous and distinct groups, revealing patterns in the data. Cluster formation occurs successively, starting with each observation as an individual cluster, then joining those with the least dissimilarity until a single cluster remains, based on the dissimilarity measure and the chaining method. Similarity was calculated using Gower's distance, which is suitable for mixed data (categorical and numerical). Average linkage was used, computing the mean distance between all observations in groups, allowing precise interpretation of each cluster. Stability of grouping was evaluated by multiscale bootstrap represented by AU p-value. Silhouette coefficient (SC) with CI 95% were calculated to represent degree of similarity.

Results and Discussion

The averages were FCR (1.973 kg), mortality rate (3.6%), WDG (0.979 kg), condemnations per respiratory issues/total slaughter (3.61%). Multivariate analysis revealed significant associations in two clusters (general AU $P = 0.98$). Cluster 1 (AU $P = 0.85$): *Mycoplasma hyopneumoniae* with bacterial agents (SC = 0.11) and condemnations by Pneumonia (SC = 0.329) were related to DWG (SC = 0.03), FCR (SC = 0.13) and mortality rates (SC = 0.10). Cluster 2 (AU $P = 0.99$): PCV2 (SC = 0.39) and its associations with *Mycoplasma hyopneumoniae* (SC = 0.39) or bacterial agents (SC = 0.38) were related to condemnations by pneumonia (0.47), pericarditis (0.49), adhesion (0.35) and purulent pleura (0.34) (general SC 0.30 CI 95% 0.28 - 0.62).

Conclusion

Multivariate methodology provided valuable insight into the association between multiple agents with complex economic consequences in real time. By integrating data, the "3D" methodology enables prioritization of areas, focusing on high-risk groups, evidence-based actions and deliver measurable improvements.

Keywords: Condemnations, Data-driven, Multivariate, Slaughter, Sustainability.

EFFECTS OF DIETARY PROBIOTICS AND ENZYME ON GROWTH PERFORMANCE, FECAL SCORES, BLOOD PARAMETERS, AND INTESTINAL MORPHOLOGY IN WEANED PIGLETS

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Introduction and Objectives

Probiotics and digestive enzymes are common feed supplements, yet their combined impact on intestinal morphology and hematology in piglets remains under-researched. This study evaluated the effects of these supplements on growth performance, fecal scores, blood profiles, and gut morphology in weaned piglets.

Materials and Methods

Ninety 25-day-old weaned piglets were assigned to three groups (n = 30/group): a basal control diet (CON), a probiotic-supplemented diet (T1: *L. acidophilus*, *B. subtilis*, *Bifidobacterium*), and an enzyme-supplemented diet (T2: carbohydrases and proteases). The trial lasted 30 days. Fecal scores were recorded daily, while growth performance (ADG, FCR), intestinal morphology (VH, CD), and hematology were assessed at day 25 (baseline) and day 45.

Results and Discussion

Diarrhea incidence was significantly lower in T1 and T2 compared to CON ($P < 0.05$). While all groups showed physiological growth in intestinal dimensions by day 45, the treatments significantly preserved mucosal integrity. Specifically, VH in the CON group decreased by 22.12% compared to baseline (350.3 ± 48.8 µm), whereas T1 maintained VH (+3.5%) and T2 showed only a marginal decrease (-2.0%) ($P < 0.05$). ADG and FCR were improved in T1 and T2 relative to CON. Hematological parameters (RBC, PLT, RETIC) remained within standard reference ranges across all groups, indicating stable health status and normal hematopoiesis.

Conclusion

Dietary supplementation with probiotics and enzymes mitigates post-weaning intestinal atrophy by maintaining villus height and reducing diarrhea incidence, thereby enhancing growth performance. These findings suggest that T1 and T2 are effective antibiotic-free strategies for nursery pig health.

Keywords: Blood parameters, Fecal scores, Growth performance, Intestinal morphology, Weaned piglets.

Acknowledgements: The authors thank Nong Lam University HCMC, Vietnam for the support with providing testing facilities.

COMPARING SEVEN PORCINE CIRCOVIRUS TYPE 2 VACCINES COMMERCIALLY ON GROWTH PERFORMANCE IN GROWER-TO-FINISHER PIGS IN THE FIELD TRIAL

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Introduction and Objectives

Porcine circovirus type 2 viruses (PCV2) are one of the most important viral pathogens affecting the global swine industry, particularly in growing - finishing pigs. They negatively impact health and productivity, resulting in substantial economic losses. A variety of commercial PCV2 vaccines is commercially available. Despite the extensive use of these vaccines, on-farm field evaluations are still required to determine which commercial PCV2 vaccine is most appropriate for a specific farm. Therefore, the objective of the present study was to compare the effectiveness of several PCV2 vaccines commercially in growing-to-finishing pigs under field conditions.

Materials and Methods

A total of 222 starter pigs (111 males and 111 females) were used in this field study. Seven PCV2 vaccines (A, B, C, D, E, F, and G) commercially available in Thailand were evaluated. Randomized completed block design was employed. All pigs were vaccinated against PCV2 at 13 weeks of age. Seven vaccines were administrated evenly within each pen (5 - 6 pigs per vaccine). Blood samples were collected at 13, 16, 19, 22, and 25 weeks of age to assess immune responses using ELISA and RT-PCR. Pigs were individually weighed at the beginning and end of the study and average daily gains (ADG) were calculated.

Results and Discussion

Initial body weight did not differ among the vaccine groups (P = 0.806). Similarly, no significant differences were observed in final body weight among groups at the end of the study (P = 0.285). ADG tended to differ among vaccine groups; however, the difference did not reach statistical significance (P = 0.090). S/P ratios at 19, 22, and 25 weeks of age in all vaccine groups, remained above the seropositive cut-off value.

Conclusion

In this field study, pigs were vaccinated at 13 weeks of age due to increased losses observed from 19 to 22 weeks. Vaccines A and G tended to improve ADG. Similarly, previous studies have reported that PCV2 vaccination at 11 weeks of age improved growth performance and reduced mortality. In conclusion, vaccine application should ultimately be based on appropriateness for a specific farm.

Keywords: Grower-to-Finisher, Porcine circovirus type 2, Performance, Vaccine.

Acknowledgements: Papon Farm Research Station, Ratchaburi, Thailand.

EFFECT OF AN INTRAMUSCULAR ILEITIS VACCINE ON GROWTH PERFORMANCE OF WEANING-TO-FINISHING PIGS

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Introduction and Objectives

Ileitis caused by Lawsonia intracellularis, is an economically important bacterial disease in starter to finisher pigs. The disease occurs in two clinical forms: acute proliferative hemorrhagic enteropathy and chronic porcine intestinal adenomatosis. Although oral live vaccines are available, their use requires antibiotic withdrawal before and after vaccination. Therefore, this study was to evaluate an intramuscular ileitis vaccine formulated with an inactivated strain.

Materials and Methods

A total of 592 three-way crossbred piglets were used in this study. Piglets were vaccinated intramuscularly against an inactivate ileitis vaccine at 3 weeks of age using a single 2-mL administered at the neck region. Piglets were weighed and allocated to 2x2 factorial in randomized complete block design (all four treatments): (T1) unvaccinated without tiamulin (UNV+NTM), (T2) unvaccinated with tiamulin (UNV+TM), (T3) vaccinated without tiamulin (VAC+NTM), and (T4) vaccinated with tiamulin (VAC+TM). Treatments were randomly assigned and blocked by pen, with 37 piglets per pen. Average daily feed intake (ADFI), average dairy growth (ADG), feed conversion ratio (FCR), Growth efficiency (G:F), feed cost per gain (FCG), and post-weaning mortality (PWM) were evaluated.

Results and Discussion

No vaccination × tiamulin interaction was detected for initial body weight, ADFI, G:F, or PWM ($P > 0.05$). However, the vaccination × tiamulin interaction significantly affected FCR and FCG ($P < 0.05$). No vaccination × tiamulin interaction was detected for final body weight and ADG. However, a significant main effect of tiamulin was observed ($P < 0.05$).

Conclusion

The present study showed a significant increase in ADG in vaccinated pigs, confirming the negative impact of L. intracellularis infection on growth rate. In contrast to previous studies, there were non-significant effects of ileitis vaccination and antibiotic feed medication on ADG and FCR in growing–finishing pigs. The vaccination × tiamulin interaction suggested that vaccination can partially compensate for the absence of antibiotic feed medication. Importantly, an inactivated intramuscular ileitis vaccination may reduce antibiotic use.

Keywords: Growth, Ileitis, Performance.

Acknowledgements: Papon Farm Research Station, Ratchaburi, Thailand.

ANALYSIS OF PRRSV PRESENCE AND CHARACTERISTICS IN BREEDING PIG FARMS THROUGH SCREENING AND DIAGNOSTIC TESTS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) has become an endemic and difficult-to-control disease in many countries, causing substantial economic losses worldwide (Neumann et al., 2005). The objective of this study was to analyze the prevalence and characteristics of PRRS virus (PRRSV) using both surveillance screening and diagnostic testing approaches (real-time PCR) in sow herds from June to December 2024 in two major pig-producing regions in Southern Vietnam.

Materials and Methods

The study was conducted in 12 sow farms across two major pig-producing regions in Southern Vietnam, including 11 clinically healthy farms and one farm with reproductive disorders, from which 1,243 pooled samples were collected through surveillance and diagnostic testing. Samples included reproductive tissues from stillborn, mummified, and aborted fetuses, weak piglets, blood from gilts, sows, and suckling piglets, and processing fluids; diagnostic samples of the same types were obtained from sows with reproductive signs, and all specimens were tested for PRRSV by real-time RT-PCR with subsequent genotyping of positive samples using RT-PCR–based assays.

Results and Discussion

A total of 1,243 pooled samples were analyzed, including 644 blood, 53 tissue, and 430 processing fluid samples under surveillance, and 60 blood and 56 tissue samples for diagnostic testing. PRRSV was detected in 115 samples (9.25%). The prevalence was significantly higher in diagnostically tested pigs than in surveillance-screened pigs (25.00 vs. 7.63%, $P < 0.001$). Blood samples showed the highest positivity in both diagnostic (38.33%) and surveillance groups (9.78%), followed by tissues (10.71 and 1.88%) and processing fluids (5.11%). In diagnostic testing, PRRSV detection was highest in gilts (88.89%), whereas surveillance data showed the highest prevalence in weaned pigs (55.56%). Viral loads did not differ significantly between groups, and genotype 2 predominated (59.13%), followed by genotype 1 (34.78%) and co-infections (6.09%).

Conclusion

PRRSV was detected in both surveillance and diagnostic herds, with significantly higher prevalence in clinically affected pigs. Genotype 2 predominated, though genotype 1 and co-infections were also present, reflecting complex viral circulation in sow farms. These findings underscore the importance of enhanced epidemiological monitoring and proactive control measures to mitigate PRRSV impact.

Keywords: Detect, Porcine reproductive and respiratory syndrome, Prevalence, Screening, Vietnam.

FIELD VALIDATION OF A NOVEL PCV2-PRRSV-SIV MULTIPLEX QPCR KIT

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Introduction and Objectives

Viral infections play a major role in PRDC, and it's reported that PCV2 circulation continues raising concerns regarding long-term control[1]. Therefore, BioChek developed a multiplex qPCR kit containing the PRRSv-, SIV- and PCV2 targets to diagnose PRDC and monitor shedding status gilts, piglets, finishers, boars and sows. Field-validation in which the multiplex qPCR kit is compared to previously generated singleplex results is a prescribed procedure at BioChek. Matrixes that can contain those 3 pathogens are included in the validation study performed by Merefelt Livestock Diagnostics.

Materials and Methods

In total 58 samples were included in this field-validation study.
34 oral-fluid (OF) samples (of which singleplex-positive: 7 PPRSv+, 11 SIV+).
15 lung-tissue (LT) samples (singleplex-positive: 6 PRRVv+, 2 SIV+, 3 PCV2+).
9 tracheobronchial swabs (TBS) (singleplex-positive: 3 PRRSv+, 5 SIV+, 1 PCV2+).
The PRRS, SIV and PCV2 singleplex qPCR kits originated from two global producers.
An automated spin-column extraction system was used while the detection was done AB7500FAST cycler.
Per target the percentage agreement between the singleplex- and multiplex results were analyzed.

Results and Discussion

PRRSv-target: agreement % was 95% (55/58). The multiplex tested 2 negative singleplex samples positive while 1 positive singleplex sample tested multiplex negative. Those 3 samples are likely borderline samples since the Cq's of the positive tests were high. PCV2-target: 100% agreement between the single-and multiplex outcomes on the LT and TBS samples. Oral-fluids were not tested in the singleplex, but the qPCR multiplex prevalence was 47% (16/34). SIV-target: agreement % was 93% (54/58). The multiplex qPCR was more sensitive vs the singleplex outcomes. 4 singleplex negative samples tested low positive (high Cq's) in the multiplex qPCR.

Conclusion

The PRRSv-PCV2 targets of the multiplex qPCR showed similar performance on all matrixes compared with the used singleplex. Regarding SIV, the multiplex was more sensitive which could be explained by the more recent primer probe design. Surprisingly, the PCV2 virus prevalence on oral fluids was high which stresses the value of having the target in the multiplex PCR. The clinical relevance still should be assessed by investigating the viral-load on individual serum or tissue samples.

Keywords: Multiplex, PRRSv, PCV2, SIV, qPCR.

CASE REPORT: REPRODUCTIVE DISORDERS CAUSED BY JAPANESE ENCEPHALITIS VIRUS AND PARVOVIRUS

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Introduction and Objectives

Japanese encephalitis (JE) usually causes no apparent clinical signs in sows. However, infection with Japanese encephalitis virus (JEV) in pregnant, non-immune sows can result in reproductive disorders, including stillbirths and neonates showing neurological symptoms around the expected farrowing date. This report describes an outbreak of abnormal births at a commercial pig farm.

Materials and Methods

Farrowing began on July 15, 2024, at a newly established commercial farm housing 200 sows. Producer reported piglets with neurological symptoms from some litters. Two piglets exhibiting neurological signs and one aborted stillborn fetus were submitted to a diagnostic laboratory for etiological investigation. In addition, on July 25, one surviving piglet with neurological symptoms was necropsied during a farm visit and submitted to the Pig Clinical Center of Azabu University for histopathological examination.

Results and Discussion

In the etiological investigation, PCR testing of a mixed sample containing liver, spleen, kidney, lung, and brain detected parvovirus in all three samples. JEV was detected in two piglets exhibiting neurological symptoms. PCV2V was detected in one sample but at a low viral load. PRRSV and leptospira virus were not detected. Histopathological examination revealed severe non-suppurative meningoencephalitis in the brain. These findings suggest that JEV and parvovirus were involved in the reproductive disorders observed in this outbreak. The failure to administer the pre-mating vaccination against JEV and parvovirus was considered the primary cause of the outbreak. At the end of July 2024 and one month later, all sows and gilts were vaccinated against JEV and parvovirus. The reproductive performance of the first six lots showed that out of 161 total farrowings, 68 resulted in total stillbirths of all piglets. All piglets that exhibited neurological symptoms died before weaning. No particular problems were observed in reproductive performance from the second parity onward after the outbreak had subsided. In 2025, the average number of piglets weaned per litter was 13.9.

Conclusions

The reproductive disorders in this case were likely caused by JEV and parvovirus.
As this was a newly established farm, all sows were in their first parity, which likely contributed to the severity of the outbreak.

Keywords: Japanese encephalitis virus, Parvovirus, Reproductive failure.

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UNDERSTANDING SOW MORTALITY IN A MIDWESTERN U.S. HERD (2024–2025): INSIGHTS FROM NECROPSY AND PATHOPHYSIOLOGY

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Introduction and Objectives

Sow mortality remains a major limitation to productivity and welfare in intensive pig production systems worldwide. Many deaths occur without systematic postmortem investigation, limiting understanding of underlying causes. This study aimed to describe annual patterns of sow mortality in a commercial Midwestern U.S. sow farm using necropsy surveillance and to investigate pathophysiological mechanisms associated with retained piglets and gastric disorders to inform strategies that improve sow welfare, longevity, and farm performance.

Materials and Methods

From September 2024 to 2025, necropsies were attempted on all found-dead sow mortalities from a single commercial Midwestern U.S. sow farm (1 herd; n = 186 necropsies, ~13% of deaths), typically within 24 hours. Farm-level data (parity, production stage, body condition score, gestation length, and age at first service) and gross findings were recorded. Causes of death were classified using laboratory testing and on-farm production data.

Results and Discussion

Based on 186 necropsies, gastric disorders were the leading cause of death (34%), followed by retained piglets (24%), cardiovascular failure (9%), and intestinal disorders and septicemia (each 8%). Approximately 60% of mortalities occurred in gilts and parity 1 - 2 sows, with 65% during the peripartum period. Gastric-related deaths were common during summer (June - August) and the peripartum period; gastric ulceration was present in 86% of sows, including 69% of non-gastric deaths, indicating physiological stress. Retained piglets occurred primarily around farrowing and seasonal transitions. Parity 1 sows retained more piglets per case, whereas older sows retained fewer piglets with prior stillbirths. Gross findings supported pathological patterns: gastric cases showed severe ulceration with hemorrhage, melena, pallor, and clots, consistent with blood loss and energy depletion, whereas retained-piglet cases were associated with prolonged or incomplete farrowing, uterine retention, postpartum decline, and generalized congestion, consistent with systemic inflammation and circulatory collapse.

Conclusion

Year-long necropsy surveillance showed that sow deaths were biologically explainable and reflected failures during physiological transitions. Retained piglets represented an acute inflammatory pathway with uterine and systemic inflammation, whereas gastric disorders reflected a chronic injury process leading to metabolic decompensation. These findings highlight the value of systematic necropsy programs to improve sow longevity.

Keywords: Gastric Ulcers, Necropsy, Retained Piglets, Sow Longevity, Sow Mortality.

Acknowledgements: This project was supported by the National Pork Board (PR-005981) and the Foundation for Food and Agriculture Research.

FIELD EFFICACY OF ENTERIROL® ILEITIS VACCINATION COMPARED WITH NON-VACCINATION IN A THAI SWINE FARM

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Introduction and Objectives

Lawsonia intracellularis, the causative agent of porcine proliferative enteropathy (PPE), is a major enteric pathogen in swine (Guedes and Gebhart, 2003). Vaccination is widely recommended for control (Riber et al., 2015). This study compared production performance between pigs with subclinical ileitis and pigs vaccinated with a commercial *L. intracellularis* vaccine.

Materials and Methods

The study was conducted on a 1900-sow farm in central Thailand with a history of subclinical ileitis. A total of 11581 pigs (4 - 23 weeks old) from 8 batches were evaluated. Four batches received a single oral ENTERIROL® ILEITIS (Boehringer Ingelheim Animal Health, USA) vaccination at 3 weeks of age, while 4 batches served as non-vaccinated controls. Statistical analyses were performed using SAS 9.4. Continuous variables were analyzed using the GLM procedure, and categorical variables using the Chi-square test, with significance set at $P < 0.05$.

Results and Discussion

A total of 8,982 non-vaccinated pigs and 2,599 pigs vaccinated with ENTERIROL® ILEITIS were evaluated for production performance under subclinical ileitis conditions. Vaccinated pigs achieved a higher body weight at slaughter compared with non-vaccinated pigs (102.8 vs. 98.2 kg), representing an increase of 4.7 kg. In addition, vaccinated pigs reached market weight 9.8 days earlier (132.2 vs. 142.0 days). Average daily gain (ADG) was markedly improved in vaccinated pigs (718.6 vs. 635.6 g/day), corresponding to an increase of 83.0 g/day. Feed conversion ratio (FCR) was slightly improved in the vaccinated group (2.4 vs. 2.5), while total feed consumption per pig was similar between groups (227.8 vs. 227.5 kg). Vaccination was associated with lower mortality (6.2 vs. 10.2%) and reduced antimicrobial costs (USD 4.8 vs. 7.5 per pig), corresponding to reductions of 4.0 percentage points and USD 2.7 per pig. Overall, ileitis vaccination improved growth performance, feed efficiency, market age, and health outcomes while reducing antimicrobial use and costs.

Conclusion

In Thai swine farms where *L. intracellularis* is highly prevalent, subclinical infection can still negatively affect production efficiency. To achieve better disease control and improve economic outcomes, vaccination of pigs against *L. intracellularis* is strongly recommended.

Keywords: Ileitis, Lawsonia intracellularis, Porcine proliferative enteropathy, Vaccine.

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DOES DOWN-TIME AFFECT THE NUMBER OF BACTERIA AND LEVELS OF ADENOSINE TRIPHOSPHATE IN THE PIG STY?

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Introduction and Objectives

Internal biosecurity is crucial for modern pig production, and the cleaning and disinfection routine often include a vacancy period ("down-time") afterwards. However, little is known regarding the effect of down-time on the bacterial load in the farrowing pen. This study investigated the results of two respective five days of down-time in a farrowing unit, by quantification of total aerobic bacteria (TAB) and adenosine triphosphate (ATP).

Materials and Methods

Samplings were made in two identical farrowing units of 12 pens each. Both units were cleaned by scraping, soaking overnight and hot-water high-pressure wash. Following cleaning, the first unit was left to dry overnight, and the second was disinfected (potassium peroxy-monosulfate based disinfectant) the next day and then left to dry overnight. The first sampling was carried out two days after washing/disinfection and the second sampling was carried out another three days later, leaving a total of five days of down-time. Sampling was carried out at two pre-determined sampling sites in each pen, A. the corner on the slatted floor and B. in the middle of the solid floor, using a pre-moistened non-woven cloth (TAB analyses; $\log_{10}$ CFU/100 cm^2) and a cotton swab (ATP analyses; $\log_{10}$ RLU/100 cm^2; Dahlin et al., 2024).

Results and Discussion

No significant differences could be seen between the two sampling occasions, for neither TAB- nor ATP-levels. When comparing sampling immediately after washing (data in manuscript) and sampling two days later, a significant TAB reduction of approximately 2 $\log_{10}$ CFU/100cm^2 could be seen ($P < 0.05$), but no significant differences in ATP were noted.

Conclusion

Our results show that washing and a certain down-time are important for reducing the bacterial load, however, a prolonged down-time do not necessarily increase the reduction. The floors' ability to dry may be an important factor to consider when deciding the length of down-time. Further, ATP and TAB levels did not correlate, and the appropriateness of the use of ATP-tools may be questioned in an environment with a high bacterial burden.

Keywords: Biosecurity, Cleaning, Down time, Vacancy period.
Acknowledgements: The authors thank Swedish Farmers' Foundation for Agricultural Research and Knowledge Centre for Animal Production (RISE, Research Institutes of Sweden) for funding.

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CAUSES AND OUTCOMES OF UNCONTROLLED INGESTION OF UNSUITABLE OBJECTS IN MINIPIGS

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Introduction and Objectives

Foreign body–related gastrointestinal disorders are relatively uncommon in conventionally housed pigs; however, minipigs kept as companion animals in domestic or garden environments are exposed to an increased risk of ingesting inappropriate materials. Owners may misjudge the digestibility and potential hazards of various objects or substances, which can complicate clinical assessment. This report describes two clinical cases illustrating how incomplete or misleading anamnestic information combined with non-specific clinical signs can delay diagnosis and treatment of gastrointestinal obstruction in pet minipigs.

Materials and Methods

Two companion minipigs were presented to veterinary clinics with acute anorexia. In the first case, the owners reported a suspected ingestion of corncobs approximately two days prior to the onset of clinical signs. In the second case, the owners assumed that the minipig had consumed chicken bones from a compost heap in the garden. Clinical examinations, diagnostic imaging, and surgical intervention were performed in both animals.

Results and Discussion

Anorexia accompanied by reduced faecal output raised suspicion of gastrointestinal obstruction in both cases. Diagnostic imaging revealed marked gastric distension on radiography and reduced intestinal motility on ultrasonographic examination. However, the suspected foreign materials reported by the owners could not be confirmed. In the first case, the underlying cause became evident only after spontaneous vomiting of a peach pit, prompting the owners to acknowledge that the minipig had unrestricted access to fallen peaches from a fruit tree. In the second case, exploratory gastrostomy revealed ingestion of large quantities of clumping cat litter. Following this finding, the owners admitted that the animal frequently rooted in and ingested material from a cat litter box. In both cases, surgical intervention via gastrotomy and enterotomy was successfully performed, and both animals recovered.

Conclusion

These cases highlight significant gaps in owner knowledge regarding minipig behaviour, feeding habits, and physiological requirements. Misinterpretation of the term “omnivore” may lead to inappropriate environmental access and feeding practices, potentially resulting in severe, life-threatening gastrointestinal disorders in companion minipigs.

Keywords: Anorexia, Foreign Body Ingestion, Gastrointestinal Obstruction, Minipig, Owner-Related Risk Factors.

VIRAL ENVIRONMENTAL CONTAMINATION IN AND AROUND MORTALITY HANDLING STRUCTURES IN WEAN-TO-FINISH FARMS

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Introduction and Objectives

Mortality due to infectious diseases requires biosecure disposal of carcasses essential to prevent pathogen spread. Although between-farm transmission routes of swine viral pathogens are well described, limited attention has been given to dead animal disposal methods as sources of environmental contamination and pathogen dissemination. Areas surrounding mortality management structures are frequently accessed by personnel, vehicles, and equipment, creating opportunities for fomite contamination. The objective of this study was to assess viral environmental contamination around dead animal disposal structures and determine whether contamination differs by mortality management method.

Materials and Methods

A cross-sectional study was conducted on 40 Midwestern US wean-to-market farms reported as porcine reproductive and respiratory syndrome virus 2 (PRRSV-2) or porcine epidemic diarrhea virus (PEDV) positive by their attending veterinarian. Environmental samples were collected from areas surrounding rendering (dead box) and composting sites (n = 20 each). Ten samples per farm were obtained using Swiffer pads from five locations: road, ground, wall, carcass, and leachate. Samples were tested by RT-PCR for PRRSV-2, PEDV, porcine deltacoronavirus (PDCoV), and transmissible gastroenteritis virus (TGEV). Samples from each farm with the lowest cycle threshold (Ct) values were submitted for virus isolation. The proportion of positive farms and mean Ct values were compared between mortality management methods using chi-square tests and t-tests.

Results and Discussion

Out of 40 farms tested, 22 (55%) had at least one positive environmental sample. Rendering sites (80%, 16/20) tested positive for at least one virus more frequently than composting sites (30%, 6/20) ($P = 0.001$). The average Ct value for PRRSV-2 was lower at rendering sites (Ct 30.4) than at composting sites (Ct 33.83) ($P = 0.012$). Leachate and carcass samples had the lowest Ct values for all tested pathogens. No viral isolates were obtained.

Conclusion

The environment around swine mortality management structures is frequently contaminated, with higher environmental contamination observed at rendering sites. Although no viral isolates were obtained, the detection of viral genetic material supports the potential for indirect transmission via contaminated surfaces, particularly through contact with carcasses and leachate. These findings highlight the importance of improved biosecurity and targeted decontamination strategies for dead animal handling structures.

Keywords: Disease spread, Mortality, Mortality handling structures, PRRSV, Viral environmental contamination.

Acknowledgements: The authors thank the Swine Health Information Center (SHIC) for funding the project.

ERADICATION OF *MYCOPLASMA HYOPNEUMONIAE* FROM A MULTI-BARN FINISHER SITE USING GOOD BIOMANAGEMENT

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Introduction and Objectives

A 1900-sow, two-site production system became *Mycoplasma hyopneumoniae* (Mhp) positive at site 1 in March 2019. Site 2, consisting of two nursery units (11,500 places) and nine finisher barns (10,000 places) located within one compound, subsequently also became positive. Site 1 implemented eradication measures including 'load-and-closure' program, double whole-herd vaccination*, and four herd antibiotic treatments (tulathromycin). Piglets received two tulathromycin treatments during lactation and continued to be weaned to site 2 every two weeks. After successful eradication of Mhp at site 1, replacement gilts were raised off-site and remained negative. The objective was to stabilize herd health at site 2, while implementing internal biosecurity to allow potential eradication despite continuous stocking.

Materials and Methods

In August 2019, five PCR-positive finishers at site 2 received an initial oral antibiotic treatment (doxycycline/tiamulin) for 14 days. Whole-herd Mhp vaccination was carried out at site 2, and all piglets were vaccinated at weaning. Nursery and finisher units were operated by separate teams who shared only shower, office, canteen, and medication facilities. A 2% peracetic acid footbath was placed at the entrance of each barn and replaced twice weekly. Each barn used dedicated equipment, except for snares and autoinjectors, which were cleaned and fitted with new needles after each use. Each barn housed one or, at most, two batches in separate rooms, with strict all-in/all-out management for each batch.

Results and Discussion

In March 2021, after 18 months without clinical signs and consistently negative Mhp PCR results from randomly selected tracheal samples, vaccination of weaned piglets at site 2 was discontinued to further assess site status. Random samples from all barns tested negative on ELISA prior to slaughter, no clinical signs were observed, and slaughter findings were unremarkable. Site 2 was subsequently confirmed Mhp-negative, allowing internal gilt production for site 1 to resume.

Conclusion

Eradication of Mhp from a continuously stocked finishing site is achievable when structural conditions support group separation and when robust biomanagement is consistently applied-such as continuous all-in/all-out management, effective vaccination strategies, and introduction of Mhp-negative piglets.

** Vaccination was performed using an inactivated Mhp vaccine formulated with an Amphigen-based adjuvant.*

Keywords: Biomanagement, Eradication, *Mycoplasma hyopneumoniae*, Vaccination.

ADVANCING PERIPARTUM SOW HEALTH AND WELFARE THROUGH STANDARDIZED NATURAL CITRUS EXTRACT DIETARY SUPPLEMENTATION IN COMMERCIAL SYSTEMS

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Introduction and Objectives

The peripartum period, particularly farrowing, represents a major physiological challenge for sows and is frequently associated with digestive disorders. These disturbances are often linked to gut microbiota dysbiosis, compromising animal health, welfare, and subsequent reproductive performance (Pearodwong et al., 2016; Ma et al., 2023). Nutritional strategies targeting the intestinal microbiota may help mitigate these effects. This study evaluated the impact of a Standardized Natural Citrus Extract (SNCE) supplementation around farrowing on sow health and performance under commercial conditions.

Materials and Methods

Fifty sows were assigned to two groups: a control group (CTL, n = 23) fed a standard diet, and a supplemented group (SNCE, n = 27) receiving 2,500 ppm SNCE from 10 days before farrowing until 5 days after. Feed intake, litter weight gain, and intestinal transit resumption (time from farrowing to first droppings) were recorded. At the end of supplementation, 8 sows per group were randomly selected for microbiota analysis.

Results and Discussion

SNCE supplementation significantly increased feed intake (8,540 vs 7,937 g/d in CTL; $P < 0.01$) and reduced the interval between farrowing and first droppings (1.35 vs 1.88 days; $P < 0.05$), indicating faster intestinal transit recovery. Microbiota analysis revealed a clear separation between groups based on 21 OTUs (ROC area = 96%), supporting a modulatory effect of SNCE on gut microbial communities. Additionally, litter weight gain between 24 h and 7 days postpartum was higher in the SNCE group (1.35 kg vs 0.93 kg; $P < 0.01$). These effects may relate to the specific composition of the SNCE, which contains citroflavonoids such as hesperidin and naringenin. Hesperidin has been shown to exert concentration-dependent myocontractile effects on porcine intestinal smooth muscle (Mendel et al., 2016), while naringenin exhibits reported laxative properties (Yin et al., 2018).

Conclusion

Overall, SNCE supplementation improved peripartum sow welfare and early litter performance, likely through modulation of gut microbiota. Enhanced feed intake, faster intestinal transit recovery, and improved early piglet growth highlight SNCE as a promising nutritional strategy to support productivity and welfare while potentially reducing reliance on medicinal interventions.

Keywords: Citrus extract, Farrowing, Microbiota management, Sows, Welfare.

Acknowledgements: The authors thank the commercial farm for assistance with the experiment. The technical support from GetPlage is also gratefully acknowledged.

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PROPOSED INTERVENTIONS FOR A SUCCESSFUL MANAGEMENT PROGRAM TO CONTROL PEDV AND KEEP A STATUS POSITIVE STABLE IN SITE 1

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Introduction and Objectives

The practice of massive exposure increases herd immunity to PEDv and has been implemented in Mexico (Trujillo et al., 2016), different protocols have been used during their implementation, which has led to considerable variation in effectiveness, generating economic losses due to continuous outbreaks at site 1.

Materials and Methods

The protocol was implemented in 60,000 sows across 18 farms, with sizes ranging from 500 to 6,500 females in Mexico. Feedback preparation: 1) Diarrhea collected from piglets less than 48 hours 2) The viability was assessed using PCR: PEDv-positive, PRRS, TGE, PDCoV, and Rotavirus-negative 3) It calculates 60 mL per animal 4) We use a new 20-liter backpack sprayer to apply directly into the mouth, pure water, disposable bags, collection buckets, and ice packs to maintain viral viability. We use only one time. This process was complemented by pre-farrowing a commercial PEDv vaccine (Zoetis, Parsippany, NJ 07054, USA). Standardized colostrum techniques ensured 100% of piglets within the first 3 hours. Massive exposure remained a key procedure for all develop Gilts to maintain stable PEDv-positive farms.

Results and Discussion

All farms were evaluated PED-ELISA, incidence before applied is around -10% and after FB obtaining positive results in 85% of samples, this management was also applied to gilts, where the massive exposure protocol was established a standardized process. Over 10-day post-feedback, PEDv morbidity was determined in all farms. A significant decrease in preweaning mortality was observed, ranging from 90% to 16.5% (Huang, et al. 2013). Implementation of the vaccination protocol-maintained mortality rates within production targets for periods exceeding 50 weeks to date. Finally, all farms, after 15 weeks of production and negative PCR PED diagnosis, were determined to have a stable PEDv-positive status.

Conclusion

The efficacy strategy in controlling PEDv across multiple farms. Coupled with the implementation of a standardized exposure protocol for gilts, showcases a proactive approach to outbreak management. Importantly, the reduction in preweaning mortality, within four weeks of post-inoculation indicates the effectiveness of the interventions. Furthermore, sustaining mortality rates within production targets for over 30 weeks highlights the robustness of the vaccination protocol.

Keywords: Colostrum, ELISA, Mortality, PEDv, Sows.

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EFFECTS OF DIETARY PROBIOTICS AND ENZYME ON GROWTH PERFORMANCE, FECAL SCORES, BLOOD PARAMETERS, AND INTESTINAL MORPHOLOGY IN WEANED PIGLETS

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Introduction and Objectives

Probiotics and digestive enzymes are common feed supplements, yet their combined impact on intestinal morphology and hematology in piglets remains under-researched. This study evaluated the effects of these supplements on growth performance, fecal scores, blood profiles, and gut morphology in weaned piglets.

Materials and Methods

Ninety 25-day-old weaned piglets were assigned to three groups (n = 30/group): a basal control diet (CON), a probiotic-supplemented diet (T1: *L. acidophilus, B. subtilis,* Bifidobacterium), and an enzyme-supplemented diet (T2: carbohydrases and proteases). The trial lasted 30 days. Fecal scores were recorded daily, while growth performance (ADG, FCR), intestinal morphology (VH, CD), and hematology were assessed at day 25 (baseline) and day 45. At each sampling time point, two piglets per group were randomly selected for intestinal morphological analysis (total n = 12). Samples from the duodenum, jejunum, and ileum were collected for measurement of villus height (VH) and crypt depth (CD) using Image-Pro Plus software equipped with a morphometric scale, following the method described by Wilson et al. (2018).

Results and Discussion

Diarrhea incidence was significantly lower in T1 and T2 compared to CON ($P < 0.05$). While all groups showed physiological growth in intestinal dimensions by day 45, the treatments significantly preserved mucosal integrity. Specifically, VH in the CON group decreased by 22.12% compared to baseline (350.3 ± 48.8 µm), whereas T1 maintained VH (+3.5%) and T2 showed only a marginal decrease (-2.0%) ($P < 0.05$). ADG and FCR were improved in T1 and T2 relative to CON. Hematological parameters (RBC, PLT, RETIC) remained within standard reference ranges across all groups, indicating stable health status and normal hematopoiesis.

Conclusion

Dietary supplementation with probiotics and enzymes mitigates post-weaning intestinal atrophy by maintaining villus height and reducing diarrhea incidence, thereby enhancing growth performance. These findings suggest that T1 and T2 are effective antibiotic-free strategies for nursery pig health.

Keywords: Blood parameters, Fecal scores, Growth performance, Intestinal morphology, Weaned piglets.

Acknowledgements: The authors thank Nong Lam University HCMC, Vietnam for the support with providing testing facilities.

LATE-LACTATION ALTRENOGEST ADMINISTRATION MITIGATES POST-WEANING OESTRUS ALTERATIONS IN LOOSE-HOUSED SOWS WITH HIGH LITTER LOSSES

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Introduction and Objectives

The progressive adoption of loose-housing systems for lactating sows in Europe aims to improve animal welfare but is often associated with increased piglet mortality due to crushing. In addition to welfare and productivity concerns, substantial litter loss may abruptly reduce suckling stimulation, potentially inducing stress-related neuroendocrine response and premature ovarian activity during lactation. This condition may compromise the normal resumption of oestrus after weaning. The present study evaluated whether altrenogest administration during late lactation influences post-weaning oestrus expression in loose-housed sows experiencing marked pre-weaning litter losses.

Materials and Methods

One hundred loose-housed sows (parity 1 - 8), temporarily confined only around parturition, were enrolled. Sows were included when cumulative litter losses before weaning reached at least 30% of an initial average of 13.8 ± 1.6 live-born piglets, occurring at 6 ± 1 day pre-weaning. Animals were randomly allocated to a Control or Treated group. Treated sows received oral altrenogest (5 mL/day) starting on the day the litter loss threshold was reached and continuing until one day prior to weaning. The weaning-to-oestrus interval (WOI) and the proportion of sows returning to oestrus within 7 days post-weaning (RO7) were recorded and analyzed using Kruskal-Wallis and chi-square tests.

Results and Discussion

Sows receiving altrenogest exhibited a significantly shorter WOI compared with controls (4.11 ± 3.8 vs 9.8 ± 14.2 days; $P = 0.011$). In addition, the proportion of sows expressing oestrus within 7 days after weaning was higher in the treated group than in the control group (97.2 vs 81.6%; $P = 0.027$). In loose-housed sows experiencing substantial litter losses, late-lactation altrenogest administration was associated with an improved and more synchronized post-weaning return to oestrus. It can be hypothesized that reduced suckling intensity following litter loss may weaken inhibitory control over gonadotrophin secretion, predisposing to ovarian activation during lactation and delayed behavioural oestrus after weaning.

Conclusion

Although endocrine pathways were not directly investigated, altrenogest treatment may have counterbalanced this premature activation, supporting a coordinated ovarian rebound at weaning. Under the conditions of this study, this approach appears promising for maintaining reproductive efficiency in welfare-oriented farrowing systems.

Keywords: Altrenogest, Lactation, Sow, Weaning-to-oestrus interval.

PARITY-RELATED RESPONSE TO ALTRENOGEST ADMINISTERED IN LATE LACTATION ON POST-WEANING FOLLICULAR DYNAMICS IN SOWS

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Introduction and Objectives

Lactation is characterized by a physiological suppression of ovarian activity driven by suckling-induced inhibition of the hypothalamic–pituitary axis. Following weaning, the resumption of gonadotrophin secretion promotes rapid follicular growth and ovulation. In high-producing sows, follicles recruited during late lactation may develop under suboptimal metabolic conditions, potentially compromising post-weaning reproductive performance. This study investigated whether altrenogest administration during late lactation influences post-weaning follicular development, with particular attention to parity-related responses.

Materials and Methods

A total of 80 sows (parity 1 - 6; lactation length: 5 weeks; litter size: 12 - 14 piglets) were randomly allocated to a Control or a Treated group. Treated sows received altrenogest orally (5 mL/day) for six consecutive days from days -7 to -2 relative to weaning. Ovarian follicular diameter was assessed by transabdominal ultrasonography (17 cm linear probe, 3.5 MHz) at weaning (Day 0) and two days post-weaning (Day 2), expressed as the mean diameter of the three largest follicles. Data were analyzed using ANCOVA with parity class (1, 2, ≥ 3). Backfat thickness, muscle depth at weaning (parity 2), and number of weaned piglets were evaluated.

Results and Discussion

Across all sows, follicular diameter increased significantly from Day 0 to Day 2 (+0.98 ± 1.17 mm; $P < 0.001$). In multiparous sows (parity ≥ 3; n = 29), altrenogest-treated animals exhibited greater post-weaning follicular growth compared with controls (1.54 ± 1.09 vs 0.58 ± 1.25 mm; $P = 0.021$). No significant treatment effect was detected in the 1st parity (n = 34; 0.92 ± 1.37 vs 1.11 ± 1.04 mm) or 2nd parity sows (n = 16; 0.82 ± 0.88 vs 0.67 ± 1.15 mm).

Conclusion

Altrenogest administration resulted in enhanced post-weaning follicular growth in multiparous sows. It is plausible that in older sows early follicular activation during lactation may lead to premature recruitment, mitigatable by progestagen supplementation. In primiparous sows, a pronounced negative energy balance and stronger physiological suppression of ovarian activity may limit any additional effect. Under the conditions of this study, late-lactation altrenogest treatment appears to promote follicular synchronization in higher-parity sows, with potential implications for post-weaning reproductive efficiency.

Keywords: Altrenogest, Follicles, Lactation, Sow.

SWINE HEALTH INTELLIGENCE CENTER: A NEW ERA IN SURVEILLANCE AND REGIONAL DETECTION OF SWINE DISEASES IN BRAZIL

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Introduction and Objectives

Effective herd health management is vital for productivity and biosecurity in large-scale swine systems, yet endemic and emerging diseases, especially those linked to the Porcine Respiratory Disease Complex (PRDC) - remain major challenges in Brazil. To overcome fragmented diagnostic data and limited epidemiological indicators, the Brazilian Agricultural Research Corporation (Embrapa), with Universidade Federal de Minas Gerais (UFMG), Iowa State University (ISU), and Brazilian Veterinary Diagnostic Laboratories (VDLs), developed the Central Intelligence in Swine Health (CISS), an integrated surveillance platform that supports risk-based decision-making and preventive strategies within One Health framework.

Materials and Methods

CISS integrates voluntary, anonymized diagnostic data from Brazilian VDLs - including PCR results, sample type, age category, origin, and production system - using LOINC and SNOMED CT standards to ensure interoperability (Linhares et al., 2022; Trevisan et al., 2024). Each record represents a farm-level batch submission and is classified as positive if at least one sample tests positive, ensuring representativeness and reducing sampling bias. A web-based dashboard enables real-time epidemiological and spatial analyses, initially focusing on Mycoplasma hyopneumoniae, with complementary assessments of PCV2 and influenza A virus, inspired by the Swine Disease Reporting System (SDRS) (Linhares et al., 2022; Trevisan et al., 2024).

Results and Discussion

From October 2019 to December 2025, CISS consolidated 14,835 PCR submissions for M. hyopneumoniae from labs, generating 1,770 standardized records. Temporal analyses showed seasonality, with peak positivity in the second semester of 2025; in September, 50% of records were positive, coinciding with increased testing demand. These findings show how integrated surveillance informs treatment, vaccination, and biosecurity decisions. Additional analyses identified high PCV2 positivity from 2020 - 2025, with PCV2d predominating and mixed infections (PCV2b + PCV2d) remaining relevant. Influenza surveillance, aligned with SDRS experience in the United States, highlights the need for intensified monitoring to mitigate zoonotic and pandemic risks. By aggregating nationwide data, CISS enabled detection of disease patterns not evident in isolated datasets and supported targeted mitigation strategies.

Conclusion

CISS advances herd health management in Brazil by transforming routine diagnostic data into standardized, aggregated, near-real-time intelligence. The platform strengthens surveillance, enables rapid visualization of pathogen detection at national and state levels, supports timely risk-based interventions, and enhances the sustainability of swine production systems.

Keywords: Brazil, Diagnostic, Herd Health, Risk Analysis, Surveillance.

Acknowledgements: The authors thank the collaborating veterinary diagnostic laboratories for voluntarily sending the results of the tested samples.

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APPLYING FARM BIOSECURITY SCORES TO CANADIAN GROW-FINISH SURVEILLANCE DATA

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Introduction and Objectives

Biosecurity is critical for disease control and an important component of antimicrobial stewardship. Biocheck.UGent™ (Bc.UG) provides a standardized and measurable approach to monitoring and improving biosecurity. The Public Health Agency of Canada's, Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) collects annual data on AMU and biosecurity on grow-finish (GF) farms. The objective of this study was to adapt the Bc.UG scoring system to existing CIPARS swine survey data to explore trends in biosecurity scores over time.

Materials and Methods

Biosecurity questions from the CIPARS annual questionnaire and Bc.UG survey were compared. Questions considered equivalent were identified and re-weighted for each sub-category, maintaining the relative weighting from Bc.UG. Survey data from 2014 to 2023 was assessed and CIPARS biosecurity scores generated using the revised scoring system.

Results and Discussion

Twelve questions from the CIPARS survey, primarily related to external biosecurity were comparable to Bc.UG. The CIPARS external biosecurity score was out of 50, with an average score from CIPARS sentinel GF farms of 24.9 in 2014 and 30.9 in 2023. Biosecurity measures that impacted changes over time included the increased use of Danish entry, visitor restrictions, and locked doors in surveyed GF farms, particularly starting in 2016. The percentage of GF farms providing boots and coveralls was > 75% throughout the period. The requirement for downtime was variable over time and the number of pig farms within 2 km was relatively consistent. The observed increase in biosecurity measures beginning in 2016 may be related to the introduction of Porcine Epidemic Diarrhea to Canada in 2014.

Conclusion

The 109 items Bc.UG survey was too extensive to integrate into routine CIPARS questionnaires, which already collected quantitative AMU, inventory, and health data. Adaptation of the Biocheck.UGent™ survey to ongoing CIPARS surveillance, provides an opportunity to monitor biosecurity trends over time, informing stewardship initiatives.

Keywords: AMU, Biosecurity, Surveillance, Trends.

Acknowledgements: The authors thank the producers and veterinarians who participate in the CIPARS Farm Swine program and the members of the CIPARS team supporting farm surveillance.

SIMULTANEOUS ERADICATION OF PRRSV AND MYCOPLASMA HYOPNEUMONIAE IN A 7200 COMMERCIAL SOW FARM IN MEXICO

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Introduction and Objectives

Sow herds negative to PRRSv and Mycoplasma hyopneumoniae (Mhyo) optimize swine performance. Hence, the objective of this study was to test and execute a protocol to eradicate PRRSV (Pepin et al., 2026) and Mhyo (Pieters et al., 2015) simultaneously.

Materials and Methods

A 7200 commercial sow farm positive to PRRSv and Mhyo with self-replacement gilts (internal GDU) was used for this prospective study. Last PRRS outbreak occurred on week 31st 2024. The 1,000-point PIC Location and Biosecurity scores were estimated. Eradication started on week 35th 2024 (W0) by closing the farm. McREBEL management (McCaw et al., 2000) and PRRSv surveillance started on W14. Time to stability (TTS) and base line production (BLP) were measured (Linhares et al., 2014). Mass vaccination against Mhyo was used twice (W41 - W44). All piglets born between W46 and W51.5 were treated with IM with tulathromycin twice. Sows were medicated PO with Tylvalosin between W48 and W51.5. Gilts started to be weaned onsite on W55. A prospective biweekly surveillance program for PRRS and Mhyo was established within the GDU to verify status.

Results and Discussion

The PIC Location and Biosecurity scores were 504 (poor) and 679 respectively (good). Main location strengths were low regional swine density. The main biosecurity risks were associated with personnel, supplies and mortality management. With an 85% probability the last PRRSV found was classified as 1B.18 variant (VanderWaal et al., 2024). The farm was closed for 54 weeks (385 days) and 37 PRRSv negative consecutive weeks were obtained (processing fluids (n = 388), tongue tips (n = 130), and tonsil swabs (n = 11)). BLP recovered at W26 of closure. On week 7th 2026 the oldest gilts were 23 weeks of age and remained PCR and ELISA negative for PRRSV and Mhyo.

Conclusion

PRRSv and Mhyo can be eliminated from sow herds simultaneously without live virus or Mhyo inoculation. However, strict biocontainment (e.g animal movement (cross-fostering) and avoiding bloodborne transmission) is required to succeed. Swine health improvement results in improved production, reduced antibiotic use, and reduced cost.

Keywords: PRRSV eradication, Mycoplasma hyopneumoniae eradication, Swine health.

Acknowledgements: The swine producer and his team.

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IMMUNOGENICITY OF SELF-VACCINATION VIA ENRICHMENT SPRAYER IN SWINE

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Introduction and Objectives

Vaccination in swine production is labor-intensive and requires individual handling, increasing stress and cost. We evaluated a pen-mounted environmental enrichment (EE) sprayer that allows pigs to self-apply liquid vaccines to oral, nasal, and ocular mucosa. This abstract summarizes two controlled studies assessing immunogenicity following self-delivery. Objectives were to determine whether pigs reliably self-administer vaccines and whether antibody responses differ between self-delivery and conventional administration across vaccine platforms. Vaccines evaluated included live oral *Salmonella* (S), *Erysipelothrix rhusiopathiae* (ERY), and *Lawsonia intracellularis* (LAW), and killed intramuscular *Mycoplasma hyopneumoniae* (MHP) and Influenza A virus (IAV).

Materials and Methods

Five vaccine platforms were evaluated in independent trials (36 pigs per trial; 12 per treatment). Pigs were randomly assigned to Control, Hand-Vaccinated, or Self-Vaccinated groups. Hand-Vaccinated pigs received vaccines per label (live oral S, ERY, LAW; killed IM MHP, IAV); Self-Vaccinated pigs received the same products via mucosal spray using the EE device. Maternal pheromone promoted interaction. Compliance was defined as at least one confirmed spray exposure per pig, verified by dye and video; all Self-Vaccinated pigs were exposed within 90 minutes. Serum and individual oral fluids were collected through 49 days post-vaccination. Antigen-specific antibodies were measured at a blinded diagnostic laboratory. Data were analyzed using mixed-effects models ($P < 0.05$).

Results and Discussion

Self-delivery of live oral S, ERY, and LAW induced serum and/or mucosal antibody responses that did not differ statistically from conventional oral administration at most time points, with earlier mucosal responses in some trials. In contrast, self-delivery of killed intramuscular MHP and IAV resulted in significantly lower antibody responses than conventional intramuscular administration and often did not differ from Controls.

Conclusion

Self-administration via an EE sprayer supported antibody responses similar to conventional oral administration for live S, ERY, and LAW but not for killed intramuscular MHP and IAV. These findings suggest vaccine platform determines suitability for behavior-driven mucosal delivery and support field studies to evaluate scalability and protective efficacy.

Keywords: Environmental enrichment device, Maternal pheromone, Self-vaccination.

Acknowledgements: We thank Dr. Luis Gimenez-Lirola for laboratory assays.

SURVEILLANCE-BASED PREVALENCE AND DIVERSITY OF PRRSV IN FINISHING PIG FARMS

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Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) has become a persistently endemic disease that is difficult to control due to the genetic diversity of the virus and its long-term persistence within pig populations (Holtkamp et al., 2013; Huang et al., 2024). This study aimed to evaluate the prevalence of PRRSV by integrating active surveillance and diagnostic detection using real-time RT-PCR in finishing pig herds during the second half of 2024 in Southern Vietnam.

Materials and Methods

The study encompassed 13 finishing pig farms (RF). Blood and tissue samples were obtained from pigs representing diverse clinical statuses, ranging from asymptomatic individuals to those with mild or severe respiratory manifestations. Sampling included both surveillance of apparently healthy pigs and diagnostic submissions from clinically affected animals. All collected samples were tested for PRRSV using real-time RT-PCR (NKPRRSV Kit, Nam Khoa, Vietnam). PRRSV-positive samples were subsequently subjected to genotype-specific RT-PCR assays to identify the circulating viral lineages.

Results and Discussion

A total of 280 samples (191 tissue, 89 blood) were analyzed, including 196 diagnostic and 84 surveillance submissions. PRRSV was detected in 152 samples (54.3%), with significantly higher prevalence in diagnostic cases (75.5%, $P < 0.001$). Tissue samples showed markedly greater positivity (72.3%) than blood (10.1%, $P < 0.001$). Detection rates varied by clinical status, peaking in pigs with severe respiratory signs and lung consolidation (90.0%), followed by mild respiratory signs with lesions (82.4%), mild signs without lesions (43.9%), and asymptomatic pigs (52.4%), indicating substantial subclinical circulation. Among positive samples, EU-type PRRSV predominated (43.4%), followed by NA-type (25.7%), with 25% showing co-circulation of both genotypes. HP+NA co-infections were rare (1.3%). Mean Ct values differed between genotypes: EU-type (27.6 ± 4.1) and NA-type (24.6 ± 3.9).

Conclusion

These findings highlight the complex epidemiological pattern of PRRSV circulation in finishing pig farms and emphasize the importance of integrated molecular surveillance for effective PRRS control.

Keywords: Detect, Porcine reproductive and respiratory syndrome, Prevalence, Screening, Vietnam.

LONGITUDINAL MONITORING OF PORCINE RESPIRATORY DISEASE COMPLEX (PRDC) ASSOCIATED PATHOGENS DURING FATTENING AND THEIR ASSOCIATION WITH CLINICAL SIGNS AND LUNG LESIONS AT SLAUGHTER

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Introduction and Objectives

PRDC is a multifactorial condition associated with variable clinical expression and pulmonary lesions detectable at slaughter. This study integrated longitudinal oral fluid (OF) monitoring, event-based lower respiratory tract sampling, and standardized lung scoring to assess pathogen dynamics and their relationship with respiratory signs and lesion severity.

Materials and Methods

Twenty-one fattening farms in Southern Germany were investigated (October 2023 - April 2024). OF were collected at beginning, middle, and end of fattening and at slaughter and analyzed by real-time qPCR for PCV 2, PRRSV, swIAV, M. hyo, and App. In farms with respiratory signs, tracheobronchial swabs (TBS) were examined by nanopore sequencing. At slaughter, 30 lungs per farm were scored (Ceva Lung Program; EP and AP indices). Lung tissue (LT) and bronchial swabs (BS) from pigs with the lowest and the highest EP indices were analyzed by PCR.

Result and Discussion

OF monitoring showed herd-level detection of App and PCV 2 in 95.2% of farms, PRRSV in 66.7%, swIAV in 38.1%, and *M. hyo* in 28.6%. Significant differences in detection patterns were pathogen-specific: PRRSV dropped to 0% by the end of fattening ($P < 0.05$), App increased during mid and late fattening ($P < 0.05$), and PCV 2 peaked at slaughter ($P < 0.05$). Respiratory signs occurred in 71.4% of farms. In affected herds, TBS sampling most frequently identified M. hyo (86.7%). Farms with respiratory signs had significantly higher numbers of pathogens detected in OF ($P < 0.05$). Postmortem, M. hyo was detected in all BS pools, whereas viral pathogens were less frequent in LT. Ct values for M. hyo differed between low and high EP score pools; no significant Ct differences were observed for other pathogens. Importantly, Principal Component Analysis–based clustering of individual (n = 630 pigs) lung scores revealed two clear distinct farm phenotypes. High-variability lung-score farms (i.e., more differences between pigs) showed higher multi-pathogen detection and more frequent clinical signs. In contrast, low-variability farms showed a more uniform lesion distribution and lower pathogen complexity.

Conclusion

Pathogen detection varied between longitudinal monitoring, clinical episodes, and postmortem assessment. Distinct lung lesion phenotypes reflected longitudinal pathogen complexity, indicating that production-phase pathogen dynamics are manifested in lesion structure at slaughter.

Keywords: Lung lesion phenotypes, Multi-pathogen detection, Porcine Respiratory Disease Complex, Oral fluid monitoring.

FIELD EVALUATION OF CO-VACCINATING OF PCV2 + *LAWSONIA INTRACELLULARIS* IM VS PCV2 ALONE IN A FINISHING BARN WITH HISTORICAL *LAWSONIA INTRACELLULARIS* INFECTION

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Introduction and Objectives

Porcine circovirus type 2 (PCV2) and Lawsonia intracellularis (LI) are among the most economically significant pathogens affecting the global swine industry. PCV2 contributes to systemic disease, immune dysregulation, and reduced growth performance, while LI - the causes impaired intestinal function, decreased feed efficiency, and variable mortality in grow-finish pigs. In herds with a documented history of LI infection, persistent subclinical enteropathy may lead to additional performance losses even when PCV2 vaccination protocols are in place. Previous field studies have shown that LI vaccination can improve feed utilization and promote more uniform growth when endemic exposure is present. Therefore, integrating LI vaccination alongside standard PCV2 immunization may offer additive or synergistic benefits in pathogen-challenged environments. This field study evaluated whether co-vaccination against PCV2 and LI could improve growth performance relative to PCV2-only vaccination in a commercial finishing barn with known historical LI pressure.

Materials and Methods

A total of 7,669 pigs housed and placed at the same time in different barns in a finishing farm were allocated into two groups: a co-vaccination (PCV2+LI) n = 3,839 and control (PCV2-only) n = 3,830. Treatment groups were assigned randomly by barn and reared under identical commercial conditions from placement to market. Historical LI ELISA indicates positivity at 11 weeks and onwards. Primary performance indicators included ADG and FCR, metrics widely used to assess economic and biological efficiency in swine production systems. Paired T-test was used to evaluate the difference.

Results and Discussion

Co-vaccinated pigs demonstrated superior growth performance numerically (ADG 0.715 vs 0.698) although not statistically significant (P = 0.141) versus the control group. Feed efficiency also improved statistically 2.27 versus 2.38 respectively (P = 0.048). These improvements align with reports that LI vaccination enhances intestinal integrity, reduces lesion severity, and mitigates performance drag in LI-endemic herds.

Conclusions

Under field conditions characterized by historical LI pressure, co-vaccination with PCV2 and LI was associated with improved ADG and feed efficiency compared with PCV2 vaccination alone. These findings support the implementation of PCV2-LI co-vaccination strategies as part of integrated health management programs to optimize finishing performance.

Keywords: Average Daily Gain, Co-vaccination, Feed Conversion Ratio, *Lawsonia intracellularis*, PCV2.

SURVEILLANCE OF *BRACHYSPIRA HYODYSENTERIAE, BRACHYSPIRA PILOSICOLI, AND LAWSONIA INTRACELULLARIS* IN BRAZILIAN HERDS

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Introduction and Objectives

Continuous surveillance of swine diseases is essential for early detection of pathogen circulation and prevention of clinical outbreak. Enteric pathogens such as Brachyspira pilosicoli, *Brachyspira hyodysenteriae,* and *Lawsonia intracellularis* can persist subclinically and compromise productivity. This study aimed to monitor the occurrence of these pathogens in commercial Brazilian swine herds and to characterize herd management practices.

Materials and Methods

Nineteen herds were enrolled in the study, and samples were collected from grow–finish pigs aged 63 to 150 days. At each visit, 35 rectal rayon swabs were obtained to ensure detection of at least one positive animal assuming a within-herd prevalence of 10 and 95% confidence. Animals from different age groups were sampled, prioritizing pigs with clinical signs to increase diagnostic sensitivity. Nucleic acids were extracted and analyzed by multiplex qPCR for detection of *B. hyodysenteriae, B. pilosicoli*, and *L. intracellularis*. Producers completed a questionnaire addressing quarantine implementation, vaccination and biosecurity practices, and surveillance for enteric pathogens within the previous two years.

Results and Discussion

The study included herds from Minas Gerais, São Paulo, and Paraná. A total of 665 qPCR analyses were performed, with positivity rates of 13.8% for *L. intracellularis*, 5.5% for *B. pilosicoli*, and 2.8% for *B. hyodysenteriae*. Co-infections in the same animal were rare (0.45%) and occurred only between L. intracellularis and B. pilosicoli. At the herd level, 42% of farms were positive for *B. pilosicoli*, 5.3% for *B. hyodysenteriae*, and 58% for *L. intracellularis*. For *L. intracellularis*, positivity was detected in 5/6 (83.3%) vaccinated farms and 6/13 (46.2%) non-vaccinated farms. At the animal level, 34/210 pigs (16.2%) from vaccinated farms tested positive, whereas 76/210 pigs (36.2%) were positive among non-vaccinated farms classified as positive. The highest detection rate for the evaluated pathogens occurred in pigs aged 90–110 days. Biosecurity practices were inconsistently applied: 26% implemented quarantine and shower-in procedures, and 53% required farm-specific clothing. None of the herds had conducted targeted surveillance in the previous two years.

Conclusion

Limited adoption of vaccination and biosecurity measures represents a major vulnerability. Integrating routine monitoring with strengthened preventive practices is essential to improve herd health and support sustainable swine production.

Keywords: Biosecurity, Enteric pathogens, qPCR, Swine health.

EFFECT OF DIFFERENT IMMUNIZATION PROTOCOLS AGAINST PORCINE PARVOVIRUS IN GILTS AND MULTIPAROUS SOWS IN MEXICO

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Introduction and Objectives

Porcine parvovirus (PPV) is a major cause of reproductive failure in swine herds, commonly associated with increased numbers of mummified fetuses resulting from infection during gestation. Prevention strategies include commercial vaccination and feedback exposure, the latter remaining a controversial practice. The objective of this study was to compare the effects of feedback and commercial vaccination on reproductive performance, particularly the occurrence of mummified fetuses, in gilts and multiparous sows under commercial production conditions.

Materials and Methods

A comparative study was conducted to evaluate productive indicators including total piglets born (TB), born alive (BA), stillborn (SB), and mummified fetuses (MF) over 104 weeks of production in gilts and multiparous sows from a 3,000-sow commercial farm divided into two populations: one consisting of 2,500 sows and the other of 500 sows. Population 1 used feedback as an exposure method against PPV, whereas the remaining population used a commercial biological product as a preventive strategy. A repeated-measures mixed model (PROC MIXED) was used for statistical analysis, considering time as a continuous variable with a 95% confidence level. Tukey's adjusted test was used to determine statistical significance. Statistical analyses were performed using SAS/STAT 9 software.

Results and Discussion

Significant differences between treatments were observed in both gilts and multiparous sows. The main affected indicator was the increase in mummified fetuses (MF), particularly observed in population 2. An increased percentage of MF was identified in both populations. Cano (2018) reported that the normal percentage of mummified fetuses ranges between 1 - 2%; however, in this study, the maximum percentage reached 52% in the population using vaccination as a preventive method against PPV. The disease typically presents in a subclinical form, with the presence of mummified fetuses of different sizes indicating fetal death occurring at different stages of gestation

Conclusion

The results indicate that preventive strategies against PPV do not always produce the expected response. Therefore, their use in swine farms should be individually evaluated and continuously monitored under farm-specific conditions.

Keywords: Parvovirus, Seroconversion, Impact.

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INVESTIGATION INTO POSSIBLE LINKS BETWEEN HIGH AVERAGE DAILY GAIN AND COMPROMISED LEG SOUNDNESS IN FINISHER PIGS

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Introduction and Objectives

Scandinavian practitioners report increasing problems with compromised leg soundness in fast-growing finisher pigs. Previously, this has been attributed to osteochondrosis (OC), and breeding has reduced occurrence (Nordbø et al., 2026). However, in recent cases no severe OC has been shown but rather lesions in tendons, ligaments and joint capsules. Furthermore, majority of affected pigs show signs of leg deformities already at placement in the finisher units or shortly after, contrasting OC that develops during later stages of production (Olstad et al., 2014). The study's objective was to assess leg soundness in problem farms, through assessments of live pigs at different stages of production, necropsies on selected cases and investigations of possible associations between average daily gain (ADG) and compromised leg soundness.

Materials and Methods

Four batches, with various genetics, 100 pigs per batch, from three farms were studied from weaning until slaughter. Each pig weighed individually, and feed-consumption on pen level noted, twice weekly for five weeks, from weaning until placement in finisher units. At placement and at four and eight weeks thereafter, the conformation of the front legs was scored by two trained research technicians on six different traits according to an established protocol. Anomalies scored 1-3p depending on severity and scores summarized. Five high-score pigs per batch were euthanized for necropsy. Descriptive statistics performed using MS-Excel.

Results and Discussion

ADG was 0.760 (0.400 - 1.060) kg, 0.760 (0.403 - 1.065) kg, 0.821 (0.532 - 1.129) kg and 0.424 (0.206 - 0.735) kg in numerical batch order. On average for all twelve assessments, 21% of pigs got 0p, 52% 1 - 2p, 22% 3 - 4p and 5% ≥ 5p. Points for individual pigs both increased and decreased between assessments although with an overall increasing trend towards slaughter, high-scores of 7 p noted in four different pigs. In necropsied pigs no findings associated with severe OC were seen, further analysis to follow.

Conclusion

Poor leg soundness without signs of severe OC was observed in about a quarter of pigs possibly affecting both animal welfare and production economy. Further statistical analyses of the data and specimens, as well as future studies, are needed to further elucidate the underlying reasons for compromised leg soundness seen in high production herds in Scandinavia.

Keywords: Animal welfare, High average daily gain, Leg soundness, Osteochondrosis, Production losses

Acknowledgements: The authors wish to thank the *Lantmännen Research Foundation* for funding and the participating farms for their cooperation.

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POSTERS

TOPIC 7: PIG PRODUCTIO AND SUSTAINABILITY (PPS)

EFFECTS OF BOAR AGE AND BREED ON SEMEN PRODUCTION TRAITS

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Introduction and Objectives

The success of artificial insemination (AI) is highly dependent on boar semen quality (Rungruangsak et al., 2021). However, semen production is influenced by various factors, including breed, age, and collection procedures (Flowers, 2022). Therefore, the objective of the present study was to investigate intrinsic factors affecting semen production in boars in a tropical environment.

Materials and Methods

A total of 331 ejaculates were collected from 26 boars in 2025 at an AI center in Thailand. Ejaculates were categorized into three age groups based on boar age at collection: MIDDLE (8-18 months, n = 127), ADULT (19-36 months, n = 135), and OLD (37-48 months, n = 74), and were obtained from Landrace (LR, n = 118), Yorkshire (YS, n = 106), and Duroc (DR, n = 107) boars. The data included date of collection, boar identity, breed, volume (mL), motility (%), and concentration ($\times 10^6$ sperm/mL). Analyses were conducted using the MIXED procedure in SAS program.

Results and Discussions

The average age of boars in this study was 24.4 ± 9.6 months, with no differences among breeds (LR: 24.9 ± 2.5; YS: 22.5 ± 2.5; DR: 22.4 ± 2.5 months, $P = 0.557$). Volume was lower in MIDDLE (207.8 ± 14.9 mL) compared with ADULT (250.8 ± 14.9 mL, $P = 0.007$) and tended to be lower than OLD (259.7 ± 14.9 mL, $P = 0.095$). A breed effect was also observed, with YS showed lower volume (194.7 ± 18.9 mL) than LR (280.8 ± 18.9 mL, $P = 0.018$) and tended to be lower than DR (242.9 ± 18.9 mL, $P = 0.055$). In addition, sperm concentration tended to be higher in MIDDLE (362.6 ± 17.7 $\times 10^6$ sperm/mL) compared with ADULT (312.7 ± 17.7 $\times 10^6$ sperm/mL, $P = 0.034$) and OLD (309.9 ± 17.7 $\times 10^6$ sperm/mL, $P = 0.328$), with no breed effect ($P = 0.724$). These results are consistent with testicular development in young sires, leading to smaller volumes and higher sperm concentrations, but lower total sperm output than in mature boars [3,4]. Mortility was reduced in MIDDLE (78.0 ± 1.7%) compared with ADULT (79.6 ± 1.7%, $P = 0.009$) and OLD (83.0 ± 1.6%, $P = 0.001$), but higher in YS (83.1 ± 1.4%) than LR (79.4 ± 1.4%, $P = 0.014$) and DR (79.2 ± 1.4%, $P = 0.013$).

Conclusion

Boar age and breed significantly influenced semen production traits at an AI center under tropical conditions. These findings support age- and breed-specific strategies for boar selection and semen utilization to optimize AI efficiency in tropical systems.

Keywords: Age, Boar, Breeds, Factors, Semen.

Acknowledgements: The data used in this study were kindly provided by Charoenphan Samchuk Farm, Thailand.

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EVALUATION OF THE EFFICACY OF A TURMERIC/SYLIMARIN-BASED ANTI-MYCOTOXIN AGENT IN MITIGATING THE NEGATIVE EFFECTS OF FUSARIUM MYCOTOXINS: AN EX VIVO TRIAL IN PORCINE ILEAL ORGANOIDS

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Introduction and Objectives

Intestinal cell layer integrity has been proven to be compromised by Fusarium-generated mycotoxins, such as deoxynivalenol (DON) and T-2 toxin, leading to an increased susceptibility of animals to pathogens and toxicants. The use of natural plant extracts is of current interest, given their favourable health properties. Turmeric (Curcuma longa) has been proven to be a free radical scavenger and also an anti-inflammatory agent capable of reducing cytokines (TNF-α, IL-6 and IL-1β). This study aims to evaluate the effectiveness of an anti-mycotoxin agent containing turmeric and milk thistle (Silybum marianum) extracts in mitigating the detrimental effects of DON and T-2 exposure in ileal porcine organoids (IPOs) monolayers within an ex vivo model.

Materials and Methods

IPOs were treated with DON (1 µM) and T-2 toxin (0.1 µM), the anti-mycotoxin agent (0.5 mg/mL), and FITC-dextran (0.5 mg/mL) for 18h. The assessments of cell viability and intestinal permeability were conducted using mitochondrial activity (PrestoBlue) and permeability/leakage (FITC-dextran) assays, respectively. The results were expressed as a percentage of the control values. The experimental data was analyzed using the analysis of variance (ANOVA) procedure (GenStat Version 21.1, 2021, Hemel Hempstead, UK), with $P \leq 0.05$ designated as the statistically significant cut-off point.

Results and Discussion

The results demonstrated that the presence of the anti-mycotoxin agent resulted in enhanced mitochondrial activity values (+65%), which led to improved cell viability when compared with the control group ($P \leq 0.05$). The significantly increased permeability of FITC-dextran ($P < 0.05$) in the DON/T-2-contaminated medium indicated leakage. However, the permeability of the medium was found to be significantly reduced by the addition of the anti-mycotoxin agent, with a marked decrease of -44% ($P < 0.05$).

Conclusion

The use of an anti-mycotoxin agent with turmeric (Curcuma longa) and milk thistle (Silybum marianum) natural extracts in its composition resulted in enhanced cellular viability and reduced intestinal permeability on mycotoxin-challenged porcine ileal organoids. The reduction of the negative effects caused by these mycotoxins could lead to improved intestinal morphology, enhanced antioxidant and anti-inflammatory capacity, potentially favouring a balanced microbiota and reduced diarrhea.

Keywords: Anti-mycotoxin agent, Cell viability, Intestinal permeability, Porcine ileal organoids.

CLOSTRIDIUM BUTYRICUM SUPPLEMENTATION IN MULTIPAROUS SOWS IMPROVES PIGLET WEIGHT

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Introduction and Objectives

Probiotics are live microorganisms that, when administered in adequate amounts, provide health and growth benefits to the host (Liao and Nyachoti, 2017). In the swine industry, probiotics are being explored as alternatives to reduce the overuse of antibiotics. Thus, the objective of this study was to determine the effects of probiotic *Clostridium butyricum* supplementation in multiparous sows from the last week of gestation to day 21 of lactation on colostrum and milk composition and piglet weight.

Materials and Methods

Thirty-eight multiparous crossbred (Landrace × Yorkshire) sows were allocated to either a control (CON; standard diet, n = 15) or treatment (TRT; standard diet supplemented with 10 g/sow/day of *C. butyricum* spores, n = 15) from the last week of gestation to day 21 of lactation (28.6 ± 5.1 days). The probiotic contained 5×10^9 CFU/g viable spores of *C. butyricum* (TopGut®, Huvepharma Ltd., Bangkok, Thailand). Litter size and weight were recorded at birth and on days 3, 10, and 21 of age. Colostrum and milk samples (collected on days 3 and 17 of lactation) were analyzed for their major compositions. Data were analyzed using a general linear mixed model in SAS.

Results and Discussion

The average sow parity was 2.9 ± 1.2, with 11.5 ± 2.3 piglets born alive per litter. Litter size from birth to day 21 and piglet birth weight were comparable between groups. Piglets nursed by TRT sows tended to be heavier on day 10 (3.1 ± 0.2 vs. 2.6 ± 0.2 kg, $P = 0.053$), while weights on days 3 and 21 were similar. Moreover, TRT sows had higher colostrum protein (17.6 ± 0.5 vs. 15.4 ± 0.5 g/100 g, $P = 0.002$) and casein (14.1 ± 0.3 vs. 12.3 ± 0.3 g/100 g, $P < 0.001$) levels than CON sows, with no differences in other milk components on days 3 and 17. As colostrum protein and casein are key contributors to early piglet growth (Rafiee-Tari et al., 2019), these increases suggest that *C. butyricum* supplementation enhances colostrum nutritional quality and may support piglet growth.

Conclusion

Supplementation with *C. butyricum* increased colostrum protein and casein content and tended to increase piglet weight during lactation.

Keywords: Clostridium butyricum, Colostrum composition, Piglets, Probiotic, Sows.

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ADJUSTMENT FACTORS FOR GROWTH TRAITS IN PIG BREEDING IN VIETNAM

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Introduction and Objectives

Key traits such as age, back fat thickness, and loin depth at 100 kg are critical for pig breeding. However, these traits cannot be measured with complete accuracy at that weight, necessitating the use of adjustment factors. Existing adjustment factors are based on the U.S. NSIF Guidelines (1987), which may not be fully applicable to Vietnamese contexts. This study aimed to recalculate adjustment factors for key growth traits in pigs using production data from Vietnam.

Materials and Methods

Data from 50,454 pigs at 22 weeks of age approximately 100 kg body weight of Landrace, Yorkshire and Duroc breeds were used to calculate adjustment factors for the growth traits.

The general principle for calculating adjustment factors is to use the linear regression equation $y = e + kx$. Where, y is the dependent variable and x is the independent variable. The change in y per unit of x is $k = (y - e)/x$. The adjustment factors a, b, c, d were calculated as $e = \bar{y} - \bar{x}\text{cov}(x, y)/\text{var}(x)$ (Lực, 1998). Where, $\bar{y}$ and $\bar{x}$ are the means of y and x, $cov(x,)$ is the covariance of *x* and *y*, and $var(x)$is the variance of x.

Results and Discussion

Adjustment formulas:

$A_{100} = A_{act} + (100 - W_{act}) \times (A_{act} - a)/W_{act}$
$BF_{100} = BF_{act} + (100 - W_{act}) \times (BF_{act} - c)/W_{act}$
$LD_{100} = LD_{act} + (100 - W_{act}) \times (LD_{act} - d)/W_{act}$

Where:

A_{act}: Actual age in day at performance test at weight W_{act}
W_{act}: Actual body weight in kg at age A_{act}
BF_{act}: Actual back fat thickness in mm at weight W_{act}
LD_{act}: Actual loin depth in mm at weight W_{act}
A_{100}: Age in day adjusted for body weight at 100 kg
BF_{100}: Back fat thickness in mm adjusted for 100 kg of body weight
LD_{100}: Loin depth in mm adjusted for body weight at 100 kg.

Adjustment factors *a* for boar 132.63, gilt 123.75 and overall 124.13; *c* by B-mode probe back fat measurement for boar 8.80, gilt 5.09 and overall 5.40; and by A-mode probe back fat measurement for boar 2.60, gilt 2.36 and overall 2.45; *d* for boar 25.29, gilt 19.02 and overall 19.69.

Conclusion

Accurate measurement of pig growth traits is vital for genetic evaluation and herd comparison. This study presents adjustment factors based on Vietnamese pig production data for use in local farms.

Keywords: Pig breeding, Genetic evaluation, Adjustment factor, growth trait.

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USING LIFE CYCLE ASSESSMENT TO EVALUATE THE ENVIRONMENTAL BENEFITS OF A MULTI-COMPONENT PROTEASE IN PIG PRODUCTION

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Introduction and Objectives

The swine industry faces growing pressure to reduce its environmental footprint while maintaining productivity and profitability. Feed production and utilization contribute substantially to greenhouse gas emissions, land use, and resource depletion, highlighting the need for nutritional strategies that enhance nutrient utilization and feed efficiency while decreasing reliance on high-impact ingredients. Exogenous proteases improve protein digestibility and amino acid utilization, enabling diet reformulation and supporting performance across production stages. This study quantified the environmental footprint of a multi-component protease in swine diets using life cycle assessment (LCA) and evaluated its effects on production performance across nursery and grower–finisher phases.

Materials and Methods

The assessment followed Livestock Environmental Assessment Partnership (LEAP) guidelines (FAO, 2021) and ISO 14040/44 standards (ISO, 2006), applying cradle-to-feed-mill and cradle-to-farm-gate boundaries with three functional units: (1) production and delivery of 1 kg protease, (2) 1 kg feed comparing conventional high-density diets with reformulated low-density diets supplemented with protease at 125 g/t, and (3) 1 kg live-weight gain across nursery and grower–finisher phases. Zootechnical effects were derived from two systematic reviews and meta-analyses: 9 trials in weaned piglets up to 24 kg body weight (2,996 pigs) and 11 trials in grower-finisher pigs from 24 kg to slaughter (1,784 pigs), encompassing commercial-type genotypes including Yorkshire-Landrace-Duroc, Large White × Landrace, and PIC-based lines.

Results and Discussion

Production and delivery of 1 kg protease generated 3.34 kg CO_2-eq, 1.18 m² crop-eq land, 5.78 g PO_4^{3-}-eq, 10 g SO_2-eq, and 850 g oil-eq fossil resources, with over 90% of impacts from raw material sourcing. Protease inclusion at 125 g/t in reformulated low-density diets reduced feed-mill impacts by up to 24% versus high-density diets. At farm level, impacts per kg live-weight gain decreased by up to 6.4% across nursery and grower-finisher phases, driven by improved feed efficiency, enhanced growth performance, and reduced use of high-impact ingredients such as soybean meal. Nationally, widespread adoption could offset an estimated 126,000 - 194,000 tons of CO_2-eq annually.

Conclusion

Supplementing multi-component protease, informed by meta-analytic performance responses, reduces environmental impacts at feed-mill and farm levels, offering a practical LCA-quantified strategy for sustainable pork production.

Keywords: Environmental footprint, Feed formulation, Multi-component protease, Net-zero emissions, Swine production.

Acknowledgements: The authors thank McGill University for technical and analytical support.

EFFECTS OF 10% BUTAPHOSPHAN AND CYANOCOBALAMIN INJECTION ON DAY 3 POST PARTUM TO IMPROVE PIGLET PRODUCTIVITY IN HYPERPROLIFIC SOW FARMS IN THAILAND

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Introduction and Objectives
Hyperprolific sow herds frequently produce large litters with considerable numbers of low-birth-weight piglets, which show reduced viability and poorer early growth. 10% butaphosphan and cyanocobalamin (Catosal), a metabolic support product containing phosphorus and vitamin B_{12}, is used to alleviate metabolic strain during early life. This study assessed two practical dosing strategies: 1.0 mL for very small piglets and 0.5 mL for improving general litter performance in commercial hyperprolific herds.

Materials and Methods
Two field trials were conducted on commercial farms in Thailand from 2023 to 2025. In Trial 1, very low-birth-weight piglets were allocated to control or treatment groups. On day 3 post partum, control piglets received 1.0 mL saline intramuscularly, while treated piglets received 1.0 mL 10% butaphosphan and cyanocobalamin intramuscularly; both groups received 2.0 mL iron injection intramuscularly. Body weights were recorded at birth and weaning (day 23). In Trial 2, piglets from hyperprolific sows were randomly assigned to control or treatment groups. On day 3, control piglets received 0.5 mL saline intramuscularly and treated piglets received 0.5 mL 10% butaphosphan and cyanocobalamin intramuscularly; both groups received 2.0 mL iron injection intramuscularly. Birth weight, weaning weight, and adjusted weaning weight (23 days) were recorded. Data were analyzed using ANOVA, with $P < 0.05$ considered significant.

Results and Discussion
In Trial 1, piglets in the 10% butaphosphan and cyanocobalamin group had lower initial weights (1.34 vs 1.46 kg; $P = 0.009$), yet achieved higher weaning weights (5.93 vs 5.39 kg; $P = 0.00045$). Average daily gain improved from 0.18 to 0.21 kg/day ($P = 0.00045$). In Trial 2, birth weights were comparable (0.94 vs 0.96 kg; $P = 0.67$). Piglets receiving 0.5 mL showed higher weaning weights (4.07 vs 3.72 kg; $P = 0.037$) and better average daily gain (0.16 vs 0.14 kg/day; $P = 0.0099$). Adjusted 23-day weaning weight was numerically higher (4.66 vs 4.26 kg; $P = 0.059$).

Conclusion
Day-3 of 10% butaphosphan and cyanocobalamin administration improved growth in hyperprolific herds. A 1.0 mL dose supported compensatory growth in low-birth-weight piglets, while 0.5 mL enhanced general litter performance, offering practical tools for improving piglet development.

Keywords: Average daily gain, 10% butaphosphan and cyanocobalamin (Catosal), Hyperprolific sows, Piglet performance, Weaning weight.

Acknowledgements: This study is supported by Elanco (Thailand).

EMERGING ALTERNATIVE FEEDSTUFFS FROM AGRO-INDUSTRIAL RESIDUES IN FATTENING PIG NUTRITION

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Introduction and Objectives

In modern animal production systems, the use of alternative feed sources is essential for reducing production costs, protecting natural resources, and improving meat quality (Saini et al., 2025). This study evaluated the impact of a unique silage produced by agro-industrial by-products (olive oil, wine-making and feta cheese production) (Petrotos et al., 2021) on growth, meat quality and health parameters of fattening pigs.

Materials and Methods

Eighteen (nine gilts/nine barrows) 120-day-old- pigs were randomly allocated to three groups and fed diets in which the innovative silage partially replaced a portion of the basal feed ingredients, at inclusion levels of 0% (Control, Group A), 5% (Group B), or 10% (Group C). After 60 days, samples of the tricepsbrachii and external abdominal oblique muscles were obtained from all animals, for chemical and microbiological analyses. Measurements included antioxidant activity, total phenolic content, fatty-acid profile, pH and meat color. Blood biochemistry was analyzed, ileal and cecal digesta were collected to assess intestinal microbiota.

Results and Discussion

Final body weight did not differ among groups while meat composition (fat, protein, collagen, ash) and pH were unaffected ($P > 0.05$). ALT levels were significantly lower in group C compared to A ($P \leq 0.05$). In the ileum, Enterobacteriaceae and Enterococci populations decreased, whereas Lactobacilli increased in B and C ($P \leq 0.05$). Cecal Enterococci were reduced in both B and C ($P \leq 0.01$). Group C showed higher total phenolic content ($P \leq 0.05$) and an improved n-6/n-3 ratio (15.09 vs. 17.54 in A). TBARS values did not differ among treatments. Campylobacter jejuni counts were lower in treatment C. Salmonella spp and Listeria monocytogenes were not detected in any sample. Meat color of tricepsbrachii was redder in both treatments B and C ($P \leq 0.05$) (Vlaicu et al., 2019).

Conclusion

The use of the novel silage based on waste by-products retrieved from the agro-food industry, did not negatively affect meat quality characteristics but in addition, it configured a favorable ratio of n-6/n-3 fatty acids in the muscle tissue, increased the concentration of total phenols and microbiologically formed a beneficial profile of eubiotic microbial organisms that were strongly correlated with the zootechnical results, health and welfare of the pigs.

Keywords: Antioxidant status, Fattening pigs, Microbial counts, Novel silage, Pork meat quality.

Acknowledgements: This research has been co-funded by European Union, European Regional Development Funds (E.R.D.F.) and by National Funds of Greece and Italy. Interreg V-A Greece-Italy, 2014-2020. Project number (MIS) 5003778, Acronym: «Inno.trition».

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FROM WASTE TO FEED: AGRO-FOOD BY-PRODUCTS AS FEED INGREDIENTS FOR PIG DIETS

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Introduction and Objectives

The search for alternative feed resources has become a priority in modern animal production systems. In this context, the present study evaluated a novel silage derived from Greek agro-industrial by-products, including olive, winery, and feta cheese wastes, as a dietary supplement for weaned pigs. The silage was incorporated into pig diets and its effects on growth performance, intestine microbiota and meat quality characteristics were assessed.

Materials and Methods

Piglets aged 34 days were assigned to three different dietary treatments, (A-control diet, B-5% silage, C-10% silage). At 74 days of age, samples of triceps brachii (shoulder), external abdominal oblique (pancetta) and biceps femoris (ham) muscles were collected from six animals per treatment, for chemical and microbiological evaluation. Antioxidant activity, total phenolic content, fatty acid composition, and pH in the meat cuts were assessed. Intestinal contents from the ileum and cecum were aseptically collected to characterize the intestinal microbial profile of the piglets.

Results and Discussion

Piglet performance indices were not negatively affected ($P > 0.050$). Clostridium spp. counts were significantly reduced in ham samples from both supplemented groups and in pancetta samples for the C-10% group. Total mesophilic counts in ham were lower in the C-10% group ($P < 0.05$). No significant differences were observed among treatments for total mesophilic count, *E. coli, Staphylococcus aureus*, Staphylococcus *spp.*, or *Campylobacter jejuni* in pancetta and shoulder samples, nor for Clostridium *spp.* in shoulder meat. Meat chemical composition differed ($P < 0.05$) in ash content of shoulder and pancetta, whereas pH values were unaffected. Dietary supplementation influenced intestinal microbiota, with shifts in anaerobic bacteria and Lactobacillus populations in both ileum and caecum ($P < 0.05$). Lipid oxidation was reduced in ham and pancetta, as indicated by lower TBARS values, while total phenolic content increased in shoulder and pancetta ($P < 0.05$). The n6/n3 fatty acid ratio was reduced and polyunsaturated fatty acids were increased in shoulder and pancetta samples of supplemented groups ($P < 0.05$).

Conclusion

The inclusion of the novel silage in the diet favorably modulated gastrointestinal microbiota and improved key meat quality characteristics, contributing to increased added value of the final product.

Keywords: Antioxidant status, Microbial counts, Novel silage, Pork meat quality, Weaned pigs

Acknowledgements: This research has been co-funded by European Union, European Regional Development Funds (E.R.D.F.) and by National Funds of Greece and Italy. Interreg V-A Greece-Italy, 2014-2020. Project number (MIS) 5003778, Acronym: «Inno.trition».

ULTRASONOGRAPHIC DETERMINATION OF FETAL AGE IN PIG FETUSES FOR ENFORCEMENT OF ANIMAL WELFARE IN TRANSPORT AND SLAUGHTER

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Introduction and Objectives

Slaughter of pregnant sows persists despite legal restrictions. In 2017, 3% of sows in Germany were pregnant at slaughter, including 0.3% in the final third of gestation (Rolzhäuser et al., 2019). Council Regulation (EC) No. 1/2005 prohibits transport beyond 90% gestation, and German law restricts slaughter in the last trimester. Accurate fetal age determination is essential for enforcement. Existing reference data for gestational age estimation in pigs is outdated and methodologically limited, particularly considering increased litter sizes and reduced individual birth weights. This study aimed to generate validated ultrasonographic fetometric reference data to support reliable gestational age assessment and animal welfare.

Materials and Methods

Seventy pregnancies (57 sows, 13 gilts) were prospectively examined on a university research farm. Animals included a low-prolificacy genotype (German Saddleback, n = 20) and medium- to high-prolificacy genotype (German Landrace and Duroc × German Landrace, n = 50). Transabdominal ultrasonography was performed throughout gestation, focusing on trimester boundaries. Two fetuses per pregnancy were assessed. Seven fetometric parameters were recorded: rostro-occipital distance, biparietal diameter, orbital diameter, sternum length, thorax diameter, body diameter, and crown–rump length (CRL). Mean values per pregnancy were analyzed. Effects of genotype, litter size, and parity were evaluated.

Results and Discussion

All fetometric parameters increased consistently with advancing gestation. CRL was the most informative parameter in early and mid-gestation, increasing from a median of 3.2 cm at the end of the first trimester to 16.3 cm at the end of the second trimester. In late gestation, CRL was no longer reliably measurable due to fetal size, whereas cranial, thoracic, and body diameters remained assessable and enabled trimester allocation. No relevant differences in fetometric growth were detected between genotypes. Litter size and parity showed no significant influence on fetal dimensions. Fetometric values were consistently lower than historical reference data, reflecting long-term genetic and management-related changes in pig production.

Conclusion

Existing reference data for fetal age estimation in pigs is outdated. This study provides in vivo ultrasonographic fetometric reference data for trimester-based gestational age determination under contemporary production conditions, supporting enforcement of animal welfare regulations regarding transport and slaughter of pregnant sows.

Keywords: Animal welfare, Fetus, Gestational age, Pig, Slaughter.

Acknowledgements: Funded by Tönnies Forschung GmbH (TF 2022/01011/004).

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LOW MATERNAL HEMOGLOBIN DURING GESTATION AFFECTS LONG-TERM PERFORMANCE OF OFFSPRING

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Introduction and Objectives

Low blood hemoglobin (Hb), commonly linked to iron deficiency, is well documented in neonatal piglets, while reduced Hb during gestation is increasingly reported in sows (McClellan et al., 2024). However, the consequences of lower maternal Hb on piglet hematological status and long-term growth remain unclear. This study evaluated the association between sow Hb concentration at mid-gestation, piglet anemia, and subsequent growth performance.

Materials and Methods

A total of 40 primiparous and multiparous sows and their offspring weaned at 21 days were monitored. Blood Hb concentrations were measured in sows and piglets. Sows were classified according to Hb concentration at 65 days of gestation (G65) with Hb < 11 g/dL used to identify sows with lower Hb status. Piglets were considered anemic when Hb was < 9 g/dL. Growth performance of offspring was recorded until slaughter. Growth performance and proportion of stillborn piglets were analyzed using linear models including sow Hb status at G65, parity and their interaction as fixed effects. Whereas piglet anemia prevalence was analyzed using generalized linear models with the same fixed effects.

Results and Discussion

At G65, 37.5% of sows had lower Hb status, increasing to 87.5% at weaning. Piglets born to sows with lower Hb at G65 tended to have a higher prevalence of anemia at birth compared with those from sows with higher Hb (56.6 vs. 43.0%; $P = 0.09$). Stillbirth proportion was significantly higher in sows with lower Hb at G65, irrespective of parity (13.3 vs. 6.6%; $P = 0.02$), while total piglets born were unaffected by sow Hb status or parity. Piglet Hb concentrations at weaning and at 67 days were not influenced by sow Hb status. However, offspring from sows with lower Hb at G65 exhibited reduced average daily gain during the fattening period compared with those from sows with higher Hb (910 vs. 958 g/day; $P < 0.05$). This delayed growth response may result from prenatal programming that limits growth efficiency during fattening phase.

Conclusion

Lower maternal hemoglobin during gestation negatively affects stillborn incidence and offspring growth, highlighting the need for nutritional strategies to support sow hemoglobin status.

Keywords: Anemic Sows, Hemoglobin Concentration, Stillborn, Performance.

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EFFECT OF SUPPLEMENTING SOWS WITH A BLEND OF MICRONUTRIENTS ON THEIR HEMATOLOGICAL STATUS AND CONSEQUENCES ON THEIR REPRODUCTIVE PERFORMANCE

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Introduction and Objectives

Iron deficiency anemia (IDA) is a prevalent condition in modern hyperprolific sows, causing a reduction in the concentration of red blood cells during gestation and insufficient recovery between reproductive cycles (McClellan, 2024). Hematological deficits in the sow can impair the uterine environment, increase farrowing complications, and reduce iron levels in neonates. This study explored whether an enhanced micronutrient premix could support sow hematology and reproduction, as well as piglet physiology.

Materials and Methods

Sixty sows were allocated to either the CONTROL (100 ppm FeSO4, inorganic Cu and Zn) or SUPPLEMENTED (150 ppm Fe glycinate, same level of Zn and Cu but as glycinates and higher levels of vitamins A, E, B2, B6, B9, B12, and C) diet, from breeding of Cycle 1 to weaning of Cycle 2. Sow hemoglobin (Hb) levels were assessed at five time points per cycle (weaning of last cycle, d28 and d77 of gestation, farrowing, and weaning). Iron intake was quantified by multiplying the feed intake by dietary iron (Fe) concentration. Litter performance, farrowing traits, piglet Hb at birth, weaning (d21) and early post-weaning growth (d42) were recorded. Subsets of piglets from both diets were followed to slaughter for long-term performance and carcass composition data.

Results and Discussion

SUPPLEMENTED sows consumed more dietary iron (+23%; $P < 0.01$) and maintained higher gestational Hb. At farrowing, only the SUPPLEMENTED group exceeded the 10 g/dL moderate IDA threshold (10.2 vs. 9.8 g/dL; $P = 0.02$). Their piglets had higher birth Hb ($P < 0.05$) and fewer anemic individuals, confirming improved maternal-fetal iron transfer. Reproductive outcomes were unchanged, though parity-specific benefits occurred. Post-weaning piglets from SUPPLEMENTED sows showed higher ADG (+8%; $P < 0.05$) and feed intake (+15%; $P < 0.01$), reflecting better early-life robustness. Finishing performance was similar between diets, but SUPPLEMENTED offspring had greater carcass leanness under restricted feeding ($P < 0.05$).

Conclusion

These findings show that targeted micronutrition improves sow hematology and provides measurable benefits to piglets from birth through weaning. The results support using bioavailable trace minerals and vitamins to mitigate maternal anemia and enhance piglet robustness in modern production systems.

Keywords: Anemic Sows, Hemoglobin Concentration, Piglet Robustness.

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EFFECT OF NUTRITIONAL STRATEGY ON THE PREVALENCE OF IRON DEFICIENCY ANEMIA IN SOWS AND CONSEQUENCES FOR THEIR OFFSPRING

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Introduction and Objectives

Iron deficiency anemia (IDA) is common in neonatal piglet and increasingly recognized as a condition in modern hyperprolific sows associated with stillbirths and prolonged farrowing (McClellan, 2024). This study explored whether supplementing gestating and lactating sows with additional iron and vitamins involved in heme synthesis (Vit C, B6, B9, B12) could reduce IDA and improve farrowing outcomes and iron status of piglets over two reproductive cycles.

Materials and Methods

Seventy-two sows (LWxLR) were allocated into one of two treatment groups for two full reproductive cycles, from breeding of Cycle 1 until weaning of Cycle 2 (40 weeks): (1) Negative Control (NC) with standard gestation and lactation diets (100 ppm added FeSO4); or (2) BLEND- diets with additional iron (200 ppm added FeSO4 + 50 ppm glycinate Fe) and heme-related vitamins. During Cycle 1, piglets received no iron supplementation to maximize detection of maternal effects; in Cycle 2, an oral iron supplement was provided to the piglets in a creep-feed from day 12 of life. Sow hemoglobin (Hb) was measured at five time points (entrance in mating room, d28 and d77 of gestation, farrowing, and weaning) per cycle while piglet Hb at birth and weaning at day 21 of life. Farrowing duration, piglet vitality scorecard, litter size, mortality, and growth were also evaluated, and all data were statistically analyzed using ANOVA or Chi-square tests.

Results and Discussion

BLEND supplementation did not significantly modify sow Hb level, though older sows, which are most prone to anemia, showed a numerical improvement at d77 of gestation. BLEND piglets, however, demonstrated higher Hb level at birth (9.8 vs 9.2 g/dL; $P < 0.0001$) with a lower proportion of anemic newborns. This advantage disappeared by weaning, particularly in Cycle 1, where the piglets did not receive iron supplementation. The litter size, vitality, mortality, and growth did not significantly differ between the treatment groups.

Conclusion

While sow performance responses were limited, maternal iron-vitamin supplementation improved neonatal iron status and reduced the risk of prolonged farrowing, with greatest potential benefits in older sows. Further studies are needed to confirm wider performance benefits in sows.

Keywords: Anemic Sows, Hemoglobin Concentration, Stillborn, Prolonged Farrowing.

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COMPARATIVE EFFECTS OF *SACCHAROMYCES CEREVISIAE* FERMENTATION-DERIVED POSTBIOTICS ON GUT HEALTH IN PIGLETS ACROSS DIFFERENT PRODUCTION SYSTEMS

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Introduction and Objectives
Pre-weaning diarrhea remains a major constraint in swine production, particularly following the global reduction in antibiotic growth promoter use. Saccharomyces cerevisiae fermentation-derived postbiotics (SCFP) have emerged as a nutritional strategy to enhance gut health and disease resilience in young pigs. However, their efficacy may depend on production conditions. This study evaluated the effects of SCFP supplementation on diarrhea incidence, intestinal morphology, and intestinal barrier-related gene expression in piglets reared under two contrasting production systems: an intensive high-biosecurity closed-farm system and a low-biosecurity smallholder system.

Materials and Methods
In each system, sows and their litters were assigned to one of three dietary treatments: Control (CON), beta-glucan (BG; 1.0 kg/mT, positive control), or SCFP (2.0 kg/mT). Experimental diets were fed to sows from insemination through weaning. Piglets received the corresponding treatments via supplemented creep feed introduced at 4 days of age and continued until weaning. The BG supplement was a commercial product used in Vietnam containing beta-glucan, mannan oligosaccharides, Lactobacillus acidophilus, and vitamin B. Diarrhea incidence was recorded daily. At weaning, 10 piglets per treatment group (n = 30 per system) were euthanized for tissue collection. Ileal samples were used for histological evaluation of villus height and crypt depth and for mRNA expression analysis of tight junction genes (Claudin-1, Occludin, ZO-1) and the cytokine IL-1β.

Results and Discussion
In the intensive system, SCFP significantly reduced diarrhea incidence and increased the expression of Claudin-1 and Occludin compared with the CON group. In the low-biosecurity smallholder system, SCFP also reduced diarrhea but did not significantly alter intestinal morphology or gene expression, likely due to high environmental pathogen pressure. BG supplementation showed intermediate, non-significant effects on diarrhea and gene expression in both systems. Across systems, no treatment affected intestinal morphology, indicating that SCFP benefits at the 0.2% inclusion level were primarily molecular.

Conclusion
SCFP effectively reduces pre-weaning diarrhea across different production environments. Its benefits are mainly mediated through molecular reinforcement of intestinal barrier function rather than through detectable structural changes. These molecular responses are system-dependent and more evident under high-biosecurity conditions. Higher inclusion levels may be required in low-biosecurity systems under conditions.

Keywords: Diarrhea, Gut barrier integrity, Saccharomyces cerevisiae, Piglet, Tight junction.

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PRODUCTIVE PERFORMANCE AND MEAT TECHNOLOGICAL TRAITS OF FEMALE PIGS SUBJECTED TO IMMUNOCASTRATION WITH A GNRH-BASED VACCINE

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Introduction and Objectives

Immunocastration is widely used in swine production as an alternative reproductive management strategy, improving growth and meat quality. In females, it may control estrus, reducing behavioral and physiological fluctuations that impair efficiency and welfare. This study evaluated the effects of immunocastration with a GnRH-based vaccine (LeanVac®, Ourofino Saúde Animal) on performance, behavior, welfare, and meat technological traits in female pigs.

Materials and Methods

Female pigs were assigned to two treatments: control (non-vaccinated) and immunocastrated (LeanVac®). Animals were housed in 42 pens (26 per pen). Treated females received two doses at 94 and 122 days of age. Estrus-related behavior was monitored continuously. Performance variables included average daily gain (ADG), daily and cumulative feed intake (FI), feed conversion ratio (FCR), and final body weight (FBW) at 155 days. Meat lipid oxidation (LO) was determined. Data were analyzed using repeated-measures ANOVA with Greenhouse–Geisser correction ($P \leq 0.05$).

Results and Discussion

ADG 14 days after the second dose was higher in the LeanVac® group than control (1.36 vs. 1.29 kg; $P = 0.00014$), consistent with evidence that suppression of reproductive hormones redirects energy to tissue growth. Non-vaccinated females showed more estrus and mounting behavior, whereas immunocastrated females were more stable. Treated animals had 2.3 kg higher FBW at 155 days, which may offset vaccination costs and provide economic benefit. FI and FCR did not differ between treatments. LO was lower in the LeanVac® group (0.08 vs. 0.11; $P < 0.0001$), indicating improved oxidative stability, an important attribute for shelf life and sensory quality.

Conclusion

Immunocastration with LeanVac® enhances growth performance in female pigs by increasing ADG and FBW without affecting FI or FCR. It also reduces lipid oxidation, enhancing meat technological quality. The use of LeanVac® in female pigs also contributes to improved behavioral stability, welfare and batch uniformity, representing an effective strategy that may reduce slaughter age while maintaining FBW

Keywords: Average daily gain, Feed efficiency, Female pig, Lipid peroxidation, Pork quality.

INSPIRED TO BOUNCE BACK: EX-POST IMPACT ANALYSIS OF THE PHILIPPINE PIG REPOPULATION PROGRAM

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Introduction and Objectives

The Integrated National Swine Production Initiatives for Recovery and Expansion (INSPIRE) is a national program of the Philippine Department of Agriculture designed to repopulate the swine industry following severe losses from African swine fever (ASF). This study aimed to: (1) conduct an ex-post impact evaluation of INSPIRE in Central Luzon, CALABARZON, and Davao Region in terms of liveweight pig production; (2) perform an economic cost–benefit analysis of INSPIRE grants for 2022–2023; and (3) estimate additional government investment requirements to restore pig production to pre-ASF (2018) levels.

Materials and Methods

Institutional data were analyzed using SARIMA modeling and financial analyses. Two counterfactual production forecasts were generated: one assuming no ASF outbreaks using quarterly data from 2000Q1–2019Q2, and another reflecting the pre-INSPIRE period using data from 2000Q1–2021Q4, which were compared with actual production data from 2021 to 2024, corresponding to the INSPIRE implementation period, to assess program impact. Cost–benefit analysis integrated information from actual production data with ARIMA-based forecasts.

Results and Discussion

The projections indicated that pig production in Central Luzon would have declined to zero (100% loss) by 2022Q2, while CALABARZON would have faced the same by 2023Q1. However, with INSPIRE implementation, total collapse was avoided. Central Luzon production only declined by 72.17%, producing 31,060 MT in 2022Q2, but recovered to 51,416 MT by 2023Q4 (+65.5%). CALABARZON production declined by only 33.68%, producing 39,807 MT in 2021Q2 and increased to 63,504 MT by 2024Q1 (3.7% growth). Davao Region exhibited a more modest response, as ASF occurred later (2021Q4) and INSPIRE was implemented on a smaller scale commensurate to the region's industry size. Nonetheless, cost–benefit and net present value analyses across regions yielded favorable ratios, indicating overall financial viability of the program.

Conclusion

INSPIRE effectively prevented a near-total collapse of pig production in key regions and restored producer confidence during 2022 - 2023. The study recommends continued implementation beyond 2025 with increased annual funding of Php 25 billion (USD 421 million) until 2028 to restore pre-ASF production levels. This study represents the first Philippine application of SARIMA time-series forecasting for evaluating a pig repopulation program, providing empirical support for government policy continuation.

Keywords: African swine fever, Cost-benefit analysis, Pig production, Pig repopulation, SARIMA.

Acknowledgements: The authors would like to acknowledge the Department of Agriculture units, offices, officials, and staff for the guidance, support, and provision of the needed data.

USE OF FIBRATES IN GILTS WITH ELECTRONIC-AUTOMATIC FEEDING: LITTER PERFORMANCE

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Introduction and Objectives

Hyperprolific sows experience an increased metabolic burden during gestation and lactation due to their large litters. This is especially true in gilts and primiparous. In this study, we investigated the influence of fibrates (Liverfine, Mefepronic acid) on litter performance in gilts with automatic feeding and increased voluntary intake.

Materials and Methods

A total of 250 gilts were used, divided into four groups: untreated control (CON; n = 50), treated with Liverfine 24 hours post-farrowing (24HAF, n = 50), treated one week before farrowing (1WBF, n = 100) and treated two weeks before farrowing (2WBF, n = 50). The sows were weighed 24 hours before farrowing and at weaning. Backfat thickness (BFT) and loin depth (LD) were also measured using ultrasound at the time of treatment, 24 hours after farrowing and at weaning. Total piglets born (TBP), alive born (ABP), stillbirths (SBP), weaned piglets (WP) and mortality rate during lactation were recorded. Piglets were weighed on the day of birth and on the day of weaning.

Results and Discussion

There were significant differences in all treated groups in the average and total litter weight at weaning ($P < 0.001$), with 4.9 and 5.5 kg more in the 1WBF and 2WBF groups, respectively. ADG was higher in the three treated groups. There were no significant differences in WP. The 24HAF group showed no difference in milk production, but the 1WBF and 2WBF groups produced between 21.4 and 20.7 kg more than control group ($P < 0.001$). Mortality was higher in the 24HAF group, but in all groups, it was less than 7%. The frequency of litters without mortality was higher in the 2WBF group (72%, $P < 0.001$). The improved hepatic lipid metabolism is clearly reflected in milk production and, therefore, in litter growth. An increase in milk production had been observed with the use of fibrates without an increase in feed intake (Ramis et al., 2022) but has been much higher in this study.

Conclusion

The use of fibrates, administered between 1 week before farrowing and at the time of farrowing, improves hepatic lipid metabolism. This advantage is maximized when animals are able to voluntarily increase their feed intake.

Keywords: Back fat thickness, Fibrate, Litter growth, Loin depth, Mefepronic acid.

Acknowledgements: The authors thank the personnel in Olimaporc farm (JISAPS) for the support during the trial and to Francisco Murciano because of the acquiring of data.

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USE OF FIBRATES IN GILTS WITH ELECTRONIC-AUTOMATIC FEEDING: REPRODUCTIVE PERFORMANCE

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Introduction and Objectives

Hyperprolific sows experience metabolic overload during gestation and lactation due to their large litters. This is especially true in gilts and primiparous sows, as they are still growing, which increases their metabolic demand. This is sometimes exacerbated by deficiencies in feed, both in terms of quality and quantity. Automatic electronic feeders allow voluntary intake to be increased on demand by up to 10%. We investigated the influence of Mefepronic acid (MA) on reproductive performance of the following gestation and the wean-to-oestrus length.

Materials and Methods

A total of 250 gilts were used in this experiment, divided into four groups: untreated control (CON; n = 50), treated with Liverfine 24 hours post-farrowing (24 HAF, n = 50), treated one week before farrowing (1 WBF, n = 100) and treated two weeks before farrowing (2 WBF, n = 50). MA was administered intramuscularly, single injection containing 1.5 g. Backfat thickness (BFT) and loin depth (LD) were measured using ultrasound at the time of treatment, 24 hours after farrowing and at weaning. The weaning-to-oestrus interval (WEI) in the experimental groups was studied, as was the prolificacy of the next birth after treatment, without the administration of any drugs.

Results and Discussion

The WEI was lower in the groups treated between 0.5 and 0.6 days for the 24 HAF and 1 WBF groups and 0.6 days higher in the 2 WBF group. Negative significant correlations were found between WEI and BFT and LD at all sampling points. An interesting finding was that 5.6% of 1WBF sows showed long WEIs, which would correspond to sows that probably came into heat during lactation due to voluntary increased intake. This would explain these long heats. Although the difference was not significant, differences were observed in the prolificacy of the next birth when comparing the CON group (15.6 TBP) with 24 HAF (16.4), 1 WBF (16.2) and 2 WBF (16.0).

Conclusion

Hepatic metabolism influences reproduction in sows, so improving it means a reduction in WEI and an improvement in prolificacy in the next litter. Let us not forget that during lactation, the follicles that will constitute the next litter are maturing. The possibility of increasing feed intake is key to optimising results.

Keywords: Back fat thickness, Fibrate, mefepronic acid, Loin depth, Weaning-to-estrus interval.

Acknowledgements: The authors thank the personnel in Olimaporc farm (JISAPS) for the support during the trial and ~~to~~ Francisco Murciano for acquiring data.

APPLICATION OF AN ANTI-GNRH VACCINE IN FATTENED IBERIAN FEMALE PIGS: ASSESSMENT OF SLAUGHTERHOUSE OUTCOMES AND MEAT QUALITY

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Introduction and Objectives
The objective of this study was to evaluate the influence of immunization against GnRH (gonadotropin-releasing hormone) in finishing Iberian gilts, fattened under commercial field conditions. For this purpose, slaughterhouse outcomes and carcass quality were analyzed and compared between immunocastrated and entire Iberian females.

Materials and Methods
Two groups of 50 Iberian gilts were studied: a control batch (C) without treatment and a vaccine batch (V) which received two doses (2ml) of Vacsincel® (Zoetis, Parsippany NJ, USA) at 27 and 31 weeks of age. Each animal was reared under identical conditions and individually ear identified. Body weight was recorded at several timepoints until slaughter at 150 kg live weight. At slaughter, live weight, carcass weight, and carcass yield were measured. Statistical analyses were performed in R® environment (R Foundation for Statistical Computing, Vienna, Austria), including mean comparisons and relevant correlations. Subcutaneous dorsal fat samples were collected for fatty acid profiling, and caudal longissimus lumborum muscle samples were analyzed for intramuscular fat profile and moisture, fat, and protein content. Stat graphics Centurion XVII was used for data analysis at the Agrarian Technological Institute, Guijuelo, Spain.

Results and Discussion
No statistically significant differences ($P > 0.10$) were found in slaughterhouse parameters between batches. However, V showed higher carcass weight, C-119.41 ± 1.60// V-120.46 ± 2.31 (+1.05) and yield, C-77.26 ± 1.34//V-77.95 ± 1.93 (+0.692). Subcutaneous fat profiles, no statistically significant differences ($P > 0.05$) were found between batches. Immunocastrated showed a tendency towards higher saturated fatty acids ($0.05 < P < 0.10$) (stearic acid, V-12.34//C-10.94, $P = 0.051$) and slightly increased linoleic acid (V-0.66//C-0.66, $P = 0.091$) (family omega-6), although no differences are detected in polyunsaturated fatty acids ($0.05 < P < 0.10$). While C batch showed a trend towards higher monounsaturated fatty acids ($0.05 < P < 0.10$). Muscle samples revealed no significant differences ($P > 0.10$) in nutritional values (intramuscular fat, moisture, protein). Intramuscular fatty acid composition showed similar conduct than in subcutaneous fat.

Conclusion
Immunocastration in Iberian female pigs showed no significant variations on slaughter outcomes and meat quality. Minor trends suggested improved carcass traits and data homogeneity. Nutritional composition and fatty acid profile remained essentially unchanged. Further studies will be needed to determine differences between groups.

Keywords: Fatty acids, Iberian females, Immunocastration, Meat quality, Slaughterhouse.

MULTI-OMICS ANALYSIS REVEALS FLAVOR DIFFERENCES BETWEEN THREE-WAY CROSSBRED PIGS AND YUXI BLACK PIGS

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Introduction and Objectives

Flavor is an important factor influencing consumers' evaluation of pork (Xiao, 2024). However, the molecular regulatory mechanism of flavor differences among different pig breeds remains unclear. Yuxi Black Pig (YX) is a distinctive high-quality native breed in China, noted for its excellent meat quality and unique flavor (Sun et al., 2025). In order to fully utilize the elite native genetic resources, we conducted a multi-omics analysis, with the expectation of uncovering more potential regulatory genes governing flavor substances.

Materials and Methods

The longissimus dorsi muscles of the Duroc-Landrace-Yorkshire three-way crossbred Pig (DLY) and YX were subjected to combined transcriptome and metabolome analysis to select key target flavor genes. The functions of the key of gene were further identified through gene overexpression or silencing.

Results and Discussion

Using transcriptomics and metabolomics techniques, the key genes and substances in the longissimus dorsi muscle of DLY and YX were identified. Between the two breeds, 1025 differential metabolites were identified, including 409 up-regulated metabolites and 616 down-regulated metabolites. KEGG enrichment showed these metabolites such as the biosynthesis of unsaturated fatty acids and fatty acid degradation. Transcriptomics revealed that the differentially expressed genes were mainly enriched in pathways such as fatty acid degradation and the PPAR signaling pathway. Multi-omics analysis further identified 9 core pathways as being associated with pork flavor, including purine metabolism, biosynthesis of unsaturated fatty acids, and fatty acid degradation signaling pathways. Finally, this study found that ACOX3 promotes lipid deposition in intramuscular preadipocytes and 3T3-L1 cells, significantly increasing the content of saturated fatty acids.

Conclusion

These results provide important insights into the flavor differences between DLY and YX and their potential molecular regulatory mechanisms and also offer theoretical references for improving the quality of pork.

Keywords: Quality of pork, Unique flavor, Native breed.
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IMPACT OF POLYPHENOL-RICH FEED ADDITIVES ON THE PERFORMANCE OF NURSERY PIGS UNDER FLUCTUATING HOUSING TEMPERATURES

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Introduction and Objectives

The piglet nursery phase is a critical stage of production. Temperature stressors promote oxidative stress, which leads to reduce growth performance and excessive economic losses (Hao et al., 2021; White et al., 2008). To alleviate stress, optimize performance, and ensure an effortless transition, the aim of this study was to explore the influence of a polyphenol rich feed additive (PFA) on nursery piglets under fluctuating temperatures in housing.

Materials and Methods

A total of 120 nursery pigs at 30 days old were randomly assigned to two dietary treatments: either a basal diet (control group) or a basal diet supplemented with PFA at the dosage of 400 g/ton of feed (PFA group). Each group contained three replicate pens, each with twenty pigs. Performance parameters including body weight (BW), average daily gain (ADG), feed conversion ratio (FCR) and mortality rate were measured from 41 to 55 and 56 to 70 days of age (Phase I and Phase II of the nursery, respectively). Thermal gradient in housing between 22 - 27 and 25 - 32 °C for nursery Phase I and Phase II respectively. Data were analyzed using ANOVA (SPSS software) with significance set at $P < 0.05$.

Results and Discussion

The PFA had a significant impact on reducing FCR in nursery, both in Phase I (control 1.32 vs PFA 1.27) and Phase II (control 1.53 vs PFA 1.47). In both Phase I and Phase II, BW and ADG were not significantly different between the control and PFA groups, although BW (control 27.39 vs PFA 28.53 kg/animal) and ADG (control 0.94 vs PFA 0.96 kg/day) were numerically higher in the PFA group in Phase II. Mortality differed between treatments (control 3.3% vs. PFA 0%) and was reported descriptively without formal statistical analysis. The results indicate that polyphenol components in PFA can improve FCR and show a trend of decreasing mortality rate as temperature fluctuates. Future trials should include more replicate pens to increase statistical power.

Conclusion

The findings of this study show that PFA can support economic efficiency and sustainability by lowering feed utilization through reduced FCR, particularly in times of fluctuating temperature.

Keywords: Nursery pigs, Performance, Polyphenol feed additive, Temperature.

Acknowledgements: The authors gratefully acknowledge the financial support from Dr. Eckel Animal Nutrition GmbH & Co. KG, Germany, which made this publication possible.

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EFFECTS OF PLANT EXTRACT SUPPLEMENTATION ON SOW MILK YIELD AND PIGLET GROWTH

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Introduction and Objectives

Lactation is a critical phase in sow productivity, during which nutrition strongly influences milk yield and composition, thereby affecting piglet growth and health. Plant extracts, such as turmeric, have been shown to enhance immune function by stimulating immunoglobulin production in colostrum and milk, supporting piglet performance during suckling and post-weaning. This study evaluated the effects of a plant extract containing turmeric and other bioactive ingredients (Fytera Care, Trouw Nutrition) on milk yield and piglet growth in multiparous sows.

Materials and Methods

A total of 157 Landrace × Yorkshire sows were blocked by parity (1 - 5 and > 5) and randomly assigned to either a basal control diet (n = 78) or the same diet supplemented with 150 g/t Fytera Care (FC; n = 79). Dietary treatments were provided from day 107 of gestation through a 21-day lactation period. Piglets received limited creep feed (200 g/day/litter mixed with 1 L of water) from day 10 until weaning. Colostrum samples were collected within 6 h postpartum, and milk samples were obtained on days 3 and 21 of lactation to determine immunoglobulin concentrations and nutrient composition. Milk yield was estimated using the method of Noblet and Etienne (1989). Piglet body weights were recorded at birth and on days 3, 10, and 21.

Results and Discussion

FC supplementation did not affect sow body weight, backfat thickness, feed intake, reproductive traits, litter characteristics at birth, or early neonatal health, indicating no alteration in maternal energy balance or early piglet viability. Milk immunoglobulin G ($P = 0.08$) and dry matter content ($P = 0.06$) tended to be higher in FC-supplemented sows at day 3 postpartum. Milk yield significantly increased from days 10 to 21 compared with the control and showed an overall upward trend across lactation. Piglets from FC-supplemented sows exhibited greater weaning weights, with individual piglets weighing on average 160 g more at weaning ($P < 0.01$) and litter weaning weight tended to by 1.75 kg per litter ($P = 0.09$).

Conclusion

Supplementation of sow diets with Fytera Care during late gestation and lactation modestly improved milk quality and enhanced milk yield and piglet growth.

Keywords: Immunoglobulin, Milk yield, Piglet growth, Milk composition, Plant extract.

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ESTIMATING GENETIC PARAMETERS AND A MULTIPLE - TRAIT SELECTION INDEX FOR AVERAGE DAILY GAIN AND FEED CONVERSION RATIO IN PUREBRED LINE PIGS

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Introduction and Objectives

Evaluating genetic parameters in purebred populations is fundamental for enhancing commercial swine productivity (Esfandyari et al., 2015; Alam et al., 2021). The sire line selection for average daily gain (ADG) and feed conversion ratio (FCR) is crucial to determine the genetic potential (Gomes et al., 2025). A multiple-trait selection index was developed to enable producers to decide on balanced selection. Therefore, this study was developed to enable estimating genetic parameters and a multiple-trait selection index for ADG and FCR in purebred line pigs.

Materials and Methods

A total of 623 purebred young pigs, Duroc (DR; 103 males and 57 females), Landrace (LR; 66 males and 108 females), and Large White (LW; 107 males and 182 females), were evaluated using the Pig Performance Tester (PPT, ProSense®, Nedap N.V.). Pigs were entered to the test at 12 weeks of age (31.74 ± 0.28 kg) and finished at 25 weeks of age (109.04 ± 0.71 kg). Diets (ME = 3,250; 3,175; 3,050 kcal/kg and %CP = 18.5, 18.0, 16.0%) were fed ad libitum. ADG and FCR were individually collected through the Nedap Velos Cloud Database. Bivariate animal models with breed and sex as fixed effects, year–month of testing entry as a random effect, were performed to estimate heritability and predicted breeding values (PBV).

Results and Discussion

The average ADGs of DR, LR, and LW pigs tested using PPT were 922.60 ± 125.55, 775.50 ± 148.56, and 785.00 ± 126.49 g/day, respectively, while the corresponding average FCR values were 2.31 ± 0.31, 2.15 ± 0.33, and 2.23 ± 0.30. The ADG and FCR heritability estimates were moderate at 0.22 and 0.15. However, The PBVs for ADG and FCR were 9.061 and 0.002. The bivariate selection index for ADG and FCR was presented to be 100 + 0.17(PBVADG) - 25.90(PBVFCR). The selection index coefficient of FCR (25.90) was higher than that of ADG (0.17), thus focusing on FCR rather than ADG will contribute more to pig selection.

Conclusion

The multiple-trait selection for ADG and FCR in purebred line pigs provided valuable insights and a practical tool for ranking animals and supported balanced genetic improvement programs.

Keywords: Estimation, Genetic parameter, Purebred sire line, Selection index.

Acknowledgements: The authors thank Papon Farm Research Station for their support and providing testing facilities.

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COMPARATIVE EVALUATION OF PROBIOTIC, BACTERIOPHAGE, AND COMBINED ADDITIVE STRATEGIES AFTER ANTIBIOTIC USE IN WEANED PIGS

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Introduction and Objectives
This study investigated whether the functional efficacy of probiotics (PRO), bacteriophages (BAC), and a phytogenic–β-glucan cocktail (COK) differs depending on the timing of administration relative to in-feed antibiotic (ANT) exposure in weaned pigs.

Materials and Methods
A total of 120 piglets were assigned to five treatments: CON (basal diet), ANT (d 0 - 7 supplementation antibiotic), ANP (d 0 - 7 supplementation antibiotic + d 8–21 supplementation probiotics), ANB (d 0 - 7 supplementation antibiotic + d 8 - 21 supplementation bacteriophage), and ANC (d 0 - 7 supplementation antibiotic + d 8 - 21 supplementation cocktail). Growth performance, fecal consistency, nutrient digestibility, blood hormones, inflammatory cytokines, and hair cortisol were evaluated over a 21-day period. No additive exerted measurable effects during the antibiotic administration period (phase 1), indicating that amoxicillin masked functional responses during early post-weaning.

Results and Discussion
Pigs receiving ANP and ANC exhibited higher overall average daily gain and average daily feed intake than CON ($P < 0.05$). The ANC group showed greater crude protein digestibility than CON and ANT during phase 3 ($P < 0.05$). ANP, ANB, and ANC supplementation increased serum IGF-1 than CON at d 21 ($P < 0.05$). Both ANP and ANC tended to attenuate inflammatory cytokines in phase 3, whereas ANB supplementation produced minimal effects ($P = 0.051$). Fecal score and hair cortisol were unaffected across treatments ($P > 0.05$).

Conclusion
These results demonstrate that functional additives provide limited benefit when co-administered with antibiotics but become effective once antibiotics are withdrawn, highlighting the importance of timing when integrating additives into antibiotic-restricted weaning programs.

Keywords: Antibiotics, Bacteriophage, Phytogenic additives, Weaned pigs.

BEYOND THE MARKET PRICE: THE TRUE PRICE OF PIG WELFARE IN A CONVENTIONAL VERSUS NEXT-GENERATION SUPPLY-CHAIN

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Introduction and Objectives

Although pig farming provides essential animal protein, it generates a range of social and environmental externalities not reflected in market price. True pricing, derived from true cost accounting, monetizes these externalities by translating non-market impacts (e.g. animal welfare) into economic values comparable to market price (Adelhart et al., 2021). As such, true pricing allows sustainability dimensions to be assessed on a common monetary scale, facilitating the comparison between production systems and the prioritization of improvement actions. This study aimed to compare the true price of animal welfare in two Italian pig supply chains: a conventional and a next-generation (NG) system, characterized by welfare standards exceeding European legal requirements.

Materials and Methods

Animal welfare was assessed using the method developed by Scherer et al. (2018), which considers animal housing, including density, and cage-free gestation and farrowing systems, among key welfare indicators. For each supply chain, the entire production cycle was considered, from the sow unit to slaughter weight (175 kg LW). Animal welfare impacts were quantified using a disability-adjusted life-years-based metric adapted from human health economics, which was monetized through the true price method to estimate the true cost of welfare (€/Kg live weight, LW) (De Groot et al., 2012).

Results and Discussion

The NG system reported cost reductions across all production phases, resulting in total savings of €27.8/kg LW. Compared to the conventional scenario, the NG true cost decreased from €38.5 to 23.3/kg LW (-€15.1/kg LW) in the farrowing site, from €23.8 to €13.0/kg LW (-€10.8/kg LW) in the weaning site, and from €7.8 to 5.7/kg LW (-€1.9/kg LW) in the fattening site. The major cost reduction occurred in the farrowing unit due to cage-free gestation and farrowing systems, while in the weaning and the fattening NG sites the lower stocking density was the key driver of true price reduction.

Conclusion

In light of the increasing consumer awareness of animal welfare and the growing demand for more ethical and sustainable farming systems, economic assessment such as true cost analysis provides a basis for evidenced-based decision-making and prioritizes sustainable development practices.

Keywords: animal welfare, sustainable development, free farrowing, True price.

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COMPARATIVE GENETIC STUDY OF ENDANGERED SPANISH AUTOCHTHONOUS PIG BREEDS: CHATO MURCIANO, NEGRO CANARIO AND PORCO CELTA

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Introduction and Objectives

Spanish autochthonous pig breeds have been endangered since the 1950s onwards. Currently, the BIO4TRACE research project aims to develop a genetic improvement programme to counteract inbreeding and safeguard the genetic identity of these breeds. The objective of this study is to analyse current inbreeding and genetic diversity using mcirosatellites. In addition, a comparative analysis is performed using results obtained from asynchronous populations of these breeds.

Materials and Methods

A total of 677 pigs from the Porco Celta (PC), 386 pigs from the Chato Murciano (CM) and 85 pigs from Negro Canario (NC) were selected. Blood samples were collected and processed at the Genomics Laboratory of the Faculty of Veterinary in Murcia. Genetic diversity was assessed using 28 microsatellite markers, with data analysis performed in GenAlEx (v6.51b2).

Results and Discussion

In PC, expected (He) and observed heterozygosity (Ho) were 0.614 and 0.611 in 2019, increasing to 0.656 and 0.670 in 2025. The results for Nei's genetic distance (Da) and Wright's Fst statistic show low genetic divergence between Porco Celta populations (Da = 0.097; Fst = 0.025). CM has shown a significant increase in genetic diversity over the studied period, with He/Ho values of 0.396 and 0.398 in 2009, 0.511 and 0.460 in 2019, and 0.560 and 0.595 in 2025. The Da and Fst values indicate progressive genetic differentiation, (Da = 0.890; Fst = 0.278). The genetic analysis conducted for NC includes only data obtained in 2025, revealing moderate levels of heterozygosity (Ho = 0.674; He = 0.698).

Conclusion

These results demonstrate a progressive increase in genetic diversity for CM and PC breeds, alongside evidence of genetic restructuring in CM. They underscore the importance of maintaining long-term genetic improvement programs to conserve endangered pig populations and preserve their breed identity, while contributing to development of more sustainable pig production.

Keywords: Genetic Heterozygosity, Microsatellites, Chato Murciano, Porco Celta, Population structure.

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ECONOMIC IMPACT OF PNEUMONIA AND PLEURISY ON LUNG DISPOSAL COSTS AND MEAT YIELD IN TWO GERMAN SLAUGHTERHOUSES

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Introduction and Objectives

Lung lesions, such as pneumonia and pleurisy, impairing animal welfare and performance are routinely assessed at slaughter. While their impact on growth and carcass quality is documented, little is known about their economic consequences and meat yield. This study aimed to evaluate the influence of lung lesions on average batch income and meat yield, focusing on premium meat cuts.

Materials and Methods

Over the course of one year, 22,586 lungs from 320 batches were assessed in two German slaughterhouses using the Ceva Lung Program (CLP). Results are given on batch level and provide indices for pneumonia (EP-Index) and pleurisy (APP-Index). Results were categorized in quartiles (low, medium low, medium high and high) and used for comparison of batch income, meat yield, and carcass weight, data which is provided by the slaughterhouse. Meat yield was measured post-evisceration using an automated Fat-O-Meter for lean meat percentage and weights of trimmed ham, loin, cutlet, and trimmed shoulder. Additionally, average carcass weight was recorded. Non-parametric tests (Kruskal-Wallis, Dunn's post-hoc) were used to assess differences in batch income and meat yield and carcass weight according to lesion severity.

Results and Discussion

Increasing EP-Index was associated with a significant decline in average batch income per pig (€227.49 vs. 202.16; $P < 0.001$). A similar trend was observed for the APP-Index with €223.22 for low lesions compared to €204.50 for high lesions ($P < 0.001$). Meat yield decreased progressively with lesion severity (low vs. high): For EP-Index, lean meat percentage dropped by 1.73 (61.31 vs. 59.58%; $P < 0.001$) and weights for trimmed ham, loin, cutlet and trimmed shoulder declined as well (e.g. trimmed ham weight: 19.34 vs 17.91 kg; $P < 0.001$). The carcass weight was similar across all lesion categories; thus, the percentage of lean meat and amount of premium meat cuts were higher in animals with low lung lesions compared to animals with high lung lesions.

Conclusion

Respiratory lesions at slaughter are linked to measurable economic losses through reduced yields of premium meat cuts. These findings highlight the importance of lung health as key factor for animal health but also the impact on carcass composition and profitability.

Keywords: Economic impact, Lung lesions, Pleurisy, Premium meat cuts, Slaughterhouse.

Acknowledgements: The authors thank the Premium Food Group for their support and the possibility to use their facilities.

COMPARISON OF TWO DIFFERENT LUNG SCORING METHODS FOR DETECTING PNEUMONIA AND PLEURISY IN SLAUGHTERHOUSES

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Introduction and Objectives

Respiratory lesions such as pneumonia and pleurisy are key indicators of pig welfare and herd health and are routinely assessed at slaughter. Multiple lung-scoring systems are used globally, but their comparability and feasibility under high-throughput conditions remain uncertain. This study aimed to compare lesion detection by the Blaha Scoring Method (BSM), a visual-only approach mandated in Germany, and the Ceva Lung Program (CLP), which combines visual inspection with palpation, under routine slaughterhouse conditions.

Materials and Methods

Lungs from 44,325 pigs (320 batches) were scored over one year in two German slaughterhouses (SH1 and SH2). All lungs were evaluated for pneumonia and pleurisy by official meat inspectors using BSM; a subset of 22,586 lungs (50.9%) was additionally assessed by a veterinarian using CLP. Because simultaneous lung-by-lung scoring was not feasible under routine slaughterhouse conditions (e.g. divided batches, empty hooks), outcomes were analysed at batch level. Lungs were classified as diseased when the score for pneumonia or pleurisy exceeded zero. Generalized linear mixed-effects models were applied to account for slaughterhouse, season, and hierarchical clustering (farm, batch).

Results and Discussion

Across all batches, CLP detected more lesions than BSM for pneumonia (25.18 vs 13.30%), and for pleurisy (24.55 vs 11.21%; both $P < 0.001$). CLP–BSM differences varied by slaughterhouse and season; in summer, the odds of detection remained significantly lower with BSM compared to CLP (OR = 0.53; 95% CI: 0.49 - 0.58, $P < 0.001$). The detection of pneumonia assessed by CLP was lower in SH2 than in SH1. The reason why CLP yielded higher prevalences was likely because it relies on both visual inspection and palpation, which might be more accurate and lead to improved discrimination from artefacts than the BSM visual only inspection. Additionally, inter-slaughterhouse variations (e.g. staff with maybe different evaluation experience and accuracy) might have impacted on the results.

Conclusion

Under routine slaughterhouse conditions, CLP yielded higher prevalences of pneumonia and pleurisy compared to BSM. Since CLP combines visual inspection with palpation it might be argued that in comparison to BSM, lesion detection is improved, suggesting greater sensitivity and robustness for herd health monitoring.

Keywords: Lung Lesions, Lung Scoring Methods, Pneumonia, Pleurisy, Slaughterhouse.

Acknowledgements: The authors thank the Premium Food Group for their support and the possibility to use their facilities.

EVALUATION OF THE EFFICACY OF FOSFOSAN® ON SOW REPRODUCTIVE PERFORMANCE AND PIGLET STRESS LEVELS

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Introduction and Objectives

An increased systemic oxidative stress is often observed during late gestation and lactation due to high energy demand, which can impair sow fertility. This study evaluated the effects of Fosfosan®, an injectable mineral formulation involved in phosphate metabolism, on farrowing performance, body condition score (BCS), conception rates, and cortisol levels in sows and piglets.

Materials and Methods

The study was conducted at Seongji Farm (380 sows). Sows were randomly allocated to two groups: an experimental group (n = 20) receiving 5 mL of Fosfosan® twice (two weeks before farrowing and at weaning) and an untreated control group (n = 18). Parameters included farrowing performance (current and subsequent parity), backfat score of sows at weaning, and conception rates. Serum cortisol levels were analyzed via ELISA. Data were analyzed using the t-test, Analysis of Variance (ANOVA), and correlation analysis, with a significance level set at ($P < 0.05$).

Results and Discussion

Numerical trends were observed in the experimental group compared to the control group, although statistical significance ($P < 0.05$) was not reached for all parameters. In the subsequent parity, the number of "Born Alive" was numerically higher in the Fosfosan® group (14.44 vs. 13.00). The conception rate was 80.0% in the experimental group and 72.2% in the control group. Regarding body condition, the experimental group maintained a higher numerical backfat score at weaning (17.2 vs. 15.1). Furthermore, a lower numerical cortisol level was observed in nursing piglets from the experimental group (3.68 ng/mL) compared to the control group (4.26 ng/mL).

Conclusion

Despite any statistical evidence, the administration of Fosfosan® appears to support long-term reproductive efficiency by numerically improving subsequent parity performance and maintaining superior sow body condition post-weaning. Furthermore, the lower cortisol levels in piglets suggest potential for stress mitigation and enhanced animal welfare. These preliminary findings indicate that Fosfosan® may serve as a valuable auxiliary tool for optimizing reproductive management and animal well-being in farrowing units. Further large-scale studies are warranted to fully validate the clinical significance of these benefits.

Keywords: Cortisol, Body condition score, Phosphate metabolism, Pregnancy rate, Sow productivity.

CO-COMPOSTING HOUSEHOLD ORGANIC WASTES WITH PIG MANURE

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Introduction and Objectives

In Mexico, some universities generate household organic waste (HOW) daily, which is not treated. As it decomposes, it produces unpleasant odors, attracting rodents and flies, and creating an unsightly appearance. To treat it, it can be co-composted in a matrix made with pig manure, which also presents its own social and environmental problems. Therefore, the objective of this study was to determine whether the composting process can adequately degrade HOW and generate mature compost.

Materials and Methods

The experiment lasted 12 weeks. Each week, 19 kg of HOW (honey-oil straw) was mixed with 8 kg of raw pig manure and 7 kg of ground oat straw. The mixture was then placed in a cylindrical container made of wire mesh, 90 cm high and 61 cm in diameter[1]. Every three days, the organic matter was removed, water was added to maintain a moisture content of 60%, and the container was refilled. After four weeks, a 600 g composite sample was obtained and analyzed for the following properties: electrical conductivity, pH, nitrogen content (Dumas method), and organic carbon content (incineration, 520 °C), as well as phosphorus, potassium, zinc, and copper levels (microwave digestion/ICP). Two additional independent composting units were then prepared from this sample.

Results and Discussion

The amounts of composted HOW, water, and immature compost harvested were 340, 272, and 186 kg, respectively. The carbon-to-nitrogen ratio obtained (10.7) indicates that the compost is stable and therefore mature. According to the Mexican Regulations[2] consulted, the mean levels (%) of N, P, and K (3.75 ± 0.36; 1.58 ± 0.37; 2.61 ± 0.38, respectively) qualify the compost as a high-quality fertilizer. The levels of Cu and Zn obtained (128 and 933 ppm, respectively) could have come from the pigs' diet and lower the compost's classification grade, but they are not toxic to the receiving soil.

Conclusions

Domestic organic waste co-composted in pig excrement degraded properly and generated a good quality agronomic fertilizer of natural origin, which will allow for the proper management of HOW that was previously unpleasant and inconvenient to handle.

Keywords: Composted, Pig farming, Sustainability.

NITROGEN PARTITIONING AND RECOVERY EFFICIENCY DURING PIG MANURE BIOCONVERSION BY BLACK SOLDIER FLY LARVAENITROGEN PARTITIONING AND RECOVERY EFFICIENCY DURING PIG MANURE BIOCONVERSION BY BLACK SOLDIER FLY LARVAE

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Introduction and Objectives

Nitrogen losses from pig manure contribute to ammonia emissions and environmental pollution in pig production systems (Philippe and Nicks, 2015). Black Soldier Fly (Hermetia illucens) larvae (BSFL) offer a promising approach to convert livestock waste into protein-rich biomass while stabilizing nutrients (Lalander et al., 2019). However, nitrogen partitioning during pig manure bioconversion remains insufficiently quantified. This study aimed to evaluate nitrogen distribution, recovery efficiency, and apparent losses during pig manure bioconversion by BSFL to assess its potential for improving nutrient management in sustainable pig production.

Materials and Methods

Fresh pig manure was used as the primary substrate and incorporated at graded inclusion levels (0, 25, 50, 75, and 100% dry matter basis) under standardized conditions (70% moisture, fixed larval density, and feeding rate) in a completely randomized design. Total nitrogen in substrates, larval biomass, and residual frass was analyzed using the Kjeldahl method. Nitrogen intake, nitrogen retained in larvae, nitrogen remaining in residue, and apparent nitrogen loss were calculated to establish a nitrogen mass balance. Nitrogen recovery efficiency (%) and nitrogen conversion ratio were determined. Data were analyzed by ANOVA and regression modeling.

Results and Discussion

Pig manure inclusion significantly affected nitrogen partitioning ($P < 0.05$). Moderate levels (25 - 50%) improved nitrogen retention in larval biomass and overall recovery efficiency, showing a quadratic response with optimal recovery at intermediate inclusion. At higher levels (≥ 75%), apparent nitrogen losses increased, likely due to ammonia volatilization and substrate imbalance. Despite this, a substantial portion of manure nitrogen was converted into larval protein, confirming the strong nutrient upcycling capacity of BSFL (Eriksson et al., 2017; Lalander et al., 2019).

Conclusion

Black Soldier Fly larvae efficiently convert pig manure nitrogen into valuable insect biomass while reducing environmental nitrogen losses. Optimizing manure inclusion improves nitrogen recovery and supports circular nutrient use in pig production. BSFL bioconversion offers a sustainable and scalable strategy for better manure management and environmental performance.

Keywords: Black Soldier Fly larvae, Pig manure, Nitrogen recovery, Nutrient partitioning, Sustainability.

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PHASE-BASED FEEDING STRATEGY TO IMPROVE SURVIVAL AND GROWTH OF BLACK SOLDIER FLY LARVAE REARED ON PIG MANURE

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Introduction and Objectives

Newly hatched Black Soldier Fly larvae frequently exhibit reduced survival when directly exposed to fresh pig manure due to unstable physicochemical conditions and elevated ammonia levels. Developmental stage strongly influences larval nutrient assimilation capacity and stress tolerance (Gobbi et al., 2013). Stage-specific feeding strategies may therefore improve early establishment and overall bioconversion performance. This study evaluated a phase-based feeding strategy designed to protect early instars while maximizing later-stage manure utilization**.**

Materials and Methods

Three feeding strategies were evaluated: (T1) immediate full exposure to pig manure (control), (T2) two-phase feeding with a carbohydrate-rich substrate during days 0–5 followed by gradual manure inclusion on days 6–14, and (T3) progressive manure inclusion at 3-day intervals. Second-instar larvae were reared for 14 days in tray-based experimental units arranged in a completely randomized design with three replicates per treatment at a standardized density of 500 larvae per tray (5 larvae cm^{-2}) and 70% substrate moisture. Measured parameters included survival rate, final body weight, biomass yield, feed conversion ratio (FCR), and substrate reduction.

Results and Discussion

Phase-based feeding significantly increased early survival (93 - 96%) compared with direct exposure (78 - 84%) ($P < 0.05$). Final larval weight improved by 15 - 20%, and FCR decreased from 2.4 - 2.7 in control to 1.8 - 2.1 in phased treatments. Gradual manure inclusion allowed early larval adaptation while maintaining high substrate reduction efficiency in later stages. Similar improvements in larval performance under staged substrate transitions have been reported in BSFL production systems (Dortmans et al., 2017).

Conclusion

Phase-based feeding enhances survival and growth of BSFL reared on pig manure under controlled conditions. Gradual manure introduction during early development represents an effective management strategy for manure-based BSFL production systems.

Keywords: Bioconversion strategy, Black Soldier Fly larvae, pig manure management, phase feeding, larval survival.

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COMPARATIVE REDUCTION OF AMMONIA AND HYDROGEN SULFIDE EMISSIONS FROM PIG MANURE USING BLACK SOLDIER FLY LARVAE, COMPOSTING AND BIOGAS TREATMENT

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Introduction and Objectives

Ammonia (NH_3) and hydrogen sulfide (H_2S) emissions from pig manure pose environmental and health risks in intensive pig production systems (Ni et al., 2012). Conventional treatments such as composting and anaerobic digestion can reduce manure volume but may still generate gaseous emissions. Black Soldier Fly (Hermetia illucens) larvae (BSFL) offer an alternative biological treatment through rapid waste conversion and nutrient retention (Mertenat et al., 2019). This study compared NH_3 and H_2S emissions from BSFL bioconversion, aerobic composting, and anaerobic digestion under standardized conditions.

Materials and Methods

Fresh pig manure with uniform nutrient composition was adjusted to 70% moisture and allocated to three treatments: (1) BSFL bioconversion (standardized larval density and feeding rate), (2) aerobic composting with periodic turning every 2 days, and (3) anaerobic digestion using a laboratory-scale biogas reactor. The experiment followed a completely randomized design with three replicates per treatment over 14 days. Gas emissions were monitored daily using calibrated electrochemical sensors in semi-closed chambers. Emission factors were calculated as cumulative mg NH_3 and mg H_2S per kg fresh manure. Manure reduction and nitrogen retention were also determined. Data were analyzed using ANOVA with significance at $P < 0.05$.

Results and Discussion

BSFL treatment showed significantly lower NH_3 emissions (250 - 320 mg/kg) compared with composting (420 - 550 mg/kg) and anaerobic digestion (360 - 470 mg/kg) ($P < 0.05$). H_2S emissions were reduced by 40 - 60% in BSFL relative to the other treatments. Manure mass reduction reached 55 - 65% with BSFL, exceeding composting and anaerobic digestion. Nitrogen retention was also highest in BSFL, indicating reduced volatilization. These results demonstrate that BSFL bioconversion more effectively alters nitrogen and sulfur pathways, resulting in lower gaseous emissions per unit of manure treated.

Conclusion

Under the experimental conditions, BSFL bioconversion was the most effective treatment for reducing NH_3 and H_2S emissions while achieving greater manure reduction compared with composting and anaerobic digestion. BSFL therefore represents a promising low-emission manure stabilization strategy for intensive pig production systems.

Keywords: Ammonia emission factor, biogas system, Black Soldier Fly larvae, hydrogen sulfide mitigation, pig manure management.

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OPTIMIZING PROTEIN-TO-FIBER RATIO IN PIG MANURE–SOYBEAN RESIDUE DIETS FOR ENHANCED BLACK SOLDIER FLY LARVAL PERFORMANCE

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Introduction and Objectives

Nutritional balance influences substrate use in Black Soldier Fly (BSFL) systems. Pig manure supplies nitrogen but is high in fiber, while soybean residue provides more digestible protein with less structure. The protein-to-fiber (P:F) ratio may therefore regulate larval growth, feed efficiency, and organic matter reduction. Yet its role in manure-based diets remains poorly quantified. This study evaluated how varying the P:F ratio in pig manure–soybean residue mixtures affects larval performance and bioconversion efficiency.

Materials and Methods

Experimental substrates were formulated by replacing soybean residue with pig manure at 0, 30, 50, 70, and 100% (DM), creating different protein-to-fiber (P:F) ratios. A completely randomized design with triplicates was applied under standardized moisture (~70%) and larval density. Larvae were reared for 14 days. Measured parameters included body weight, biomass yield, survival, FCR, substrate reduction, and WRI. Substrate protein and fiber were analyzed to determine P:F ratio, and polynomial regression was used to identify the optimal range.

Results and Discussion

Larval growth responded non-linearly to dietary P:F ratio ($P < 0.05$). Intermediate ratios (~1.2 - 1.5) produced the highest biomass (110 - 140 kg/ton), >90% survival, and lowest FCR (1.7 - 2.0). Both low P:F (high fiber) and high P:F (excess protein) reduced efficiency and substrate reduction. These findings suggest that balanced nitrogen relative to structural carbohydrates improves digestion and nutrient assimilation, consistent with previous studies on macronutrient composition in BSFL diets (Lee et al., 2004; Oonincx et al., 2015).

Conclusion

The protein-to-fiber ratio is a critical nutritional determinant of BSFL growth and bioconversion efficiency in pig manure–soybean residue systems. Maintaining a moderate P:F ratio (1.2 - 1.5) optimizes biomass yield and feed conversion efficiency. Nutritional balancing offers a practical strategy to enhance manure valorization in BSFL production.

Keywords: Black Soldier Fly larvae, Feed conversion efficiency, Pig manure, Protein-to-fiber ratio, Soybean residue

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TOLERANCE THRESHOLDS OF EARLY-STAGE BLACK SOLDIER FLY LARVAE TO AMMONIA AND HYDROGEN SULFIDE DURING PIG MANURE EXPOSURE

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Introduction and Objectives

Fresh pig manure may contain high ammonia (NH_3) and hydrogen sulfide (H_2S), which can impair insect respiration and metabolism. Ammonia toxicity arises from free ammonia diffusion across membranes, disrupting physiological processes (Anthonisen et al., 1976). While BSFL are adapted to organic waste environments, early instars may be more vulnerable to gaseous stress. However, tolerance thresholds remain unclear. This study determined lethal and sublethal NH_3 and H_2S limits for early-stage larvae and compared their sensitivity with later developmental stages.

Materials and Methods

Larvae at 2–3 days (early instar) and 7–8 days (late instar) were exposed to controlled NH_3 (0, 50, 100, 200 ppm) and H_2S (0, 10, 25, 50 ppm) concentrations in sealed chamber systems containing standardized pig manure substrate. Exposure lasted 72 hours. Survival rate, feeding activity, body weight change, and behavioral responses were recorded. Probit regression analysis was applied to estimate median lethal concentration (LC_{50}) and sublethal threshold levels.

Results and Discussion

Early instars showed significantly lower tolerance than late instars ($P < 0.05$). The 72-hour LC_{50} for NH_3 was 145 - 175 ppm in early larvae and 250 - 290 ppm in late larvae, while for H_2S it ranged from 30 - 38 ppm and 48 - 62 ppm, respectively. Sublethal effects, including reduced feeding and mobility, occurred above 80 ppm NH_3 and 15 ppm H_2S. These results indicate that gas accumulation in fresh manure can impair larval establishment, consistent with physicochemical stress effects reported in BSFL (Miranda et al., 2020).

Conclusion

Early-stage BSFL are significantly more sensitive to NH_3 and H_2S than later instars. Maintaining NH_3 concentrations below 80 ppm and H_2S below 15 ppm during early rearing is recommended to improve survival and productivity in pig manure-based systems. Establishing stage-specific gas tolerance thresholds provides a scientific basis for optimizing manure management strategies in BSFL production.

Keywords: Ammonia toxicity, Black Soldier Fly larvae, gas tolerance threshold, hydrogen sulfide exposure, pig manure

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BIOCONVERSION EFFICIENCY OF BLACK SOLDIER FLY LARVAE FED FRESH PIG MANURE UNDER DIFFERENT MOISTURE LEVELS AND FEEDING REGIMES

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Introduction and Objectives

Efficient manure valorization depends on controlling key biological and physicochemical factors. Black Soldier Fly (Hermetia illucens) larvae (BSFL) can rapidly convert organic waste into protein-rich biomass (Diener et al., 2009). Substrate moisture strongly affects larval feeding, microbial activity, and degradation processes (Holmes et al., 2013), while feeding regime may influence aeration and nutrient dynamics. However, their combined effects on fresh pig manure bioconversion remain unclear. This study evaluated the interaction between moisture level and feeding strategy on larval growth, waste reduction, and nutrient conversion efficiency.

Materials and Methods

Fresh pig manure was adjusted to 60, 70, and 80% moisture and tested under two feeding regimes: single-batch feeding, where the entire substrate was provided at the start of the experiment, and incremental feeding, where substrate was supplied at defined intervals throughout the rearing period. Treatments were arranged in a 3 × 2 factorial completely randomized design with three replicates per treatment using tray-based experimental units containing 500 second-instar larvae each (5 larvae cm^{-2}). Larvae were reared for a standardized 14-day period under controlled moisture conditions. Measured parameters included larval weight, biomass yield, survival rate, feed conversion ratio (FCR), substrate reduction, and nitrogen conversion efficiency. Data were analyzed using two-way ANOVA.

Results and Discussion

Moisture and feeding regime significantly influenced bioconversion efficiency ($P < 0.05$). Optimal results were achieved at 70% moisture with incremental feeding, yielding 100 - 130 kg larvae per ton, > 90% survival, FCR of 1.8 - 2.1, and 60 - 70% substrate reduction. Higher moisture (80%) likely limited oxygen diffusion, while lower moisture (60%) reduced substrate utilization. Incremental feeding improved nitrogen conversion (40 - 55%), highlighting the importance of substrate conditions and feeding management in BSFL efficiency.

Conclusion

Substrate moisture and feeding regime are critical operational determinants of BSFL bioconversion efficiency. Maintaining moisture at approximately 70% combined with incremental feeding maximizes biomass production and waste reduction during fresh pig manure treatment, supporting optimized manure management strategies in pig production systems.

Keywords: Black Soldier Fly larvae, bioconversion performance, feeding strategy, substrate moisture, waste reduction efficiency.

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INTEGRATION OF BLACK SOLDIER FLY LARVAE INTO CIRCULAR PIG MANURE MANAGEMENT SYSTEMS: SYSTEM-LEVEL RESOURCE RECOVERY AND SUSTAINABILITY IMPACT

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Introduction and Objectives

Pig manure management in intensive systems commonly relies on storage and land application, resulting in nutrient losses and limited resource recovery (Philippe and Nicks, 2015). Transition toward circular nutrient use is essential for sustainable pig production. Black Soldier Fly (Hermetia illucens) larvae (BSFL) can convert manure into protein-rich biomass and stabilized residue (Lalander et al., 2019). This study evaluated BSFL-based manure treatment using a system-level resource recovery framework, focusing on nutrient redistribution, soybean meal protein substitution potential, and quantified indicators of manure reduction and nitrogen recovery.

Materials and Methods

Fresh pig manure from a commercial farm was evaluated in a completely randomized design with three systems: (T1) conventional storage; (T2) BSFL bioconversion; and (T3) an integrated circular scenario consisting of experimentally implemented BSFL treatment combined with mass-flow-based estimation of larval protein reintegration into pig feed and fertilizer characterization of frass. Substitution and reintegration were modeled based on measured outputs and were not physically tested in feeding trials. Each treatment included three independent bioconversion bins (50 kg manure per bin; total 150 kg per system). For BSFL treatments, moisture was adjusted to 70% and larvae stocked at about 5,000/kg substrate for 10 - 12 days. Manure reduction, larval yield, crude protein, and total nitrogen partitioning were measured. Apparent nitrogen losses were estimated using total-N mass balance (initial manure vs larvae + frass + residual substrate), without direct gaseous emission measurements.

Results and Discussion

BSFL reduced manure mass by 50 - 60%, producing 80 - 120 kg larvae per ton of manure with 38 - 45% crude protein. Per ton of manure, 20 - 25% of total nitrogen was recovered in larvae and 45 - 55% retained in frass, resulting in overall useful nitrogen recovery of 65 - 80%. Apparent nitrogen losses were 25 - 35% lower than conventional storage based on mass balance comparison. Recovered insect protein showed the potential to substitute 10 - 20% of soybean meal protein in pig diets based on crude protein equivalence only. Frass met fertilizer-quality characteristics and represents a recyclable organic amendment.

Conclusion

BSFL integration shifts manure management toward resource recovery by reducing waste volume, improving nitrogen retention, and generating valuable protein and fertilizer streams within pig production systems.

Keywords: Black Soldier Fly larvae, circular pig production, manure integration, nutrient recovery,

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EFFECT OF PROBIOTIC INOCULATION ON PIG MANURE BIOCONVERSION EFFICIENCY AND LARVAL BIOMASS YIELD IN BLACK SOLDIER FLY PRODUCTION

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Introduction and Objectives

Microbial communities are key drivers of organic matter degradation during Black Soldier Fly (Hermetia illucens) larvae (BSFL) bioconversion. Interactions between substrate microbes and larval physiology may influence nutrient availability and conversion efficiency. Pig manure hosts diverse native microbes, but imbalances may hinder degradation and increase ammonia formation. Probiotic inoculation with beneficial bacteria such as *Bacillus spp.* and *Lactobacillus spp.* can enhance substrate fermentation (Moura et al., 2018). This study evaluated the effects of probiotic inoculation on larval performance, biomass yield, and substrate stabilization.

Materials and Methods

Fresh pig manure was treated under standardized conditions (≈70% moisture) in tray-based experimental units arranged in a completely randomized design with four treatments: control, 0.5, 1.0, and 1.5% probiotic inoculum (w/w) containing Bacillus subtilis and Lactobacillus plantarum. Each treatment included three replicates with 500 second-instar larvae per tray (5 larvae cm^{-2}). Larvae were reared for 14 days. Measured parameters included larval weight, biomass yield, survival, feed conversion ratio (FCR), and substrate reduction. Nitrogen in larvae and frass was analyzed to evaluate nutrient conversion. No microbiological or fermentation parameters were directly measured. Data were subjected to ANOVA and regression analysis.

Results and Discussion

Probiotic inoculation significantly enhanced bioconversion performance ($P < 0.05$). The 1.0% level yielded the highest biomass (120 - 145 kg larvae/ton manure), > 92% survival, and the lowest FCR (1.6 - 1.9) compared with control (2.2 - 2.6). Substrate reduction increased from 55 - 60% to 68 - 73%. Observed performance improvements may be associated with probiotic-mediated changes in substrate characteristics; however, mechanistic effects on microbial community dynamics or larval gut microbiota were not directly evaluated. Within the tested range and experimental conditions, the 1.0% inclusion level showed superior performance.

Conclusion

Probiotic supplementation at approximately 1.0% improved pig manure bioconversion efficiency and larval biomass yield under controlled short-term conditions. Further studies incorporating microbiological measurements and larger-scale validation are required to confirm mechanistic effects and broader applicability.

Keywords: Biomass yield, Black Soldier Fly larvae, Microbial enhancement, Pig manure, Probiotic inoculation

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MODEL-BASED OPTIMIZATION OF PIG MANURE INCLUSION LEVEL FOR MAXIMIZING GROWTH PERFORMANCE AND WASTE REDUCTION IN BLACK SOLDIER FLY LARVAE

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Introduction and Objectives

Efficient valorization of pig manure is essential to improve sustainability in pig production systems. Black Soldier Fly (Hermetia illucens) larvae (BSFL) have demonstrated strong capacity to convert organic waste into insect biomass while reducing manure volume (Lalander et al., 2019). However, determining the biologically optimal manure inclusion level remains critical for maximizing growth performance and bioconversion efficiency. This study aimed to establish an optimal pig manure inclusion level in BSFL substrates using regression modeling to improve biomass yield and waste reduction efficiency.

Materials and Methods

Fresh pig manure was incorporated into experimental substrates at 0, 25, 50, 75, and 100% (dry matter basis). Moisture content (70%), larval density (500 second-instar larvae per tray; 5 larvae cm^{-2}), and feeding rate were standardized. The experiment was conducted in tray-based experimental units arranged in a completely randomized design with three replicates per treatment. Larval growth parameters (final body weight, average daily gain, survival rate), feed conversion ratio (FCR), and substrate reduction were recorded. Polynomial regression and broken-line analysis were applied to determine the response curve and estimate the optimal manure inclusion level. Statistical analyses were performed using ANOVA and nonlinear modeling.

Results and Discussion

Pig manure inclusion significantly affected larval growth performance and nitrogen partitioning ($P < 0.05$). Intermediate inclusion levels (25 - 50%) improved biomass yield, survival, and feed conversion efficiency compared with control and high-manure treatments. Polynomial regression estimated an optimal manure inclusion level of approximately 48 - 52% for maximizing growth performance and waste reduction. Higher levels (≥ 75%) increased apparent nitrogen losses, potentially associated with ammonia volatilization and substrate imbalance. Despite this, a substantial share of manure nitrogen was converted into larval protein, confirming the strong nutrient upcycling potential of BSFL (Eriksson et al., 2017; Lalander et al., 2019).

Conclusion

Model-based analysis indicates that moderate pig manure inclusion levels optimize BSFL growth performance and nitrogen recovery under the present experimental conditions. BSFL bioconversion shows promise as a sustainable manure management strategy, although further validation under scaled production systems is warranted.

Keywords: Black Soldier Fly larvae, pig manure, nitrogen recovery, nutrient partitioning, Sustainability

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OPTIMIZING PIG MANURE INCLUSION LEVEL TO ENHANCE NUTRIENT RECOVERY AND PROTEIN PRODUCTION THROUGH BLACK SOLDIER FLY LARVAE BIOCONVERSION

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Introduction and Objectives

Pig production generates large amounts of manure, contributing to nitrogen losses, ammonia emissions, and environmental pressure. Black Soldier Fly (Hermetia illucens) larvae (BSFL) offer a promising solution by converting organic waste into valuable protein and organic fertilizer while improving resource recovery and reducing emissions. This study aimed to determine the optimal inclusion level of pig manure in BSFL substrates to maximize larval growth performance, nitrogen recovery, protein yield, thereby contributing to sustainable pig production systems.

Materials and Methods

Fresh pig manure collected from fattening pigs was incorporated into experimental substrates at 0.25, 50, 75, and 100% (dry matter basis), adjusted to 70% moisture prior to larval introduction. Treatments were arranged in tray-based experimental units under a completely randomized design with three replicates per treatment. Each replicate contained 500 second-instar larvae introduced using gravimetric counting, mortality rate was calculated as the proportion of dead larvae at harvest relative to the initial number. Larval density and feeding rate were standardized across treatments. Larval growth performance (final body weight, ADG, survival rate), feed conversion ratio (FCR), waste reduction efficiency were evaluated. Nitrogen intake, nitrogen retention in larval biomass, residual nitrogen in frass were quantified to estimate nitrogen recovery efficiency. Data were analyzed using ANOVA and polynomial regression to identify the biologically optimal manure inclusion level.

Results and Discussion

Pig-manure inclusion significantly affected larval performance and nutrient utilization ($P < 0.05$). Moderate inclusion levels (25 - 50%) improved final body weight and FCR, comparing both control and high-manure treatments. Biomass yield and protein production per unit of manure exhibited quadratic response, with the predicted optimal inclusion level ranging 45 - 55%. Nitrogen recovery into larval biomass represented substantial proportion of total substrate nitrogen, demonstrating efficient nutrient upcycling from pig manure into insect-derived protein. However, excessive manure inclusion (≥75%) was associated with reduced protein conversion efficiency, potentially linked to substrate nutrient imbalance and elevated ammonia accumulation. Waste reduction efficiency remained consistently high across treatments.

Conclusion

Manure inclusion level of approximately 50% represents the optimal condition for maximizing BSFL productivity, nitrogen recovery, and protein production while maintaining larval survival.

Keywords: Black Soldier Fly larvae, Pig manure, Protein production, Nutrient recovery, Sustainability.

Acknowledgements: The authors acknowledge financial support from the Department of Science and Technology of BRVT province, Vietnam (Contract No. 10/2024/HĐ-QKHCN, dated December 23, 2024), and infrastructural support from the Research and Technology Transfer Center, Nong Lam University, HCMC, Vietnam.

STAGE-SPECIFIC OPTIMIZATION OF CARBON-TO-NITROGEN RATIO FOR ENHANCED GROWTH AND BIOCONVERSION EFFICIENCY IN BLACK SOLDIER FLY LARVAE FED PIG MANURE

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Introduction and Objectives

Carbon-to-nitrogen (C/N) ratio regulates nitrogen availability, microbial activity, and ammonia formation in organic substrates. In BSFL systems, nitrogen levels influence larval growth and survival, especially during early stages with low ammonia tolerance. While C/N balance is well established in composting, stage-specific requirements for BSFL on pig manure remain unclear. This study evaluated optimal C/N ratios for early and late larval stages to improve survival, biomass yield, and bioconversion efficiency.

Materials and Methods

Pig manure was adjusted to three C/N ratios (15:1, 20:1, and 25:1) using carbohydrate-rich amendments. Larvae were divided into early stage (days 0 - 5) and late stage (days 6–14). Growth performance, survival rate, feed conversion ratio (FCR), substrate reduction percentage, and ammonia concentration were monitored. Polynomial regression analysis was applied to determine stage-specific optimal C/N ratios.

Results and Discussion

Early-stage larvae showed higher survival and weight gain at C/N ratios of 22 - 25:1, likely due to reduced ammonia levels. Late-stage larvae achieved greater biomass and lower FCR at moderate ratios (18 - 22:1), with peak substrate reduction at intermediate C/N levels. These results indicate that early larvae benefit from carbon-rich substrates that buffer nitrogen toxicity, while later stages require balanced nitrogen for protein synthesis, consistent with substrate-dependent growth responses reported in BSFL (Jucker et al., 2017; Rehman et al., 2019).

Conclusion

Optimal C/N ratio in pig manure-based BSFL systems is stage-dependent. Maintaining higher C/N during early larval development and moderate C/N during later stages enhances survival, growth, and substrate reduction efficiency.

Keywords: Bioconversion efficiency, Black Soldier Fly larvae, Carbon-to-nitrogen ratio, Pig manure, Nitrogen balance.

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EARLY GROWTH OR LIFETIME EFFICIENCY? COMPARING PIETRAIN AND DUROC AS TERMINAL SIRES IN THREE-WAY FINISHING PIGS

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Introduction and Objectives

Terminal sire selection strongly influences biological efficiency in three-way commercial pig production. Pietrain is associated with rapid early lean growth, whereas Duroc is considered more persistent and adaptable. Whether early growth advantage results in superior lifetime efficiency under tropical commercial conditions remains uncertain. This study evaluated the effects of terminal sire, diet, and sex on growth trajectory, feed efficiency, and fat deposition of three-way crossbred pigs raised under commercial conditions in Vietnam.

Materials and Methods

A total of 365 pigs (Duroc-sired: n = 184; Pietrain-sired: n = 181) were evaluated in a 2 × 3 × 2 factorial design with sire line, diet (Control, T1, T2), and sex as factors. T2 was a higher-energy, slightly lower-fiber diet than Control and T1. Traits recorded were initial body weight (BW0), average daily gain during phases 1 and 2 (ADG1, ADG2), average daily feed intake (ADFI1), feed conversion ratio (FCR1, FCR2), final body weight (BW-End), and backfat thickness (BF). Data were analyzed using linear mixed models in R (version 4.5.0) with Tukey-adjusted comparisons ($P < 0.05$).

Results and Discussion

Pietrain-sired pigs had greater BW0 ($P < 0.01$) and higher ADG1 (738 vs. 708 g/day; $P < 0.05$), with higher ADFI1 (1.49 vs. 1.42 kg/day; $P < 0,05$). However, no significant differences were detected in ADG2, FCR1, FCR2, or BW-End ($P > 0.05$, respectively). Despite lower BW0, Duroc-sired pigs reached comparable final weight, indicating similar cumulative feed efficiency and growth persistence.

Backfat thickness did not differ between sire lines. Sex effects were significant: males were 6–7 kg heavier and exhibited 1.7–2.5 mm greater backfat than females ($P < 0.05$). Diet affected performance independently; T2 reduced ADG1 ($P < 0.01$) but improved FCR2 ($P < 0.05$). No sire × diet interaction was detected.

Conclusion

Pietrain conferred an early growth advantage but did not improve lifetime efficiency. BW-End, FCR, and BF were comparable between sire lines. Duroc demonstrated growth persistence despite lower initial weight. In this study, no terminal sire showed clear overall superiority; selection should align with production objectives and environmental conditions to optimize overall system efficiency.

Keywords: Growth persistence, Feed efficiency, Terminal sire, Three-way crossbred pigs, Tropical production.

ECONOMIC AND LIFE-CYCLE ASSESSMENT OF PIG MANURE BIOCONVERSION USING BLACK SOLDIER FLY LARVAE IN SMALLHOLDER FARMS IN VIETNAM

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Introduction and Objectives

Smallholder pig farms in Vietnam produce large amounts of manure, often managed through direct land application or simple storage with limited value recovery. Sustainable solutions must address both environmental and economic outcomes. Black Soldier Fly (Hermetia illucens) larvae (BSFL) offer a decentralized approach for converting manure into protein and organic fertilizer (Čičková et al., 2015). However, economic and life-cycle assessments at smallholder scale are limited. This study evaluated the economic viability and environmental impacts of BSFL-based manure treatment compared with conventional practices in southern Vietnam.

Materials and Methods

Field data were collected from representative smallholder pig farms (30–100 pigs) applying either conventional manure storage or BSFL treatment systems. Economic analysis included capital investment, operational costs, labor requirements, biomass revenue, and net profit per ton of manure treated. Life-cycle assessment (LCA) was conducted using a cradle-to-gate boundary, evaluating global warming potential (GWP), acidification potential (AP), and eutrophication potential (EP). Environmental impact categories were calculated following ISO 14040/44 guidelines. Sensitivity analysis was performed to assess feed substitution credit from larval protein replacing soybean meal.

Results and Discussion

BSFL treatment produced 90 - 130 kg fresh larvae per ton of manure, generating additional income from biomass and frass. Net profit ranged from 18 - 32 USD per ton, with a payback period of 1.5 - 2.5 years for small-scale units. Life-cycle assessment showed 25 - 40% lower GWP due to reduced methane emissions and protein substitution. Acidification decreased by ~30% and eutrophication by 20 - 35%. Profitability and environmental benefits were mainly influenced by larval price and feed substitution rate, indicating improved resource efficiency and sustainability at smallholder level.

Conclusion

Black Soldier Fly larvae bioconversion is economically viable and environmentally advantageous for pig manure management in Vietnamese smallholder farms. Integrated economic and life-cycle evaluation demonstrates its potential to support circular agriculture and climate-resilient livestock production systems.

Keywords: Black Soldier Fly larvae, circular agriculture, economic feasibility, life-cycle assessment, pig manure management.

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PHYSIOLOGICAL AND BEHAVIORAL STRESS RESPONSES OF BLACK SOLDIER FLY LARVAE UNDER SHORT-TERM AMMONIA AND HYDROGEN SULFIDE EXPOSURE

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Introduction and Objectives

In pig manure-based rearing systems, transient accumulation of ammonia (NH_3) and hydrogen sulfide (H_2S) may induce sublethal stress in Black Soldier Fly (Hermetia illucens) larvae (BSFL). Ammonia can diffuse across biological membranes and disrupt cellular metabolism, while hydrogen sulfide interferes with mitochondrial respiration (Randall and Tsui, 2002; Reiffenstein et al., 1992). Although lethal toxicity thresholds are important, sublethal behavioral suppression may significantly reduce feeding efficiency and growth performance. However, recovery dynamics of BSFL following short-term gaseous exposure remain insufficiently documented. This study aimed to evaluate behavioral suppression and post-exposure recovery of early-stage BSFL subjected to controlled NH_3 and H_2S concentrations.

Materials and Methods

Three-day-old larvae were exposed for 24 hours to sublethal NH_3 (50 and 100 ppm) and H_2S (10 and 20 ppm) concentrations in enclosed manure-based chambers. After exposure, larvae were transferred to fresh, gas-free substrate and monitored for 72 hours. Measured parameters included feeding rate (substrate consumption per larva), mobility index, weight gain, time-to-resume feeding, and survival rate. Growth recovery (%) was calculated relative to non-exposed controls.

Results and Discussion

Short-term exposure significantly reduced feeding activity by 25 - 40% and mobility by 30 - 45% during the exposure period ($P < 0.05$), without causing high mortality. Larvae exposed to 100 ppm NH_3 or 20 ppm H_2S required 24 - 36 hours to resume normal feeding. Despite temporary suppression, most larvae recovered 85 - 95% of control growth within 72 hours. However, repeated exposure scenarios resulted in cumulative growth reduction. These findings suggest that NH_3 and H_2S primarily induce reversible metabolic suppression rather than immediate lethality, consistent with documented respiratory inhibition mechanisms of these gases (Reiffenstein et al., 1992).

Conclusion

Short-term exposure to elevated NH_3 and H_2S induces significant but largely reversible behavioral and growth suppression in early-stage BSFL. Understanding stress and recovery dynamics provides practical insight for managing transient gas accumulation in pig manure-based production systems.

Keywords: Black Soldier Fly larvae, ammonia stress, hydrogen sulfide exposure, behavioral suppression, pig manure.

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ECONOMIC PERFORMANCE AND COST STRUCTURE OF SMALLHOLDER PIGLET PRODUCTION SYSTEMS

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Introduction and Objectives

Pig production in Mexico has grown steadily; however, regional dependence persists despite high internal mobilization volumes. In the State of Mexico, 99.4% of mobilized pigs are destined for slaughter, highlighting structural imbalances within local production systems. Smallholder piglet production may contribute to strengthening regional supply chains. This study aimed to analyze the economic costs and benefits of small-scale piglet production systems in selected municipalities of the State of Mexico and to evaluate profitability under alternative accounting scenarios incorporating opportunity costs.

Materials and Methods

Data were obtained through structured questionnaires applied to 113 small-scale producers across 27 municipalities during the 2024 production cycle. Production systems were family-based, operating on average with two breeding sows and eleven live piglets per litter. Unit production cost per weaned piglet was estimated using established cost calculation methodologies. Four economic scenarios were evaluated: (I) excluding opportunity costs of capital and family labor; (II) including capital opportunity cost (COL) only; (III) including family labor opportunity cost (COMOF) only; and (IV) including both COL and COMOF. Capital opportunity cost was calculated using the 28-day Mexican Treasury bill rate for 2024 (8.25% annual). Differences among scenarios were analyzed using one-way ANOVA and Tukey tests ($P < 0.05$).

Results and Discussion

Significant differences were observed among scenarios in production cost ($P = 0.0142$), net profit ($P < 0.0001$), and benefit–cost ratio ($P = 0.003$). Scenario I showed the lowest cost (MXN 765.87 ± 355.58) and the highest profit (MXN 534.13 ± 355.58), with a B/C ratio of 1.03 ± 0.80. In contrast, Scenario IV showed the highest cost (MXN 930.16 ± 417.11) and the lowest profit (MXN 369.84 ± 417.11), with a B/C ratio of 0.67 ± 0.68, below the economic viability threshold (B/C ≥ 1). The progressive inclusion of opportunity costs substantially reduced profitability and revealed economic vulnerability in smallholder systems.

Conclusion

Incorporating opportunity costs significantly modifies profitability estimates in small-scale piglet production. Although simplified accounting suggests economic viability, full-cost evaluation indicates structural constraints that limit sustainability. Strengthening technical management strategies and cost optimization measures is essential to improve competitiveness and resilience in smallholder pig production systems.

Keywords: Cost structure, Economic sustainability, Piglet production, Profitability, Smallholder system.

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DEVELOPMENT OF PLANT-DERIVED FORMULATIONS FOR THE PREVENTION AND TREATMENT OF DIARRHEA IN PIGLETS

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Introduction and Objectives

Plant-derived compounds administered through the diet may influence the gastrointestinal system of animals and humans. Consequently, phytochemicals have attracted increasing attention as alternatives to antibiotics in livestock production. In our study, three plant-based formulations prepared from selected plant species were developed and evaluated as alternatives for the prevention and treatment of diarrhea in piglets.

Materials and Methods

Materials from Curcuma longa (1), Cynara scolymus (2), Phyllanthus amarus (3), Andrographis paniculata (4), and Coscinium fenestratum(5) were collected from different provinces and commercial sources. Quantitative analyses for bioactive compounds (curcumin, cynarin, phyllanthin, andrographolide, and berberine, respectively) were performed using HPLC and other analytical methods. Qualified materials were used to formulate the preparations, which were subsequently evaluated for their in vitro and in vivo effects (in medium-sized farms with hundreds of piglets for each group). Pilot-scale extraction was conducted to produce the required input materials (number 1 in powder form and the others in extract forms) for final formulations.

Results and Discussion

PremixHad was formulated from components 1 - 3, PremixHerb 1 from components 1 - 5, and PremixHerb 2 from components 1 - 4; all formulations included a carrier and differed in ingredient proportions. All products were safe in mice. In suckling piglets, supplementation (100–300 g per ton of feed) showed positive effect on intestinal microbiota and morphology. In weaned piglets, the formulations improved body weight gain (by an average of 5.3%) and reduced the incidence of diarrhea by approximately two-thirds compared with the control groups. PremixHerb 1, PremixHerb 2 and their production processes have been granted exclusive patents by the Intellectual Property Office of Vietnam (IP Vietnam).

Conclusion

The developed formulations, prepared from five selected medicinal plants with adequate levels of target bioactive compounds, demonstrated safety and beneficial effects on intestinal microbiota, intestinal morphology, growth performance, and diarrhea control in piglets, indicating that these formulations are promising phytogenic feed additives for use in swine production.

Keywords: Bioactive compounds, Diarrhea control, Piglets, Phytogenic feed additive formulations.

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POSTERS

TOPIC 8: AIOT IN PIG HEALTH AND PRODUCTION (AIOT)

TOWARD EARLY DETECTION OF NEWBORN PIGLETS USING VOCALIZATION ANALYSIS

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Introduction and Objectives

Piglets that fail to locate and access the sow's teats in the early postnatal period are at particularly high risk of starvation, hypothermia, and death (Farmer et al., 2022). However, early identification of such piglets is difficult under conventional management, since fixed cameras cannot capture piglets behind the sow and the resulting camera images' quality is often low especially in the night time (Kong et al., 2025).

Materials and Methods

In this study, we propose a novel monitoring system that detects piglets by analyzing their vocalizations. The system is based on continuous acoustic monitoring in the farrowing environment, combined with signal processing techniques to identify vocal features which are characterized with non-audible frequency components (more than 20 kHz) as well as audible frequency components (less than 20 kHz). Random Forest is applied for learning and an integrated system for vocalization is uniquely developed with a multi-channel noise reduction technique. When such vocalizations are successfully detected, an alert will be transmitted wirelessly to caregivers.

Results and Discussion

Field experiments were conducted in farrowing facilities during the suckling period of newborn piglets. Piglet vocalizations were recorded using microphones installed near the farrowing crates, and data from 9 sows were collected immediately after birth (total 1,686 minutes). We utilized a six microphones array created in the authors' lab. Acoustic features of piglets were extracted and used to distinguish them from those of the sow. The proposed method demonstrated recall 89 percent, precision 66.8 percent and F1-score 0.76 for piglets (where the training and test split was 80/20 percent) under practically noisy farm conditions. The performance is better than that of the existing camera monitoring system.

Conclusion

The proposed analysis system will notify caregivers shortly after detecting newborn piglet vocalizations, allowing rapid assistance such as guiding piglets to teats or providing supplemental care. Such a system may support improved management and potentially enhance the survival of newborn piglets. By focusing on piglet vocal behavior, the system provides a non-contact and stress-free solution that can be integrated into existing farrowing management practices. This technology may also contribute to more sustainable pig production.

Keywords: Monitoring system, Noise reduction, Non-audible frequency components, Random Forest, Vocalization.

Acknowledgements: This work was conducted as a part of the livestock promotion project funded by the Japan Racing Association (JRA).

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PILOT STUDY: TAIL LESION CLASSIFICATION WITH A NEURAL NETWORK COMPARED TO VETERINARY ASSESSMENT

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Introduction and Objectives

Diagnosing tail lesions and assessing transport fitness in slaughter pigs remains challenging in Danish pig production and is expected to become more challenging with upcoming restrictions on tail docking. We hypothesized that an artificial intelligence (AI)-based decision-support tool could improve consistency in tail lesion assessment. This pilot study aimed to evaluate the potential of an image-based neural network (CNN) for transport fitness classification compared with assessments made by a trained veterinarian.

Materials and Methods

Video recordings of tail lesions were obtained during live animal assessments performed by a trained veterinarian. Following clinical examination, pigs were classified into three transport fitness categories: fit, fit with special care, and unfit. Tails were recorded before and after cleaning. CNN training was done using an unbalanced dataset comprising video sequences from 58 pigs (clean tail records n = 87; unclean tail records n = 91) and was labelled according to veterinary assessments. An independent dataset for external evaluation comprised video sequences from 121 pigs (clean tail records n = 105; unclean tail records n = 86). CNN classifications were compared with the subjective veterinary assessments, which served as the reference standard for model evaluation.

Results and Discussion

Agreement beyond chance between CNN and veterinary transport fitness classifications was low but higher for cleaned than for uncleaned tail recordings (48.6 vs. 37.2%; Cohen's kappa 0.15 vs. 0.06). Cleaning also improved sensitivity for identifying tails classified as unfit (0.68) and fit with special care (0.19), regardless of the very low sensitivity. The latter result reflects a visual and clinical ambiguity in this intermediate category. CNNs tended to overclassify tails as unfit, with lower specificity for the unfit category (≤ 0.44) than for fit and fit with special care (≤ 0.78 and ≤ 0.71).

Conclusion

The CNN showed insufficient performance for reliable transport fitness decision-making. Limited video quality and challenges in translating on-farm clinical assessments to video-based evaluation likely contributed to the low agreement. Future studies should include larger datasets, improved video acquisition protocols, and stricter process control during AI training to further evaluate the potential of AI-assisted transport fitness assessment in slaughter pigs.

Keywords: Artificial Intelligence, Neural Network, Tail Lesions, Transportability.

Acknowledgements: The authors thank the Danish Agriculture and Food Council for funding, hiring the expert that build the neural network, and for kindly lending out personnel to help video recording.

AIOT APPLIED FOR BIOPIG FARMS IN DIGITAL DATA ANALYSIS FOR PIG FARM CONDITIONS AND DIGITAL NETWORK IN VIETNAM

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Introduction and Objectives

This study assesses pig farm conditions using AIoT and AI applications within a digital network in Vietnam's livestock sector. The objective was to evaluate real-time environmental monitoring, risk classification, and data-driven decision support in commercial BioPig production.

Materials and Methods

The Farmbiotech Defense System (FDS)- an AIoT platform with sensors for temperature, humidity, NH_3, CO_2, animal activity, feed and water intake- transmitted data every 15 minutes via Wi-Fi/LoRaWAN/4G to the cloud for automatic THI, dew point, air quality calculation, risk classification, and mobile alerts. A 6-month trial (July - Dec 2025) on two commercial BioPig farms compared two pens per farm (100 finishing pigs/pen): one with FDS (AIoT group) and one control (conventional). Both groups (total 400 pigs) had identical feeding/veterinary protocols. Environmental data were continuously recorded; respiratory disease was assessed blinded; feed waste and labor time were logged. Data were analyzed by t-test ($P < 0.05$).

Results and Discussion

FDS operated stably, collecting ~2,800 data points/day/farm. FDS pens had more stable THI (24.7 ± 0.9 vs 25.9 ± 1.4). Of 127 environmental alerts (ventilation, NH_3, temperature), 70% matched on-farm events; temperature alerts preceded clinical signs by 4 - 6h. AIoT monitoring proved feasible in Vietnamese commercial farms, significantly reducing feed waste and labor time. Growth and health improvements were positive but not significant within 6 months, suggesting longer studies. Alert reliability requires refinement to reduce false positives.

Conclusion

This pilot study shows that AIoT systems like FDS can be successfully deployed in Vietnamese pig farms to improve environmental monitoring, reduce feed waste, and save labor. While preliminary results are encouraging, longer-term studies with larger sample sizes are necessary to quantify impacts on productivity and health. The approach aligns with national goals for sustainable and data-driven livestock production.

Keywords: AIoT, Digital farming, Pig health, Precision livestock, Smart farming farmbiotech defense system (FDS).

Acknowledgements: The authors also acknowledge the support and participation of teaching staff from Hue University, who received advanced training in AIoT and digital networking applications during this study.

ARTIFICIAL INTELLIGENCE A.I. APPLICATIONS FOR PRRS HEALTH MANAGEMENT IN COLOMBIA

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Introduction and Objectives

PRRS management is complicated by territorial heterogeneity, animal mobilization, and the coexistence of production systems with varying biosecurity levels, necessitating the use of instruments that enable effective health management. This study aimed to develop an AI-based decision-support system integrating quantitative risk modeling and knowledge-assisted reasoning to strengthen PRRS health management at the municipal level.

Materials and Methods

The system integrates official 2.023 - 2.024 datasets, including records of 5.181 georeferenced commercial farms, 208.770 mobilization flows of 11.570.395 animals, PRRS seroprevalence data based on 750 positive cases of 3.868 samples collected in 301 farms in 16 departments, and a hierarchical Health Risk Model combining Hazard, Vulnerability and Exposure components generating Sanitary Risk Index (IRS). The AI architecture comprised two agents with an independent Retrieval-Augmented Generation (RAG) pipelines to improve the accuracy of large language models and guarantee responses based on retrieved evidence reducing hallucinations. The first agent explains municipal PRRS risk by interpreting the quantitative model outputs and retrieving supporting evidence on the highest contributing factors from a curated risk-oriented knowledge base built upon 38 scientific references. The second agent generates actionable mitigation recommendations by retrieving prevention protocols and biosecurity guidelines from a separate knowledge base supported by 21 mitigation-focused records. Both agents were deployed on Amazon Bedrock using Claude 3.5 Sonnet with Titan Embeddings V2 and OpenSearch Serverless, ensuring evidence-grounded responses with source attribution and expert validation. About prediction, thematic evaluation was conducted by the Colombian swine industry, determining a certainty of 95.20% regarding the non-occurrence.

Results and Discussion

The tool transforms numerical risk metrics of the Health Risk Model into actionable decision-support components. The Risk Explanation Agent can generate up to 824 individualized explanations, one for each municipality with commercial swine production, ensuring full territorial interpretability of the IRS (53.07%). The Mitigation Agent produces at least five context-specific recommendations per user query in 7 seconds, strengthening response capacity.

Conclusion

Integrating Health Risk Models with knowledge-based A.I. tools reduce dependence on manual analysis, support decision-making and contributes to more efficient, targeted, and adaptive epidemiological surveillance for Colombian swine production.

Keywords: Artificial Intelligence, A.I.-agents, PRRS, Health Management.

Acknowledgements: The authors would like to express their sincere gratitude to DataLab-UNAL (Andres Torres, David Gonzalez and Erika Camacho) and Porkcolombia-FNP (Enrique Medina) for their significant contribution to this project.

DATA ANALYTICS AND ARTIFICIAL INTELLIGENCE APPLICATIONS FOR HEALTH RISK MANAGEMENT OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME (PRRS) IN COLOMBIA

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Introduction and Objectives

Traditional disease surveillance approaches are characterized as reactive and static, which present limitations for efficient health management. Transitioning from reactive to proactive surveillance is essential to better inform decisions on managing and mitigating the negative impact of a disease. The objective of this study was to develop a set of tools based on data analytics and A.I. applied to PRRS, to support Health Risk Management in Colombia.

Materials and Methods

PRRS Health Risk integrated official 2.023 - 2.024 datasets, including 5.181 georeferenced commercial farm records, 208.770 mobilization flows of 11.570.395 animals and 3.868 epidemiological samples collected in 301 farms in 16 departments. Data updates are semiannual or annual depending on their availability, but it could be more frequent depending on the information accessibility. Factors, Categories, and Components to derive a risk level per municipality, which was adjusted based on the effective mitigation capacity for each risk factor whose epidemiological influence has been recognized as relevant by Expert Criteria. This adjustment yielded a risk value adjusted for specific capacities: $FR_i^{\text{aj}}(m) = \max(FR_i(m) - Mit_i(m), 0)$. The model is used FRiaj(m) to group, weight, and combine them into Categories, which are then regrouped into the Hazard and Vulnerability Components to generate territorial layers through map algebra for Factors, Categories, and Components. Data analytics techniques were applied for normalization, weighting, and spatial pattern identification. The system incorporates AI-based decision-support logic through an intelligent user interface that enables interactive exploration of scenarios and risk drivers via Dashboard.

Results and Discussion

The model integrates risk with mitigation capacity for each municipality, developing indicators that reflect the territory's actual hazard and vulnerability. The highest values are concentrated in territories where significant hazard levels converge, limiting Health Management capacity. In contrast, some municipalities with moderate Hazard levels may exhibit a lower adjusted risk due to better institutional capacities, diagnostic infrastructure, and/or more robust health practices.

Conclusion

The tool set synthesizes PRRS Health Risk and the territory's relative capacity to mitigate its effects. These instruments support decisions on prevention, mitigation, and control by identifying territories in which Hazard and Vulnerability, constrained by response capacity, generate scenarios of greater health fragility.

Keywords: Health Risk Management, PRRS, Data Analytics, Dynamic Modeling.

Acknowledgements: The authors would like to express their sincere gratitude to DataLab-UNAL (Andres Daza Johanna Avila and Andres Torres) for their significant contribution to this project.

DATA-DRIVEN OPTIMIZATION OF YOUNG BOAR SELECTION IN AI CENTERS USING LOGISTIC REGRESSION AND ARTIFICIAL NEURAL NETWORKS

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Introduction and Objectives

Semen collection planning still relies mainly on descriptive historical parameters rather than predictive modeling. This study aimed to develop and validate a data-driven framework integrating logistic regression and artificial neural networks (ANN) to optimize semen production, particularly in young boars (6 - 7 months).

Materials and Methods

A dataset of 63,011 ejaculates (experimental unit) from 4,226 boars across five AI centers was analyzed, accounting for repeated measures per boar. Volume (mL), concentration (10^6 spermatozoa/mL, spz/mL), and pathology (%) were binarized using biologically relevant thresholds and modeled against service interval, age, and genetic index using logistic regression. Classifier performance was reported using accuracy, precision, sensitivity, and specificity instead of percentage "confidence" within a confusion-matrix framework. Monte Carlo simulation (10,000 virtual collections per scenario) estimated expected gains, and Wilcoxon tests ($\alpha = 0.05$) compared strategies. An ANN (H2O.ai) with constraints on genetic index and age was trained to predict total sperm count using previous production metrics, concentration, age, service interval, and genetic index. Field validation compared Period I (120 days, uncontrolled planning) with Period II (64 days, ANN-guided planning) in one AI center (~280 boars), with timing chosen to reduce seasonal confounding.

Results and Discussion

Logistic regression showed moderate accuracy and precision, supporting its use as a screening tool. Monte Carlo simulations indicated average gains of about +15 mL in volume and $+2 \times 10^9$ total spz per ejaculate under optimized selection ($P < 0.05$). The ANN achieved acceptable prediction error and moderate R^2, sufficient to rank boars by expected sperm output. In young boars, ANN-guided planning improved semen traits: motility (1–5 scale) increased from 4.39 ± 1.36 to 4.88 ± 0.96, pathology decreased from 22.60 ± 13.95% to 18.65 ± 5.89%, and volume rose from 120.10 ± 73.78 to 174.38 ± 97.60 mL (≈ +45%), all $P < 0.05$. Total and pure semen concentration increased by approximately 8 - 15% ($P < 0.05$).

Conclusion

Combining logistic regression and ANN-based ranking enables predictive semen planning aligned with genetic merit while handling repeated ejaculates per boar. This data-driven strategy improves early boar performance and supports stable productivity in AI centers.

Keywords: Boar, Artificial insemination, Machine learning, Artificial neural network, Genetic index.

POSTERS

TOPIC 9: NUTRITION AND GUT MICROBIOTA (NGM)

THE ROLE OF ZINC OXIDE AND ITS PHYSICO-CHEMICAL PROPERTIES IN ENHANCING PIGLET HEALTH AND GROWTH

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Introduction and Objectives

This study aimed to characterize the physico-chemical and antibacterial properties of two zinc oxide (ZnO) sources and to evaluate their physiological effects in piglets under conditions with or without a dietary challenge induced by the withdrawal of feed additives.

Materials and Methods

Two ZnO sources were evaluated: potentiated ZnO (pZnO) and activated ZnO (aZnO). Physical properties were determined by particle size (laser diffraction), bulk density (Carney flowmeter), and specific surface area (SSA; nitrogen adsorption). Antibacterial activity was assessed in vitro using *E. coli* ETEC F18 in a liquid medium (pH 6.7; 8 h incubation). Due to solubility limits, 160 µg Zn/mL was used to monitor bacterial growth by optical density (690 nm) every hour; data were analyzed by T-test. For the in vivo study, 560 piglets (Topigs TN70 × DB Duroc; 26 d weaning, 10.9 ± 0.9 kg) were distributed in a 2 × 2 factorial design: Zn source (aZnO or pZnO) × dietary challenge (with or without 0.5% citric acid + 0.2% encapsulated essential oils/organic acids). Each treatment had eight replicates (~17 piglets). Performance was recorded until 65 d of age and analyzed by two-way ANOVA.

Results and Discussion

Marked differences were found between sources: median particle size (pZnO = 126 µm; aZnO = 16 µm), bulk density (1 vs 2 g/mL), and SSA (45 vs 0.04 m²/g), meaning > 1000-fold higher surface area for pZnO. In vitro, bacterial growth was higher ($P < 0.01$) with aZnO, with E. coli proliferation delayed from 3 h to 5 h with pZnO. In vivo, pZnO tended to improve ADG (624 vs 595 g/d; $P < 0.10$), with 7% and 3% higher growth under challenge and non-challenge conditions, respectively. Feed intake was unaffected by Zn source but tended to be higher without challenge (946 vs 903 g/d; $P < 0.10$).

Conclusion

Potentiated ZnO improved growth tendency and reduced costs compared with activated ZnO. The enhanced antibacterial effect and greater specific surface area of pZnO likely explain its superior support for intestinal health and piglet performance.

Keywords: *E. coli*, Piglet, Performance, ZnO.

DEOXYNIVALENOL AND ENNIATINS AFFECT GROWTH PERFORMANCE AND GUT HEALTH IN PIGLETS: THE BENEFICIAL EFFECT OF AN ALGOCLAY-BASED DETOXIFIER

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Introduction and Objectives

Deoxynivalenol (DON) exposure of piglets, showed elevated gut inflammation markers (Grave et al., 2021). The effects of dietary exposure to DON and enniatins (ENNs), were assessed on growth performance, inflammation, oxidative stress, and tight junction integrity markers. A secondary objective was to evaluate the efficacy of an algoclay-based detoxifier as a nutritional strategy to mitigate these effects.

Materials and Methods

Naturally contaminated corn and barley served as sources of DON and ENNs, respectively. A total of 180 piglets were assigned to three dietary treatments (60 per group, 10 pens of six animals): a CONTROL diet with low contamination (DON: 20 ppb; ENN: 20 ppb), a high DON+ENN diet (DON: 700 ppb; ENN: 800 ppb), and a contaminated diet supplemented with ALGOCLAY, 1.5 g/kg of feed. Diets were fed for 14 days, followed by a marginally contaminated diet until day 35 to assess lasting effects. Growth performance (ADG, FCR) was measured during exposure (days 0 - 14), post-exposure (days 14 - 35), and overall (days 0 - 35). After six days of exposure, intestinal and brain tissues were collected to assess mRNA expression of key markers linked to inflammation and barrier integrity.

Results and Discussion

Piglets fed the DON+ENN-contaminated diet required eight times more antibiotic treatments than controls, indicating impaired immune defense and higher disease susceptibility. Supplementation with ALGOCLAY reduced antibiotic use by 31%. During the first 14 days, DON+ENN exposure tended to decrease ADG and increase FCR ($P = 0.09$). Although partial recovery occurred after switching to a marginally contaminated diet, ADG remained lower than controls by day 35 ($P < 0.03$), showing persistent effects. At the molecular level, DON+ENN exposure downregulated ZO-1 ($P < 0.01$) and upregulated IL-8 ($P < 0.001$) in the jejunum, while IL-1β increased in the colon ($P < 0.01$), indicating inflammation and barrier disruption. In the hippocampus, reduced expression of occludin and the serotonin transporter ($P < 0.02$) suggested altered gut-brain communication.

Conclusion

In **Conclusion**, DON and ENN exposure impaired piglet performance and induced both intestinal and neurological alterations, affecting the gut-brain axis. The algoclay-based decontaminant demonstrated protective effects on gut health and inflammation and represents a viable strategy to mitigate the adverse outcomes of dietary mycotoxin exposure.

Keywords: Emerging toxins, Algae, Molds, Detoxification, Barley.

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SUPPLEMENTATION OF ENZYMATICALLY HYDROLYZED YEAST (CELMANAX™) DURING LATE GESTATION AND LACTATION IMPROVES PIGLET VITALITY AND WEANING PERFORMANCE: A FIELD STUDY IN A COMMERCIAL FARM

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Introduction and Objectives

Low birth weight piglets are a common problem that can occur in pig production worldwide. It is one of the leading causes of death in the first week after birth (Theil et al., 2014). Hydrolyzed yeast (HY) provides bioactive compounds contribute to sows' and piglets' health by modulating physiological functions such as nutrient digestibility, gut microbiota balance, and immune function (Jiang et al., 2015). This study aimed to evaluate the effects of enzymatically HY (EHY) (Celmanax™) supplementation on piglet survival and weaning performance under real-world conditions.

Materials and Methods

A Cambodian wean-to-finish pig farm was selected for this study. The treatment group was fed the same feeding program with a control diet (16% protein and 3,300 kcal/kg) containing EHY 200 g/ton of feed, according to manufacturer, in late gestation (day 85) and lactation. The production data in the farrowing unit were recorded: farrowing date, number of piglets born alive, litter birth weight, weaning date, number of pigs weaned, and weaning weight. All data were analyzed statistically by the Shapiro-Wilk test and the Mann-Whitney U test, or Welch's T-Test using Jamovi version 2.6.44.0 (https://www.jamovi.org).

Results and Discussion

A total of 193 sows were randomly assigned to control (60) and treatment (133) groups. Total piglets born alive (12.6 ± 2.91, 12.5 ± 2.79; $P = 0.521$), litter birth weight (16.1 ± 4.6, 15.8 ± 3.579; $P = 0.375$), lactation length (21.9 ± 1.53, 19.3 ± 1.92; $P = 1.000$), and pre-weaning mortality (14.7 ± 30.1, 6.38 ± 28.7; $P = 0.963$) were not statistically different. While weaning performance, pigs weaned/litter (10.1 ± 2.19, 11.2 ± 2.43; $P = 0.001$), litter weaning weight (44.3 ± 8.17, 53.3 ± 15.2; $P < 0.001$), and litter weight gain (1,291 ± 445, 1,989 ± 903; $P < 0.001$) of the EHY supplemented group were very significantly different. Sows receiving EHY in their diets had numerically lower pre-weaning mortality. The supplementation with EHY increased litter weight gain (approximately 50%) and weaning weight (approximately 0.3 kg/piglet). Higher weaning weights result in stronger piglets and a shorter time to market weight, resulting in increased profits.

Conclusion

The supplementation of EHY (Celmanax™) at 200 g/ton in sow diets during late gestation and lactation significantly improved piglet survival and weaning quality.

Keywords: Enzymatically hydrolyzed yeast, Piglet vitality, Weaning performance.

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DIETARY ENZYMATICALLY HYDROLYZED YEAST (CELMANAX™) DURING LATE GESTATION AND LACTATION ENHANCES SOW COLOSTRUM YIELD AND PIGLET PERFORMANCE UNDER FARM CONDITIONS

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Introduction and Objectives

Genetic improvements have resulted in high litter sizes but have also led to higher neonatal mortality. So, ensuring the piglet's survival during the first 24 hours after birth is crucial. Colostrum intake can reduce mortality rate and increase weaning weight. Nutritional additives such as hydrolyzed yeast (HY) are known to enhance gut health, immune response, and nutrient absorption (Tan et al., 2021). This study aimed to evaluate the effects of enzymatically hydrolyzed yeast (Celmanax™) (EHY) supplementation during late gestation and lactation on colostrum yield and piglet performance under commercial farm conditions.

Materials and Methods

Totally 196 sows from a commercial wean-to-finish farm in Cambodia were randomized into 2 groups, control (60) and treatment (136) based on the structure of pig building and amount of product. Both groups were fed the same feed formula (16% protein and 3,300 kcal/kg). The treatment group was fed EHY (200 g/ton of feed as manufacturer recommendation) from 85d gestation to weaning. We collected data: number of piglets born alive, litter birth weight, litter body weight at 24 hours after birth. The colostrum yield was calculated as described by Theil et al. (2014). The data were performed the Shapiro-Wilk test and the Mann-Whitney U test or Welch's T-Test using Jamovi version 2.6.44.0 (https://www.jamovi.org).

Results and Discussion

No significant differences of control and treatment groups were observed in the number of piglets born alive (12.6 ± 2.91, 12.3 ± 3.07; $P = 0.724$), litter birth weight (16.1 ± 4.69, 15.5 ± 3.90; $P = 0.473$), and average birth weight (1.29 ± 0.282, 1.28 ± 0.194; $P = 0.590$). However, the treatment group exhibited significantly higher 24h body weight (16.0 ± 4.45, 16.7 ± 4.15; $P = 0.034$) and average 24h piglet body weight (1.29 ± 0.274, 1.38 ± 0.206; $P = 0.008$). Colostrum yield (g/litter) was significantly greater in the supplemented group (3,121±1,629, 4,671±1,742; $P < 0.001$). This study showed that supplementation with EHY increased early piglet weight gain, indicating improved colostrum availability in the sows. These effects may be due to EHY bioactive compounds that modulate immune response and improve nutrient transfer to the offspring.

Conclusion

Feeding EHY (Celmanax™) at 200 g/ton to sows during gestation and lactation significantly enhanced colostrum yield and piglet body weight 24h after birth without affecting birth parameters.

Keywords: Colostrum yield, Enzymatically hydrolyzed yeast, Piglet performance, Sows.

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SUGARCANE YEAST EXTRACT REPLACES SPRAY-DRIED PLASMA IN WEANED PIGLETS' PRE-STARTER DIETS, AND MAINTAINS MICROBIOTA STABILITY AND PERFORMANCE

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Introduction and Objectives

Spray-dried plasma (SDP) is commonly included in pre-starter diets to stimulate feed intake (FI), improve efficiency, and immune status in weaned piglets. However, its cost, availability, and demand for animal-free ingredients have driven the search for alternatives. Yeast extract (YE) from *Saccharomyces cerevisiae*, rich in functional peptides, amino acids, and nucleotides, is a potential SPD replacement without impairing performance or gut health. This study evaluated the partial replacement of SDP with YE in pre-starter diets on performance, gut health and microbiota in weaned piglets.

Materials and Methods

A total of 350 piglets were blocked by body weight (BW) and sex and assigned to five diets: control diet containing 3 and 1.5% SDP in pre-starter I and II (CN), CN with 1% YE on-top, and diets replacing 16.7, 33.3, and 50% of SDP with 0.5, 1.0, and 1.5% YE, respectively. FI and fecal score (FS) were recorded daily, and BW weekly. On day 21, samples (n = 10/treatment) were collected for intestinal histomorphometry, plasma cytokines, fecal myeloperoxidase, and gut microbiota diversity. Performance and histomorphometry were analyzed using ANOVA and Tukey's test. Microbiota diversity was evaluated using Mann-Whitney and perMANOVA. Myeloperoxidase and cytokines were analyzed using Kruskal-Wallis and Dunn's post hoc tests. Significance was declared when $P < 0.05$.

Results and Discussion

In pre-starter I, FI was higher in CN compared to 1.5% YE ($P < 0.05$), but no differences were found in BW, average daily gain, or feed conversion in either pre-starter I, II or overall phases ($P > 0.05$), indicating YE provided functional peptide and nucleotide fractions supporting growth similarly to SDP. FS did not differ ($P > 0.05$), suggesting YE did not increase diarrhea incidence. Histomorphometry confirmed gut integrity maintenance in YE treatments. Microbiota α and β-diversities did not differ ($P > 0.05$), indicating structural stability. Likewise, fecal myeloperoxidase and plasma TNF-α, IL-1β, IL-18, IL-12, IFN-γ were unaffected ($P > 0.05$), suggesting preserved inflammatory balance.

Conclusion

Under the conditions of this study, sugarcane yeast extract can partially replace spray-dried plasma in pre-starter diets for weaned piglets while maintaining growth performance, gut health, and microbiome stability.

Keywords: Alternative Protein, Gut Microbiota, Saccharomyces cerevisiae, Performance, Piglets.

EFFECT ON MORTALITY AND PERFORMANCE OF PIGLETS SUPPLEMENTED WITH A *CLOSTRIDIUM BUTYRICUM* PROBIOTIC FROM WEANING UNTIL 45 DAYS POST-WEANING IN A COMMERCIAL FARM

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Introduction and Objectives

Probiotics showed potential to modulate the inflammatory response and to improve pig intestinal health. They are also related to the production of short-chain fatty acids in the intestinal lumen by bacterial fermentation of undigested dietary carbohydrates. The multiple positive direct and indirect effects of butyrate are well documented: it is a major metabolite for the colonic epithelial cells (Bedford & Gong, 2018), and it can improve post-weaning pig growth and increase feed digestibility (Bergman, 1990). In this study, we evaluate the mortality and performance of piglets on a diet supplemented with a butyrate-producing *C. butyricum* probiotic (Miya-Gold®/Top Gut®) during the first 45 days post-weaning.

Material and Methods

435 weaned piglets from three production batches were divided into two groups. From 30 days of age, a 3-phase diet in meal-form was provided. All animals were individually weighted at the start and the end of the trial. *C. butyricum* spores were added to the treatment group diet at $5.0x10^8$ CFU/kg from day 31 to day 41 and 2.5×10^8 CFU/kg from day 42 onwards. In case of mortality, the date of mortality, weight and average daily weight gain until death were registered.

Results and Discussion

Significant differences ($P < 0.005$) in mortality weights were demonstrated; 10.8 ± 1.36 and 4.88 ± 0.51 in the control and treated groups, respectively. Average daily gain improved significantly ($P < 0.005$) from 0.560 ± 0.011 to 0.604 ± 0.011 in the control and treated groups, respectively in the period from 53 to 72 days of age. The control group showed higher mortality weights due to a digestive and respiratory syndrome, while the treated ones died during the first weeks as runts.

Conclusion

The inclusion of *C. butyricum* spores in the diet of weaned piglets generates a statistically better average daily weight gain from 53 to 72 days of age. The inclusion of *C. butyricum* spores in the diets of just weaned piglets demonstrated statistical differences in mortality, weight, and performance.

Keywords: Butyrate, *Clostridium butyricum*, Probiotics.

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ASSESSMENT OF THE BIOACTIVE MINERAL-BASED PRODUCT (OPTIMIZE®) FOR IMPROVING SOW PRODUCTIVITY

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Introduction and Objectives

Hyper-prolific sows are common in modern pig production, but higher productivity increases the risk of oxidative stress, which can compromise embryo quality, survival, and piglet development. Oxidative stress impairs reproduction by triggering harmful cytokines, leading to embryonic loss or reduced litter quality (Yang et al., 2023). Optimize®, a bioactive mineral product containing FeO, Fe_2O_3, Al_2O_3, and MgO, releases reactive ions that neutralize free radicals generated by oxidative stress, thereby mitigating its negative effects, supporting reproductive health, and enhancing sow performance (Holck et al., 2019; Song et al., 2021). This study evaluated the effects of dietary Optimize supplementation on sow reproductive performance in Vietnam field conditions.

Materials and Methods

A total of 602 crossbred sows (Landrace × Yorkshire), parity 1–6, were randomly allocated into two groups with equivalent parity distribution. Due to field production conditions, the group sizes were unequal, with 285 sows in the Control group and 317 sows in the Optimize group. The Control group received no supplementation, while the Optimize group was supplemented with Optimize at 5 g/sow/day during gestation and 10 g/sow/day during lactation using the top-dressing method. Sow performance parameters, including total born, born alive and piglets weaned per litter, were recorded and analyzed by ANOVA (significance at $P < 0.05$).

Results and Discussion

Results showed that sows receiving Optimize exhibited significant improvements in performance compared to the Control group ($P < 0.05$), including total born (14.53 vs 12.75 piglets), born alive (12.97 vs 11.42 piglets), and piglets weaned per litter (12.36 vs 10.71 piglets). Although cross-fostering was applied during the trial, making pre-weaning mortality data less accurate, improvements in born alive and piglets weaned per litter suggest a notable reduction in mortality in the Optimize group compared to the Control group (4.7 vs 6.22%).

Conclusion

Dietary supplementation with Optimize significantly improved reproductive performance and piglet productivity in sows under field conditions in Vietnam. Sows receiving Optimize showed higher total born, born alive, and piglets weaned per litter compared to the Control group. These results indicate that Optimize effectively supports sow health and reduces pre-weaning mortality, contributing to enhanced overall productivity in intensive pig production systems.

Keywords: Bioactive mineral-based feed additive, Nutrition, Oxidative stress, Sow performance.

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EFFECTS OF A BIOACTIVE MINERAL-BASED ADDITIVE (OPTIMIZE®) ON GROWTH PERFORMANCE AND CARCASS TRAITS OF FATTENING PIGS UNDER FIELD CONDITIONS

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Introduction and Objectives

Mineral oxides have been associated with antimicrobial properties through redox reactions and reactive species generation (Williams et al., 2011; Guo et al., 2021). Such mechanisms may influence gut health and nutrient utilization, potentially affecting pig productivity. Optimize® is a bioactive mineral complex containing FeO, Fe_2O_3, Al_2O_3, and MgO, which can release reactive ions under gastrointestinal conditions. While theoretical benefits have been proposed, evidence under commercial swine production remains limited. This study aimed to evaluate the effects of dietary Optimize supplementation on growth performance and carcass traits of finishing pigs under field conditions in Vietnam.

Materials and Methods

A total of 640 mixed-sex pigs, average body weight (BW) 60 kg, were fed for 60 days. Animals were housed in a mechanically ventilated closed housing system at 24 - 28°C with a stocking density of ~0.8 m^2/pig and fed through circular hoppers with commercial bagged pelleted feed (CP 13%, ME 2,900 kcal/kg, CF 8%); both feed and water were provided ad libitum. Sixteen pens (8 per treatment, 40 pigs/pen) served as experimental units. Pigs were sorted by gender and weight, then pens were blocked by body weight and randomly assigned to Control or Optimize diets using a randomized complete block design. Data collected included BW, feed intake, FCR, and carcass traits from 48 carcasses (3 pigs/pen). Statistical analysis used ANOVA (significance at $P < 0.05$).

Results and Discussion

Pigs supplemented with Optimize showed higher final BW (108.3 vs. 106.5 kg; SEM = 0.89, $P = 0.002$), improved ADG (942.2 vs. 909.7 g/day; SEM = 16.7, $P = 0.002$), and better FCR (2.96 vs. 3.03; SEM = 0.02, $P = 0.00$) than Control. Carcass traits improved with greater yield (76.0 vs. 74.3%; SEM = 1.78, $P = 0.00$), lean percentage (57.6 vs. 56.2%; SEM = 1.49, $P = 0.00$), lower backfat (16.3 vs. 17.4 mm; SEM = 1.97, $P = 0.00$), and reduced drip loss (4.95 vs. 6.78%; SEM = 2.14, $P = 0.00$).

Conclusion

Supplementation with Optimize improved growth rate, feed efficiency, and key carcass traits in fattening pigs, confirming its positive impact on growth performance and carcass quality under field conditions.

Keywords: Bioactive mineral-based feed additive, Carcass trait, Feed efficiency, Finishing pigs, Growth performance.

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DYNAMICS OF THE PIGLET FECAL MICROBIOME DURING LACTATION WITH AND WITHOUT *BACILLUS* SP. PROBIOTIC SUPPLEMENTATION

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Introduction and Objectives

Given the importance of fecal microbiome dynamics in piglets during lactation, particularly under tropical production conditions, understanding these shifts can offer valuable insights for optimizing nutrition, microbial interventions, and overall health management in swine herds (Saladrigas-García et al., 2022). Accordingly, the present study examines the temporal changes in the piglet fecal microbiome throughout lactation, comparing those receiving Bacillus sp. probiotic supplementation with those that did not.

Materials and Methods

Fecal samples (n = 90) from 30 piglets collected on days 3, 7, and 21 were analyzed by 16S rRNA sequencing. Piglets were assigned to control (n = 15) or treatment (n = 15) groups, with the treatment group receiving Bacillus subtilis and B. amyloliquefaciens probiotics (1.1×10^9 CFU/g) in creep feed from days 3–21 and no antibiotics used. Alpha and beta diversity were assessed using Kruskal–Wallis and PERMANOVA, respectively, while bacterial abundances were analyzed using GLM procedure with groups and sample days as the fixed effects in SAS 9.4.

Results and Discussion

Piglet fecal microbiota richness increased from ~100 to 400 ASVs during lactation and was dominated by Firmicutes (52.2%), Bacteroidota (30.1%), and Proteobacteria (6.9%). Early-life genera (e.g., Bacteroides, Enterococcus, and Fusobacterium) declined over time, whereas Christensenellaceae_R-7_group, Muribaculaceae, and Phascolarctobacterium increased ($P < 0.05$), indicating progressive microbiome maturation with reduced maternal influence. Although no differences in alpha diversity were observed between groups on days 3 and 7 ($P > 0.05$), the treatment group showed higher alpha diversity on day 21 (e.g., Chao1 ($P = 0.028$), Shannon ($P = 0.022$), and observed features indices ($P = 0.031$)). Beta diversity did not differ between groups at any time point ($P > 0.05$). In addition, the relative abundance of Bacteroides was greater in the treatment group on day 21 (7.5 vs. 3.7%, $P = 0.028$), suggesting that Bacillus supplementation might promote beneficial taxa such as Bacteroides, which Tan et al. (2019) revealed as a next-generation probiotic.

Conclusion

The piglet microbiome continued to mature with increasing richness and reduced maternal influence. Bacillus sp. supplementation led to higher diversity and higher Bacteroides on day 21, but these changes were too modest to alter overall community composition.

Keywords: Bacteroides, Dominant bacteria, Gut health, Feed additive, Suckling piglet.

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BIOAVAILABILITY OF ZINC CHELATE OF SMALL PEPTIDES IN GROWING PIGS COMPARED TO ZINC SULFATE

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Introduction and Objectives
Zinc (Zn) is an essential trace element required for growth, bone development, and numerous metabolic processes that support animal health. However, the bioavailability of dietary zinc can vary depending on its source. The aim of this study is to compare an organic zinc source (zinc chelate of small peptides) to an inorganic source (zinc sulfate, $ZnSO_4$).

Materials and Methods
Ninety male pigs (Landrace × Large White; 63 days old; 25.44 ± 0.30 kg) were assigned to a randomized complete block design based on initial body weight in a 2 × 4 + 1 factorial arrangement, including two zinc sources (Zn chelate or $ZnSO_4$), four dietary zinc levels (30, 60, 90, and 120 mg Zn/kg), and a negative control without supplemental zinc, with 10 pigs per treatment over a 60-day period. Zinc digestibility was assessed using acid-insoluble ash as an internal marker, and relative bioavailability was determined by linear slope-ratio regression, with data analyzed using zinc source and level as fixed effects, block as a random effect, and linear and quadratic contrasts to evaluate dose–response relationships.

Results and Discussion
Compared with unsupplemented pigs, zinc supplementation improved growth performance ($P \leq 0.05$). During days 0 - 30, pigs fed zinc chelate showed quadratic responses for ADG and feed efficiency and linear increases in final body weight and feed intake ($P \leq 0.05$). From days 30 - 60, both zinc sources induced linear and quadratic improvements in final body weight, ADG, and feed efficiency ($P \leq 0.05$). Pigs fed zinc chelate tended to exhibit lower fecal zinc excretion, higher liver zinc concentrations, and greater bone zinc content ($P \leq 0.05$) compared with those fed $ZnSO_4$. Serum zinc increased over time in all supplemented pigs ($P \leq 0.05$), with a tendency toward higher concentrations in pigs fed zinc chelate. Apparent total tract digestibility of zinc increased linearly ($P \leq 0.05$), with positive values observed only for the organic zinc source.

Conclusion
The findings suggest that the novel Zn chelate of small peptides is more efficient than $ZnSO_4$ and can be supplemented in smaller amounts to achieve the same results, contributing to both animal productivity and environmental sustainability.

Keywords: Bioavailability, Mineral retention, Organic zinc, Performance, Sustainability.

EFFECT OF AN ALGOCLAY COMPLEX ON PERFORMANCE OF PIGS FED REDUCED ENERGY, PROTEIN AND AMINO-ACIDS LEVELS

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Introduction and Objectives

For decades, pig production has relied on nutrient-dense diets to maximize performance. Modern production systems now emphasize precision nutrition to sustain high productivity while reducing feed costs. Enhancing diet digestibility is one approach, as improving nutrient utilization enables diet dilution without compromising growth. This study assessed whether an algoclay complex can increase diet digestibility and consequently preserve pig performance under reduced dietary energy, protein, and amino-acid levels.

Materials and Methods

A total of 390 pigs (Danbred × Duroc), 56 days old and weighing 16.6 ± 1.09 kg, were allotted to 30 pens with 13 pigs per pen in an environmentally controlled facility. The feeding program included three experimental phases: Grower 1 (30 - 60 kg), Grower 2 (60 - 90 kg), and Finisher (90 - 110 kg). Diets were based on wheat, barley, and soybean meal. From 56 to 84 days of age, all pigs received a standard diet before being assigned to one of three treatments: T1: standard diet meeting pigs' nutritional requirements; T2: 3% diluted standard diet supplemented with the algoclay complex; T3: 6% diluted standard diet supplemented with the algoclay complex. Performance (body weight, ADG, feed intake, and FCR) was monitored throughout the trial and an economic analysis evaluated the profitability of including the algoclay complex in nutrient-diluted diets.

Results and Discussion

Reducing dietary energy, protein, and amino-acid levels compensated for the cost of the algoclay complex and lowered feed expenses without affecting pigs' final weight (108.4 kg for pigs of the control group vs. 109.7 kg for pigs from T2 and T3, $P = 0.939$, NS). Consequently, pigs in the 3% (T2) and 6% (T3) diluted-diet groups achieved higher benefits over feed cost than the control group (T1), with gains of 1.2 and 4 USD per pig, respectively, demonstrating the strong economic efficiency of the algoclay complex.

Conclusion

In this study, the algoclay complex seems to improve the utilization of nutrient-diluted diets. Pigs fed the 3% (T2) or 6% (T3) diluted-diets maintained performance comparable to the control group while delivering higher economic returns (+ 3.3 and + 4%, ROI of 2 and 6, respectively).

Keywords: Digestibility, Growth performance, Nutrient diluted, Precision nutrition, Sustainability.

THE EFFECT OF ENERGY SUPPLEMENTS ON NEWBORN PIGLETS AT LOW ENERGY LEVELS

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Introduction and Objectives

The body reserve of piglets at birth is the immediate source of energy. In moderate climate conditions, a 1.0 kg piglet has an energy requirement of 900 - 950 kJ. This demand is partly covered by body reserves (about 420 kJ/kg bodyweight) and colostrum, as these sources are lacking to maintain its live weight. Insufficient energy supply is considered the leading cause of piglet losses in the first two days of life (Dividich et al. 2005). The aim of energy supplements is to activate piglets, enable suckling, thereby ensuring efficient colostrum intake and facilitating passive immune transfer. The purpose of this trial was to investigate the effect of such an energy supplement on piglet performance.

Materials and Methods

26 sows and their litters were randomly allotted into a control and trial group, ensuring a similar parity distribution between groups. A total of 444 piglets were weighed individually on their day of birth within 4 - 6 hours after birth. The control group received no supplementation. In the trial group, only piglets with birth weight below 1.2 kg received 2 ml of the energy supplement MiaKick (MIAVIT GmbH) orally after weighing. Those piglets weighing less than 0.9 kg received a second dose of MiaKick on the second day of life. All piglets were weighed at birth and again at weaning.

Results and Discussion

Variance analysis of weaning weight, with birth weight included as a fixed covariate and litter treated as a random effect, indicated a significantly higher weaning weight of + 0.34 kg in the trial group (5.78 kg) compared to the control group (5.43 kg) (P = 0.05). Litter homogeneity, assessed by the coefficient of variation, was slightly higher in the trial group at birth (14.0 vs. 13.1%) and visibly lower at weaning (21.1 vs. 24.8%), though differences were not statistically significant (F-test).

Conclusion

The trial was conducted to determine the effect of an additional energy supply to piglets directly after birth on performance and litter homogeneity. The results prove positive effects on weight gain (+ 0.34 kg in the trial group).

Keywords: Energy lack, Piglet survival, Booster.

Acknowledgements: We thank the Scientific Committee and the reviewers for their constructive suggestions. This abstract has been revised to improve the statistical methodology and clarity. This was done in response to the Committee's request, while maintaining the original study design and length restrictions for the abstract.

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EFFECT OF A COMBINATION OF ENCAPSULATED AND GROUND PHYTOGENS ON DIGESTIVE PARAMETERS IN PIGLETS

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Introduction and Objectives

The intestine is crucial for animal health, well-being and performance. During weaning, the intestine is challenged due to changes in environment and feed. Natural feed additives like *Miarom Intest C* provide a specific combination of diverse phytogenics, either encapsulated or ground, including active components from caraway, star anise, chamomile, ginger, cinnamon, and oregano. This formulation ensures release throughout the entire intestine, supporting intestinal health. The study aimed to determine its influence on performance and faecal parameters of piglets.

Materials and Methods

Freshly weaned piglets (Duroc x DanBred) were allotted into three groups to test *Miarom Intest C* (MIAVIT) "on-top" at two dosages. The control group received no supplementation. The low-dose (MIC-L) group received 100 mg/kg feed throughout the study, while the high-dose group received 200 mg/kg feed in starter I and 100 mg/kg feed in starter II. Each group included 9 piglets per pen and 12 replicates. The piglets were weighed individually on day 0, 14, 28 and 42. The faecal score was visually determined once a week. Faecal samples from MIC-H and the control group, eight samples each, were taken at day 12 and conserved using Biofreeze (Alimetrics) until the analysis.

Results and Discussion

There were no significant differences regarding performance or fecal scores, which is due to the high performance and hygiene standards of the farm. Group MIC-L showed the numerically highest performance values. No differences were observed in total faecal bacterial counts or in specific bacterial taxa between the control and supplemented groups. The relative number of specific bacterial taxa shows that most microbes have not been identified. The relative amount of acetic acid was significantly higher (65.1 vs. 58.4% acetic acid of total amount of SCFA) in the supplemented group, which indicates better fibre fermenation. Valeric acids, a derivate of protein fermentation, was significantly lower (in the supplemented group 1.31 vs. 2.69% valeric acid of total amount of SCFA). These reduced values indicate improved protein digestion in the small intestine, as less undigested protein reaches the large intestine for fermentation.

Conclusion

The product influenced the microbiota positively, which is reflected in changes in SCFA.

Keywords: Microbiota modulation, Feed additives, Volatile fatty acids.

SUPPLEMENTING SOWS WITH EUBIOTIC LIGNOCELLULOSE IN LATE GESTATION IMPROVES FARROWING AND LITTER PERFORMANCE IN PRACTICAL CONDITIONS

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Introduction and Objectives

Among the most critical stressors for gestating sows are oxidative stress from rapid tissue growth and nutritional factors like feed restriction and low-fiber diets, which can impair placental function and fetal development. While dietary fiber benefits for gestating sows are gaining recognition, different values of specific fiber types remain less understood. For example, feed-grade lignocellulose is mainly known for reducing constipation in sows. Eubiotic lignocellulose, unlike conventional lignocellulose, contains partly fermentable fiber and phenolic compounds that enhance SCFA production and improve metabolic and oxidative status, reducing stress and improving farrowing ease and litter performance. A field study investigated these effects.

Materials and Methods

The trial was carried out in March of 2025 on a commercial sow farm with 95 sows (parity 3 - 7); 47 sows in the control (NC) and 48 in the treatment group (ELC). NC sows received the standard gestation diet, while ELC sows additionally received 75 g eubiotic lignocellulose/sow/day from day 87 of gestation until farrowing. Each sow was considered one repetition, and data were collected on farrowing duration, litter size, and birth weight.

Results and Discussion

Even though ELC sows had on average 0.6 more live-born piglets per litter (12 vs. 11.4), the average farrowing duration was reduced by 45 minutes (243 vs. 288 min). The portion of weak piglets was reduced from 9.7% in NC to 1.6% in ELC group and the average birth weight was increased from 1.43 to 1.49 kg. The results show that the more favorable and uniform birth weight distribution within the ELC litters, with fewer piglets in the low weight categories < 1.2 kg and more piglets in the higher weight categories > 1.4 kg.

Conclusion

Sows supplemented with eubiotic lignocellulose had a quicker farrowing process, but larger and heavier litters. This shows the physiological benefits of eubiotic lignocellulose in the demanding late phase of gestation.

Keywords: Dietary Fiber, Eubiosis, Piglet Health, Sow Productivity.

PROTECK IMPROVED SOW PRODUCTIVITY UNDER ITALIAN FIELD CONDITIONS

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Introduction and Objectives

A bioactive mineral-based feed additive (BMF) is a mined mineral from a unique location that has demonstrated a positive impact on the microbiota of pigs. Feeding BMF to sows throughout gestation and lactation resulted in 0.7 extra piglets weaned per litter combined with an increased glutathione peroxidase activity (GPx) in blood serum from sows taken at day 114 of gestation. This improved oxidative stress status may contribute to better piglet quality (Al-Gubory et al., 2010). The objective was to determine the effect of BMF on litter performance and reactive oxygen metabolites (ROM) as a measurable indicator of GPx activity.

Materials & Methods

A 1400-sow farrow-to-finish farm (Mantova, Italy) with TN70 sows was enrolled in a sequential study (control, n = 3,954; BMF, n = 855). The BMF (Proteck; Elanco AH, Indianapolis, IN, USA) was fed at 2 kg per tonne of feed. Monthly blood samples (n = 220 in total) were collected from sows in late gestation (d 114) for d-ROM analysis. Sow reproductive performance parameters were recorded throughout the study. Data were analyzed using JMP 17.0 at a significance level of 0.05.

Results

The d-ROM levels were significantly ($P < 0.05$) reduced from 36.16 mg H2O2/dL (n = 145) in the Control group to 23.30 mg H2O2/dL (n = 75) in the BMF group. The proportion of sows with a low oxidative stress level significantly ($P < 0.05$) increased from 9% in the Control group to 51% in the BMF group. The number of stillborn piglets per litter significantly ($P < 0.05$) reduced by 0.133, and the number of mummified piglets per litter significantly ($P < 0.05$) reduced by 0.16 in the BMF group. In the BMF fed group, an additional 0.245 piglets were weaned per litter ($P < 0.01$).

Discussion & Conclusions

The present longitudinal field study demonstrated that feeding BMF to sows during the entire production cycle resulted in an increase of 0.245 piglets per sow per litter or 0.588 piglets per sow per year. Feeding the BMF decreased d-ROM by 35% resulting in an overall decreased oxidative stress level within the sows.

Keywords: Sow productivity, field trial, Italy, Proteck.

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MICROENCAPSULATED ORGANIC ACIDS AND ESSENTIAL OILS DELIVER MEASURABLE GAINS IN SOW PRODUCTIVITY AND PIGLET PERFORMANCE UNDER COMMERCIAL FARM CONDITIONS

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Introduction and Objectives

Increasing restrictions on in-feed antibiotic use in breeding herds, driven by antimicrobial resistance concerns and regulatory pressure, have intensified the search for nutritional strategies that support intestinal health, sow resilience, and piglet survival (Dos Santos et al., 2023). Organic acids (OA) and essential oils (EO) exhibit antimicrobial and anti-inflammatory properties, but their efficacy may be limited by rapid degradation in the upper gastrointestinal tract. Microencapsulation protects OA and EO in a lipid matrix for targeted hindgut release. This study evaluated the effects of a microencapsulated OA+EO on sow and piglet performance under commercial conditions.

Materials and Methods

A total of 332 Large White × Landrace sows on a commercial farm were randomly assigned across four batches to a control group (basal diet; n = 166) or treatment group receiving microencapsulated OA+EO at 10 g/sow/day (n = 166). Allocation balanced groups for parity and pre-farrowing body condition. Diets were fed from 7 days pre-farrowing to 28 days post-farrowing. Measurements included sow body condition score (BCS), backfat thickness (BF), shoulder ulcer incidence and score, feed intake, reproductive traits, and piglet performance (birth and weaning weight, preweaning mortality, diarrhea incidence, average daily litter weight gain). Diarrhea incidence and pre-weaning mortality were analyzed using Chi-square tests; other parameters used t-tests.

Results and Discussion

Sows fed microencapsulated OA+EO showed improved body condition at weaning, with higher BCS (2.93 vs. 2.84), reduced BCS loss (-0.23 vs. -0.26), and lower BF loss (-2.14 vs. -2.70 mm) compared with controls ($P < 0.05$). Welfare indicators improved, with reduced shoulder ulcer incidence (0.55% vs. 0.81%) and lower scores (0.91 vs. 1.36). Treated sows had higher feed intake during lactation (5.51 vs. 5.40 kg/d). Reproductive parameters were not affected. Piglets from OA+EO-fed sows demonstrated superior performance, including more pigs weaned per litter (11.83 vs. 11.37), higher weaning weight (6.11 vs. 5.90 kg), greater average daily litter weight gain (1963 vs. 1801 g/d), and reduced diarrhea and mortality rates ($P < 0.05$).

Conclusion

Supplementation with microencapsulated OA+EO improved sow condition, welfare, and feed intake while enhancing piglet growth and survivability, supporting its use as an effective strategy to reduce reliance on in-feed antibiotics in lactating sows.

Keywords: Antibiotic alternatives, Organic acids, Essential oils, Piglet performance, Sow productivity.
Acknowledgements: The authors thank the Chulalongkorn University, Bangkok, Thailand for the support with providing testing facilities.

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DUAL-STRAIN BACILLUS-BASED PROBIOTIC ENHANCES GUT INTEGRITY AND REDUCES THERAPEUTIC ANTIBIOTIC USE IN NURSERY PIGS

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Introduction and Objectives
Reducing antibiotic use in swine production while maintaining performance and gut health is a global priority. SolPreme® is a dual-strain Bacillus-based probiotic designed to enhance nutrient digestibility and intestinal resilience in weaned pigs. This study evaluated the effects of SolPreme® on growth performance, intestinal morphology, gut permeability, and therapeutic antibiotic use in nursery pigs.

Materials and Methods
Two consecutive 35-day trials were conducted with 640 crossbred weaned pigs [(Yorkshire-Landrace) × Duroc; 28 ± 1 days old; 6.88 ± 0.66 kg initial BW] in a randomized complete block design. Pigs were assigned to Control (basal diet) or SolPreme® (1.1E+09 CFU/kg feed), with 40 pens/treatment and 8 pigs/pen (equal sex ratio). Parameters included BW, ADG, ADFI, FCR, mortality, diarrhea incidence (score 0-3), and frequency of antibiotic treatment. In trial 2, serum samples (20 pigs/treatment) were collected to assess intestinal permeability 4 hours after oral administration of FITC-dextran (4 mg/kg BW, time 0) at 28 and 38 days of age. Ileal morphology (villus height, crypt depth, VH/CD) was measured at 63 days of age. Performance data were analyzed by ANOVA (MIXED, SAS), while mortality and diarrhea were analyzed by Chi-square; significance was set at $P < 0.05$ and trends at $P < 0.10$.

Results and Discussion
SolPreme® improved BW at 63 days of age (19.68 vs.19.27; $P = 0.007$), ADG (361.19 vs. 346.51 g/d; $P = 0.003$), and FCR (1.615 vs. 1.668; $P < 0.001$). Diarrhea incidence over the entire period (5.77% vs. 8.42%) and antibiotic treatment frequency (7.44% vs. 10.37%) were lower ($P < 0.001$) in the SolPreme® group than in the control group. SolPreme® increased ileal VH (454 vs. 408 µm; $P = 0.013$) with a trend for higher VH/CD (1.60 vs. 1.42; $P = 0.072$) as compared with control. Serum FITC-dextran did not differ between groups at weaning, however the SolPreme® group tended to have lower levels at 38 days of age (10 days post-weaning, 77.6 vs. 92.3 µg/mL; $P = 0.057$), indicating improved barrier integrity.

Conclusion
SolPreme® inclusion in nursery pig diets supported gut structure and barrier function, with associated improvements in digestive health and performance, supporting its role in antibiotic reduction strategies.

Keywords: Antibiotic reduction, Bacillus, Gut health, Nursery pigs, Probiotic.

REPLACING CHOLECALCIFEROL WITH 25-HYDROXYVITAMIN D3 IN PIG DIETS: INFLUENCES ON VITAMIN D METABOLISM AND MUSCLE DEVELOPMENT

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Introduction and Objectives

In pig diets, vitamin D_3 (D_3) is often replaced with the more efficiently absorbed metabolite 25-hydroxyvitamin D_3 ($25(OH)D_3$). This study investigated potential effects of the vitamin D source on systemic vitamin D metabolism and muscle gene expression in growing–finishing pigs.

Materials and Methods

Twenty pigs (21.8 ± 4.8 kg BW) were assigned to two treatments during the growing-finishing phase: vitamin D_3 (2000 IU/kg feed) or $25(OH)D_3$ (50 µg/kg feed). At slaughter (113.8 ± 11.5 kg), blood samples and tissues (liver, renal cortex, and M. *Longissimus dorsi*) were collected. Plasma concentrations of vitamin D metabolites were determined, and relative gene expression of enzymes involved in vitamin D metabolism and muscle development was analyzed by qPCR. Sex was considered in the statistical analyses due to observed sex-related differences.

Results and Discussion

Plasma vitamin D_3 was detected only in pigs fed D_3 (5.8 ± 2.36 ng/mL). Plasma $25(OH)D_3$ and $24,25(OH)_2D_3$ concentrations were significantly higher in the $25(OH)D_3$ group (46.0 ± 8.73 vs. 22.8 ± 5.08 ng/mL and 17.1 ± 84.15 vs. 7.48 ± 1.62 ng/mL, respectively), while $1,25(OH)_2D_3$ and 3-epi-$25(OH)D_3$ did not differ between treatments. Hepatic RNA expression of CYP2R1, CYP27A1, and CYP2D25, coding for enzymes that convert vitamin D3 to $25(OH)D_3$, and renal expression of CYP27B1, crucial for the synthesis of 1,25(OH)2D3, were unaffected. In contrast, renal CYP24A1 was upregulated in the $25(OH)D_3$ group (2.69 ± 1.48 vs. 1.21 ± 0.74). Gene expressions of MSTN and MYOG did not differ between the groups. In pigs fed D_3, MSTN expression was negatively correlated with plasma $1,25(OH)_2D_3$ (r: -0.74) and 3-epi-$25(OH)D_3$ (r: -0.76), suggesting a relationship between vitamin D metabolism and muscle growth regulation. Females exhibited higher plasma albumin concentrations than males (4.00 ± 0.10 vs. 3.71 ± 0.10 g/dL), regardless of treatment. Albumin was associated with muscle gene expression in males, showing positive correlations with MSTN in pigs fed D_3 (r: 0.95) and with MYOG in pigs fed $25(OH)D_3$ (r: 0.96).

Conclusion

Although inactivation of vitamin D metabolites is induced, neither hepatic conversion of D_3 to $25(OH)D_3$ nor renal synthesis of $1,25(OH)2D_3$ seem to be affected by offering $25(OH)D_3$. The results also indicate an interaction between vitamin D metabolism and muscle physiology.

Keywords: Calcidiol, qPCR, Swine, Vitamin D3.

EVALUATING SERUM AND URINARY CALCIUM AND PHOSPHORUS FOR DETECTING PHOSPHORUS DEFICIENCY IN PIGS

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Introduction and Objectives

Ante-mortem assessment of circulating and urinary calcium (Ca) and phosphorus (P) status remains underutilized, despite the potential for dietary mineral supply. Therefore, our objective was to evaluate serum and urinary Ca and P for detecting phosphorus deficiency in growing pigs.

Materials and Methods

Twenty-four mixed sex pigs (22.5 ± 0.4 kg BW) were enrolled in a 28-day study and assigned to one of three dietary treatments (n = 8/trt). The diets were isocaloric and equal in total calcium but varied in digestible phosphorus (digP) and were fed ad libitum. These included: 1) control 0.30% digP diet formulated with monocalcium phosphate (Con); 2) 0.30% digP diet formulated with 350 FTU/kg phytase (Phy); and 3) a 0.10% digP deficient diet without monocalcium phosphate or phytase (Def). After 21 days, pigs were placed into metabolism stalls for 7 days to conduct total urine and fecal balance. Body weights were recorded on days 0 and 28, and serum collected on day 28. Serum and urine samples were analyzed for Ca, creatinine, and P via IDEXX Catalyst One Chemistry Analyzer. Feed and fecal samples were analyzed for Ca and P via ICP. Data were analyzed using mixed-effect models with pigs as the experimental unit.

Results and Discussion

Pig body weight was reduced in Def compared to Con and Phy (38.3, 49.6, and 46.9 kg, respectively; $P = 0.041$). Calcium retention was higher in Con and Phy compared to Def (10.22, 7.21 and 3.87 g/d, respectively; $P < 0.001$). Phosphorus retention was elevated in Con and Phy compared to Def (11.95, 7.68, and 2.73 g/d, respectively; $P < 0.001$). Def serum Ca was elevated compared to Phy and Con (12.99, 11.24, and 10.75 mg/dL, respectively; $P < 0.001$); while urinary Ca:creatinine ratio did not differ between dietary treatments ($P = 0.278$). Def reduced serum P compared to Phy and Con (5.49, 9.32, and 10.05 mg/dL, respectively; $P < 0.001$). Urinary P:creatinine ratio was reduced in Def and Phy compared to Con (0.03, 0.08, and 0.72, respectively; $P < 0.001$).

Conclusion

Phosphorus deficiency disrupts growth and mineral homeostasis, resulting in measurable serum and urinary changes. Incorporating these samples into routine diagnostics may enable earlier identification of phosphorus deficiency before skeletal issues arise.

Keywords: Calcium, Phosphorus, Serum, Urine.

A PHYTOBIOTIC MIXTURE ADDED IN THE WEANED PIGS DIET MODIFIES FECAL MICROBIOTA AND PROMOTES TAXA TOWARDS AN EUBIOTIC STATE

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Introduction and Objectives

Gut microbiota composition reshaping, with phytobiotic extracts diet enrichment is challenging. These changes could improve animals' health and productivity for a long-lasting period (Rodrigues et al., 2022). The current pilot study evaluated the impact of diet supplementation with a phytobiotic mixture (PM) on weaned pigs' fecal microbiota and the duration of the induced change. The PM consisted of encapsulated essential oil from the Greek Origanum vulgare subsp. hirtum, Crithmum maritimum L. essential oil, and in powdered form Camelina sativa L. and Allium sativum L.

Materials and Methods

Seventeen 34-day-old weaned pigs were randomly divided into two groups. For 43 days one group (A) received basal diet and the other (B) was fed with PM-enriched diet. Each ear-tagged pig was kept in a separate pen and served as an experimental replicate. Fresh fecal sampling was performed three times during the experiment, at the age of 77 days (t1) when the supplemented diet was ceased, 7 days later (t2) and 67 days later (t3). Next generation sequencing (NGS) was implemented to study fresh fecal microbiota, using bacterial 16S rRNA gene amplicon sequencing (V4), followed by bioinformatic analysis (Tzora et al., 2022). Evaluation of fecal microbiota alpha-diversity (species richness) was based on the Normalized Richness index. Taxa relative abundance differences were assessed with Wilcoxon rank-sum test.

Results and Discussion

At the end of the trial (t1) and one week later (t2), alpha diversity of fecal microbiota was found to be decreased in group B compared to group A ($P < 0.05$). Significant differences in taxa's relative abundance that exist both in group A and B at t1 and t2, not at t3 were also revealed. Among increased taxa in group B at t1 ($P < 0.05$) were genera Blautia, Coprococcus, Faecalibacterium with known probiotic characteristics and potential positive impact on pig's health. Specifically, Prevotella copri (OTU 57) that was increased is an important candidate as a next-generation probiotic (NGP) (Zang et al., 2024).

Conclusion

In group B PM supplementation significantly decreased alpha diversity in fecal microbiota but the alterations in relative abundance promoted beneficial bacteria. However, once the PM was removed, the impact disappeared.

Keywords: a-diversity, Amplicon sequencing, Fecal microbiota, Phytobiotic mixture, Weaned pigs.

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PREVALENCE OF BENEFICIAL BACTERIAL TAXA IN FECAL MICROBIOTA OF WEANED PIGS UNDER A DIET SUPPLEMENTED WITH A PHYTOBIOTIC MIXTURE

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Introduction and Objectives

Gut microbiota has been associated with intestine health and functionality, providing indices for animals' well-being (Wang et al., 2022). This preliminary study investigated bacterial taxa changes in prevalence in weaned pig's fecal microbiota, fed with a diet enriched with a phytobiotic mixture (PM) consisting of encapsulated oregano essential oil, from Origanum vulgare subsp. hirtum, Crithmum maritimum L. essential oil, and powdered Camelina sativa L. and Allium sativum L. (garlic).

Materials and Methods

Seventeen (17) weaned pigs (34 days) were randomly assigned to two groups. Group A received a basal diet (control) and group B was fed a PM-enriched diet for 43 days. Each ear-tagged pig/pen was an experimental unit. High-throughput sequencing of bacterial 16S rRNA gene amplicon (V4) was performed for fecal DNA accompanied by bioinformatic analysis (Tzora et al., 2022). Changes in prevalence were examined with Fisher's exact test (corrected for multiple testing using the Benjamini-Hochberg method) at the age of 77 days (t1) when the enriched diet was ceased 7 days later (t2) and 67 days later (t3).

Results and Discussion

At (t1) and (t2), differences between the two groups ($P < 0.05$) were disclosed regarding the prevalence of bacterial taxa. At t1 taxa with higher prevalence in group B were Streptococcus and a genus of Ruminococcaceae family and Gemmiger gallinarum/formicilis (OTU 84) and Blautia luti/provencensis/wexlerae (OTU 15). Members of Ruminococcaceae produce enzymes that degrade carbohydrates (Niu et al., 2022). Blautia has probiotic properties. Faecalibacterium prausnitzii (OTU 244) was exclusively found in group B. It produces anti-inflammatory metabolites and butyrate that can modulate the intestinal immune system, and has been proposed as a potential treatment, being a next-generation probiotic (NGP) (Maioli et al., 2021). At t2, Methanobacteriaceae, Eubacterium coprostanoligenes group genus and Methanobrevibacter, were found only in control.

Conclusion

Prevalence analysis highlighted bacterial taxa with more consistent presence in pigs' fecal microbiota fed with PM-diet, even though the sample size limits the generalizability. When PM-diet ceased differentiations disappeared, maybe due to microbiota resilience and/or diet kinetics. The detected taxa possess beneficial characteristics.

Keywords: Bacterial taxa prevalence, Fecal microbiota, Next generation sequencing, Phytobiotic mixture, Weaned pigs

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CHANGES IN FECAL CORE MICROBIOTA AND BETA DIVERSITY OF WEANED PIGS AFTER WITHDRAWAL OF A PHYTOBIOTIC-ENRICHED DIET

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Introduction and Objectives

Core microbiome refers to a collection of microbial taxa, along with their genomic and functional traits, that are uniquely representative of a particular host (Neu et al., 2021). The composition of fecal microbiota, b-diversity, as well as the core microbiota in weaned pigs fed a basal diet or supplemented with a phytobiotic mixture (PM) consisting of encapsulated oregano essential oil, derived from Origanum vulgare subsp. hirtum and Crithmum maritimum L. essential oil, Camelina sativa L. and Allium sativum L. (garlic) in powdered form were studied.

Materials and Methods

Weaned pigs (17) 34 days old, were randomly allocated to two groups. Group A (control) was fed with a basal diet and in group's B diet was added a PM for 43 days. Amplicon sequencing of the bacterial 16S rRNA gene (V4) was performed from fecal DNA accompanied by bioinformatic analysis (Tzora et al., 2022). The microbiota composition, the core genera and OTUs and b-diversity, were determined at the age of 77 days (t1) when the enriched diet came to an end, 7 days later (t2) and 67 days later (t3).

Results and Discussion

Statistically significant differences in b-diversity, indicating bacterial community composition, between the two groups were observed at t1 and t2 timepoints (PERMANOVA, $P < 0.05$), but not at t3 timepoint. The pigs' core fecal microbiota under experimental diet at t1 included the genera Clostridium, Coprococcus and Blautia that breakdown dietary fibers and resistance starches leading to short chain fatty acids formation, fundamental for energy homeostasis (Yang et al., 2018). The number of shared genera and OTUs between the core fecal microbiota of pigs under experimental diet and those under control diet increased steadily over time (10 genera and 8 OTUs (t1), 14 genera and 16 OTUs (t2) and 22 genera and 28 OTUs (t3).

Conclusion

Following the cessation of administration of the PM microbiota compositional differences were eliminated. This is also reflected by the increase of common taxa between the core microbiota of the two groups. Beneficial core bacterial genera are potentially targets of regulation through modified nutrition with substrates that favor their flourishing.

Keywords: B-diversity, Core microbiota, Fecal microbiota, Phytobiotic mixture, Weaned pigs.

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A MULTICOMPONENT PROTEASE MAINTAINS PERFORMANCE AND IMPROVES CARCASS TRAITS, OUTPERFORMING OTHER PROTEASES

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Introduction and Objectives

Reducing dietary protein and feed costs during grower–finisher phases are achieved using exogenous proteases with different outcomes in performance and carcass traits. A Multicomponent Protease was compared with different proteases to evaluate their effects on growth performance and carcass traits of growing-finishing pigs fed nutrient-reduced diets.

Materials and Methods

Four hundred PIC Camborough × PIC337 pigs (50% males and females), 63 days old and weighing ≈ 20.2 kg were housed in 40 floor pens and assigned to five treatments (8 replicates/treatment; 10 pigs/pen) until 157 days of age (≈ 130 kg). Treatments consisted of a standard diet (Control) and four nutrient-reduced diets supplemented with different proteases (Multicomponent Protease, Protease A, Protease B, and Protease C), with nutrient reductions based on matrices and dosages recommended by each enzyme manufacturer. The Multicomponent Protease is composed of three proteases originating from the same bacterial fermentation. A three-phase feeding program (Grower 1, Grower 2, and Finisher) was used. Growth performance was evaluated at the end of each phase, and loin depth and backfat thickness were assessed at day 157. Data were blocked by sex and analyzed by ANOVA, with loin depth analyzed by ANCOVA using body weight as a covariate. Means were compared by Fisher's test ($P \leq 0.05$).

Results and Discussion

Pigs fed the Control diet, and the Multicomponent Protease-supplemented diet showed the lowest feed conversion ratio (1.82) compared with the other proteases (1.85, 1.87 and 1.85 for Protease A, B and C, respectively), while average daily gain did not differ among treatments (1189 g/d average). Pigs fed the Multicomponent Protease had the greatest loin depth (69.7 mm), indicating higher carcass lean meat, with no differences among treatments in the proportion of pigs with backfat thickness >16 mm, a threshold penalized in the local market. The broader proteolytic activity of the Multicomponent Protease, combined with a more appropriate nutrient uplift, may explain the improved performance and carcass traits.

Conclusion

The Multicomponent Protease maintained growth performance at Control levels, improving FCR by up to 5 points over other proteases, and enhanced carcass traits in growing-finishing pigs, allowing feed cost savings without compromising performance.

Keywords: Cost effectiveness, Carcass traits, Growing-finishing pigs, Multicomponent protease, Swine production.

DIETARY USE OF GREEK PHYTOGENIC MIXTURES AND THEIR BIOLOGICAL EFFECTS ON WEANED PIGS

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Introduction and Objectives

Contemporary consumer demand for meat produced with reduced antibiotic use presents major challenges for animal production systems. The use of indigenous aromatic and medicinal plants or their derivatives offers a promising approach to support animal health. This study evaluated the effects of a phytobiotic mixture containing *Origanum vulgare* subsp. *hirtum* and *Crithmum maritimum* L. essential oils, *Allium sativum* L. and *Camelina sativa* L. Crantz in flour form, on pig performance, health indicators, and meat quality.

Materials and Methods

45 weaned pigs were randomly assigned to three dietary treatments (single dietary phase) for 40 days: a control group (CONT) and two phytobiotic-supplemented groups (PM-A and PM-B). PM groups were fed diets containing 0.2% of the quadruple phytobiotic mixture with different oregano essential oil levels (PM-A: 200 mL/t feed; PM-B: 400 mL/t feed). All diets were isonitrogenous and isocaloric. Muscle samples (triceps brachii, external abdominal oblique and biceps femoris) were collected (d74 of age) for chemical and microbiological analyses, and meat quality parameters were assessed. Hematological and biochemical analysis was performed. Ileal and cecal digesta were collected to evaluate the intestinal microbial profile.

Results and Discussion

No significant differences ($P > 0.05$) in body weight, growth performance, meat proximate composition, hematological and biochemical parameters were observed. In the ileum, total aerobic bacteria were increased in the PM-A group, whereas *Escherichia coli* counts were significantly reduced in the PM-B group ($P < 0.05$). In the caecum, PM-B group showed decreased *Enterobacteriaceae* and *Lactobacillaceae* populations and PM-A group decreased *Lactobacillaceae* populations ($P < 0.05$). Lipid oxidation was significantly reduced ($P < 0.05$) in triceps brachii and biceps femoris muscles of both PM groups (day 0), and in triceps brachii and external abdominal muscles (day 7). Both treatments increased ΣPUFA, h/H, and PUFA/SFA ratios in biceps femoris and external abdominal oblique cuts ($P < 0.05$). Increased redness (a* value) in biceps femoris and triceps brachii and decreased yellowness (b* value) in biceps femoris were noticed ($P < 0.05$).

Conclusion

The two investigated herbal mixtures, rich in diverse bioactive compounds, can be effectively used in weaned pigs' diets, showing positive effects on intestinal microbial modulation, oxidative stability, fatty acid profile, and pork meat color characteristics.

Keywords: Antioxidant status, Gut microbiology, Meat quality, Phytobiotic mixture, Weaned pigs.

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MULTIPLE MYCOTOXINS DETECTED IN WHEAT, SOY, DISTILLERS' GRAINS AND SWINE FINISHED FEED SAMPLES FROM THAILAND AND VIETNAM IN 2025

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Introduction and Objectives

Wheat, soy, and distillers' dried grains with solubles (DDGS) are some of the most important raw materials used in swine nutrition in Thailand and Vietnam. The aim of the present study was to quantify mycotoxins in wheat (30 samples), soy (25 samples), DDGS (25 samples) and swine finished feed samples (71) received from different regions of Thailand and Vietnam between Jan - Nov 2025, using LC-MS/MS Triple Quadrupole (Waters Xevo TQ-XS) based multi-mycotoxin method for analysis of aflatoxins (AFB_1, AFB_2, AFG_1, AFG_2), deoxynivalenol (DON), fumonisins (FB_1, FB_2), ochratoxin A (OTA), T-2 toxin, and zearalenone (ZEN).

Materials and Methods

The samples were delivered to Betagro Science Center, Thailand, between Jan–Nov 2025. These samples were extracted and analysed using LC-MS/MS based method adopted from Farkaš et al., 2025 (recoveries in the range of 93.6%–114.2%).

Results and Discussion

Analysis of wheat samples showed that DON, (average 517 ppb), and ZEN (average 71 ppb), were detected in 63% and 33% samples, respectively. 73% of soy samples were not contaminated with mycotoxins whereas 17% contained 1 mycotoxin. 91% of DDGS samples were contaminated with more than 1 mycotoxin. AFB_1 (average 242 ppb), DON (average 1,721 ppb), FB_1 (average 573 ppb), OTA (average 83 ppb), T-2 toxin (average 24 ppb) and ZEN (average 169 ppb) were detected on 36, 77, 9132, 27, and 55% of DDGS samples respectively. 87% of swine finished feed samples were contaminated with more than one mycotoxin. AFB_1 with an average of 5 ppb, DON, 308 ppb, FB1, 217 ppb, OTA, 4 ppb, and ZEN with an average of 323 ppb were detected in 11, 72, 94, 59, and 7% of the swine finished feed samples respectively.

Conclusions

During 2025, the analysis of wheat, soy, DDGS, and swine finished feed samples from Thailand and Vietnam showed that wheat, DDGS and swine feed were contaminated with multiple mycotoxins. Co-occurrence has significant implications for food and feed safety, as combined exposure to multiple mycotoxins can lead to synergistic toxic effects, increasing human and animal health risks.

Keywords: Wheat, DDGS, Swine feed, Mycotoxin risk, Feed safety.

THE INFLUENCE OF NUTRITION ON HEMOGLOBIN LEVELS IN SOWS AND GILTS

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Introduction and Objectives

Anemia was mainly associated with infection by *Mycoplasma suis*, however, this infection is probably widespread and enzootic (Brissonnier et al., 2020). Due to genetic progress, which has led to a significant increase in the number of piglets per litter, there has been an increase in the nutritional demands of sows.

Materials and Methods

An incidence of anemic sows was observed in autumn 2025 on 2400 DanBred sows farm with SPF status. Sows didn´t have diarrhea and showed no signs of systemic illness. In ten pale late pregnant sows, hemoglobin was measured using the HemoCue. Blood samples were taken from a vein in the earlobe in October 2025 and further tested for *M. suis*, PRRS, PCV2, PCV3. Eight weeks ago, the folic acid content in feed for pregnant sows was reduced from 6 mg/1 kg of feed to 2 mg/1 kg. Immediately the content of folic acid was increased to 6 mg/L kg again and the proportion of organic iron was significantly raised. No antibiotic treatment was administered. Ten weeks after the feed adjustment, blood samples from sows and gilts were taken and examined in the same way.

Results and Discussion

Anemia was confirmed during the first hemoglobin measurement. The average hemoglobin level was 81,2 g/l, and extreme anemia below 60 g/l was found in four of the sows. In a pooled blood sample *M. suis* was confirmed by PCR.

There was a marked improvement ten weeks after the feed change. Almost all animals had hemoglobin within the physiological range. Three pooled blood samples were tested for *M. suis*, of which two were positive. In both cases, other laboratory tests were negative.

No Category Hemoglobin average Hemoglobin range

10 Gilts 5 month old 106.9 g/l; 86 - 119 g/L.
10 Gilts 4 weeks after insemination 132.2 g/L; 118 - 151 g/L.
10 Gilts 2 - 3 weeks before farrowing 119.2 g/L; 104 - 129 g/L.
10 Sows 4 weeks after insemination 111.4 g/L; 98 - 121 g/l.
10 Sows 2 - 3 weeks before farrowing 117.6 g/L; 110 - 126 g/L.

Conclusion

The field study confirmed the significant impact of adequate nutrition on the incidence of anemia in sows.

Keywords: Anemia, Folic acid, Hemoglobin, Pregnancy.

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HARNESSING MICROBIOME METABOLISM: PRECISION BIOTIC STABILIZES PIG PERFORMANCE UNDER SOCIAL STRESS

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Introduction and Objectives

Stress-induced abnormal behavior increases energy expenditure and diverts nutrients away from growth, thereby reducing feed efficiency and resource utilization. Recent publications (Ren et al., 2025) reported this issue could be at least partially remedied using precision biotics (PB) in addition to improving pig welfare. This study evaluated PB supplementation for mitigating anticipated performance deficits, nutrient digestibility impairments, and metabolic disruptions caused by social stress in grower-finisher pigs.

Materials and Methods

A total of 288 pigs (PIC L1050 × L337; 144 barrows, 144 gilts; initial BW 33.00 ± 1.97 kg) were assigned to four diets: two controls (NCN, NCY) and two supplemented with 250 ppm precision biotics (PBN, PBY). The 10-week trial included a social stress challenge on day 49 for NCY and PBY groups via pig exchanges. Measurements included apparent total tract digestibility, fecal short-chain fatty acids (SCFAs: acetic acid, propionic acid, butyric acid, caproic acid [CA], etc.), and blood nitrogen metabolism parameters. Data were analyzed using JMP Pro v16.0 (SAS Institute Inc.), with significance at $P < 0.05$.

Results and Discussion

Within main factor analysis, PB supplementation increased fecal CA concentration (0.71 vs. 0.43 mmol/kg DM; $P = 0.019$), a metabolite associated with gut health through pathogen inhibition. PB also reduced FCR ($P = 0.01$) and increased average daily gain ($P < 0.01$) during the post-challenge period (Ren et al., 2026). No significant differences were observed in nutrient digestibility or blood parameters, indicating PB's mechanism may be independent of absorption. Positive trends were noted in PBY (mmol/kg DM intake): + 59% CA ($P = 0.10$) compared with NCY. It's worth highlighting that these values of the PB group approached those observed under non-challenged conditions, suggesting that PB supports microbial fermentation and energy recovery during social stress.

Conclusion

PB supplementation helps stabilize gut microbiota function, particularly SCFA-producing pathways, thereby optimizing energy metabolism in pigs under social stress. By enhancing the extraction of energy from feed nutrients, PB offers a leverage point to improve feed efficiency and producer profitability.

Keywords: Precision biotics, Grower-finisher Pigs, Microbiome Metabolism.

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PIGLETS BENEFIT FROM MILK REPLACER, EVEN IN MODERATELY-SIZED LITTERS

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Introduction and Objectives

Even in moderatly-sized litters (≤ 15 piglets at d4), sow milk production is often insufficient for optimal piglet growth (Ngo et al., 2012). Still, the use of piglet milk replacer (PMR) in moderately sized litters remains debated. Therefore, the aim of this practical study was to investigate the effect of providing PMR to piglets in moderately sized litters on sow performance and piglet performance up until slaughter.

Materials and Methods

480 TN70 sows were allocated to two treatments at farrowing: Control (n = 233) and PMR (n = 247). PMR piglets received PMR from d4 to d19 via an automated cup system, while Control piglets relied exclusively on sow milk. All piglets had access to dry feed from d6 onwards. At d4, piglets were tagged with an RFID eartag. Piglets were weighed individually at d4 and d21 (weaning). At d67 and at slaughter, pen weights were recorded (13 and 10 pigs per pen, respectively). The effect of PMR supplementation was tested using the GLM procedure (SAS 9.4).

Results and Discussion

The number of piglets per sow at d4 did not differ between Control and PMR sows (14.73 vs 14.85; $P > 0.1$). PMR sows weaned 0.33 piglet more per litter compared to Control sows (14.03 vs 13.70; $P < 0.01$). Body weight at d4 did not differ between Control and PMR piglets (1.88 vs 1.91 kg; $P > 0.1$), but PMR piglets were significantly heavier at weaning (+0.28 kg; $P < 0.01$) and at d67 (+0.85 kg; $P < 0.01$). At these timepoints, the proportion of small piglets was lower in the PMR group compared to the Control group ($P < 0.01$). Although body weight at slaughter was identical (126.2 kg; $P > 0.1$), PMR pigs reached this weight 3.3d earlier than Control pigs (166.3 vs 169.6 days; $P < 0.001$).

Conclusion

Even in moderately sized litters, provision of PMR significantly improved results in the farrowing house with more piglets weaned and heavier weaning weights. Moreover, these benefits persisted in the nursery phase and resulted in shorter time to slaughter. Altogether, the obtained results correspond with a ROI of 4.3 within a year, proving that automated PMR provision is an effective strategy to improve piglet performance with an interesting economical return.

Keywords: Milk replacer, Piglet performance, Pre-weaning nutrition, Sow performance.

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MORE EATERS, HEAVIER PIGLETS; THE BENEFITS OF MILK REPLACER SUPPLEMENTATION IN SUCKLING PIGLETS

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Introduction and Objectives

At weaning, piglets undergo major environmental and nutritional changes which often result in reduced feed intake, gastrointestinal problems and growth retardation. Encouraging piglets to consume solid feed before weaning is crucial for a smooth transition. Milk replacers, being more similar to sow's milk than creep feed, may stimulate early intake and train suckling piglets to explore new feed sources. This study evaluated the effect of piglet milk replacer supplementation on feed intake, number of eaters, and pre-weaning performance.

Materials and Methods

A practical trial was conducted on a commercial sow farm including 800 piglets from 59 litters (TN70 x Tempo). Piglets were allocated per litter to either a control group (sow's milk + creep feed twice daily) or a milk replacer group (sow's milk + creep feed + piglet milk replacer). Milk replacer was offered ad libitum via an automated cup system from four days of age until 2 days before weaning (~21 days). Feed intake was measured per litter. Piglets were weighed to record individual body weights at four days of age and at weaning. Rectal swabs at weaning were used to classify piglets as eaters (brown, textured faeces) or non-eaters (yellow, smooth faeces). The effect of milk replacer supplementation on feed intake and body weights was tested using GLM procedure, effect on the prevalence of (non-)eaters with Chi² test (SAS 9.4).

Results and Discussion

Milk replacer supplementation significantly increased the proportion of eaters (67.3 vs. 50.5%, $P < 0.0001$) and reduced non-eaters (6.4 vs. 20.5%, $P < 0.0001$) compared with control. Dry feed intake pre-weaning was higher in supplemented piglets (152 vs. 119 g per piglet, $P < 0.0001$), in addition to an average milk replacer intake corresponding to 206 g dry matter per piglet. Weaning weights were improved (6.25 vs. 5.37 kg, $P < 0.0001$). These results indicate that milk replacer supplementation effectively stimulates early feed intake and enhances pre-weaning growth performance.

Conclusion

Pre-weaning milk replacer supplementation promotes early feed intake, increases the number of eaters, and improves weaning weight, supporting a smoother transition and more resilient piglets at weaning.

Keywords: Creep feed intake, Milk replacer, Pre-weaning nutrition, Weaning transition.

EFFECT OF A BIOACTIVE BENTONITE SUPPLEMENTATION ON SOW PERFORMANCE BY PARITY IN A COMMERCIAL FARM IN MEXICO

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Introduction and Objectives

Bioactive bentonite (BB) has been shown to induce changes in sow microbiota and mitigate indicators of oxidative stress, leading to a tendency for an increased number of weaned pigs (Holck et al., 2019; Song et al., 2021). The objective of this analysis was to evaluate the effect of this bioactive bentonite (Proteck, manufactured for Elanco) on sow reproductive performance across different parities.

Material and Methods

A before/after comparison study was implemented in a commercial farm setting (1,600 sows, Jalisco, Mexico). Control (CON) groups received standard gestation and lactation diets, while experimental groups received similar diets supplemented with BB (2.0 kg/MT) from insemination-to-weaning. Sow performance parameters-total born (TB), born alive (BA), weaned-piglets (WP), and adjusted litter weight (kg) at 21d (ALW)-were compared over similar timeframes: BB groups (February-August 2023) versus CON groups (February - August 2022). A total of 4,303 sows were included across both timeframes. Performance data were obtained from PigCHAMP reports, categorized by parity (P). Statistical analyses considered parity and WP per litter effects, using the weekly insemination batch as the experimental unit. Differences were evaluated using Student's t-test and Dunnett's test for least squares means, with significance set at $P < 0.05$ and trends at $P < 0.10$ (JMP 18.1.0).

Results and Discussion

Overall, inclusion of BB significantly increased: TB = 15.4 vs 14.7 ($P < 0.0002$), BA = 13.6 vs 13.1($P = 0.003$), WP = 12.0 vs 11.3 (P = 0.0001), ALW = 68.8 vs 65.9 kg ($P < 0.01$). When analyzed by parity: P1=Showed increases for BB vs CON in TB (+1.25; $P < 0.0001$), BA (+0.97; $P = 0.004$), WP (+0.72; P = 0.004), and ALW (+ 3.3 kg; $P < 0.02$). P2-P3 an increase was observed for WP (+0.55; $P = 0.001$) and ALW (+2.3 kg; $P < 0.007$). For P4 - P7, an increase was observed for TB (+1.13; $P < 0.0008$), BA (+ 0.98; $P = 0.0007$), WP (+ 0.67; $P < 0.0001$), and ALW (+1.8 kg; $P < 0.02$).

Conclusion

Although no other factors that might confound results (mycotoxins in feed, seasonal variables, and major changes on diets, and/or management during this before/after study) were recorded, sows supplemented with BB resulted in productive improvements in TB, BA, WP, and ALW, particularly in P1 and P4+ sows. A significant response in WP and ALW was also noted in P2-P3 sows. Sow performance in this study agrees with results reported by Lopez & Armenta (2025).

Keywords: Bioactive bentonite, Born alive, Litter weight, Oxidative stress, Weaned piglets.

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FUMONISIN MANAGEMENT WITH ENZYMATIC BIOTRANSFORMATION

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Introduction and Objectives

Fumonisin contamination poses a prevalent challenge, resulting in the disruption of sphingolipid biosynthesis. Current strategies utilize organic or inorganic adsorbents to mitigate this issue. Enzymatic hydrolysis of fumonisins (FB) primarily occurs under neutral to alkaline pH conditions. However, achieving significant *in vivo* efficacy requires the use of enzymes active at lower pH levels, allowing effective hydrolysis in the gastrointestinal tract. The effectiveness of such fumonisin esterase was investigated in both piglets and sows.

Materials and Methods

Altogether 36 female crossbred weaned piglets and 18 sows were involved in the trial. Animals in the Positive control group (PC) received normal diet contaminated with 5 mg/kg FB; animals in the trial group (T) received the 60 U/kg fumonisin esterase enzyme and FB, while animals in the negative control group (NC) received normal diet. The trial lasted 28 days, fecal and blood samples were collected and analyzed for FBs and hydrolyzed fumonisins (HFB) and sphingolipid profile with an HPLC-FLD and UPLC-MS/MS method, respectively.

Results and Discussion

The amounts of the FBs and FB metabolites were significantly different by the end of the trial between the treatment groups. The HFB content was significantly higher in T compared to the PC (P = 0.000 for both piglets and sows). The FB content of the feces was highest in the PC, with 14.16 µg/g (piglets) or 16.03 µg/g (sows), indicating the enrichment of FB in the feces. FB content of the feces in T was significantly lower compared to the PC, with 0.84 µg/g (P = 0.000) for the piglets and 1.10 µg/g (P = 0.000) for the sows. The sphinganine/sphingosine ratio in T was reduced to 0.17 (both for piglets and sows) to the NC levels (0.16 for both piglets and sows), compared to the 0.28 (piglets) or 0.27 (sows) results of the PC (P = 0.000).

Conclusions

Fumonisin esterase metabolized the 5 mg/kg fumonisin content of the feed to HFB. Moreover, fumonisin esterase significantly improved the sphingolipid profile of both piglets and sows consuming a fumonisin contaminated diet. The utilization of enzymatic mycotoxin management strategies represents a viable alternative for mitigating fumonisin contamination.

Keywords: Fumonisin, Hydrolyzed fumonisin, Sphingolipid profile.

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ALTERNATIVE TO ZNO: PHYTOBIOTICS TO PREVENT WEANING DIARRHEA

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Introduction and Objectives

The use of zinc oxide (ZnO) in weaned piglets has been associated with the emergence of antibiotic resistance and significant environmental concerns, prompting regulatory bans on high concentrations of ZnO in swine diets. An alternative strategy for replacing ZnO in swine production involves enhancing biosecurity measures alongside dietary supplementation. A phytobiotic mixture (PM) with curcumin and fenugreek was developed as a possible substitute for antimicrobial agents. The current *in vivo* study assessed its efficacy on the incidence of diarrhea and overall performance in a commercial farm.

Materials and Methods

Altogether 288 weaned piglets (144 males and 144 females) were allocated to 2 Trial and 2 Control barns, including 8 pens in both treatment groups (18 piglets/pen) balanced for litter of origin and sex. The Control group received a mixture of ZnCl2-CuSO4 in the drinking water in the first week of the trial, while Trial group received the PM feed additive in 3 kg/t dosage during the whole trial period. Fecal consistency was scored daily using a 1 - 4 scale at pen level. Statistical evaluation was done by t-test for continuous variables and Mann-Whitney U test was applied for fecal scores and Fisher's exact test for incidence/duration of diarrhea. The statistical analyses used the pen as experimental unit.

Results and Discussion

Both fecal scores (median Test = 2.5 vs Control = 3) and incidence/duration of diarrhea (T = 6 vs C = 37) were significantly lower in the Test group ($P < 0.0001$). Average daily gains and feed conversions were significantly improved in the Test groups. (ADG: T = 196.1 ± 15.5 g vs C = 152.9 ± 23.8 g; $P = 0.001$; FCR: T = 1.73 ± 0.14 vs C = 2.19 ± 0.31; $P = 0.002$). No medication was required in the Trial pens, while antibiotic medication due to diarrhea outbreaks was required in the Control units.

Conclusions

Results indicate that the curcumin–fenugreek based phytobiotic mixture reduces post-weaning diarrhea and the necessity for antimicrobial treatments while simultaneously maintains optimal growth rates during the weaning phase.

Keywords: Weaning diarrhea, ZnO removal, Phytobiotics.

Acknowledgements: Part of the research was funded by the Cooperative Doctoral Scholarship KDP-2021 offered by the National Research, Development and Innovation Office, Hungary.

MILK FAT GLOBULE MEMBRANE (MFGM) ENSURES A SMOOTH TRANSITION DURING WEANING

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Introduction and Objectives

The idea is rising that brain and nervous function are tied to the gut microbiome and involves epigenetic and immunoregulatory changes. Scientific research indicates that MFGM has the potential to benefit the brain-gut axis through better cognitive and gut development and reduced infection. MFGM is a natural bioactive component of cow's milk. Orally administrating MFGM during the first postnatal week improved the growth performance of neonatal piglets on 21 d (Wu et al., 2020). The hypothesis is that supplementation of these natural bioactive milk molecules in piglet feed strengthens piglets to transition smoothly through weaning.

Materials and Methods

In two trials, 21day old, weaned piglets were randomly assigned to the two treatments (Control and MFGM) based on sow origin, sex and body weight (block) to examine the effect of MFGM containing supplement (2 kg/T) on piglet performance. In trial 1, 256 piglets (Danbred x Pietrain), 8 replicates with 16 piglets per pen were enrolled for 49 days. MFGM was supplemented in weaner and starter diets. In trial 2, 288 piglets (TN70 x Pietrain), 8 and 16 replicates with 12 piglets per pen in Control and MFGM treatments, respectively were followed for 37 days. MFGM was supplemented in the weaner diet. In both trials, weaner diets were fed the first 14 days and thereafter starter diets were fed. Diets were barley, wheat, and soya-based, without medication nor pharmaceutical levels of ZnO. Measurements were body weight at the start, 14 days, and end of the trial and feed intake per pen.

Results and Discussion

No differences were reported in mortality or morbidity in both trials. In both trials, the final weight was improved ($P < 0.05$) with 1.5 and 0.8 kg in the MFGM treatments, respectively. Furthermore, in both trials feed intake was increased with 4 and 3% in the MFGM treatments, respectively. Moreover, feed conversion rate was improved in both trials with 4 ($P < 0.05$) and 1% in the MFGM treatments, respectively.

Conclusion

MFGM supplementation in piglet diets improves growth performance and feed efficiency, thereby ensuring a smooth transition at weaning.

Keywords: Milk Fat Globule Membranes, Nursery performance, Piglet.

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APPLICATION OF A B-MANNANASE ENZYME IN DIETS WITH REDUCED NET ENERGY DURING THE EARLIER FATTENING PERIOD RESULTED IN EQUAL PERFORMANCE AND AN ADDITIONAL ECONOMIC BENEFIT

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Introduction and Objectives

β-Mannans are strongly anti-nutritive polysaccharide fibers found in most vegetable feed ingredients. The estimated content of soluble β-mannans in common fattening diets is only 0.20 - 0.35%, and in vitro studies have demonstrated that as little as 0.05% soluble β-mannan in feed can elicit a strong innate immune response. Hemicell HT (Elanco) is a β-mannanase enzyme for animal feed that breaks down β-mannans. The aim was to evaluate the impact of a 45 and 63 kcal net energy reduction on performance in first phase fatteners.

Materials and Methods

A 36-day feeding trial was conducted on a commercial fattening facility with DanBred x Belgian Piétrain pigs starting at 10 weeks of age. Pigs were randomly allocated to one of the 3 treatment groups: Control, 45 kcal NE reduction + Hemicell HT, 63 kcal NE reduction + Hemicell HT. Standard production data were collected. The data were analysed using JMP 17.1 statistical program.

Results and Discussion

During the first phase of fattening (36 d), no significant differences among the 3 treatment groups were observed concerning feed consumption, growth, feed conversion, average daily weight gain or mortality. Overall, production cost per pig during the first phase of fattening was €0.23 lower in the 45 kcal NE reduction and € 0.30 in the 63 kcal NE reduction group.

Conclusions

The trial demonstrated that both a NE reduction of 45 and 63 kcal/kg with supplementation of Hemicell HT resulted in similar performance results as the pigs fed the Control diet with the full NE content. Therefore, supplementation of Hemicell HT to fattening diets can help in cost reduction of the formulated feed through a decrease of 45 - 63 kcal NE per kg of feed.

Keywords: Fattening pigs, Hemicell HT, β-Mannanase, Net energy reduction.

MELANOSIS COLI IN THE SLAUGHTERED PIGS IN THAILAND

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Introduction and Objectives

Melanosis coli (MC) is a condition characterized by the presence of brown pigment-laden macrophages in the lamina propria of the large intestinal mucosa. It has been associated with long-term use of laxative in human patients (Zhang et al., 2023). In pigs, many cases of MC were diagnosed in fattening pigs with evidence of oxidative damage of pigment-laden macrophages and intestinal epitheliums (Rodrigues et al., 2021). In this study, we aim to investigate the association between MC and the occurrence of *Lawsonia intracellularis, Brachyspira hyodysenteriae*, and *Salmonella spp*.

Materials and Methods

A total of 14 intestinal samples (13 cases with MC and a normal case) were collected from six farms. Pool samples consisting of colon, rectum and adjacent lymph nodes were submitted for multiplex PCR to detect *Lawsonia intracellularis, Brachyspira hyodysentery* and Salmonella *spp*. at the Veterinary Diagnostic Laboratory, Faculty of Veterinary Science, Chulalongkorn University. All samples were also examined grossly and processed for histopathology.

Results and Discussion

Pathological examination of the large intestine revealed varying degrees of mucosal discoloration, ranging from whitish tan in a normal case, greyish in mild cases to blackish in severe cases especially in colon and rectum. Histopathologically, macrophages laden with brown pigment were readily observed in the lamina propria in severe cases. Multiplex PCR detected *Lawsonia intracellularis* in 6 cases - 5 from MC-affected farms and 1 from a non-affected farm. PCR results for *Brachyspira hyodysenteriae* and Salmonella *spp.* were negative in all samples. It has been noted that *L. intracellularis* could be detected in healthy pigs. Pathological examination did not show any inflammation related to infection either in MC cases or in a normal case.

Conclusion

Based on our observations, MC in pigs is not associated with the occurrence of *Lawsonia intracellularis*, *Brachyspira hyodysentery* and *Salmonella* spp.

Keywords: *Brachyspira, Lawsonia,* Melanosis coli, *Salmonella.*

Acknowledgements: This research was funded by the Faculty of Veterinary Science, Chulalongkorn University (NO. RI 11/2566). The authors thank all pig farms for providing samples.

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SUPPLEMENTATION PREGNANT SOWS WITH MULTI-SPECIES PROBIOTICS PROMOTE SERUM AND COLOSTRUM IMMUNOGLOBULINS LEVEL AFTER VACCINATION WITH F4 FIMBRIAE EXTRACT *ESCHERICHIA COLI* VACCINE

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Introduction and Objectives

Enterotoxigenic-*Escherichia coli* is pathogen causing diarrhea in piglets. Using antibiotics led to antibiotic resistance (Nguyet et al., 2022). Virulence factors, such as fimbriae, play an essential role in pathogenesis and being used for producing vaccine. Thus, we studied a synergistic effect of supplementation multispecies probiotics (BACTOSAC - Tablet) following vaccination sow with crude F4-fimbriae-vaccine which has been proved against ETEC (Nguyet et al., 2024). BACTOSAC-Tablet is composed of multi-strains probiotic: *Lactobacillus* spp., *Bacillus* spp., *Pediococcus* spp. and *Saccharomyces* spp. which improving colostrum IgA production and health in sows and piglets (Innamma et al., 2023).

Materials and Methods

Twenty pregnant-sows were vaccinated with F4-fimbriae-vaccine twice at 4- and 2-week before-farrowing; thereafter, vaccinated-12th wk-pregnant-sows (n = 10) were fed with 1 tablet-5 grams of BACTOSAC-Tablet, once daily, until farrowing, vaccinated-control group was not supplemented (n = 10). The sow serum was collected pre-vaccination, 2- and 4-weeks post-vaccination, colostrum at 6 hours post-farrowing, piglet's serum from both groups (2 piglets/sow) were collected on 3 days-old to measure F4-specific IgG, F4-specific IgA using in-house-ELISA (Nguyet et al., 2024).

Results and Discussion

At 2-and 4-weeks post-vaccination showed that titer of F4-specific IgG in sow serum in vaccinated-group plus BACTOSAC-Tablet was significantly higher than vaccinated-control group (182,170 vs 127,532; 547,884 vs 512,000, respectively) ($P < 0.01$). However, titer of F4-specific IgA in sow serum in vaccinated-group plus BACTOSAC-Tablet was not different from vaccinated-control group. Colostrum titer of F4-specific IgG and IgA in vaccinated-group plus BACTOSAC-Tablet was significantly higher than vaccinated-control group (2,240,000 vs 1,130,667; 80,000 vs 50,222, respectively) ($P < 0.01$). Piglet serum titer of F4-specific IgG and IgA in vaccinated-group plus BACTOSAC-Tablet was significantly higher than vaccinated-control group (687,200 vs 472,800; 3,125 vs 838, respectively) ($P < 0.01$). These effects may be associated with probiotic-induced modulation of mucosal immune trafficking pathways in the sow udder subsequently promoting immunoglobulin transfer into colostrum as suggested by previous studies (Bourges et al., 2008; Innamma and Kaeoket, 2025).

Conclusion

Multispecies probiotics supplementation in sow post-vaccination with crude F4-fimbriae-vaccine not only improved titer of F4-specific IgG in sow serum but also titer of F4-specific IgG and IgA in colostrum and piglet's serum.

Keywords: Colostrum, *Escherichia coli,* Immunoglobulins, Piglet, Probiotic.
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PRODUCTIVE EFFECTS OF DIETARY SUPPLEMENTATION WITH POLYPHENOLS IN GESTATING SOWS

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Introduction and Objectives

Nutritional strategies focused on reducing oxidative stress during gestation have been shown to enhance reproductive performance (Li et al., 2022). This study evaluated the effects of dietary polyphenol supplementation during gestation on reproductive performance and litter quality and size in hyperprolific sows, including a temporal longitudinal comparison with farrowings without supplementation.

Materials and Methods

A total of 47 hyperprolific sows (Landrace × Large White, DanBred) were assigned to two dietary treatments: CTRL (basal diet supplemented with a blend of hydrophilic and lipophilic polyphenols, including hydroxytyrosol and carnosic acid, provided at a fixed inclusion rate of 150 g per tonne of feed throughout gestation; n = 23). Reproductive performance and litter traits were recorded during the trial. Longitudinal data from previous and subsequent farrowings of the same sows without dietary supplementation were used for comparison.

Results and Discussion

Sows receiving polyphenol supplementation (AOX) showed a significantly higher number of total born piglets compared with control sows (20.28 vs. 17.55; $P < 0.03$), as well as a higher number of live-born piglets (17.79 vs. 15.59; $P < 0.009$). No differences were observed between treatments in the number or percentage of stillborn or mummified piglets. Control sows exhibited a higher proportion of small litters (<16 total born piglets) and a lower frequency of large litters (>19 live-born piglets) compared with AOX sows ($P < 0.05$). Mean individual birth weight did not differ between treatments (1.27 vs. 1.28 kg); however, total litter weight was significantly higher in the AOX group (24.71 vs. 21.08 kg; $P < 0.02$). AOX sows also showed a lower proportion of piglets weighing <1.1 kg and a higher proportion >1.5 kg compared with control sows ($P < 0.05$). Longitudinal analysis showed a higher number of live-born piglets during the experimental period compared with the previous farrowing (17.91 vs. 15.91; $P < 0.05$), with no residual effects in the subsequent farrowing.

Conclusion

Dietary polyphenol supplementation during gestation improves reproductive performance and litter quality in hyperprolific sows during the supplementation period, with no residual effects on subsequent reproductive cycles. Complementary studies from this group address the underlying genetic mechanisms.

Keywords: Gestating sows; Polyphenols; Reproductive performance; Litter quality.

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EFFECTS OF DIETARY ENERGY AND PROTEIN LEVEL IN LACTATION PERIOD ON REPRODUCTIVE PERFORMANCE, MILK COMPOSITION, METABOLIC AND REDOX STATUS OF SOWS

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Introduction and Objectives

High-yielding sows are prone to body weight loss during lactation due to limited feed intake, which affects the growth of piglets and their own health. Therefore, this study aims to investigate the effects of increasing energy and/or protein during lactation on the reproductive performance, milk composition, plasma metabolites, redox status and intestinal microbiota of sows.

Materials and Methods

During a 21-d lactation, a total of 232 multiparous French sows were randomly assigned to 4 dietary treatments (58 sows per treatment) according to their parity, body weight and backfat receiving diet with net energy at 2.38 Mcal/kg and crude protein (CP) at 17.46% (CON), diet with net energy at 2.38 Mcal/kg and CP at 19.21% (HCP), diet with net energy at 2.61 Mcal/kg and CP at 17.46% (HE), diet with net energy 2.61 Mcal/kg and CP at 19.21% (HE-HCP), respectively.

Results and Discussion

The results showed that sows fed HCP diet had lower average daily feed intake ($P < 0.05$), along with lower average daily gain and weaning weight of suckling piglets ($P < 0.05$). Meanwhile, sows fed HCP diet had lower apparent total tract digestibility (ATTD) of DM, GE, CP ($P < 0.05$), milk protein level ($P = 0.093$), plasma activity of T-SOD (P = 0.075), but increased plasma levels of urea ($P < 0.05$), leptin ($P < 0.05$) and cholecystokinin ($P = 0.068$). In contrast, HE diet had higher body weight loss, along with lower ATTD of dry matter (DM), gross energy (GE) and CP ($P < 0.05$). Meanwhile, sows fed HE diet had increased levels of milk fat and dry matter ($P < 0.05$), and levels of plasma non-esterified fatty acid ($P = 0.052$) and H_2O_2 ($P = 0.074$), and decreased activity of T-AOC ($P < 0.05$).

Conclusion

In conclusion, piglets from sows fed HP diet had lower ADG and weaning weight, which could be associated with the lower ADFI and NE intake of sows, as well as the lower digestibility of CP and GE. Moreover, sows fed HE diet still had lower digestibility of CP and GE, but the ADG and weaning weight of piglets were not markedly affected, which may be ascribed to the higher NE intake during lactation, and the increased concentrations of milk fat and dry matter.

Keywords: Lactation, Net energy, Protein, Pig, Reproduction.

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EFFECTS OF FEATHER AND CHICKEN HYDROLYSATES ON PIGLET NUTRITION, GUT HEALTH, AND IMMUNE RESPONSE

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Introduction and Objectives

The valorization of poultry by-products as alternative protein sources aligns with circular economy principles and sustainable livestock production. Feather hydrolysate (HFP) and chicken hydrolysate (HCP) are rich in bioactive peptides and amino acids, but their optimal inclusion levels and immunological impacts in piglets remain insufficiently characterized (Rossi et al., 2021; Campos et al., 2020). This study evaluated the effects of dietary inclusion of HFP and HCP on intestinal health, oxidative stress, and immune modulation in weaned piglets challenged with Escherichia coli, aiming to optimize protein inclusion while enhancing sustainability and animal health.

Materials and Methods

Fifty weaned piglets were assigned to five dietary treatments: basal diet (control), basal diet supplemented with 10 or 20% HCP, and basal diet supplemented with 10 or 20% HFP. After four weeks of dietary treatment, piglets were orally challenged with *E. coli*. Growth performance, intestinal morphology, oxidative stress markers (TBARS, GPx, SOD), lymphocyte subpopulations, cytokine profiles, and mucosal immunoglobulins (SIgA and IgM) were evaluated.

Results and Discussion

Diets containing 10% HFP or HCP improved intestinal morphology, increasing villus height and villus height-to-crypt depth ratio, and supported mucosal immune parameters, including SIgA production. These diets also contributed to balanced oxidative status without inducing systemic inflammation. In contrast, inclusion of 20% HFP resulted in increased oxidative stress, evidenced by elevated lipid peroxidation markers, alterations in immune cell populations, and signs of intestinal inflammation. Although 20% HFP enhanced SIgA levels, this response was associated with prolonged inflammatory stimulation rather than protective immune modulation. Controlled immune activation and improved gut integrity observed at 10% inclusion suggest enhanced resilience to *E. coli* challenge while minimizing inflammatory energy costs.

Conclusion

Feather and chicken hydrolysates represent promising sustainable protein alternatives for piglet nutrition when included at appropriate levels. Inclusion at 10% supports intestinal integrity and immune homeostasis, whereas higher inclusion levels, particularly 20% HFP, may compromise gut health and induce oxidative and inflammatory stress. These findings reinforce the importance of optimized dietary formulation when incorporating poultry by-products into piglet diets.

Keywords: Chicken hydrolysate, Circular economy, Feather hydrolysate, Immune response, Piglets
Acknowledgements: The authors acknowledge Embrapa Swine and Poultry for institutional support and funding.

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MITIGATING EFFECTS OF A MULTICOMPONENT MYCOTOXIN DETOXIFYING AGENT AGAINST COMBINED DIETARY EXPOSURE TO MULTIPLE MYCOTOXINS IN PIGS

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Introduction and Objectives

Mycotoxins are toxic fungal metabolites in feed that cause significant health effects in pigs. Simultaneous dietary exposure to multiple mycotoxins in pigs has been reported as prevalent (Akinmoladun et al., 2025). The efficacy of a multicomponent mycotoxin detoxifying agent (MMDA) combining minerals, microbial concoction, yeast cell wall, and herbal extracts against combined dietary exposure to multiple mycotoxins in pigs was tested in vivo and results are presented.

Materials and Methods

Five in vivo trials in pigs under multi-mycotoxin dietary exposure have been performed, with dietary MMDA supplementation at 1.5 or 3 kg/t of feed. Mycotoxin challenges in the respective trials were: trial 1: 1.2 - 1.5 mg deoxynivalenol (DON) and 0.9 mg zearalenone (ZEN)/kg feed in piglets; trials 2 and 3: 0.5 mg T-2 toxin and 0.35 mg ZEN/kg feed in piglets (trial 2) or 2 mg T-2 toxin and 1 mg ZEN/kg feed in sows (trial 3); trial 4: 0.5 mg ochratoxin A (OTA) and 1 mg ZEN/kg feed in piglets; trial 5: 0.5 mg aflatoxin B1 (AFB1), 0.5 mg fumonisin B1 (FB1) and 0.35 mg ZEN/kg feed in piglets. Health and performance parameters, mycotoxin residues in tissues, and blood biochemistry/hematology parameters were evaluated.

Results and Discussion

A significant growth improvement ($P < 0.05$) was reported in groups which received the detoxifying agent at 3 kg MMDA/t of feed, i.e. 9.5% improvement of feed conversion ratio in trial 1, or 14.3% improvement of body weight gain in trial 5. Significant reduction of mycotoxin residues in tissues of piglets which received 3 kg MMDA/t of feed was detected also, i.e. 53.3% reduction of T-2 residues in kidneys in trial 2, or 26.8%, or reduction of ZEN and its metabolites in liver samples in trial 4.

Conclusion

A mode of action of the detoxifying agent including adsorption, biotransformation, immune and liver support is suggested. Findings support that the MMDA significantly reduces the bioavailability and impact of mycotoxin exposure in pigs and can be used as an effective mitigating tool against combined mycotoxin exposure in pig production.

Keywords: Health and performance, Mycotoxins, Mycotoxin detoxification, Swine.

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NATURAL 1, 25-DIHYDROXY VITAMIN D3 GLYCOSIDES SUPPLEMENTATION IMPROVED SOW FARROWING TIME AND IMMUNOGLOBULIN G

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Introduction and Objectives

Reproductive performance in sows is the crucial factor for successful pig production. Adequate vitamin D is essential for maintaining reproductive function of sow. 1,25-dihydroxyvitamin D3 glycosides is the most active form of vitamin D in animals. The aim of this study was to evaluate the effect of dietary supplementation with natural 1,25-dihydroxyvitamin D_3 glycosides (1,25 $(OH)_2$D3-glycoside) on farrowing time and immunoglobulin G levels in sow.

Materials and Methods

Sixty multiparous sows were randomly allocated to four dietary treatments: a control group fed a basal diet, and three supplemented groups receiving 1,25-$(OH)_2D_3$ glycoside at 50/100 ppm (gestation/lactation), 75/125 ppm, or 75 ppm combined with Sangrovit Extra (100 ppm) throughout gestation and lactation. Farrowing duration was recorded, and blood samples were collected on gestational day 105 to determine IgG concentrations.

Results and Discussion

Sow dietary supplementation with 1,25-$(OH)_2D_3$ glycosides can reduce total farrowing duration compared with the control group ($P < 0.05$). The active form of vitamin D plays a key role in calcium homeostasis and uterine contractility, helping to prevent uterine atony and accelerate parturition (Madsen et al., 2023; Bosch et al., 2023). In addition, supplementation can increase circulating IgG levels in sows ($P < 0.05$). Vitamin D is a well-known modulator of innate and adaptive immunity, influencing dendritic cells, T cells, and B-cell antibody production (Alswailmi et al., 2021).

Conclusion

Supplementation of natural,25-dihydroxyvitamin D3 glycosides can enhance farrowing duration and increase immunoglobulin G levels in sows.

Keywords: Natural 1,25-dihydroxyvitamin D_3, farrowing time, reproductive performance, sow.

Acknowledgements: The authors thank Chiang Mai University, Thailand for providing support in testing facilities.

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MULTI-OMICS INTEGRATION REVEALS THE SHORT-TERM AND LONG-TERM IMPACTS OF FORMULA MILK ON GUT-MUSCLE-GROWTH AXIS IN PIGLETS

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Introduction and Objectives

Early nutrition critically influences piglet development. Genetic selection for larger litters has outpaced lactation capacity, reducing milk intake and compromising piglet growth and survival (Kobek-kjeldager et al., 2020). Formula milk offers a nutritional solution. The early postnatal period represents a critical window for gastrointestinal and skeletal muscle development. This study investigates short- and long-term effects of formula feeding on these systems.

Materials and Methods

One hundred forty-four piglets were assigned to SOW group with sow milk, or FM-7 and FM-14 groups weaned at 7 or 14 days with formula milk. Intestinal morphology, nutrient digestibility, barrier gene expression, microbiota composition by 16S rRNA sequencing, and transcriptome by RNA-seq were analyzed. Blood parameters, carcass composition, myofiber characteristics, and longissimus dorsi transcriptome and metabolome were determined using RNA-seq and LC-MS.

Results and Discussion

In short term, FM-7 piglets exhibited impaired growth and intestinal function, with lower body weight at 21 days compared to FM-14 and SOW piglets, which could be associated with the higher diarrhea index, lower ileal villus-to-crypt ratio and lactase activity, as well as the down-regulated tight junction proteins Claudin1 and Occludin. Systemic inflammation was evident through elevated plasma C3 and CRP, increased leukocytes and monocytes, and up-regulated IL-6, IL-1β, and TNF-α. Transcriptomic-microbiome analysis revealed complement system activation correlating with altered Escherichia_Shigella and Enterobacteriaceae. Muscle development showed lower muscle weight and carcass fat, increased fast-twitch fiber density with smaller diameter, and AMPK/FoxO pathway activation indicating excessive catabolism. However, FM-14 piglets demonstrated comparable short-term performance to SOW group and superior long-term outcomes, achieving 2.00 kg higher body weight at 70 days (P = 0.02), alongside enhanced nutrient digestibility, up-regulated lipid digestion genes and anti-inflammatory metabolites, and down-regulated pro-inflammatory genes.

Conclusion

This study demonstrates that weaning at 7 days with formula milk impairs short-term growth performance, intestinal function, and muscle development, while weaning at 14 days shows comparable outcomes to sow-rearing. Notably, early weaned piglets fed with formula milk exhibit compensatory growth and metabolic adaptation over the long term. These findings provide evidence for optimizing early weaning timing and nutritional strategies in piglets, highlighting their adaptive capacity to early nutritional interventions.

Keywords: Body composition, Formula milk, Gut microbiota, Muscle development, Pigs

Acknowledgements: The authors thank the Institute of Animal Nutrition, Sichuan Agricultural University, China for the support with providing testing facilities.

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EFFECT OF MATERNAL IMPRINTING ON THE COMPOSITION OF PIGLET MICROBIOTA AT BIRTH AND WEANING

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Introduction and Objectives

Current production faces the challenge of managing hyperprolific sows, with low-weight piglets, higher pre-weaning mortality and poorer yields. To produce without antibiotics, we need nutritional strategies that guarantee digestive health at all stages. Microbiota is established in the first days of life under the influence of diet, age, and maternal and genetic factors. Despite advances, questions remain about maternal microbial colonisation in piglets during lactation. The objective was to verify the imprinting of piglets with maternal microbiomes.

Materials and Methods

Twenty farms with white and Iberian sows in Spain and Portugal were sampled, comprising some 45,000 breeding animals. From each farm, 20 (C) sows that had recently farrowed from different parities were selected. Feces from the sows and a pool of 5 piglets from each litter were sampled at 3 days of age (L1) and at weaning (L2). The feces were immediately frozen. Once the DNA was isolated, massive sequencing of segments V1 to V9 of the 16s ribosomal gene was performed. Relative abundance and diversity were estimated using the Simpson and Shannon indices (alpha-diversity).

Results and Discussion

On all farms, the most abundant phylum in sows is Firmicutes, but at the genus level, Christensenellaceae and Escherichia predominate, and at the species level, Escherichia coli generally predominates, although there were farms where Methanobrevibacter smithii, Bifidobacterium thermophilum, Clostridium sensu stricto, Lactobacillus amylovorus, or Ruminococcus flavefaciens predominated. However, in peripartum piglets, proteobacteria and the Escherichia genus predominate on all farms, except for one where Coriobacteriacea predominates. Before weaning, Coriobacteriacea is the most abundant genus, followed by Christensenellaceae and Escherichia. This suggests that, given the protein-rich milk diet that the animals receive, proteobacteria have an adaptive advantage over the others, and diversity in peripartum piglets is significantly lower.

Conclusion

We can determine that on the farms studied, the microbiota of weaned piglets is significantly more diverse than that of peripartum piglets, and much more similar to that of their mothers. Further research is needed to determine whether modifying the microbiota of sows through nutritional supplementation allows us to modify the way piglets are imprinted in the peripartum period.

Keywords: Alpha-diversity, Imprinting, Microbiome.

EFFECTS OF PEAT PELLET PROVISION ON PIGLET GROWTH, HEALTH, AND POST-WEANING DIARRHEA

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Introduction and Objectives

The weaning period represents a major challenge for piglets, associated with impaired growth and intestinal disturbances. Peat-derived products containing humic acids have gained attention for beneficial intestinal effects. We evaluated the association between peat provision, growth, medications, and diarrhea in piglets.

Materials and Methods

Forty sows and their litters were divided into peat or control groups and provided daily with peat pellets (ProHumi®, Hankkija, Finland) or sawdust from one week before farrowing through lactation (0.5 L/day; PEAT n = 160; CONTROL n = 160). Mean total born was comparable (CONTROL: 20.1 ± 0.3; PEAT: 19.9 ± 0.3). Piglets were weaned at ~28 days, then PEAT piglets received ProHumi® (1.5 L/day) until day 64, whereas CONTROL piglets received sawdust. Body weight was recorded on days 1–2, 26, 36, and 64. Medical treatment (treated piglets/litter size) was from sow cards and analysed using a general linear model adjusting for litter size. Post-weaning diarrhea was recorded as presence/absence of liquid feces at day 33 and compared using a chi-square test. Growth data were analysed using linear mixed-effects models, while descriptive statistics are presented as mean ± SD.

Results and Discussion

PEAT piglets were heavier than CONTROL at all points (kg; day 1 - 2: 1.92 ± 0.35 vs. 1.79 ± 0.32; day 26: 8.00 ± 1.10 vs. 7.46 ± 1.09; day 36: 9.96 ± 1.41 vs. 9.22 ± 1.30; day 64: 26.21 ± 3.79 vs. 25.10 ± 3.42; $P < 0.001$). Average daily gain was higher in the PEAT group, between days 1 - 26 (0.205 vs. 0.179 kg/day, $P < 0.001$) and days 26 - 36 (0.177 vs. 0.147 kg/day, $P < 0.05$), whereas there were no differences during later period (days 36 - 64; $P = 0.8$). Piglets' medical treatment rate during the pre-weaning period was lower in the PEAT group compared with CONTROL (0.104 ± 0.021 vs. 0.172 ± 0.033; $P = 0.05$). Diarrhea incidence 8 days after weaning was higher in CONTROL piglets (18.1%) than in PEAT piglets (8.1%; $P < 0.05$).

Conclusion

Providing peat pellets on the floor was associated with greater early post-weaning growth, reduced medical treatment during lactation, and lower diarrhea in post-weaning.

Keywords: Growth performance, Peat, Piglets, Postnatal development, Weaning transition.

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REPLACING ADDED FAT WITH A GLUCONEOGENIC AND PHYTOGENIC ADDITIVE IN LATE NURSERY PIG DIETS

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Introduction and Objectives

SOLERGY is a novel feed additive combining gluconeogenic precursors and phytogenic compounds, designed to optimize metabolic efficiency (Madesh et al., 2025). The objective of this study was to evaluate the growth performance and economic implications of replacing graded levels of choice white grease (CWG) with SOLERGY in late nursery piglet diets.

Materials and Methods

A total of 600 piglets (PIC 800 × DNA 241; initial BW 11.82 ± 1.26 kg) were utilized in a randomized complete block design with 4 treatments and 15 replicates (10 pigs/pen) over a 20-day late nursery period. A positive Control diet was formulated with 1.0% added CWG. Three experimental diets (LS, MS, HS) replaced 33, 67, and 100% of the added fat, respectively, by incorporating the additive (up to 1.0 kg/ton) and inert filler, based on an applied metabolizable energy matrix of 78.0 Mcal/kg for the additive. Performance data were analyzed using the GLM procedure of SAS and Tukey test. Economic analysis calculated formulation savings based on ingredient prices at the time of the trial (CWG: 1.05 USD/kg; Additive: 4.00 USD/kg).

Results and Discussion

Non-significant differences ($P > 0.05$) were detected in growth parameters among treatments. Piglets fed the HS diet achieved a final BW of 23.23 kg, compared to 23.45 kg for the Control ($P = 0.625$). Average daily gain (0.576 vs. 0.585 kg/d; $P = 0.729$) and Feed:Gain ratio (1.51 vs. 1.48; $P = 0.127$) did not differ significantly between the HS and Control groups. Furthermore, average daily feed intake did not differ between treatments (0.876 vs 0.866 kg/d; $P = 0.941$), indicating that dietary fat removal and additive inclusion did not adversely affect voluntary feed intake or energy satiety. The HS treatment yielded a formulation cost reduction of 6.10 USD/ton compared to the Control (510 USD/ton), primarily driven by the removal of high-cost CWG.

Conclusion

The results indicate that the inclusion of the gluconeogenic-phytogenic additive allowed full replacement of 1% added fat with no detectable impairment in growth performance during the late nursery phase. This approach has a potential to reduce formulation cost when fat ingredient prices are high.

Keywords: Energy, Fat replacement, Gluconeogenesis, Nursery piglets, Phytogenics.

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GUT MICROBIOTA DYNAMICS AND PROBIOTIC INFLUENCE DURING LACTATION: POTENTIAL IMPLICATIONS TO SOW PERFORMANCE IN A EUROPEAN COHORT

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Introduction and Objectives

The gut microbiota plays a critical role in sow health and nutrient utilization, influencing reproductive performance. This study aimed to characterize fecal microbiota of European sows on day 21 of lactation and identify taxa associated with performance and probiotic administration.

Materials and Methods

Fecal samples and reproductive performance data were collected from 359 multiparous sows across 26 farms in eight swine-producing countries in Europe on day 21 of lactation (minimum 12 sows per farm). The probiotic SolPreme® was included in sow diets from nine farms. Microbiota composition was analyzed using 16S rRNA gene long-read amplicon sequencing, followed by OTU clustering and relative abundance profiling. Associations with reproductive performance and probiotic administration were assessed.

Results and Discussion

A core microbiota, defined as OTUs present in more than 90% of sows with abundance greater than 0.5% of the total abundance, was identified across samples, with the five most abundant OTUs being *Clostridium*, *Terrisporobacter*, *Turicibacter* sp., *Lactobacillus amylovorus*, and *Corynebacterium glucuronolyticum*. *Tepidibacter* was negatively associated with high reproductive performance (> 37 weaned piglets per sow per year; $P < 0.001$, LFC2.2). Probiotic-fed sows exhibited higher relative abundance of *Terrisporobacter* (LFC1.5), *Terrisporobacter petrolearius* (LFC1.3), *Clostridium* (LFC1.1), *Parabacteroides* (LFC1.8), *and Candidatus Saccharimonas* (LFC1.0) ($P < 0.001$). Late lactation represents a period of high nutrient demand and fiber intake. Enrichment of *Terrisporobacter* and *Clostridium* in probiotic-fed sows may support fiber degradation and short-chain fatty acid (SCFA) production, enhancing energy availability (Liu et al., 2022). Similarly, *Parabacteroides* is recognized for anti-inflammatory properties and SCFA generation, suggesting a beneficial role in gut health (Wang et al*.,* 2025). Conversely, the presence of *Tepidibacter*, though not well characterized, may indicate a gut environment prone to dysbiosis and intestinal inflammation, potentially impairing nutrient absorption and reducing productivity (Li et al., 2025).

Conclusion

On day 21 of lactation, sows share a core microbiota, while specific OTUs associate with performance and probiotic supplementation. The observed enrichment of *Terrisporobacter* and *Parabacteroides* in SolPreme®-administered sows suggests improved fiber utilization and gut resilience during lactation. Further studies should confirm functional outcomes, and link microbiota shifts to productivity.

Keywords: Sow gut microbiota, Probiotic, Bacillus, Reproductive performance, Fiber utilization

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COMPARATIVE EFFECTS OF DIFFERENT FORMS OF DIETARY SUPPLEMENTAL SELENIUM IN HOT ENVIRONMENT-INDUCED ENDOPLASMIC RETICULUM STRESS IN PIGS

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Introduction and Objectives

Heat stress (HS) compromises pig production by inducing endoplasmic reticulum (ER) stress. Selenium (Se) is crucial for antioxidant defense, but the efficacy of different Se forms against HS remains unclear. This study compared the protective effects of inorganic and organic Se sources on HS-induced ER stress and performance in pigs.

Materials and Methods

Forty 2.5-month-old growing pigs were fed during a hot summer (avg. 31.6°C) with either a Se-deficient basal diet (BD), or BD supplemented (0.3 mg Se/kg) with sodium selenite (SeNa), seleno-yeast (SeY), or 2-hydroxy-4-methylselenobutanoic acid (SeO) for 84 days. Growth performance, feed efficiency (FCR), antioxidant status, tissue Se content, selenoprotein and ER stress marker expression in liver/muscle, and meat quality were analyzed.

Results and Discussion

All Se forms improved FCR, with organic Se (SeY, SeO) showing greater efficacy than SeNa ($P < 0.05$). Organic Se significantly enhanced Se retention in plasma, muscle, and liver ($P < 0.05$), boosted antioxidant capacity (elevated GPX, SOD, GSH, $P < 0.05$; reduced MDA, $P < 0.01$), and upregulated key selenoproteins (e.g., GPX4, SELENOT, $P < 0.05$). Crucially, organic Se more effectively downregulated ER stress markers (ATF4, ATF6, GRP78, CHOP, P-eIF2α) in tissues ($P < 0.05$). Regarding meat quality, organic Se (SeY and SeO) reduced drip loss by 25.94 and 27.19%, respectively, compared to the basal diet ($P < 0.05$) and favorably altered muscle fiber type gene expression.

Conclusion

Dietary organic Se (SeY, SeO) is superior to inorganic SeNa in mitigating HS-induced ER stress in pigs, likely via enhanced selenoprotein-mediated antioxidant protection. This translates to improved growth performance and pork water-holding capacity, supporting the use of organic Se in swine nutrition for HS management.

Keywords: Endoplasmic reticulum stress, Heat stress, Organic selenium, Pork quality, Selenoprotein.

EFFECT OF SACCHAROMYCES CEREVISIAE BOULARDII CNCM I-1079 ON GROWTH PERFORMANCE AND GUT HEALTH IN POST-WEANING PIGLETS

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Introduction and Objectives

Post-weaning piglets face significant challenges related to gut health and systemic inflammation, which can impair growth and feed efficiency. Probiotic yeast supplementation has been proposed as a strategy to improve intestinal integrity and performance during this critical period. This study aimed to evaluate the effects of LEVUCELL SB (LSB, Saccharomyces cerevisiae var. Boulardii CNCM I-1079) (Bautista-Marín, S. et al., 2020) on zootechnical performance and biomarkers of gut health in post-weaning piglets under commercial conditions.

Materials and Methods

The trial was conducted on an experimental farm in Belgium (Innsolpig) in May - June 2025 with 447 piglets (Topigs TN70 x German genetics), aged 21 days, allocated into 32 pens (14 piglets/pen) and divided into 2 groups:

- Control: Basal Phase 1 (days 0 to 14) and Phase 2 diets (days 15 to 49).
- LSB Group: Same diets supplemented with LSB (200 gr/tn in Phase 1, 100 gr/tn in Phase 2).

The trial lasted 49 days post-weaning. Performance parameters (Body weight (BW), Average Daily Gain (ADG), Feed Conversion ratio (FCR)) were recorded at days 0, 14 and 49. Gut health was assessed via fecal Calprotectin (day 35) and salivary Haptoglobin (day 49) as biomarkers of intestinal and systemic inflammation.

Results and Discussion

Piglets supplemented with LSB showed significant improvements in growth performance: BW at day 49 was + 1.49 kg. higher than Control (23.2 vs. 21.79 kg, $P < 0,05$), ADG increased by + 15% in Phase 1 ($P < 0.005$), and by + 9% in Phase 2 ($P < 0.01$). Feed efficiency improved, with FCR reduced during both phases compared to Control (relative values: 93.2% ($P < 0,05$) and 95.3% ($P < 0.0005$) respectively for Phase 1 and 2). Biomarker analyses indicated better gut health: Fecal Calprotectin decreased by 32% (945 vs. 1,387 µg/g; $P < 0.1$) and salivary Haptoglobin by 51% (7.26 vs. 14.83 µg/mL; $P < 0.005$), suggesting reduced intestinal and systemic inflammation. These findings confirm the dual benefit of LSB on performance and health during the post-weaning period.

Conclusion

LSB supplementation improves growth performance and feed efficiency while reducing inflammatory biomarkers, supporting its role as a nutritional strategy to enhance gut health and resilience in post-weaning piglets.

Keywords: Calprotectin, Haptoglobin, Piglets, Post-weaning, Yeast.

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REGULATORY EFFECTS OF SACCHAROMYCES CEREVISIAE BOULARDII CNCM I-1079 AND A COMBINATION OF INACTIVATED YEAST FRACTIONS ON GROWTH PERFORMANCE, DIARRHEA INCIDENCE AND GUT HEALTH IN WEANED PIGLETS UNDER ETEC K-88 CHALLENGE

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Introduction and Objectives

Post-weaning piglets are prone to enteric disorders linked to impaired intestinal barrier and dysbiosis. Enterotoxigenic *Escherichia coli* (ETEC) K88 infection worsens these issues, causing diarrhea and growth retardation. This study evaluated yeast-based supplements LEVUCELL SB (Saccharomyces cerevisiae var. Boulardii CNCM I-1079) and YANG (inactivated yeast fractions) on growth performance, diarrhea incidence, intestinal integrity, microbiota, and inflammatory responses in weaned piglets.

Materials and Methods

Three experiments were conducted with piglets randomly allocated to treatments:

Exp. 1: 72 piglets (AIW: CON 8.84 kg; Treatment 8.88 kg) received either basal diet (CON) or basal diet + Levucell SB + Yang for 28 days. Exp. 2: 18 piglets (AIW ≈ 8.13 kg) divided into CON (n = 6), K88 (n = 6), and Y+K88 (n = 6; diet + Levucell SB + Yang). On day 14 post-weaning, K88 and Y+K88 were orally challenged with 5×10^9 CFU/mL ETEC K88; lasted 14 days post-challenge. Exp. 3: 18 piglets (AIW ≈ 9.8 kg) divided as above; challenged with 1×10^9 CFU/mL ETEC K88 one day post-weaning; lasted 7 days post-challenge.

Results and Discussion

Yeast supplementation improved ADG (348 vs. 410 g/d; $P < 0.05$), reduced diarrhea (6.4 vs. 4.2%; $P < 0.01$) and serum LPS (22.8 vs. 19.8 EU/mL; $P < 0.05$) in Exp. 1. In Exp. 2 and 3, LEVUCELL SB + YANG mitigated ETEC-induced diarrhea (83.3 vs. 33.3%, Exp. 2; 66.7 vs. 33.3%, Exp. 3; $P < 0.05$), enhanced tight junction integrity, and lowered TNF-α (Exp. 2: 14.3 vs. 9.0 pg/mL; Exp. 3: 7.8 vs. 6.7 pg/mL; $P < 0.01$). Microbiota analysis showed increased SCFA (Exp. 3: 3291 vs. 4038 µg/g; $P < 0.05$), restoration of beneficial bacteria, and reduced E. coli colonization (Exp. 2: 5.1 vs. 4.9 Log_{10} CFU/g; Exp. 3: 5.0 vs. 4.8 Log_{10} CFU/g; $P < 0.05$).

Conclusion

LEVUCELL SB and YANG improved growth and gut health in weaned piglets by reinforcing intestinal barrier, modulating microbiota, reducing systemic LPS, and attenuating inflammation under ETEC challenge.

Keywords: Enterotoxigenic *E. coli* K-88, Gut microbiota, Intestinal barrier function, Short-chain fatty acids.

NUTRIENT COMPOSITION OF SWILL FED TO PERI-URBAN FREE-ROAMING PIGS IN GERT SIBANDE, SOUTH AFRICA

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Introduction and Objectives

The rising cost of conventional animal feeds has emerged as a significant limitation for smallholder farmers, resulting in increased reliance on locally accessible alternative feeds in peri-urban areas. Therefore, this study was to investigate the variation in nutritional composition of four distinct swill types and to evaluate the nutrient composition of swill against the recommended nutritional needs for pig feeds in peri-urban pig farming in the Gert Sibande District.

Materials and Methods

All pig farmers (124) included in the study fed swill, supplemented with other feed sources such as commercial feeds, mixed home-formulated feeds, and other alternative feeds. The body condition score (BCS) was assessed based on the visual appearance criteria established by American Mini Pig Association (www.americaminipigassociation.com). Fourteen swill samples, originating from households, schools, restaurants, and wholesalers, were collected from pig producers in peri-urban areas. The samples were analyzed for standard nutritional profiles, and mean outputs (descriptive and analytical statistics) were generated using the Statistical Package for Social Sciences. Correlation between swill feeding and body condition score, as well as between swill feeding and age group, were evaluated using the chi-square (χ^2) test.

Results and Discussion

Swill feeding was most prevalent among pigs aged 9 - 12 months (39.2%), followed by pigs aged 1 - 4 months (32.2%) and those aged 5 - 8 months (22.6%). The majority of swill-fed pigs exhibited ideal body condition (39.9%), followed by those classified as thin (34.3%), fat (13.8%), and emaciated (10.2%). The swill samples were high in moisture (household: 80.14%, school: 80.27%, restaurant: 54.36%, wholesaler: 56.63%), and low in dry matter (household: 19.86%, school: 19.73%, restaurant: 45.64%, wholesaler: 43.37%), compared to standard feeds. Excess crude protein and fibre contents and imbalanced macro-mineral compositions (calcium, phosphorus, and sodium contents) were observed. The moisture, dry matter, and crude fibre contents fell outside the recommended range.

Conclusion

Swill feeding was predominantly observed in older pigs and typically correlated with ideal BCS, but many exhibited thinness or emaciation. Nutritional analysis indicated elevated moisture content, diminished dry matter, and imbalance in protein, fiber, and macro-minerals, signifying deficiency. Appropriate supplementation and management are essential to promote growth and BCS across various age groups.

Keywords: Diet, Feed formulation, Nutrient composition, Pig nutrition, Proximate analysis.

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EFFECTS OF GESTATIONAL POLYPHENOL SUPPLEMENTATION ON PLACENTAL GENE EXPRESSION IN SOWS

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Introduction and Objectives

Gestation in hyperprolific sows entails high maternal–fetal metabolic demands, with the placenta acting as a key regulator of nutrient, oxygen, and molecular signal exchange. Nutritional strategies targeting placental function have emerged as a promising approach to improve reproductive efficiency. Although gestational polyphenol supplementation has been associated with improved reproductive outcomes, the molecular pathways involved remain poorly not fully understood. The objective of this exploratory study was to characterize the placental transcriptomic response to maternal polyphenol supplementation during gestation, which led to better reproductive outcomes compared with a non-supplemented control group, as reported in a separate abstract submitted to the IPVS Congress 2026.

Materials and Methods

Placental samples were collected at parturition from multiparous Landrace × Large White (DanBred) sows assigned to a control group (CTRL; n = 3) or a polyphenol-supplemented group (AOX; n = 4). Samples were stabilized in RNAlater and stored at -80 °C. Total RNA was extracted, quality-assessed, and used to generate transcriptomic profiles using GeneChip® Porcine Genome microarrays, enabling evaluation of over 20,000 genes. Differential gene expressions were assessed using unadjusted p-values ($P < 0.05$) combined with a fold-change threshold ($|\log2FC| > 1$) as an exploratory approach. Selected results were validated by RT-qPCR.

Results and Discussion

Comparison between AOX and CTRL identified 380 differentially expressed genes (DEG), with a predominance of upregulated genes in the AOX group (54%, 203 genes). Polyphenol supplementation induced a moderate and targeted remodeling of placental gene expression. Functional enrichment analyses showed that genes associated with AOX supplementation were mainly involved in protein phosphorylation, post-translational modification, and intracellular signaling. Biological pathways related to circulatory system development and cellular communication were also enriched, suggesting potential effects on placental vascular regulation and signaling efficiency. These results are based solely on transcriptomic data and do not constitute direct functional evidence; reproductive outcomes were evaluated in a separate study.

Conclusion

Maternal polyphenol supplementation during gestation induces specific transcriptomic changes in the sow placenta, primarily affecting signaling and protein modification processes. These findings support the potential of polyphenols as a targeted nutritional strategy to modulate placental function alleviating oxidative stress in hyperprolific sows.

Keywords: Gestating sows, Polyphenols, Placenta, Transcriptomics, Reproductive performance.

Acknowledgements: The authors thank Miavit GmbH for providing the polyphenol blend MiaPhenol used in this study.

PHYTOBIOTIC-PREBIOTIC MODULATION OF THE GUT MICROBIOTA AND POTENTIAL SHORT-CHAIN FATTY ACID PRODUCTION IN GROWING PIGS

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Introduction and Objectives

Optimizing gut health through precision nutritional interventions is an important component of sustainable swine production under antimicrobial-reduction strategies. This study evaluated the effects of a phytobiotic–prebiotic blend composed of chicory, carob seed, and fenugreek (Neosantrix) on fecal microbiome composition and predicted metabolic functionality in growing pigs. The objective was to characterize microbial shifts and infer functional pathways potentially associated with saccharolytic metabolism using microbiome-based approaches.

Materials and Methods

A controlled feeding trial was conducted with 20 crossbred gilts (39.1 ± 3.1 kg) assigned to a basal diet (Control) or the same diet supplemented with Neosantrix at 1 kg/ton (Treatment). Fecal samples were collected at days 0 and 36 for 16S rRNA gene sequencing (V3 - V4 region, Illumina NextSeq 2000). Microbiome analysis included DADA2-based taxonomic profiling and functional inference using PICRUSt2. Statistical analyses comprised diversity metrics, differential abundance testing (FDR-adjusted $P < 0.05$), and exploratory multivariate analysis using PLS-DA with cross-validation.

Results and Discussion

The Treatment group altered gut microbiome composition (PERMANOVA: $P < 0.01$, $R^2 = 0.20$) without affecting microbial diversity (Shannon index: $P = 0.18$). The treatment showed enrichment of taxa commonly associated with fermentative metabolism, including Phascolarctobacterium ($P < 0.01$), Ruminococcaceae ($P < 0.01$), Lachnospiraceae ($P < 0.05$ - 0.01), Lactobacillus gasseri ($P < 0.05$), Bifidobacterium ($P < 0.05$), and Methanosphaera ($P < 0.05$), alongside a reduction of potentially pathogenic families (Bacteroidaceae: $P < 0.01$; Campylobacteraceae: $P < 0.001$). PICRUSt2-based functional prediction suggested potential enrichment of carbohydrate metabolism pathways, including glycolysis, the TCA cycle, and short-chain fatty acid–related biosynthetic routes; however, these inferred pathways require validation through direct metabolite quantification. Exploratory multivariate and machine-learning analyses demonstrated moderate discrimination between groups (AUROC = 0.85); however, these results should be interpreted with caution given the limited sample size.

Conclusion

Dietary supplementation with a phytobiotic–prebiotic blend was associated with changes in the porcine gut microbiome, characterized by enriching fermentative-associated taxa and reducing potentially pathogenic bacteria. These preliminary microbiome-based findings, derived from predictive functional analyses, provide a foundation for further investigation of phytobiotic-prebiotic strategies for gut health modulation in antimicrobial-reduction contexts.

Keywords: Microbiome, Phytobiotic-prebiotic, Short-chain fatty acids, Swine.

COMPARISON OF EFFECTS OF A PHYTOGENIC SUPPLEMENTATION AND ZINC OXIDE ON PERFORMANCE AND DIGESTIVE HEALTH OF WEANED PIGLETS

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Introduction and Objectives

The post-weaning period represents a major challenge in pig production due to the immaturity of the digestive tract and the immune gap in piglets. Phytogenic feed additives have emerged as promising strategies to support digestive health and performance through nutritional modulation. The objective of this study was to evaluate the effects of a phytogenic supplementation based on plant extracts on growth performance and digestive health of weaned piglets, in comparison with a negative control diet and a zinc oxide–supplemented diet.

Materials and Methods

The trial was conducted on a commercial pig farm in Spain using 378 piglets weaned at 28 days of age. Piglets were allocated into three dietary groups with 9 replicates of 14 piglets per group: a negative control group without supplementation, a zinc oxide group receiving 3 kg/t of ZnO (2,500 ppm) during the prestarter phase, and a phytogenic group supplemented with 2 kg/t of a plant-based additive. Main zootechnical parameters were monitored. Digestive health was assessed through daily faecal consistency scoring and recording of veterinary treatments.

Results and Discussion

During the pre-starter period, piglets receiving the phytogenic supplementation showed significantly improved growth performance compared to the negative control, with a 64% increase in ADG ($P < 0.0001$), and a tendency toward higher ADG compared to the zinc oxide group (+ 11%; $P = 0.0826$). Feed efficiency was also markedly improved, with a 49% improvement in FCR compared to the control and performance comparable to or better than zinc oxide ($P < 0.0001$). No liquid feces were observed in the phytogenic group throughout the post-weaning period. In parallel, veterinary drug use was reduced by 87% in the phytogenic group, reflecting improved digestive stability.

Conclusion

The phytogenic supplementation evaluated in this study significantly improved growth performance and feed efficiency of weaned piglets while promoting digestive health. By preventing severe digestive disorders and reducing the need for veterinary treatments. These findings support the use of phytogenic feed additives as a sustainable nutritional approach to enhance gut health and performance in weaned piglets, offering a viable alternative to zinc oxide in modern pig production systems.

Keywords: Performance, Phytogenic, Zinc.

KEY ASPECTS OF INTESTINAL INTEGRITY AT PIGLET WEANING: INSIGHTS FROM PRINCIPAL COMPONENT ANALYSIS

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Introduction and Objectives

Weaning is a critical stage in pig production, characterised by abrupt changes in diet, environment, and management that frequently lead to intestinal inflammation, impaired barrier function, microbiota dysbiosis, and post-weaning diarrhoea (de Groot et al., 2021; Ramis et al., 2023). In antibiotic-free production systems, these challenges are particularly relevant, as intestinal health relies mainly on the balance between immune activation, epithelial integrity, and microbiota stability. This study aimed to identify the main factors associated with intestinal integrity in weaned piglets by applying principal component analysis (PCA) to inflammatory biomarkers and tight junction proteins.

Materials and Methods

A total of 160 piglets from four commercial farms (n = 40 each) were selected at weaning. Faecal samples were collected and analyzed by PCR to quantify the expression of tight junction proteins (zonulin and occludin) and inflammatory markers (calprotectin, IFNγ, and TGFβ). Data were analyzed using PCA with XLSTAT software. Sampling adequacy was assessed using the Kaiser-Meyer-Olkin index and Bartlett's test of sphericity, retaining variables with KMO values above 0.5.

Results and Discussion

The PCA identified three components explaining 67.36% of the total variability. Weaning was associated with increased IFNγ and TGFβ expression, reflecting immune activation and intestinal inflammation. Calprotectin showed a positive correlation with occludin expression, suggesting epithelial regeneration in response to inflammatory damage. Zonulin displayed a high loading on an independent component, highlighting its specific role in regulating intestinal permeability.

Conclusion

Weaning induces marked alterations in intestinal integrity, characterised by inflammation, increased permeability, and immune activation. In antibiotic-free systems, maintaining a balance between inflammation, epithelial repair, and microbiota stability is essential to preserve intestinal health and performance.

Keywords: Antibiotic-free, Intestinal integrity, Microbiota, Piglets, Weaning.

Acknowledgements: The authors thank the personnel working in the farms where piglets were sampled.

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DIETARY *WEISSELLA CIBARIA* AND *LATILACTOBACILLUS* SAKEI IMPROVE GROWTH PERFORMANCE AND INTESTINAL MICROBIAL BALANCE IN GROWING PIGS

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Introduction and Objectives

Improving growth performance and gut health while reducing environmental emissions is a major goal in sustainable swine production. Probiotics are increasingly used as alternatives to antibiotic growth promoters due to their positive effects on nutrient digestibility, immune status, gut microbiota, and noxious gas reduction. *Weissella cibaria* and *Latilactobacillus sakei* are lactic acid bacteria with probiotic potential, including antimicrobial activity and intestinal health modulation, yet their combined effect in growing pigs is limited therefore, this study aims to assess its effects on growth performance, nutrient digestibility, blood profiles, noxious gas emissions, and fecal microbiota.

Materials and Methods

Ethical approval of this study was granted by Institutional Animal Care and Use Committee of Dankook University, Korea the Republic, and n = 252 ([Yorkshire × Landrace] × Duroc) growing pigs (26.82 ± 1.24 kg) used in a 6-week trial. All pigs were randomly assigned to 1 of 3 dietary treatments: CON, Basal diet; TRT1, CON + 0.3% *W. cibaria* SC51-2 (2.4E + 10 (CFU/mL); TRT 2, CON + 0.3% *L. sakei* SC83-3 (2.7E + 09 (CFU/mL) with 21 replicates of 4 pigs/ pen. Data was analyzed in a randomized complete block design using one-way ANOVA in the GLM procedure of SAS (SAS Institute, NC, USA), and $P < 0.05$ was set as significant.

Results and Discussion

At the end of week 6, pigs fed *L. sakei SC83-3* showed significantly increased ($P < 0.05$) daily gain and dry matter digestibility compared to CON. Also, pigs fed *W. cibaria* SC51-2 and *L. sakei* SC83 showed increased ($P < 0.05$) fecal *Lactobacillus* and reduced *E. coli* populations, indicating improved gut microbial balance, which partly explained the enhanced growth performance. In contrast, no significant effects were observed on noxious gas emissions or blood parameters, suggesting that the probiotics primarily influenced intestinal function rather than systemic metabolism or environmental outputs.

Conclusion

To our knowledge, this study provides new evidence supporting the beneficial effects of probiotic supplementation in pigs. Based on the results, we infer that inclusion of 0.3% W. cibaria SC51-2 and L. sakei SC83-3 in growing pigs' diets would be beneficial for improving their performance.

Keywords: Fecal microbiota, Gas emission, Growing pigs, Nutrient digestibility, Probiotics.

BASED ON MULTI-OMICS ANALYSIS, THE DIFFERENCES IN MEAT FLAVOR COMPONENTS AND REGULATORY MECHANISMS BETWEEN NINGXIANG PIGS AND DUROC×LANDRACE×YORKSHIRE (DLY) PIGS WERE REVEALED

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Introduction and Objectives

As the largest pork producer and consumer, China hosts diverse indigenous pig breeds. Ningxiang pigs are renowned for superior meat quality with high intramuscular fat and distinctive flavor, while commercial Duroc×Landrace×Yorkshire (DLY) pigs exhibit rapid growth but inferior flavor characteristics (Ma et al., 2022; Tao et al., 2023). This study aimed to: 1) compare fatty acid and amino acid compositions in longissimus dorsi; 2) identify key flavor-related metabolites and genes via multi-omics; and 3) validate candidate genes functionally.

Materials and Methods

Longissimus dorsi samples were collected from gender-balanced, 6-month-old Ningxiang and DLY pigs (n = 6 per breed, ~ 120 kg) raised under identical conditions. Fatty acids were analyzed by GC-MS following GB 5009.168-2016, and amino acids by automatic analyzer (GB 5009.124-2016). Metabolomics used LC-MS (Waters UPLC Xevo G2-XS QTOF), while transcriptomics employed Illumina NovaSeq with differential expression criteria of fold change ≥ 2 and FDR < 0.01. Weighted Gene Co-expression Network Analysis (WGCNA) identified flavor-related modules. GMPR was selected for CRISPR/Cas9 validation based on its strong correlation with inosine acid ($|r| > 0.6$) and hub status in WGCNA.

Results and Discussion

Nutritional analysis showed that the contents of saturated fatty acids (SFA) and umami amino acids in Ningxiang pigs were significantly higher than in DLY pigs, while essential amino acids (EAA) were higher in DLY pigs. Metabolomics identified 844 differential metabolites, with Ningxiang pigs enriched in umami nucleotides (e.g., inosine acid), antioxidant precursors, and fatty acid intermediates. Transcriptome analysis revealed up-regulation of genes related to fatty acid degradation (e.g., ACSL1, CPT1B, ACADM) and purine metabolism (e.g., GMPR, PDE4D, ADCY2) in Ningxiang pigs. WGCNA of transcriptomes highlighted a module correlated with flavor traits, with GMPR as a hub gene. Knockout of GMPR in myoblasts altered lipid accumulation, confirming its role in flavor regulation.

Conclusion

These findings indicate that fatty acid degradation and purine metabolism are pivotal pathways enhancing the flavor profile of Ningxiang pork. Functional validation revealed that GMPR knockout affected lipid accumulation, confirming its importance in flavor-related pathways. Despite inferior growth performance, Ningxiang pigs excel in producing richer flavors and more stable meat quality at the molecular level.

Keywords: Ningxiang pig, DLY crossbred pig, Multi-omics analysis, Fatty acid degradation, GMPR.

Acknowledgements: The authors thank the Huazhong Agricultural University, China for the support with providing testing facilities.

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FLEXIBLE NURSERY DIETS: A MULTIDIMENSIONAL APPROACH TO ENHANCE PRODUCTIVITY AND COST-EFFICIENCY IN TROPICAL SWINE PRODUCTION

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Introduction and Objectives

Early post-weaning nutrition strongly influences gut microbial development, intestinal function, and growth performance in pigs. Under tropical conditions, heat stress and ingredient price volatility necessitate flexible feed formulation, which may affect gut microbial stability. This study evaluated whether nutritionally equivalent nursery diets with diverse ingredients can maintain gut health, performance, and cost efficiency within an integrated feeding system.

Materials and Methods

A total of 280 weaned piglets (24 days of age) were allocated to 20 pens in a commercial-scale nursery trial conducted under tropical conditions. Experimental diets were formulated to similar nutrient specifications but differed in ingredient composition to reflect practical formulation flexibility and variation in fermentable substrates available for gut microbiota. Feed nutrient profiles were verified using near-infrared spectroscopy (NIRS). Pellet physical quality parameters (PDI, hardness, and fines content) were measured due to their known influence on feed intake behavior, digestive processes, and hindgut fermentation. Growth performance, general health status, and fecal consistency were monitored throughout the 42-day nursery period, with the pen considered the experimental unit.

Results and Discussion

NIRS analysis confirmed that all diets met formulated nutrient targets, with crude protein contents ranging from 19.53 to 21.11%. Pellet physical quality remained within commercially acceptable ranges (PDI 89.40 - 91.20%, hardness 2.60 - 3.20 kg, fines 1.80 - 2.00%), supporting uniform feed intake and digestive function. Growth performance did not differ significantly among dietary treatments ($P > 0.05$). Final body weight ranged from 23.29 to 26.38 kg, with average daily gain of 0.38 - 0.46 kg/day and feed conversion ratio of 1.33 - 1.59. Mean fecal scores ranged from 1.06 to 1.53, indicating stable gastrointestinal conditions. Feed cost per kilogram of body weight gain ranged from 14,336 to 17,083 VND/kg, with several flexible formulation diets achieving lower costs while maintaining comparable performance and gut health indicators.

Conclusion

These results demonstrate that nutritionally balanced nursery diets formulated with flexible ingredient compositions can support gut health, and growth performance while improving economic efficiency under tropical commercial conditions. An integrated, system-based feed formulation strategy represents a practical and sustainable approach for modern swine production systems facing ingredient variability and economic constraints.

Keywords: Gut health; Nursery pigs; Dietary flexibility; Pellet quality; Feed formulation.

Acknowledgements: The authors thank the staff of the commercial swine farm and feed mill for their technical support and cooperation during this study.

DIETARY PROTEIN OPTIMIZATION MAINTAINS GROWTH PERFORMANCE AND ECONOMIC EFFICIENCY IN GROWER–FINISHER PIGS

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Introduction and Objectives

This study evaluated how dietary crude protein (CP) levels and antibiotic growth promoter (AGP) supplementation affected growth, health, and economic efficiency in grower-finisher pigs.

Materials and Methods

256 crossbred pigs (Yorkshire×Landrace×Duroc) were allocated to a 2 × 2 factorial design. The study compared two dietary CP levels, high (18.3% grower, 15.5% finisher) and low (16.3% grower, 14.8% finisher), and two AGP regimens (with and without AGP). Pigs averaged 23 kg at the start of the grower phase and were followed to approximately 110 kg market weight. Pigs were housed in pens of 16 animals, with four replicates/ treatment, monitored throughout the grower and finisher phases. Diets were formulated based on corn-soybean meals, with crude protein levels adjusted by varying soybean meal inclusion and supplementing with crystalline amino acids to maintain amino acid balance, according to internal nutritional guidelines routinely applied in commercial swine production. All diets were isoenergetic. Standardized ileal digestible (SID) lysine levels and SID lysine-to-energy ratios were kept consistent across treatments. The number of animals and replicates provided sufficient experimental power to detect meaningful differences in growth performance and feed efficiency.

Results and Discussion

No interactions between CP and AGP were seen for growth performance or health indicators. Reducing dietary CP while maintaining balanced essential amino acid levels did not impair growth performance. AGP supplementation did not affect performance during the grower phase. However, it improved average daily gain (ADG) and feed efficiency ($P < 0.05$) during the finisher phase. Mortality and removal rates were low and unaffected by diet. Dietary crude protein level did not change feed cost per kilogram of weight gain in either phase ($P > 0.05$). AGP supplementation increased feed cost per kilogram of gain across both phases ($P < 0.05$). Despite better growth efficiency during the finisher phase, AGP supplementation did not improve economic efficiency.

Conclusion

These findings suggest that optimizing dietary protein levels with an adequate amino acid balance can maintain growth performance and improve economic efficiency under tropical commercial conditions. AGP supplementation, while improving growth efficiency during the finisher phase, increased feed costs, offsetting potential economic benefits and thereby limiting overall economic efficiency.

Keywords: Antibiotic growth promoter, Crude protein, Feed efficiency, Pigs, Tropical conditions.

Acknowledgements: The authors thank the staff of the commercial swine farm and feed mill for their technical support and cooperation during this study.

GROWTH PERFORMANCE, WHITE BLOOD CELL PARAMETERS AND MICROBES ARE NOT DIFFERENT AMONG FOUR LEVELS OF DIETARY INDIGENOUS MICROORGANISMS IN GROWING-FATTENING PIGS

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Introduction and Objectives

Excessive antibiotic use in livestock threatens public health (Tang et al., 2017), necessitating sustainable alternatives like probiotics (Patyra et al., 2023). Indigenous microorganisms (IMOs) are advantageous due to their low cost, biodiversity, and local adaptability. This study evaluated the effects of dietary IMO supplementation on growth performance, feed efficiency, white blood cell counts, and microbial parameters in growing-fattening pigs.

Materials and Methods

Eighty Kagoshima Berkshire × Binh Thuan pigs (85 days old; 15.27 ± 0.20 kg) were allotted to four dietary treatments (0, 0.5, 1, and 1.5% IMOs) in a randomized complete block design based on weight. Each treatment had two replicate pens (10 pigs/pen; 5 barrows, 5 gilts). The IMOs were prepared on-farm two weeks before the trial.

Results and Discussion

Dietary IMO supplementation had no significant effect on body weight ($P > 0.05$), though ADG and ADFI showed increasing trends with higher IMO levels ($P > 0.05$). From days 0-30, FCR improved significantly ($P < 0.001$), with the lowest value at 1.5% IMO (3.23) versus control (4.08); no differences were noted thereafter. IMO diets significantly decreased fecal pathogens (Coliform, *E. coli*, and Clostridium) ($P > 0.05$) while increasing lactic acid bacteria ($P < 0.001$). Furthermore, slightly higher white blood cell profiles suggest potential immunomodulatory effects, contributing to an enhanced gastrointestinal immune barrier in pigs.

Conclusion

Indigenous microorganisms supplementation did not significantly reduce fecal pathogens or growth performance. However, it increased beneficial lactic acid bacteria and improved early-phase FCR (0 - 30 days), suggesting potential benefits for gut health and initial feed efficiency.

Keywords: Indigenous microorganisms, growth performance, White blood cell.

Acknowledgements: The authors thank the Research and Technology Transfer Center, Nong Lam University HCMC, Vietnam for the support of providing testing facilities.

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BRANCHED-CHAIN AMINO ACID OPTIMUM RATIO IN TRANSITION DIETS ON SOW'S BODY WEIGHT LOSS AND PIGLET'S GROWTH PERFORMANCE

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Introduction and Objectives

Branched-chain amino acids (BCAAs) including L-valine (Val), L-leucine (Leu), and L-isoleucine (Ile), play a crucial role in mammary gland development and are important substrates for colostrum and milk protein synthesis which begins upon entry into the transition period (TP) (Li et al., 2009). As sows becoming hyperprolific, little is known regarding the BCAAs optimal ratio relative to lysine in transition diets. Therefore, the aim of the study was to evaluate the BCAAs optimal ratio relative to lysine in transition diets on sow's body weight loss and piglet's growth performance.

Materials and Methods

Forty-eight primiparous and multiparous sows were employed from day 106 of gestation to day 10 of lactation. Box-Behnken design (BBD) response surface design was applied. Gestating sows were randomly allotted, divided into 16 runs with 14 dietary treatments were formulated according to BBD. All dietary treatments were applied on TP. Sow body weights (BW) during TP and at weaning were recorded. Suckling piglet's BW during TP and at weaning was recorded and average daily gains (ADG) were calculated.

Results and Discussion

BW and BW loss during TP were not statistically significant ($P > 0.05$). Suckling piglet's BWs during TP were statistically significant ($P < 0.05$). ADGs during TP and at weaning were statistically significant ($P < 0.05$). During TP, as more Val included, ADG linearly higher ($P < 0.05$) whereas more inclusion levels of Leu and Ile tended to higher ADG ($P < 0.10$). Interaction effect of Val × Leu was found in ADG ($P < 0.001$), but not for that of Leu × Ile. At weaning, as more Leu included, ADG linearly was higher ($P < 0.05$). Interaction effects of Val × Leu and Leu × Ile were found in ADG ($P < 0.001$). During TP, the predicted optimal levels of Val, Leu and Ile were 183.94, 489.41, and 246.86%.

Conclusion

This study found increased suckling piglet's ADG during TP and at weaning. Similarly, to previous report, Increasing BCAAs level enhanced the growth performance of suckling piglets with higher ADG (Rezaei et al., 2022). At optimal ratio relative to lysine, BCAAs mitigated sow's BW loss improved piglet' growth performance.

Keywords: Bach-chain amino acids, Body weight Loss, Performance, Sow, Transition.

Acknowledgements: The study was funded by Papon farm.

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EFFECTS OF DIETARY VALINE SUPPLEMENTATION DURING MID-GESTATION TO LACTATION ON REPRODUCTIVE PERFORMANCE AND LITTER GROWTH IN HYPERPROLIFIC SOWS

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Introduction and Objectives

Gestation and lactation diets impact sow productivity and subsequent litter performance, substantially elevating amino acid requirements for mammary development and colostrum synthesis (Theil et al., 2022). Valine, the second-limiting branched-chain amino acid for milk protein synthesis, stimulates mammary epithelial cell proliferation (Gao et al., 2019). However, optimal dietary valine levels remain inconsistent and uncleared across studies. This study investigated the effects of dietary total valine fed from mid-gestation through lactation on sow reproductive performance and litter growth.

Materials and Methods

Thirty-nine crossbred sows (Large White × Landrace, parity from 0 to 4) were randomly allocated to three treatments (N=13 per treatment) in a completely randomized design: T1, T2, T3 receiving 0.70%, 1.20% and 1.70% total valine, fed from day 63 of gestation until weaning (25 days of lactation). Experimental diets were formulated for three phases: gestation, transition (10 days pre-farrowing to 10 days post-farrowing), and lactation. Sows with ideal body condition and no udder damage were selected. Sow and individual piglet body weights (BW) were recorded at birth, day 10, and weaning. Sow's health problems were observed throughout the experiment.

Results and Discussion

One sow health problem was observed throughout the experiment. Litter size and sex ratio were similar among treatments ($P > 0.05$). The supplementation had no significant effect ($P > 0.05$) on sow BW loss during lactation. T2 showed non statistical increase piglet birth BW ($P = 0.361$), weaning BW ($P = 0.672$), and average daily gain from birth to weaning ($P = 0.926$) as well as litter birth BW ($P = 0.624$), litter weaning BW ($P = 0.912$), and pre-weaning mortality ($P = 0.735$). The baseline valine level in T1 (0.70% total valine, equivalent to 45.1 g/day SID valine at 6.89 kg ADFI) represented 88-107% of NRC (2012) recommendations, suggesting adequacy for lactation performance.

Conclusion

Increasing dietary total valine at 1.20 and 1.70% (Val:Lys ratio approximately 1.50:1 or 2.15:1) provided non statistically significant benefits for piglet growth and survival in hyperprolific sows. These findings suggest that 0.70% total dietary valine (0.86 Val:Lys ratio) appears adequate for optimal lactation performance for modern hyperprolific sows during mid-gestation to lactation under tropical conditions.

Keywords: Amino acid, Gestation, Hyperprolific, Lactation, Valine.

Acknowledgements: The authors thank the National Swine Research and Training Center and Papon Farm.

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EFFECT OF DIETARY 14-EPIMER OF 25-HYDROXYCHOLECALCIFEROL ON PLASMA 25-HYDROXYCHOLECALCIFEROL LEVELS IN GILTS AND PRIMIPAROUS SOWS

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Introduction and Objectives

Vitamin D_3 (VD3) is a fat-soluble prohormone that is metabolically converted to its circulating intermediate, 25-hydroxycholecalciferol (25-OHD3). The hormonally active form 1,25-(OH)2D3 regulates calcium and phosphorus homeostasis, leading to improved skeletal integrity in developing gilts, and enhanced lifetime reproductive efficiency in sows (Coffey et al., 2012). Through biotechnological advances, 14-epi-25-OHD3 has been developed as a dietary source of VD3. However, evidence regarding their ability to maintain 25-OHD3 status under physiologically demanding conditions such as lactation, remains limited. Therefore, this study evaluated the effects of dietary 14-epi-25-OHD3 on the reproductive performance of primiparous sows.

Materials and Methods

Primiparous sows (n-180) were randomly allotted to pre-gestation, gestation and lactation diets formulated to attain 2,000 IU/kg dietary equivalent of either regular VD3 (control, T1), 25 µg of 14-epi-25-OHD3 (Bio-D®, T2), or 50 µg 25-OHD3 (Hy-D®, T3). Diets were offered *ad libitum* from 10 weeks of age through first parity weaning. Sows' blood samples were collected on days 5 and 25 of lactation for plasma 25-OHD3 analysis. Post-farrowing performance measures included body weight, feed intake, number born alive, removals, and weaned piglets.

Results and Discussion

Feed consumption reached 6 kg/day during lactation, resulting in 599.32, 524.32, and 351.26% increases in plasma 25-OHD_3 in T1, T2, and T3, respectively, between days 5 and 25 ($P < 0.001$). Stillborn rates were 10.36, 8.15, and 4.58% in T1, T2, and T3, respectively ($P = 0.015$). There were significant differences in total born ($P = 0.001$), born alive ($P = 0.048$), and changes in sow body weight ($P = 0.011$) across treatments. Sows in T2 experienced greater body weight loss; however, this did not adversely affect piglet vitality, consistent with previous reports indicating that moderate maternal weight loss during lactation does not necessarily compromise neonatal viability (Højgaard et al., 2020).

Conclusion

A half dose of 14-epi-25-OHD3 was sufficient to maintain plasma 25-hydroxycholecalciferol concentrations and to support optimal productive performance in gilts and primiparous sows, achieving outcomes comparable to those obtained with the standard dose of 25-OHD3.

Keywords: 14-epimer, 25-hydroxycholecalciferol, Gilt, Sow, Vitamin D3.

Acknowledgements: The study was funded by Huvepharma®.

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PARABIOTICS SUPPLEMENTATION IMPROVES GUT HEALTH IN *E. COLI*-CHALLENGED WEANED PIGS

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Introduction and Objectives

Nutritional modulation of gut microbiota and intestinal immunity is a key strategy to mitigate post-weaning disorders in pigs. Parabiotics offer improved stability compared with probiotics, yet evidence for Enterococcus faecalis-based parabiotics combined with other gut-modulating components remains limited. This study evaluated the effects of dietary supplementation with an *E. faecalis*–based parabiotic alone or combined with Bacillus subtilis, β-glucan, and mannan-oligosaccharides on growth performance, gut health, immune responses, and fecal microbiota in Escherichia coli–challenged weaned pigs.

Materials and Methods

Twenty-four weaned pigs were assigned to six treatments for 17 days: basal diet (PC), *E. coli* challenge (NC), NC with 0.10% heat-killed *E. faecalis* (T1), and NC with 0.05, 0.075, or 0.10% of a parabiotic-based additive composed of heat-killed *E. faecalis*, B. subtilis, β-glucan, and mannan-oligosaccharides (T2 - T4). Growth performance, fecal score, nutrient digestibility, serum immune, intestinal morphology, tight junction-related gene expression, and fecal microbiota composition were evaluated.

Results and Discussion

The E. coli challenge impaired growth performance, nutrient digestibility, and intestinal morphology while increasing diarrhea incidence and inflammatory markers ($P < 0.05$). Combined parabiotic supplementation alleviated these effects, with the greatest improvements observed at the highest inclusion level. The T4 group showed higher average daily gain and lower feed conversion ratio compared with the NC group ($P < 0.05$). Dry matter, gross energy, and crude protein digestibility were significantly improved, accompanied by reduced white blood cell counts and interleukin-6 concentrations and increased immunoglobulin A and G levels ($P < 0.05$). Intestinal barrier integrity was enhanced, as indicated by increased villus height-to-crypt depth ratio and claudin-1 expression. These improvements in growth performance and nutrient utilization were associated with enhanced intestinal integrity and attenuated systemic inflammation, as evidenced by intestinal morphological and immune-related indices measured in the present study. Overall microbial diversity was not altered; however, specific taxonomic shifts, including increased Blautia, were observed.

Conclusion

Dietary supplementation with an *E. faecalis*-based parabiotic combined with *B. subtilis* and immunomodulatory polysaccharides improved growth performance and nutrient utilization in *E. coli*-challenged weaned pigs, which was associated with enhanced intestinal integrity and moderated immune responses rather than major alterations in overall microbial diversity.

Keywords: Weaning pigs, Parabiotics, Gut health, Intestinal integrity, *Escherichia coli.*

EFFECTS OF AQUEOUS SELENIUM NANOPARTICLES IN DIETS ON PERFORMANCE OF SOWS

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Introduction and Objectives

Sows' productivity has changed drastically recently, especially in litter size. Greater productivity heightens catabolic activity and reactive oxygen species, causing oxidative stress during farrowing and nursing. This stress impairs milk yield, reproduction, and sow longevity (Zhao et al., 2011). Selenium (Se) supplementation provides antioxidant protection, strengthening cellular defense (Lubinski et al., 2018). The objective of this study was to evaluate the effects of dietary aqueous selenium nanoparticles on sow performance.

Materials and Methods

A total of 38 sows (Landrace x Yorkshire), from 2 to 5 litters, were randomly allocated to two treatments on a commercial farm. In the control group, 17 sows were fed a commercial diet without supplementation, whereas 21 sows in the AMMS group received 1 mL of AMMS Se™ per sow per day. The AMMS Se™ product was top-dressed onto the feed during the morning meal for 7 days prior to farrowing and throughout the lactation period until weaning. Parameters including total piglets born, piglets born alive, piglets weaned per litter, birth weight, weaning weight, and sow feed intake were recorded and compared between treatments using ANOVA, with statistical significance set at $P < 0.05$.

Results and Discussion

Feeding AMMS Se™ diets to sows did not significantly change ($P > 0.05$) the performance parameters. However, sows fed the aqueous selenium tend to improve the number of piglets born alive (11.95 vs 11.18 piglets), piglets weaned per litter (10.71 vs 10.11 piglets), weaned weight (5.69 vs 5.32 kg), and reduce mortality (16.59 vs 20.91%) and significantly improve ($P < 0.05$) the number of days to return to heat (4.43 vs 5.06 days). Sows fed the AMMS Se™ saved the feed cost by 6.15% per weaned piglet and 12.22% per kg weaning weight compared to control feed.

Conclusions

Feeding AMMS Se™ diets to sows improves the weaning weight by 368 g per weaned piglet, increases the number of weaned piglets per litter by 0.6, shortens the days to return to heat by 0.5 days, and improves the feed cost by 6.15% per weaned piglet and 12.22% per kg of weaning weight.

Keywords: Aqueous Selenium, Oxidative Stress, Sow performance.

Acknowledgements: The authors express their appreciation to Biotech (Lu'an) Co., Ltd. for providing AMMS Se™ and funds for conducting this experiment.

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COMPARISON OF A BACTERIAL XYLANASE WITH FUNGAL NON-STARCH POLYSACCHARIDE (NSP) ENZYMES ON GROWTH PERFORMANCE IN PIGLETS AND ECONOMIC IMPACT

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Introduction and Objectives

Bacterial xylanase has been shown to improve growth performance and nutrient digestibility in pigs by reducing the viscosity of the soluble arabinoxylans and breaking down insoluble fibre structures to release entrapped nutrients (Boudry et al., 2022). β-glucanases similarly support NSP degradation in barley-based diets by hydrolysing β-glucans (Choi et al., 2024), although these fibres may still offer physiological benefits (Metzler-Zebeli et al., 2013). This study aimed to compare the effects of a bacterial xylanase to a fungal NSP enzyme complex (Xylanase + β-glucanase), on piglet growth performance and economic outcomes.

Materials and Methods

A total of 350 Victoria x Belpi piglets (7.78 kg, weaned at 26 days old) were housed in 10 pens (35 mixed sex piglets per pen) and assigned to two treatment groups: bacterial xylanase (bXYL) at 100 g/T (10 IU/kg) and a fungal NSP enzyme complex (fNSP) at 50 g/T (6250 U/g xylanase and 4300 U/g β-glucanase). The trial was conducted over a pre-starter phase (Day 1 - 14) and a starter phase (Day 14 - 42) with barley-wheat-corn-based diets specific to each phase. BW and ADFI were measured on days 0, 14, and 42, and the economic outcomes were calculated. Data were analysed using SAS GLM, with significance at $P \leq 0.05$.

Results and Discussion

By Day 42, piglets fed bXYL had significantly higher BW of 26.98 ± 2.18 kg ($P = 0.04$) and ADG of 457 ± 13g/d ($P = 0.02$), than those receiving fNSP (BW: 25.72 ± 2.48kg; ADG: 427 ± 29g/d). ADFI (728 ± 42 g/d vs 713 ± 33 g/d) and FCR (1.592 ± 0.07 vs 1.672 ± 0.07) also tended to improve with bXYL supplementation ($P > 0.05$). Economically, bXYL delivered a feed gain of €28/year per piglet place with 7.45 cycles/year - a 35% increase over fNSP - and reduced feed cost/kg of growth (€0.805 vs 0.844), considering feed costs per piglet and value increase of a piglet per kg of growth, highlighting its superior economic efficiency.

Conclusion

The supplementation of a bacterial xylanase in barley-based diets improved growth performance of piglets and delivered strong economic benefits compared with fungal NSP enzyme complex, yielding 35% higher feed profit and 5% reduction in feed costs.

Keywords: Bacterial xylanase, Barley, Economic benefit, Growth performance, Weaned piglets.

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EFFECTS OF PHYTOGENIC SUPPLEMENTATION ON PIGLETS PERFORMANCE IN THE PRESENCE OF FEED CONTAMINATED WITH VERY HIGH LEVELS OF MYCOTOXINS

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Introduction and Objectives

Feed contaminated by mycotoxins remains a typical issue whose impacts on performance are often difficult to quantify. This is the case for swine, which is a species sensitive to mycotoxins. This trial evaluated effects of a dietary supplementation of phytogenic extracts on the performance of piglets in the presence of feed contaminated with a mycotoxin blend and compared them to a clay-enzymes-based binder and a control lot.

Materials and Methods

24 piglets weaned at 28 days old, randomly divided in 3 lots (C, B, I) of 8 piglets were followed for 28 days starting at 35 days old. Control lot (C) received a feed with mycotoxin's contaminations and without supplementation. Feed level contamination was 0.5 ppm Aflatoxins + 25 ppm Fumonisins + 4 ppm Deoxynivalenol (DON) during the whole trial. Both other lots were fed with the same contaminated feed supplemented: a clay and enzymes-based binder have been added at the recommended dose of 0.1% to lot B (Binder) and the phytogenic product has been added at 0.025% to lot I (INEDIA®). Group-fed system housing and Bonferroni model were used for analysis.

Results and Discussion

DFI (daily feed intake) (kg/piglet/day) was higher in lot I (0.733) compared to lot B (0.708) and lot C (0.667) ($P \leq 0.05$). Same positive trend about ADG (average daily gain) (g/piglet/day) for lot I (423) compared to lot B (394) and lot C (392). The villi height/crypt depth ratio of the trial lot (I) is higher (2.17) than the other groups (control C 1.64 and 'binder' group B 1.91, $P \leq 0.05$). This result demonstrated an improvement in the structure of the intestinal mucosa with wider surface.

Conclusion

These preliminary results support the relevance of phytogenic supplementation in piglets exposed to high dietary mycotoxin levels. Improved feed intake, growth performance, and villus height/crypt depth ratio indicate positive effects on intestinal morphology. Suggesting a better preservation of gut structure and contributing to greater resilience to mycotoxin challenge. Under severe polycontamination, INEDIA® showed a more pronounced beneficial effect than a clay–enzyme binder in limiting performance impairment and intestinal alterations.

Keywords: Performance, Phytogenic, Mycotoxin, Resilience.

EFFECT OF NUTRITIONAL PROTEIN GEL SUPPLEMENTATION IN SUCKLING PIGS ON GROWTH PERFORMANCE AND PIGLET PRE-WEANING MORTALITY: A MULTI-TRIAL ANALYSIS

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Introduction and Objectives

Improving piglet survival and early growth performance remains a major challenge in swine production, especially among low-birthweight piglets that are at increased risk of pre-weaning mortality (Douglas et al., 2014). Early-life nutritional strategies are commonly implemented to support these vulnerable populations (Tucker et al., 2021). Porcistart® is a nutritional protein gel formulated to provide piglets with essential energy and nutrients. Enriched with whey protein, butyric acid, caffeine, vitamins, and minerals to support piglet growth and their gut health. The present study assesses the effectiveness of Porcistart® relative to a standard control by analyzing pooled data from seven independent trials. The aim was to evaluate the effects of Porcistart® on growth performance and pre-weaning mortality, and to examine whether these effects varied according to piglet birthweight.

Materials and Methods

Data from seven independent trials (n = 3,067) were pooled to assess the effectiveness of Porcistart® treatment (n = 2,127) in comparison with a Control group (n = 940). Growth performance parameters including birthweight, weaning weight, and average daily gain were analyzed using the General Linear Model (GLM) in SAS. Mortality outcomes were assessed using a Chi-square test, with statistical significance defined as $P < 0.05$.

Results and Discussion

Across all trials, piglets receiving Porcistart® had a significantly lower overall mortality rate compared with controls ($P = 0.0159$). In terms of growth performance, Porcistart® supported the development of small piglets, allowing them to attain weaning weights (5.61 kg) that were not statistically different from those of Normal piglets receiving the same treatment (6.52 kg; $P = 0.1367$).

Conclusion

This study demonstrated that administering Porcistart® as a nutritional intervention during the first days of piglets' lives reduces mortality and improves growth performance by helping close the growth gap between smaller piglets and larger piglets.

Keywords: Birthweight, Mortality, Piglet, Supplementation, Weaning weight.

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POSTBIOTIC SUPPLEMENTATION THROUGHOUT POSTNATAL LIFE IMPROVES BODY WEIGHT AND LARGE GUT DEVELOPMENT OF PIGS AFFECTED BY INTRAUTERINE GROWTH RESTRICTION

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Introduction and Objectives

Intrauterine growth restriction (IUGR) is a condition in which individuals do not reach their potential growth, presenting low birthweight and impaired postnatal performance. Studies reported that IUGR pigs remain lighter than normal birthweight pigs until finishing phase (Santos et al., 2022). Supplementation with postbiotics has been used as growth promoter (Chen et al, 2021). Thus, the aim of this study was to investigate the effect of a concentrated yeast-derived postbiotic (PB) on body weight and organ development of IUGR pigs.

Materials and Methods

Sows (n = 242) were selected at GD76 and sorted into two groups: Control diet (C) and supplemented daily with 30g of PB on top (S). One piglet born with normal birthweight (NBW, 1.6 - 1.9kg) and one piglet born with IUGR (0.7 - 1.0kg) were selected from each sow. At 0, 26, 70, and 150 days the piglets were weighed and measured. After weaning, half of each group switched diets. On 0, 26 and 70 days, a subset of n = 8 piglets/birthweight/group were randomly selected for euthanasia, and the organs weighed.

Results and Discussion

NBW_C and NBW_S piglets were heavier and presented larger organs than their IUGR littermates ($P < 0.05$). At 26 days, IUGR_S group presented higher body weight, biometric measurements, and heavier large gut than IUGR_C group ($P < 0.05$). At 70 days, the IUGR_SC group presented the lowest body weight ($P < 0.05$). Supplementation did not affect biometrics, but liver weight was higher in the NBW_SC group ($P < 0.05$). At 150 days, the IUGR_SS group presented body weight similar to all the NBW groups ($P > 0.05$), and higher than all the other IUGR groups ($P < 0.05$).

Conclusion

Supplementation with PB improved body weight and organ development of IUGR pigs, especially in pigs supplemented throughout postnatal life. Postbiotic withdraw was critical, and more studies on pig physiology are crucial for efficient nutritional interventions.

Keywords: IUGR, Postbiotic supplementation, Body weight, Organ development, Postnatal growth

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GUT MICROBIOTA REGULATE TRYPTOPHAN METABOLISM TO AFFECT SOW UTERINE HEALTH

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Introduction and Objectives

Sow endometritis causes infertility and culling (Nash et al., 2025). Gut microbiota influence uterine health via tryptophan metabolism through the gut–organ axis (Jia et al., 2024). This study evaluated the association between gut–uterus tryptophan metabolism and endometritis, and explored the protective effects of 3-indolepropionic acid (IPA).

Materials and Methods

Sow endometritis was characterized by a high uterine abundance of pathogenic bacteria (≥ 10^6 CFU/mL), postpartum hyperthermia, and severe lochial discharge. Uterine lavage fluid was collected postpartum from 186 healthy and diseased sows across two farms for partial 16S sequencing; serum from 20 healthy and diseased sows was analyzed by LC-MS/MS. At one farm, 120 primiparous sows at 95 days of gestation were selected: 60 received a basal diet, and 60 received the basal diet supplemented with 0.02% IPA from gestation day 95 to 7 days postpartum. Recorded parameters included farrowing performance, blood samples from the anterior vena cava (n = 40), vulval discharge status (7 days postpartum), body temperature (7 days postpartum), piglet weaning data, and post-weaning estrus rate. Furthermore, a mouse model was used: mice received 10 mg/kg IPA by gavage for 7 consecutive days, and on day 8, endometritis was induced by intravaginal lipopolysaccharide (LPS) infusion.

Results and Discussion

In diseased sows, the relative abundance of pathogenic bacteria (Escherichia coli, Enterococcus faecalis, Streptococcus spp.) in uterine lavage fluid was significantly increased, and serum levels of tryptophan metabolites were markedly reduced. Dietary IPA supplementation significantly reduced the incidence of postpartum lochia (by 35%) and hyperthermia (by 20%), decreased serum levels of inflammatory cytokines (IL-6, IL-1β, TNF-α; $P < 0.05$), shortened farrowing duration (by 0.8 h), increased the number of piglets born alive per litter (by 1.6 piglets), and improved post-weaning estrus and mating rates. In mice with endometritis, the abundance of tryptophan-metabolizing gut bacteria was downregulated, and serum IPA concentration was significantly decreased. consistent with the findings in sows. The underlying mechanisms require further investigation.

Conclusion

Depleted tryptophan-metabolizing gut microbiota and reduced tryptophan metabolites contribute to endometritis. IPA supplementation mitigates endometrial inflammation.

Keywords: Sow endometritis, Gut microbiota, Tryptophan metabolism, 3 Indolepropionic acid, Reproductive performance.

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DIETARY CO-EXPOSURE TO DEOXYNIVALENOL, ZEARALENONE AND OCHRATOXIN A AT EU GUIDANCE LEVELS INDUCES DISTINCT SYSTEMIC AND HISTOPATHOLOGICAL CHANGES IN PIGS

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Introduction and Objectives

Mycotoxin contamination is a major concern in swine production, with exposure linked to impaired growth and immunosuppression. While regulatory thresholds exist for individual mycotoxins, the effects of concurrent multi-mycotoxin exposure remain poorly understood. The European Union (EU) has set feed guidance levels for pigs of 0.9 ppm for deoxynivalenol (DON), 0.1 ppm (piglets and gilts) for zearalenone (ZEN), and 0.05 ppm for ochratoxin A (OTA) (EC, 2006). This study is the first to evaluate simultaneous dietary exposure to DON, ZEN, and OTA at or near these EU guidance levels in weaned pigs.

Materials and Methods

Sixty-four weaned pigs (28 days of age) were assigned to two dietary treatments for 14 days. Thirty-two animals received a control diet with trace mycotoxins (0.03 ppm DON and 0.6 ppm fumonisins, well below EU guidance levels, thus unlikely to confound results), and 32 received a contaminated diet (1.19 ppm DON, 0.09 ppm ZEN, 0.05 ppm OTA). Tissue samples (liver, jejunum, ileum, colon, uterus, ovaries, kidneys) were collected from 16 animals per group for histopathological evaluation. Systemic exposure was assessed via dried blood spots (DBS) on days 1, 7, and 14, analyzed by LC-MS/MS. Histopathological data were analyzed by chi-square test; DBS data by repeated-measures ANOVA.

Results and Discussion

Periportal inflammatory findings were observed in 81.25% (13/16) of contaminated-group liver samples versus 31.25% (5/16) in controls ($P < 0.01$). Renal lesions (glomerular alterations and tubular degeneration) appeared in 31.25% (5/16) of samples from animals receiving contaminated feed versus none in controls ($P < 0.01$). Ileal epithelial degeneration and necrosis occurred in 62.5% (10/16) of the contaminated group samples versus 6.25% (1/16) of controls ($P < 0.01$). Pigs receiving contaminated feed also showed greater systemic exposure to DON and OTA, suggesting additive or interactive toxicokinetic effects.

Conclusion

This study provides the first evidence that concurrent exposure to three mycotoxins at or near EU guidance levels results in aggravated pathological outcomes. Findings align with known individual toxicities - intestinal barrier disruption (DON), nephrotoxicity (OTA), potential hepatic effects (ZEN) – but suggest interactive potentiation, underscoring the need for multi-mycotoxin risk assessment and feed and blood monitoring.

Keywords: Deoxynivalenol, Dried blood spots, Mycotoxins, Ochratoxin A, Zearalenone.

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FEED ADDITIVE SUPPLEMENTATION REDUCES FARROWING DURATION AND IMPROVES PRODUCTION PERFORMANCE IN HYPERPROLIFIC SOWS

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Introduction and Objective

Hyperprolific sows are frequently associated with prolonged farrowing duration, which increases the risk of stillbirth. Extended farrowing may also negatively affect milk production, leading to higher pre-weaning mortality (Bosch et al., 2022). Therefore, this study aimed to evaluate the effects of a nutritional feed additive on farrowing performance and production efficiency in a commercial sow herd.

Materials and Methods

A total of 108 multiparous sows were allocated into two groups: control (n = 55) and treatment (n = 53), in a commercial farm housing approximately 2,500 sows. Both groups were maintained in the same environmentally controlled farrowing house equipped with an evaporative cooling system. The treatment group received GF-Sow Booster® at 20 g/sow/day once daily from 7 days before farrowing until weaning at 25 days, whereas the control group received no supplementation. The feed additive is a proprietary nutritional supplement formulated with energy substrates, antioxidant components, and functional additives designed to support metabolic status during late gestation and lactation. Farrowing duration, inter-piglet birth interval, and production performance parameters were recorded. Data were analyzed using a t-test in R Studio.

Results and Discussion

Sows in the treatment group exhibited a shorter farrowing duration (240.77 ± 119.19 min) compared with the control group (317.96 ± 154.65 min; p = 0.007). Accordingly, the average inter-piglet birth interval was reduced in the treatment group (12.29 ± 6.16 min) compared with the control group (16.54 ± 9.65 min; P = 0.007). Litter size did not differ between groups (20.00 ± 3.31 vs. 19.76 ± 3.14). However, the treatment group showed higher numbers of weaned piglets and greater weaning weights, resulting in a higher average daily litter weight gain (3,258.11 ± 778.40 g/day) compared with the control group (3,093.22 ± 807.36 g/day).

Conclusion

Supplementation with the nutritional additive reduced farrowing duration and improved subsequent production performance in hyperprolific sows. These findings suggest that targeted nutritional strategies during late gestation and lactation may enhance productivity and efficiency in commercial breeding systems.

Keywords: Commercial swine production, Farrowing duration, Nutritional supplementation, Reproductive efficiency.

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IMPACT OF AN INTESTINAL HEALTH PROGRAM ON GUT MICROBIOTA DIVERSITY AND IMMUNE RESPONSE IN A PIG FARM IN WESTERN MEXICO

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Introduction and Objectives

Intestinal Health Programs (IHP) have been associated with a decrease in cases of enteritis and dysbiosis, as well as an increase in serum IgG concentration (Zheng et al., 2021; Xiong et al., 2019). IHP may include the use of probiotics and additives, such as phytobiotics and short-chain fatty acids, among others (Upadhaya et al., 2022). The objective of this study was to evaluate the microbiota diversity and the health of animals by quantifying serum IgG, IgA, and IgM in the intestines of pigs with and without IHP.

Materials and Methods

All animal protocols were authorized by the Internal Committee for the Care and Use of Laboratory Animals of the FESC, UNAM (CICUAE-FESC C23_33). Thirty-two pigs were evaluated, 16 farm pigs with IHP (with additives and probiotics) and 16 farm pigs without IHP, located in the state of Jalisco, Mexico. Blood and intestinal contents samples were taken from pigs at different ages (3, 5, 7, and 10 weeks). Samples of caecal contents were collected for characterize the microbiota using 16S rRNA gene (V3-V4) sequencing. Serum IgG concentration was quantified using the Pig IgG ELISA kit (ab291065, Abcam). Data processing consisted of descriptive analysis, Student's t-test for comparison of means, and Welch's test for adjustment.

Results and Discussion

At the phylum level, caecal microbiota relative abundance was higher in IHP-treated animals, with the most pronounced differences observed at 5, 7, and 10 weeks of age ($P < 0.05$). Seven-week-old pigs with IHP showed a 10% increase in IgG production when compared to the same-aged group without IHP ($P < 0.05$). Three-, five-, and ten-week-old pigs showed no differences when comparing animals with IHP and without IHP ($P > 0.05$). These results are consistent with reported in literature (Zeng et al., 2021; Wang et al., 2024), who state that 7 weeks of age is a critical period for the establishment of the immune system in the intestines of pigs.

Conclusion

IHP use improves the relative abundance of the caecal microbiota and, the immune response in pigs, which could improve overall pig health and make pig production systems more efficient.

Keywords: Additives, Pigs, Microbiota, Gut health.

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MULTI-STRAINED PROBIOTICS MODULATE THE GUT-MUSCLE AXIS TO INCREASE MUSCLE MASS AND FEED EFFICIENCY IN PIGS

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Introduction and Objectives

Production of pork is directly linked to skeletal muscle growth and anabolic metabolic processes, such as muscle protein synthesis, in pigs. Probiotics are recognized for their role in modulating gut microbiota and host metabolism, which may potentially influence carcass quality. The objective of the present study was to investigate growth performance, gut microbiome, serum metabolome, short-chain fatty acids (SCFAs) production, and carcass traits of pigs fed with a multi-strained probiotic product (SYNLAC LeanAd, SYNBIO TECH INC.).

Materials and Methods

A total of 144 commercial weaning piglets (28 days old) were randomly allocated to two groups (n = 18 per pen, 4 pens per group) and fed diets with (LeanAd) or without (Control) probiotic supplementation (0.1%; 1.0 x 109 CFU/g) for 18 weeks. Microbiome analysis, serum metabolic profiling, and gene expression analysis of the PI3K/Akt/mTOR pathway were conducted to assess the effects of supplementation.

Results and Discussion

Results showed that LeanAd supplementation significantly improved feed efficiency and increased muscle mass in the loin eye, arm shoulder, and blade shoulder ($P < 0.05$). Microbiome analysis revealed a significant enrichment of SCFA-producing taxa, including Acidaminococcus, Allisonella, Dialister, and Megasphaera, which correlated with a significant increase in cecal butyrate levels. Moreover, pigs from the LeanAd group had significantly ($P < 0.05$) higher serum insulin levels and upregulated key genes in the PI3K/Akt/mTOR pathway, including igf1r, insr, and pi3k. The expression of the bile acid receptor, tgr5, was significantly ($P < 0.05$) increased in LeanAd pigs.

Conclusion

These findings demonstrate that dietary supplementation with SYNLAC LeanAd can enhance muscle deposition and carcass traits. This is achieved by modulating the gut-muscle axis, which elevates SCFA production, activates the PI3K/Akt/mTOR signaling pathway, and regulates bile acid metabolism.

Keywords: Gut-muscle axis, Probiotics, Muscle mass, PI3K/Akt/mTOR, Short-chain fatty acids

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LONGITUDINAL CHARACTERIZATION OF PIGLET FECAL MICROBIOME FROM LACTATION TO THE END OF THE NURSERY PHASE

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Introduction and Objectives

The gut microbiome plays a key role in nutrient metabolism and host physiology. In piglets, early-life microbial colonization may influence growth performance and health status (Wang et al., 2025). This study longitudinally characterized fecal microbiota from lactation to the end of the nursery phase and explored differences between piglets stratified by final bodyweight.

Materials and Methods

Fourteen crossbred piglets (Landrace × Large White × Duroc) from a single sow were included in this study population. Fecal swabs were collected on May 23, 2025 (14 days pre-weaning), at weaning, and at 7, 14, 28, and 42 days post-weaning (six time points). Bacterial DNA was extracted (Qiagen DNeasy PowerSoil Pro Kit) and subjected to 16S rRNA gene sequencing (Illumina MiSeq), with bioinformatic analysis performed using QIIME2 (Bolyen *et al.*, 2019). After weaning, piglets were housed individually to monitor growth performance. At 42 days post-weaning, piglets were stratified into high (> 20 kg, n = 9) and low (< 20 kg, n = 5) bodyweight groups using a predefined cut-off.

Results and Discussion

At 42 days post-weaning, piglets were stratified into high (>20 kg, n = 9) and low (< 20 kg, n = 5) bodyweight groups. Beta diversity analysis (Bray-Curtis) revealed temporal shifts in microbial composition. Significant differences in community structure were detected at weaning (D0; PERMANOVA, $P = 0.011$) and 7 days post-weaning (D7; $P = 0.046$), but not during lactation (wk2; $P = 0.569$) or later nursery stages (D14 - D42; all $P > 0.05$), including day 42 ($P = 0.199$). Shannon diversity did not differ between groups ($P = 0.156$). Descriptive differences in relative abundance were observed: Akkermansia muciniphila and Faecalicatena spp. were relatively higher in lower-bodyweight piglets early, whereas Limosilactobacillus mucosae, Blautia, and Prevotella were more abundant in heavier piglets. No significant correlations were found between dominant genera and bodyweight (Spearman, $P > 0.05$).

Conclusion

Gut microbiota composition changed across developmental stages. Transient differences in community structure occurred during the weaning transition, but no significant differences were detected at nursery end, suggesting early post-weaning as a potential window for microbial divergence between growth groups.

Keywords: Gut microbiota, Lactation period, Nursery phase, Piglet fecal.

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EFFECTS OF DIETARY CHLORHEXIDINE NANOPARTICLES ON FECAL MICROBIAL DIVERSITY IN WEANED PIGLETS

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Introduction and Objectives

The increasing global concern regarding antimicrobial resistance has intensified the search for alternatives to antibiotics growth promoters in animal production. Chlorhexidine has emerged as a promising alternative due to its broad antimicrobial activity, which is enhanced by nanotechnology (Michalak et al., 2022). Therefore, this pioneering study aimed to evaluate the effects of dietary nano-chlorhexidine on the fecal microbiota of weaned piglets.

Materials and Methods

The 42-day experiment involved 120 weaned piglets, assigned to five groups in a randomized block design (initial weight and sex), with eight replications per treatment: CON (negative control, no additive), HALQ (addition of 120 mg/kg halquinol in feed), and C25, C50, C75 (addition of 25, 50, and 75 mg/kg nano-chlorhexidine in feed, respectively). At trial completion, six piglets per group, with body weights closest to the treatment mean, were selected for rectal swab microbiota analysis (n = six piglets per treatment). The sequencing sample size was limited by financial constraints and the exploratory nature of this early-stage project. Bacterial DNA was extracted using the ZymoBIOMICS DNA Miniprep Kit. The V3 - V4 region of the 16S rRNA gene was amplified and sequencing data were processed in QIIME software (v2022.2.0). Alpha diversity was assessed using the Kruskal-Wallis test with false discovery rate correction, while beta diversity was evaluated using PERMANOVA. A significance level of 5% was adopted for statistical analyses.

Results and Discussion

No significant differences in alpha diversity (Shannon and Fischer indices) were observed among the groups ($P = 0.131$ and $P = 0.457$, respectively). The analysis showed no significant differences in microbial community composition between treatments ($F = 1.14$, $R^2 = 0.15$, $P = 0.29$). The lack of significant effects may be partially attributed to the health status of the piglets and the limited number of replicates per treatment, which may have reduced the ability to detect subtle microbial shifts.

Conclusion

Dietary nano-chlorhexidine at the evaluated inclusion did not lead to detectable alterations in the fecal microbiota of weaned piglets. As an innovative approach, further research is required to evaluate the safety and efficacy of chlorhexidine nanoparticles as potential alternatives to antibiotics growth promoters.

Keywords: Antibiotics growth-promoters, Antimicrobial resistance, Gut health, Swine nutrition.

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EFFECTS OF COMBINATION OF ORGANOSULFUR AND COPPER-EXCHANGED CLAY IN DIETS TO REPLACE ANTIBIOTIC GROWTH PROMOTER ON PERFORMANCE OF PIGS

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Introduction and Objectives

Withdrawing antimicrobial growth promoters (AGPs) from pig diets may increase diarrhea and disease incidences (Upadhaya and Kim 2021). A holistic approach is needed to support gut health by maintaining microbial balance and boosting antioxidant capacity. Organosulfur compounds from onions and garlic provide strong antioxidants and antimicrobial effects, while a specific clay that is combined with copper ions through cation exchange technology shows improved bacterial balance. This trial aimed to evaluate the efficacy of combining organosulfur and this specific clay in pig diets.

Materials and Methods

A total of 225 pigs with an average live weight of 15.06 kg were randomly allocated into three diet treatments, three replicates per treatment and 25 pigs per replicate. Three experimental diets included the control diet (CON) supplemented with 120 ppm of haquinol and the BL1 diet supplemented with organosulfur (0.005%) and specific clay (0.04%). The BL2 diet was the BL1 diet supplemented with yeast (0.1%). All pigs were fed to ad libitum. Live weight was monitored on 6 pigs per replicate, identified by ear tags, on the 1st, 22nd, 82nd, and 110th days of the trial, and feed intake was recorded daily. On the 110th day, two pigs per treatment were randomly selected to evaluate carcass dressing and carcass quality. All data were subjected to Minitab Version 17 for statistical analysis.

Results and Discussion

Growing pigs fed the BL1 or BL2 diets did not show any significant differences ($P > 0.05$) in live weight, average daily gain, feed intake, and feed efficiency when compared to pigs fed the CON diet during the trial. Meat color, dressing carcass percentage and drip loss of pigs fed the BL1 or BL2 diets were similar to those of pigs fed the CON diet. Economic profits of pigs fed the BL1 and BL2 diets was higher than that of pigs fed the CON diet at 9.8 and 5.7%, respectively.

Conclusions

Pigs fed diets supplemented with organosulfur and copper-exchanged clay either alone or in combination with yeast showed comparable growth performance, feed efficiency, dressing percentage, and drip loss to those on the antibiotic-supplemented diet, while yielding higher economic profits.

Keywords: AGP, Fattening, Growth performance, Carcass quality.

Acknowledgements: The authors express their appreciation to Archer Daniels Midland (ADM) Animal Nutrition for providing products and funds for conducting this experiment.

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EFFECT OF BACILLUS SUBTILIS DSM 29784 ON PERFORMANCE OF POST-WEANING PIGLETS

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Introduction and Objectives

Weaning is a critical and stressful period for piglets, often causing reduced feed intake, digestive disturbances, and impaired growth. Historically, antibiotics were used both as growth promoters and as therapeutics, but their use is now increasingly restricted. This highlights the need for non-antibiotic strategies that support gut health and growth performance after weaning. The present study investigates the effects of Bacillus subtilis DSM29784 (Bs) on piglet health and productivity.

Materials and Methods

A total of 240 castrated male piglets (Landrace × Large White), weaned at 26 days, were allocated to four treatments in a randomized complete block design (10 replicates; 6 pigs/pen). For 42 days, T1 received a basal antibiotic-free diet; T2 received the basal diet plus antibiotics (Tiamulin 200 ppm, Colistin 200 ppm, Amoxicillin 350 ppm); and T3 and T4 received the basal diet supplemented with Bs at 10 or 100 g/ton (10^{10} CFU/g). Average daily gain (ADG), feed conversion ratio (FCR), and diarrhea were measured. Blood was analyzed for cortisol, myeloperoxidase (MPO), and calprotectin at D10 after weaning. Data was evaluated by ANOVA.

Results and Discussion

Diarrhea severity was mild across treatments (scores 1.01 - 1.05) and no mortality occurred. From D0–D42, ADG increased significantly in all treated groups (T2: 585; T3: 468; T4: 474 g/day) compared with the control (438 g/day; $P < 0.01$). Feed-to-gain improved from 0.667 (control) to 0.704, 0.692, and 0.696 in T2–T4, respectively ($P < 0.01$). Cortisol, MPO, and calprotectin were unaffected by treatment, indicating a low stress for the animals at 10d after weaning. Under present conditions, probiotic supplementation improved ADG by 7 - 8% and FCR by 3 - 4% compared to the control group. Feed cost/kg gain was reduced by 0.37% (T4) - 3.4% (T3) in the probiotic groups vs control.

Conclusion

Bs clearly enhances growth and feed efficiency in piglets after weaning, even under mild stress conditions, although it does not fully recover antibiotic-driven improvements. Increasing the dose did not yield significant additional performance benefits, indicating that the low dose is sufficient. Overall, Bs supports productive, welfare-focused, and regulation-compliant swine production, reinforcing its value as a practical alternative in modern systems.

Keywords: Gut health, Probiotic, Post-weaning.

VITAMIN OPTIMIZATION MITIGATES THE IMPACT OF SHORT-TERM HEAT STRESS ON PIG GROWTH PERFORMANCE

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Introduction and Objectives

Heat stress (HS) challenges pigs' ability to maintain euthermia, disrupting metabolic, physiological, and immune functions and ultimately reducing growth performance and welfare. Modern high-performing pigs may have higher vitamin requirements than those outlined in NRC (2012), particularly when exposed to environmental stressors. This study evaluated whether elevated vitamin supplementation following the Optimum Vitamin Nutrition (OVN, 2023) concept could improve resilience and performance of growing–finishing pigs subjected to short-term HS.

Materials and Methods

A total of 288 pigs (26.1 ± 1.75 kg) were housed in 48 pens (6 pigs/pen) and randomly assigned to three vitamin treatments: NRC levels (T1), commercial industry levels (T2; Yang et al., 2021), and OVN levels (T3). Pigs received grower diets from days 1–35 and finisher diets from days 36 - 70 under thermoneutral conditions (20 - 22°C in the grower phase; 18–20 °C in the finisher phase). A controlled diurnal heat-stress challenge was applied on days 54 - 56 (6 h at 30 - 32°C; 18 h at 28°C). Body weight, feed intake, lesions, lameness, and daily fecal score (0 - 3) were recorded. Rectal temperature (Tr) and respiration rate (RR) were measured during heat stress to confirm physiological response. Data were analyzed using JMP 16 with pen as the experimental unit.

Results and Discussion

The HS protocol effectively induced heat load, as shown by increased Tr and RR ($P < 0.05$). Despite HS, pigs continued to gain weight between days 52 and 57. OVN-supplemented pigs tended to have higher average daily gain during HS (1087 g/d) compared with NRC (945 g/d) and commercial levels (1019 g/d) ($P = 0.08$). Feed intake was unaffected, but OVN improved feed conversion ratio in the finisher phase (2.78 vs. 2.88 for commercial levels and 2.85 for NRC; $P = 0.05$). Fecal score increased during HS (1.73) relative to grower (1.19) and finisher (1.37) phases, with no treatment differences. Ear lesions and lameness remained low, whereas tail lesions increased over time ($P < 0.05$).

Conclusion

Elevated vitamin supplementation following the OVN concept improved resilience and helped maintain growth performance of pigs exposed to short-term HS compared with NRC and commercial vitamin levels.

Keywords: Heat stress, Resilience, Growth performance, Fecal score, Vitamins.

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EFFECTS OF DIETARY SUPPLEMENTATION WITH ENTEROSURE™ ON GROWTH PERFORMANCES OF POSTWEANING PIGS

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Introduction and Objectives

Antimicrobial resistance is a major challenge in pig production worldwide. Consequently, non-antibiotic strategies such as probiotics have gained attention as sustainable alternatives to improve pig health and performance. Bacillus-based probiotics produce bioactive metabolites with antimicrobial properties. Previous research demonstrated that metabolites produced by *Bacillus* strains in ENTEROSURE™ inhibited enterotoxigenic *Escherichia coli* (ETEC) isolated from pig farms in Thailand. This study evaluated the effects of dietary supplementation with a *Bacillus*-based probiotic blend (ENTEROSURE™) on growth performance and health parameters of postweaning pigs under commercial farm conditions in Thailand.

Materials and Methods

The trial was conducted on a commercial farrow-to-finish farm (600 sows) in Chonburi Province, Thailand. A total of 280 healthy weaned piglets (Large White × Duroc × Landrace), 28 days old, were randomly assigned to a control group receiving a basal diet (n = 140) or a treatment group receiving the same diet supplemented with ENTEROSURE™ Dry at 0.05% (1 kg/ton) for 42 days. Pigs were housed in an environmentally controlled facility with *ad libitum* access to feed and water. Growth performance parameters, including average daily gain (ADG), average daily feed intake (ADFI), and feed conversion ratio (FCR), were calculated. Diarrhea incidence, mortality, and culling were recorded daily. The experimental unit was the individual pen. Data were analyzed using Student's t-test ($P < 0.05$).

Results and Discussion

The treatment group showed higher ADG (549.69 ± 8.22 g/day) than the control group (419.27 ± 1.41 g/day). ADFI was significantly greater in the treatment group (771.68 ± 3.48 g/day) compared to the control group (560.76 ± 0.10 g/day) ($P < 0.05$). FCR was slightly higher in the treatment group (1.43 ± 0.03) than controls (1.34 ± 0.02). Mortality and culling rates were reduced by 2.14 and 2.86%, respectively, in the treatment group. Diarrhea incidence was significantly lower in supplemented pigs (5.24 ± 0.91%) than controls (24.74 ± 6.83%) ($P < 0.05$), possibly reflecting the previously reported anti-ETEC activity of ENTEROSURE™ metabolites (3).

Conclusion

ENTEROSURE™ supplementation improved growth performance and reduced postweaning diarrhea, supporting its use as a non-antibiotic strategy in commercial pig production in Thailand.

Keywords: ENTEROSURE™, Dietary, Growth performances, Postweaning pigs, Supplementation.

NUTRITIONAL INTERVENTION USING A SEMI-SOLID SUPPLEMENT TO MITIGATE POST-WEANING GROWTH DEPRESSION IN UNDERWEIGHT PIGLETS

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Introduction and Objectives

Post-weaning growth set back is a significant challenge in modern swine production, particularly for piglets with low weaning weights. These animals often face delayed gut development and insufficient nutrient intake during the first week post-weaning (Wensley et al., 2021). This study aimed to evaluate the impact of a specialized semi-solid nutritional supplement (Porcistart®) on productive performance and survival rate of underweight piglets during the post weaning period. The product is formulated as a functional supplement that contains 32 easily digestible ingredients (Bousquet et al, 2019), including medium- and short-chain fatty acids such as butyric acid, which promotes gut maturation, controls pathogenic bacteria, and stimulates feed intake.

Materials and Methods

A cohort of 524 weaned piglets (mean BW: 3.8 - 4.1 kg) was utilized in a randomized controlled field trial. Animals were assigned to: (1) Control (n = 261; conventional nursery management and liquid milk replacer), or (2) Treatment (n = 263; 30 - 50 g/head/day of Porcistart® for five consecutive days post-weaning). Longitudinal growth performance was monitored via body weight measurements up to 10 weeks of age, with ADG normalized across trial sites. Mortality was recorded throughout the nursery phase. Continuous data were analyzed using a two-tailed Student's T-test, while categorical mortality data were subjected to Fisher's Exact Test in R. Statistical significance was established at $P < 0.05$.

Results and Discussion

The Treatment group demonstrated a significantly superior ADG of 330 + 150 g/day compared to 271 + 156 g/day in the Control cohort ($P = 0.047$), representing a 21.7% improvement in growth velocity and in final bodyweight at end of nursury. Furthermore, mortality was significantly reduced in treated piglets (3.13%) relative to controls (7.63%; $P = 0.02$). The administration of the semi-solid supplement may help mitigate post-weaning growth depression in low birth weight piglets, resulting in significantly higher ADG and improved survival rate compared to the control group.

Conclusion

The observed improvement in growth is hypothesized to be linked to the stabilization of the gut barrier and maturation of enterocytes. However, this hypothesis remains speculative, as no direct measures of gut morphology, microbial profile, or specific barrier integrity markers were collected in this study.

Keywords: Post-weaning Set-back, Survival rate, Underweight piglets.

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GAMMA AMINOBUTYRIC ACID SUPPLEMENT IN GESTATING AND LACTATING SOW FEED FOR IMPROVING SOW AND PIGLET PERFORMANCE

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Introduction and Objectives

Gamma Aminobutyric Acid (GABA) is an inhibitory neurotransmitter and a mediator linking gut microbiotas and mental health. Previous study showed the improvement of sow performance and the trend to improve Wean to Service (WTS) days of sows supplemented GABA in gestating and lactating feed at 100 ppm (Makhanon et.al., 2025). This field study aimed to find GABA efficacy to sow performance in a commercial farm in Philippines and to evaluate the result of increasing the concentration of GABA in gestating feed (Liu et.al., 2022).

Materials and Methods

After mating, 300 gestating sows (Sow: LL x LW, & Boar: Duroc, Danish) in the same unit were divided into three groups equally. GABA feed supplement from two months of gestation at the concentration of 0, 100, and 200 ppm until farrowing as control, G100 and G200 groups, respectively. After farrowing the supplement in lactating feed was continue at 100 ppm GABA on G100 and G200 groups until weaning, the average piglets/litter were 11.88 pigs in control and 12.16 pigs in G100 and G200. The average lactating days of control, G100 and G200 are 24.79 ± 1.55 d vs 26.33 ± 1.71 d vs 23.91 ± 1.22 d. Data collection including piglet born and born alive, birth weight and weaning weight, and WTS days, were recorded. Statistical analysis was at $P < 0.05$.

Results and Discussion

This study illustrated that average birth weight of G100 was significantly higher than control and G200 (1.55 ± 0.15 vs 1.50 ± 0.15 vs 1.53 ± 0.17 kg, $P < 0.05$). The lactating performance illustrated that the litter and average wean weight and weight gain of G100 and G200 were higher than control, $P < 0.05$. WTS days of sows in control group was shorter than G100 (5.01 ± 1.74 d vs 6.17 ± 4.62 d, $P < 0.05$) and no difference to G200 (5.01 ± 1.74 d vs 5.32 ± 3.42 d, $P > 0.05$).

Conclusion

GABA supplement in gestating sows can significantly increase the average birth weight of piglets. GABA supplement at 100 ppm in lactating sows can improve wean weight and weight gain of piglets, significantly. This study has no effect of GABA supplement to WTS days in sows which is different from the previous study (Makhanon et.al., 2025).

Keywords: GABA, gestating and lactating sow, Feed supplement.
Acknowledgements: The author would like to thank Charoen Pokphand Foods Philippines Corporation to facilitate the study.

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MATERNAL IMMUNOMODULATORY FUNCTIONAL AMINO ACIDS SUPPLEMENTATION CAN BE ASSOCIATED WITH ZONE-DEPENDENT HEPATOCYTE NUCLEAR MODULATION IN SWINE OFFSPRING

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Introduction and Objectives

Functional amino acids supplemented during gestation may support fetal development and optimize postnatal performance. The liver is a key organ for nutrient metabolism and alterations in its early development may influence metabolic efficiency. This study aimed to evaluate whether maternal functional amino acids supplementation throughout gestation may influence hepatic function, by measuring nuclear morphometry, in swine offspring across productive stages.

Materials and Methods

Thirty gestating sows were allocated into two experimental groups: CC (gestation diet) and TT (gestation diet + 40 g/sow/day functional amino acid supplementation throughout gestation). Male offspring were euthanized at 26 (post-weaning), 70 (nursery), and 145 (finisher) days (n = 5 animals/group/age). Liver samples were fixed in 4% paraformaldehyde and processed for histological analysis. Hepatocyte nuclear area was measured using QuPath® in periportal and centrilobular regions. Five 40 × photomicrographs/region/animal were obtained, and all visible nuclei measured to determine mean nuclear area per zone and total parenchyma. Data were analyzed by ANOVA and means compared by Tukey-Kramer test ($P < 0.05$).

Results and Discussion

Nuclear morphometry revealed age- and zone-dependent differences between groups. At 26 days, TT animals exhibited reduced periportal nuclear areas ($P < 0.05$), suggesting moderated metabolic activity after weaning, and at 145 days, showed greater total and centrilobular nuclear areas ($P < 0.05$), indicating enhanced metabolic capacity at the finisher phase. Kinetics analysis demonstrated oscillatory nuclear behavior in CC animals, with peak total nuclear area at 70 days followed by reduction at the finisher phase. In contrast, TT animals maintained more consistent total and centrilobular nuclear areas across stages, while periportal nuclear areas increased after weaning and remained stable thereafter. Maternal dietary protein levels during gestation have been associated with persistent alterations in hepatic gene expression related to energy metabolism in offspring. Such transcriptional modulation may reflect sustained changes in hepatocellular metabolic activity, which could be structurally manifested as differences in nuclear morphometry. Therefore, the observed variations in hepatocyte nuclear area may represent a phenotypic expression of nutrition-induced hepatic programming.

Conclusion

Given the liver's central role in nutrient utilization and feed efficiency, enhanced hepatocellular activity at the finisher phase may contribute to improved metabolic capacity and productive performance in swine offspring.

Keywords: Feed efficiency, Hepatic metabolism, Nutrient utilization, Prenatal nutrition, Productive performanc.

Acknowledgements: The authors acknowledge Agroceres Multimix for financial support, CNPq and FAPEMIG for providing scholarships.

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COLON MORPHOLOGICAL ALTERATIONS IN THE OFFSPRING OF SOWS SUPPLEMENTED WITH FUNCTIONAL AMINO ACIDS DURING GESTATION

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Introduction and Objectives

Gestating sows' supplementation with alternative nutritional substances, such as functional amino acids, is recommended to ensure optimal conceptus development. The impact of such supplementation on offspring colonic development is essential, due to the role of colonic morphology for water and minerals absorption, and microbial interaction environment. This study aimed to investigate colonic morphological alterations in the offspring from sows supplemented with immunomodulatory functional amino acids during gestation.

Materials and Methods

Thirty gestating sows were allocated into two experimental groups: CC (control diet during gestation) and T114 (control diet + 40 g/sow/day of an immunomodulatory functional amino acid supplement throughout gestation). Male offspring were selected and euthanized at 26 (post-weaning), 70 (nursery), and 145 days (finisher) (n = 6 animals/group/age). Colon samples were collected, fixed in paraformaldehyde 4% and processed for histological analysis. Photomicrographs (20x) of 30 crypts were obtained per animal, and their width, depth, epithelial and mucosal height, goblet cells/crypt and crypts density were measured using the software ImagePro Plus®. Data were tested for normality using the Shapiro-Wilk test and were analyzed through analysis of variance and means compared using Tukey-Krammer post-test ($P < 0.05$).

Results and Discussion

At 25 days of age, offspring from supplemented sows showed greater crypt depth, higher number of goblet cells, and increased mucosal height ($P < 0.05$), suggesting enhanced mucosal development and secretory capacity early after weaning. In contrast, crypt density was higher in the control group ($P < 0.05$), possibly reflecting a compensatory increase in crypt number rather than structural maturation. At 70 days of age, pigs from the T114 group exhibited greater epithelial height ($P < 0.05$), indicating sustained effects of gestational supplementation on epithelial growth during the nursery phase. At 145 days of age, crypt width and epithelial height remained higher in the T114 group, suggesting long-term modulation of colonic architecture. Overall, gestational supplementation with an immunomodulatory functional amino acid promoted age-dependent morphological adaptations in the colon, potentially favoring epithelial integrity and mucosal functionality throughout postnatal development.

Conclusion

Gestational supplementation with immunomodulatory functional amino acids positively modulated colonic morphology, promoting sustained epithelial development and mucosal integrity, which suggests potential improvements in gut resilience and long-term intestinal functionality.

Keywords: Functional amino acids, Colon morphology, Sow nutrition.

Acknowledgements: The authors acknowledge Agroceres Multimix for financial support, and CAPES and CNPq for scholarships.

POOLED ANALYSIS OF TWO PROTECTED BENZOIC ACID STUDIES ON WEANED PIG PERFORMANCE WITHOUT PHARMACOLOGICAL ZINC OXIDE

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Introduction and Objectives

Organic acids enhance nutrient utilization, positively impact gut microbiota, and improve weaned pig performance (Suiryanrayna et al., 2015). Protected benzoic acid (PBA; PROVENIA® Feed Solution) provides enhanced delivery of benzoic acid to the small intestine and hindgut, thus positively influencing the microbial populations and supporting gut health. Individual studies have shown positive growth response of nursery pigs to PBA (Correa et al., 2021; Peric et al., 2023). Therefore, a meta-analysis of two trials on the effect of PBA on growth performance of nursery pigs was conducted.

Materials and Methods

A pooled-analysis was conducted combining data from two nursery pig trials. In Trial 1, 364 pigs were assigned to two dietary treatments (0 or 2.5 kg/MT PBA) with 14 pens per treatment for 40 days. In Trial 2, 654 pigs were assigned to the same treatments with 34 pens per treatment for 35 days. Diets did not contain pharmacological levels of ZnO. Overall phase represents d 0 - 35 and 0 - 40, whereas combined phases represent d 0 - 7, 7 - 14, 14 - 35 and 14 - 40. Data were analyzed using mixed models in JMP Pro 19. Pen was the experimental unit with treatment, phase, trial, and their interaction as fixed effects, and pen as random effect.

Results and Discussion

Inclusion of PBA in the diets increased the average daily gain (ADG) from d 0 - 7 by 28.3% (0.154 vs 0.120 kg/d, $P = 0.0001$) and d 7 - 14 by 18.1% (0.365 vs 0.309 kg/d, $P = 0.0335$). Across the overall phase, PBA improved ADG by 8.3% (0.433 vs 0.400 kg/d, $P = 0.0284$) and by 11.1% (0.351 vs 0.316 kg/d, $P = 0.0139$) across the combined phases. Feed conversion ratio (FCR) was improved with PBA from d 0 - 7 by 23.3% (1.503 vs 1.960, $P < 0.0001$) and by 10.3% (1.442 vs 1.608, $P < 0.0001$) across the combined phases. The FCR for d 7 - 14 was 1.327 and 1.392 ($P = 0.3423$) and across the overall phases was 1.457 and 1.510 ($P = 0.1308$), for pigs fed diet with and without PBA, respectively. In addition, inclusion of PBA tended to decrease mortality (0.98 vs 2.36%, $P = 0.0971$).

Conclusion

The result of this meta-analysis supports using protected benzoic acid to improve weight gain in weaned pigs.

Keywords: Benzoic acid, Growth performance, Nursery pigs, Organic acid.

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METHIONINE HYDROXY ANALOGUE BIS-CHELATED TRACE MINERALS POSITIVELY IMPACT GROWTH PERFORMANCE OF NURSERY PIGS

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Introduction and Objectives

Trace minerals are essential for growth, immune function, and metabolism in nursery pigs. Bioavailability of inorganic trace minerals (ITM) can be reduced by antagonisms within the gastrointestinal tract. In contrast, methionine hydroxy analogue bis-chelate (MHAC; Mintrex® Trace Minerals), have been shown to enhance mineral bioavailability not only for Zn, Cu and Mn but for other minerals including Ca and P and have been shown to improve pig performance (Peric et al., 2023). The objective was to compare the effects of ITM and MHAC on nursery pig performance and removals.

Materials and Methods

In Exp. A, 1,152 nursery pigs were allocated to 24 pens/treatment. Dietary treatment provided Zn, Cu, and Mn at 100, 130, and 40 mg/kg from d 0 to 14 and 100, 80, and 40 mg/kg from d 14 to 35, either as ITM modified oxides or MHAC. In Exp. B, 364 nursery pigs were assigned to 14 pens/treatment. The same mineral levels as Exp. A were provided either as ITM sulfates or MHAC from d 0 to14 and d 14 to 40. The methionine concentration was formulated to be equivalent in the ITM and MHAC diets. Data for these trials were analyzed using PROC MIXED (SAS v9.4).

Results and Discussion

In Exp. A, feed conversion ratio (FCR) was improved in pigs fed MHAC compared with ITM modified oxides from d 14 to 35 (1.424 vs 1.471; $P = 0.014$) and overall from d 0 to 35 (1.377 vs 1.411; $P = 0.020$). Mortality plus removals were 0.17% for ITM and 1.2% for MHAC fed pigs. In Exp. B, MHAC improved FCR compared with ITM sulfates from d 14 to 40 (1.452 vs 1.543; $P = 0.024$) and overall from d 0 to 40 (1.427 vs 1.476; $P = 0.030$). Fewer pigs were removed (1.10 vs 5.49%; $P = 0.016$), and mortality plus removals were numerically lower (2.74 vs 7.69%; $P = 0.096$) in MHAC fed pigs. Both experiments indicated better feed utilization with MHAC.

Conclusion

Trace mineral source influenced nursery pig performance. Improved feed efficiency and reduced removals highlight the value of MHAC bis-chelated trace minerals in supporting growth and health post-weaning.

Keywords: Copper, Manganese, Organic minerals, Swine, Zinc.

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COMPARATIVE ANALYSIS OF ENZYME - ZEARALENONE INTERACTIONS TO IDENTIFY DETOXIFICATION STRATEGIES

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Introduction and Objectives

Zearalenone (ZEN) is a common feed contaminant causing estrogenic effects and reproductive disorders in pigs (Lv et al., 2025). Enzymatic detoxification, which converts ZEN into non-toxic metabolites, is a promising mitigation strategy (Fruhauf et al., 2019), but substrate specificity limits its effectiveness. This study compares established ZEN hydrolases with structurally distinct α/β-hydrolases to identify features critical for ZEN degradation.

Materials and Methods

Several α/β-hydrolases (EC 3.1.1.B12), like CrZHD (*Clonostachys rosea*) and ReZHD (*Rhodococcus erythropolis*), efficiently hydrolyze ZEN. We studied two potential ZEN-degrading enzymes with distinct structures: *Streptomyces exfoliatus* lipase (SeLIP) and *Thermobifida cellulosilytica* cutinase (TcCUT). All were recombinantly expressed and assessed for thermal stability. General esterase activity was measured using *p*-nitrophenyl acetate (*p*NPA) at pH 7.0, 25°C, and hydrolysed zearalenone (HZEN) product formation was evaluated via LC-MS/MS at pH 8.0, 37°C. Additionally, *in silio* molecular docking was performed to investigate the mechanism of ZEN hydrolysis, highlighting the critical role of substrate specificity in enzymatic detoxification.

Results and Discussion

CrZHD and ReZHD enzymes resulted in complete ZEN conversion, whereas SeLIP and TcCUT were not able to degrade ZEN. The catalytic efficiency (k_{cat}/K_m) of CrZHD was 6.3×10^4 $M^{-1}s^{-1}$, whereas that of RezHD was 1.4×10^5 $M^{-1}s^{-1}$. LC–MS/MS analysis further revealed that the enzymatic reaction led to the formation of HZEN, a non-estrogenic product. In contrast, when using *p*NPA as the substrate, the four enzymes exhibited highly variable catalytic efficiencies, ranging from 4 to 214 M^{-1} s^{-1}. The structural basis of these differences was further investigated by molecular docking, which demonstrated that the lack of a cap-domain structural element in SeLIP and TcCUT prevents proper binding of ZEN and its correct positioning within the active site.

Conclusion

This study demonstrates that efficient ZEN degradation requires highly specific structural features that are not shared by general lipases, cutinases, or esterases. Our results confirm that established ZHD enzymes outperform structurally different α/β-hydrolases. Structure-function analysis is therefore essential for rational screening and engineering of future ZEN-detoxifying biocatalysts for feed safety applications.

Keywords: Mycotoxin detoxification, Enzyme-based feed additives, Enzymatic biotransformation, Zearalenone (ZEN), Zearalenone hydrolase.

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EFFECTS OF FAT-PROTECTED CALCIUM BUTYRATE ON GROWTH PERFORMANCE AND SERUM BIOCHEMICAL MARKERS IN STARTER PIGLET

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Introduction and Objectives

The systemic metabolic effects of calcium butyrate-based feed additives remain poorly characterised during the starter phase despite frequent use (Piva et al., 2002; Bedford & Gong, 2018). This study evaluated the effects of supplementing starter pigs with a fat-protected calcium butyrate source (CaB) on blood biochemical and enzymatic indicators of nutrient metabolism and growth performance.

Materials and Methods

Clinically healthy hybrid piglets (Large White × Landrace; n = 30/treatment; individually housed) were allocated at 50 days of age to: 1) Control (basal diet); 2) CaB group (basal diet + globa.max B700 (Global Nutrition International, France) at 1.5 kg/t) for 33 days. Live weight gain and feed intake were recorded. The basal diet was formulated to meet or exceed NRC (2012) nutrient requirements for starter pigs, with balanced Ca:P ratio and adequate crude protein and metabolizable energy. On day 33, blood samples were collected for serum biochemistry, enzyme activity, and vitamins A and E determination. Data were evaluated for normality and homogeneity of variance; where necessary, log transformation was applied prior to analysis. Data were analysed using Student's T-test and P-values for biochemical and enzyme variables adjusted using the Benjamini–Hochberg false discovery rate procedure. Significance was declared at $P < 0.05$.

Results and Discussion

Vitamins A and E were unaffected ($P > 0.05$). CaB increased serum urea (+16.2%) and reduced inorganic phosphorus (-10.2%) without altering total calcium ($P < 0.05$). Alkaline phosphatase increased (+17.2%) and creatine kinase decreased (-21.2%) ($P < 0.05$), suggesting altered mineral metabolism and reduced muscle enzyme leakage. Glucose, cholesterol, non-esterified fatty acids, AST, and ALT were unchanged. CaB increased average daily gain by 4.9% (0.623 vs. 0.594 kg/day; $P < 0.05$), while FCR was unaffected.

Conclusion

Calcium butyrate increased growth rate without affecting feed efficiency and was associated with changes in circulating nitrogen and calcium–phosphorus biomarkers and reduced creatine kinase activity. These findings indicate systemic metabolic responses during the starter phase; further studies including mineral retention and digestibility assessments are needed to clarify mechanisms.

Keywords: Blood biochemistry, Calcium butyrate, Growth performance, Metabolism, Starter piglets.

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EFFECT OF NEONATAL SUPPLEMENTATION OF HYPERTONIC SOLUTION ON PIGLETS PERFORMANCE FROM BIRTH TO 45 DAYS POST-WEANING

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Introduction and Objectives

Lactation is a critical phase when piglets are highly vulnerable, requiring adequate nutrients to sustain early growth, especially in hyperprolific sows (Chisoro et al., 2023). The aim of this study was to determine the effects of hypertonic solution (GreenTONIC) supplementation on piglet performance and their metabolic, immune, inflammatory, and survival response in piglets until 45 days of age.

Material and Methods

Thirty sows (Danish genetic) were randomly assigned to a control group (standard management, n = 15) or an experimental group (GreenTONIC, 40 g/L; administered at 0.5 L/litter/day from days 2 to 8, and two-days pre-weaning, and 1.5 L/10 piglets/day at weaning for two subsequent days). Performance (birth weight, BW21, BW45, ADG), health (diarrhea incidence, pre- and post-weaning mortality), microbiological (*E. coli* count), and immunological (fecal calprotectin) were measured at 45 days of age. Data were analyzed with PROC MIXED for repeated measures of SAS System, and differences were declared at $P < 0.05$ by pdiff option.

Results and Discussions

Piglets supplemented with GreenTONIC had significantly higher body weights at weaning (+475 g; $P = 0.001$) and at 45 days (+412 g; $P = 0.023$), as well as higher ADG from 1 - 21 days (+25 g/piglet/day; $P < 0.0001$) and from 1 - 45 days (+10 g/day; $P = 0.008$). Supplementation reduced the incidence of pre-weaning diarrhea (-15.3%) and pre-weaning mortality (-4.85%). A decrease in *E. coli* fecal counts at day 1 and 45 was observed, reflecting improved intestinal immune status. The increased calprotectin concentrations were not associated with signs of inflammatory damage. In terms of productivity, supplemented piglets gained an average of +446 g additionally up to 45 days of age. The economic analysis showed a ROI of more than 3:1, due to increased survival and improved production performance.

Conclusions

Hypertonic solution (GreenTONIC) increased piglet survival, decreasing the occurrence of diarrhea and improving intestinal health in lactation and allowing piglets to reach the end of the transition period expressing their growth performance in a more remarkable way.

Keywords: Newborn piglets, Hypertonic solutions, Oral supplementation, Growth performance, Gut health.

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DIETARY BUTYRATE GLYCERIDES PREVENTED GROWTH RETARDATION AND ALTERED INTESTINAL MICROBIOTA IN LIPOPOLYSACCHARID-CHALLENGED WEANED PIGS

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Introduction and Objectives

Early weaning of piglets is often associated with reduced feed intake and increased intestinal dysfunction. Butyrate glycerides (BG) have been documented to enhance piglet performance and gut development. The objectives of this study were to evaluate 1) growth responses of weaned pigs to BG supplementation with or without antibiotics (AB), and 2) potential mechanisms by which BG modulates intestinal responses during a lipopolysaccharide (LPS) challenge.

Materials and Methods

A total of 240 piglets (Duroc × Large White × Landrace) were weaned at 21 days of age and allocated to one of four dietary treatments: a basal control diet, basal diet with AB (+AB), basal diet with BG (+BG), or basal diet with both AB and BG (+AB+BG). Growth performance was recorded. At 49 days of age, 12 healthy male piglets from the control and +BG treatments were intraperitoneally injected with Escherichia coli LPS (25 μg/kg BW) or sterile saline (n = 6 per group) and euthanized 4 h post-injection. Blood samples, ileal mucosa, colonic tissue, and cecal contents were collected for analysis of inflammatory cytokines, intestinal morphology, goblet cell counts, short-chain fatty acids and bacterial populations.

Results and Discussion

Piglets fed diets with BG had higher feed intake and a lower percentage of negative growth animals during the first week after weaning compared with control. An interaction between BG and AB was observed for feed intake in the first two weeks, which may be associated with the changes of intestinal microbiota. The LPS challenge increased systemic inflammatory markers and disrupted hindgut fermentation, as reflected by reductions in acetate, while the BG supplementation attenuated these inflammatory responses and tended to increase ileal villus height. The supplementation of BG also influenced microbial indices: LPS increased E. coli abundance, while BG reduced the magnitude of this response and increased total bacterial counts, suggesting improved fermentation capacity.

Conclusion

Supplementation of BG improved early post-weaning feed intake in piglets and reduced the incidence of negative growth. When piglets are subjected to a LPS challenge, BG contribute to improved host resilience by modulating inflammatory cytokines, intestinal morphology and mucosal protection.

Keywords: Butyrate glycerides, Piglets, Gut health, Intestinal morphology, Gut microbiota.

EFFECTS OF LAURIC AND CAPRIC ACIDS ON GUT MICROBIOTA, MICROBIAL FERMENTATION, AND NUTRIENT DIGESTIBILITY IN PIGS FROM THE MEKONG DELTA UNDER *IN VITRO* CONDITIONS

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Materials and Methods

In vitro fermentation used large intestinal inocula from pigs (Williams et al., 2005). Six treatments included control, amoxicillin (2.0 µg/mL), and capric (CA) and lauric acids (LA) at 0.5% and 1.5% (n = 3). Samples were incubated anaerobically at 39°C for 12 h. NH_3, pH, volatile fatty acids (VFA), microbiota (Escherichia coli, Lactobacillus, Bifidobacterium), and dry matter digestibility (DMD) were analyzed.

Results and Discussion

NH_3 concentration differed ($P < 0.01$), with the highest values at 0.5% CA (11.67 ± 0.88 ppm) and 0.5% LA (13.67 ± 0.88 ppm) compared to the control (9.00 ± 0.58 ppm), whereas amoxicillin (4.17 ± 0.44 ppm), 1.5% CA (5.33 ± 0.88 ppm), and 1.5% LA (4.67 ± 0.67 ppm) significantly reduced NH_3. VFA differed ($P < 0.001$), with the highest value at 0.5% CA (0.10 ± 0.00) and the lowest at 1.5% CA (0.03 ± 0.00), indicating altered fermentation patterns. DMD increased to 1.5% (1.5% LA: 35.43 ± 2.29%; 1.5% CA: 34.33 ± 0.88%) compared to the control (31.17 ± 1.05%), whereas 0.5% treatments showed no improvement ($P < 0.01$). Microbial populations differed ($P < 0.001$). *Lactobacillus* and *Bifidobacterium* increased at 1.5% CA and LA, while 0.5% treatments showed minimal or inconsistent effects. *Escherichia coli* was reduced at 1.5% CA (73.33 ± 0.88) and LA (53.33 ± 3.18), as well as amoxicillin (25.33 ± 5.36), compared to the control (121.67 ± 4.80), while 0.5% had no significant effect. These results indicate that low LA and CA levels exert non-selective antimicrobial effects, whereas higher levels selectively inhibit ammonia-producing bacteria such as Escherichia coli, thereby reducing NH_3 and promoting beneficial microbial populations (Jackman et al., 2020).

Conclusions

0.5% CA and LA increased NH_3 without improving digestibility or microbiota, whereas 1.5% reduced NH_3, enhanced DMD, increased beneficial bacteria, and suppressed Escherichia coli, demonstrating a dose-dependent effect of CA and LA in modulating fermentation and microbial balance.

Keywords: Capric acid; Gut microbiota; In vitro fermentation; Lauric acid; Nutrient digestibility.

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POSTERS

TOPIC 10: ONEHEALTH, AMR AND PIG WELFARE (OAW)

PAIN CONTROL IN PIGLET TAIL DOCKING: A BEHAVIORAL AND THERMOGRAPHIC APPROACH USING ANESTHESIA AND ANALGESIA

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Introduction and Objectives

Tail biting is a multifactorial behavioral disorder that compromises animal welfare and causes significant economic losses in pig production. This study aimed to evaluate the effectiveness of anesthetic and analgesic protocols in alleviating pain in piglets undergoing tail docking.

Materials and Methods

The experiment was conducted on a commercial pig farm in Brazil, involving 25 litters. From each litter, three piglets were selected, totaling 75 animals. Each piglet received a different treatment: T1-tail docking without anesthesia or analgesia; T2-tail docking with anesthesia; and T3-tail docking with both anesthesia and analgesia. The anesthetic protocol consisted of lidocaine and bupivacaine, while Meloxicam 0.2% was used as the analgesic. Tail docking was performed within the first three days of life, following current legislation, by removing the distal third of the tail. Pain assessment was based on behavioral observation using the UPAPS scale and tail temperature measurement with a thermal imaging camera (FLIR TG165). Evaluations occurred at four time points: 24 hours before docking (1), 1 minute after (2), 1 hour and 30 minutes after (3), and 24 hours post-procedure (4). At each time point, piglets were filmed for 4 minutes, and tail temperature was recorded. A blinded observer analyzed the videos, totaling 300 minutes of observation. Pain scores were assigned based on observed behaviors.

Results and Discussion

No significant differences were found between treatments for tail temperature ($P = 0.09309$) or pain score ($P = 0.3293$). However, significant differences were observed across time points for both parameters: temperature ($P = 0.0144$) and pain score ($P < 0.0001$), particularly between moments 2, 3, and 4. Tail temperature increased progressively, consistent with the inflammatory process, while pain scores decreased over time, as expected after caudectomy. Although piglets experienced pain and inflammation, the effectiveness of the anesthetic and analgesic protocol could not be clearly determined.

Conclusion

These findings align with previous studies reporting limitations in behavioral indicators for pain assessment. Further research with larger sample sizes and additional pain indicators is recommended to refine analgesic protocols and improve animal welfare.

Keywords: Analgesic protocols, Pain assessment, Piglets, Tail Docking.

Acknowledgements: The authors thank the Pamplona ALimentos S/A, Brazil for the support with providing testing facilities.

SILVER NANOPARTICLES SUCCESSFULLY CONTROLED ANTIBIOTIC-RESISTANCE LEPTOSPIROSIS IN A SOUTH AFRICAN SOW HERD

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Introduction and Objectives

Antimicrobial resistance (AMR) in swine production is primarily driven by antibiotic overuse/misuse, alongside inadequate biosecurity measures (Muwonge et al., 2025). To understand the severity of AMR, WOAH warns that the food security of 2 billion people will be threatened, and cause US$ 100 trillion in economic loss by 2050 due to AMR across the animal industry (World Organisation for Animal Health, 2025). This field case evaluated oral silver nanoparticles (AgNPs) as a non-antibiotic alternative for leptospirosis that was unresponsive to two commonly used antibiotics in a commercial South African sow herd.

Materials and Methods

An 800-sow farrow-to-finish farm in KwaZulu-Natal, South Africa, suffered persistent abortions due to confirmed leptospirosis infection. Standard biosecurity measures plus two cycles of in-feed tetracyclines (4 kg/tonne) and amoxicillin (2 kg/tonne), 2 weeks on/2 weeks off, failed. The sow herd then received silver nanoparticles (AgNPs) at 400 g/tonne of feed for 2 weeks on/2 weeks off, repeated once after one month.

Results and Discussion

In the leptospirosis infection, two commonly used antibiotics, namely tetracyclines and amoxicillin, along with standard biosecurity measures. failed to reduce the abortion rate and effectively treat the sow population. However, after treatment with AgNPs (400g/tonne, 14 days, repeated once), abortions dropped from between 4 - 8% to between 0 - 0.75% within 7 days of starting AgNP treatment and returned to baseline levels that were sustained for at least six months post-treatment. AgNPs have demonstrated potent bactericidal activity against Leptospira spp. At low concentrations (Hodkovicova et al., 2025), consistent with the rapid clinical resolution observed in this herd. Readily available commercial AgNP feed-additive formulations support the feasibility of rapid, practical deployment of this non-antibiotic strategy against antibiotic-resistant bacteria in commercial pig production.

Conclusion

Oral silver nanoparticle supplementation rapidly resolved persistent abortions caused by antibiotic-resistant Leptospira infection in an 800-sow herd, offering a promising non-antibiotic strategy for managing resistant bacterial diseases in swine.

Keywords: Antimicrobial resistance, Field case, Leptospirosis, Silver nanoparticles.

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GENOMIC CHARACTERIZATION OF EXTENDED-SPECTRUM BETA-LACTAMASE (ESBL)-PRODUCING MULTIDRUG-RESISTANT *ESCHERICHIA COLI* FROM HUNGARIAN SWINE HERDS

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Introduction and Objectives

Antimicrobial resistance (AMR) remains one of the most pressing global threats to public and animal health. In Hungary, the swine sector is the largest consumer of antibiotics. Escherichia coli is a key indicator organism in AMR monitoring due to its dual role as a commensal and opportunistic pathogen, and its capacity to acquire and horizontally transfer a wide array of resistance genes. This study aimed to investigate the resistance profiles of multidrug-resistant (MDR) *E. coli* strains isolated from large-scale swine farms, with a particular focus on extended-spectrum β-lactamase (ESBL) production.

Materials and Methods

A total of 203 *E. coli* isolates were collected from four pig farms and tested for antimicrobial susceptibility using minimum inhibitory concentration (MIC) methods. ESBL and β-lactamase production were confirmed in 127 (62.6%) and 110 (54.2%) strains, respectively. Whole genome sequencing (WGS) was performed on 116 isolates to identify genotypic resistance determinants.

Results and Discussion

WGS identified 82 distinct resistance genes, with a total of 5,427 occurrences across the dataset. ESBL genes included CTX-M-1, CTX-M-32, CTX-M-55, CTX-M-8 and TEM-1, TEM-150, found in 43.1% (50/116) of strains. In phenotypically ESBL-positive but genotypically negative strains, chromosomal ampC and ampH were present in 99.1%, indicating β-lactamase overexpression. Additional mechanisms included aminoglycoside-modifying enzymes (20.7%), tetracycline resistance genes (tetA-D, 25.9%), plasmid-mediated quinolone resistance (qnrB5, 1.7%), and universal efflux pump genes (100%). Chromosomal colistin resistance determinants (pmrF, eptA, ugd) were found in all isolates; plasmid-mediated mcr-1 was detected in 2.6%. Macrolide and phenicol resistance were conferred by mphA, mphB, floR, and catI.

Conclusion

Our findings reveal that MDR E. coli populations in Hungarian swine farms harbor a complex resistome comprising both mobile genetic elements and chromosomally encoded adaptive mechanisms. This interplay reinforces bacterial survival under antimicrobial pressure and poses not only animal health challenges but also zoonotic risks. The results highlight the urgent need for continuous surveillance and prudent antimicrobial use in livestock systems.

Keywords: Antimicrobial resistance, Escherichia coli, Extended-spectrum beta-lactamase, Swine, Whole genome sequencing.

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ANTIMICROBIAL SUSCEPTIBILITY OF STREPTOCOCCUS STRAINSISOLATED FROM LARGE-SCALE SWINE HERDS IN HUNGARY

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Introduction and Objectives

The swine industry is one of the largest antibiotic-consuming sectors globally, playing a central role in the emergence and spread of antimicrobial resistance (AMR). Among the bacterial pathogens, *Streptococcus* species are of particular concern due to their zoonotic potential and their role as opportunistic agents in pig production. Changes in their antibiotic susceptibility present significant animal health challenges, particularly during piglet rearing and fattening. This study aimed to assess the antimicrobial susceptibility profile of Streptococcus strains isolated from large-scale Hungarian pig farms using minimum inhibitory concentration (MIC)-based methods.

Materials and Methods

A total of 252 Streptococcus isolates were collected from 17 high-capacity swine farms across Hungary. Antimicrobial susceptibility testing was performed against 15 antibiotics using MIC determination following standardized protocols.

Results and Discussion

High levels of susceptibility were found for florfenicol (100%, 252/252), cefquinome (98%, 247/252), ceftiofur (95%, 239/252), imipenem (91%, 230/252), and enrofloxacin (88%, 223/252). In contrast, only 23% of strains were susceptible to oxytetracycline (58/252) and doxycycline (58/252), and even lower levels were observed for tilmicosin (15%, 37/252), tulathromycin (32%, 81/252), and lincomycin (10%, 26/252). This reflects a concerning resistance pattern, particularly against macrolides and lincosamides—commonly used in the treatment of respiratory and systemic infections. For other compounds, susceptibility to potentiated sulfonamides was 63% (160/252), tiamulin 17% (43/252), penicillin and amoxicillin-clavulanic acid both at 73% (184/252), while amoxicillin showed 81% susceptibility (203/252). These findings raise questions about the selective pressures shaping resistance in *Streptococcus* populations. Low susceptibility to tetracyclines and macrolides may reflect overuse, while retained efficacy of florfenicol and certain β-lactams suggests potential for rational use, though emerging resistance remains a concern.

Conclusion

Our findings highlight the widespread resistance to several commonly used antibiotics, particularly tetracyclines and macrolides, among Streptococcus isolates from Hungarian pig herds. The observed resistance profiles emphasize the urgent need for targeted, evidence-based antimicrobial use, and underscore the importance of continuous microbiological surveillance to combat AMR in swine production systems.

Keywords: Antimicrobial resistance, Minimum inhibitory concentration, Streptococcus, Swine.

Acknowledgements: Project no. RRF-2.3.1-21-2022-00001 was implemented with the support provided by the Recovery and Resilience Facility (RRF), financed under the National Recovery Fund budget estimate, RRF-2.3.1-21 funding scheme.

RISK FACTORS FOR ANTIBIOTIC TREATMENT OF PREWEANING DIARRHEA

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Introduction and Objectives

Neonatal diarrhea in pigs is common and can lead to mortality and may require antibiotics. In this study, we used survival analysis to investigate risk factors related to two separate outcomes: diarrhea, and diarrhea treatment in the preweaning period.

Materials and Methods

A total of 2,699 pigs from a single Danish herd, were followed from birth and until weaning at 4 weeks of age. Weekly recordings of fecal consistency for diarrhea assessment (Eriksen et al, 2024) and daily recordings of diarrhea treatments were obtained. Only pigs with clinical signs (unthriftiness/dehydration/depression), in addition to diarrhea, received treatment by injection of oxytetracyline. Batch treatments were not allowed. We evaluated the association between diarrhea/diarrhea treatment and the following explanatory-variables: sow parity (1 - 6) or parity group (gilt or multiparous), litter size, birthweight, intrauterine growth restriction (IUGR), sex, imputed CHCF1 and FUT1 genotype. Variables with a significant association on univariable analysis ($P > 0.05$) were included in a multivariable model, with batch and sow as random effects.

Results and Discussion

Forty-two percent of the pigs had at least one observation of diarrhea in the preweaning period, and most cases (95.1%) occurred within the first 4 days of life. Eleven percent of the pigs required diarrhea treatment in the preweaning period, and most treatments (80.1%) were performed within the first 4 days of life. Parity level was highly associated with diarrhea risk. For each increase in parity level the risk of diarrhea was reduced by 14% (hazard ratio (HR) = 0.86, 95% CI [0.79; 0.94], $P = 0.001$). Pigs born from multiparous sows had 68% lower risk of diarrhea treatment compared to those born from gilts (HR = 0.32, 95% CI [0.18; 0.55], $P > 0.0001$). Further, each 100 g increase in birthweight reduced risk of diarrhea treatment with 24% (HR = 0.76, 95% CI [0.72; 0.80], $P > 0.0001$). In this study, litter size, IUGR, sex, and the CHCF1 and FUT1 genotypes showed no significant association with the investigated outcomes.

Conclusion

In conclusion, pigs from gilt litters were at higher risk of getting diarrhea treatment and increasing parity levels were associated with reduced risk of diarrhea. Low birthweight pigs were at increased risk of diarrhea treatment.

Keywords: Antimicrobial resistance, Neonatal diarrhea.
Acknowledgements: Rasmus Jelle Syhler provided valuable technical assistance in the cohort study. The study was funded by Novo Nordic Foundation, grant number: NNFSA210073688.

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ROLE OF CHCF1 GENOTYPES IN RESISTANCE TO ETEC F4-MEDIATED POST-WEANING DIARRHEA

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Introduction and Objectives

Antibiotic treatment of post-weaning diarrhea (PWD) is a major contributor to antibiotic use in Danish pig production. We previously showed a complete association between the genetic marker, CHCF1, and susceptibility to enterotoxigenic E. coli (ETEC) F4 in experimental trials (Rydal et al., 2023). In this study, the objective was to investigate the relationship between CHCF1 genotypes and PWD outbreaks in herds with a history of ETEC F4-mediated diarrhea. Additionally, to estimate the potential reduction in PWD prevalence if the pig population consisted exclusively of CHCF1 resistant pigs.

Materials and Methods

Three Danish herds (n total = 890 pigs examined) were included in the study. Weaning ages ranged from 3–4 weeks. The PWD prevalence was determined in the first week after weaning, based on a random sample of ~ 300 pigs per herd. We CHCF1 genotyped a subsample of 12 pigs with diarrhea and 12 pigs without diarrhea at each herd. We defined ETEC F4-mediated diarrhea as clinical signs of the disease and PCR/culture-verified presence of ETEC F4 and ≥ 50% hemolytic E. coli-like colonies. Based on the subsamples of pigs, we estimated the attribution of CHCF1 homozygous resistant (RR) and heterozygous susceptible (RS) genotypes to the overall PWD prevalence at each herd. Finally, we estimated the potential reduction in overall PWD prevalence provided that the population of pigs would comprise only CHCF1 RR pigs.

Results and Discussion

The overall mean PWD prevalence across herds was 16% (SD ± 1.3%). ETEC F4-mediated diarrhea occurred exclusively in CHCF1 RS pigs, resulting in a higher PWD prevalence among RS pigs compared to RR pigs. We estimated that given the population consisted exclusively of CHCF1 RR pigs, the mean PWD prevalence would be reduced by 27.5 % (SD ± 12.5%).

Conclusion

The study suggests that a reduction in PWD can be achieved in ETEC F4 affected herds, if pigs with CHCF1 RR genotype are selected as opposed to the CHCF RS genotype. Our calculation assumes that the PWD prevalence in CHCF1 RR pigs was unaffected by the presence of CHCF1 RS pigs in the population.

Keywords: CHCF1, ETEC F4, Genetic markers, Post-weaning diarrhea.

Acknowledgements: The authors would like to thank Rasmus Jelle Syhler for technical assistance on sampling days. The study was funded by Novo Nordic Foundation, grant number: NNFSA210073688.

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IN-VITRO INTERACTION OF A NOVEL FEED ADDITIVE - UNEVEN MEDIUM CHAIN FATTY ACIDS AND MACRO MOLECULES AGAINST COMMON PATHOGEN GRAM-POSITIVE BACTERIA IN SWINE PRODUCTION

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Introduction and Objectives

Gastrointestinal diseases pose a serious threat to commercial swine production. Gram-positive bacteria such as *Streptococcus agalactiae* (septicaemia, pneumonia, different systematic diseases), *Streptococcus suis* (sudden deaths in young animals, severe illnesses), *Staphylococcus aureus* (high resistant MRSA), *Clostridium perfringens* (severe diarrhoea, necrotic enteritis) pose a danger for the health and productivity in modern swine production. In the past this hazard was controlled by the prophylactic use of antibiotics. However, animal production is viewed critically for its usage of antibiotics, both from consumers and regulatory authorities. As a result, various feed additives have been studied as alternatives. Currently, there is growing interest in natural bioactive compounds, which are characterized by high food safety as well as consumer acceptance. Medium chain fatty acids (MCFA) naturally optimize livestock production, especially due to improved animal performance and animal health status. They efficiently support gut health in animals, by a strong antimicrobial effect against pathogen bacteria and improving the gut morphology. Data on uneven MCFA are still scarce. This formed the impetus of the trial.

Material and Methods

In this in-vitro experiment, a highly concentrated product (pwrPlanz® EMC, ADDCON), which consists of a mixture of uneven MCFA and macro molecules, was subjected to minimum inhibitory concentration (MIC) tests against the most common pathogenic Gram-positive bacteria in swine production. The MIC was tested in the range from 0.01 to 1.00%, expressed as g/L. The following bacteria strains were used: *Streptococcus agalactiae* ATCC 279556, *Streptococcus suis*, *Clostridium perfringens* ATCC 13124 and a multi resistant *Staphylococcus aureus* (MRSA) strain.

Results and Discussion

In vitro antimicrobial MIC-tests showed a strong effect of EMC against the Gram-positive bacteria *Streptococcus agalactiae* 0.50 g/L, *Streptococcus suis* 1.25 g/L, *Clostridium perfringens* 0.13 g/L and MRSA *Staphylococcus aureus* 2.5 g/L. Based on the *in vitro* MIC results, EMC can be considered an important tool in any antibiotic reduction strategies, thus supporting sustainable animal production**.**

Conclusion

This report presents valuable information on the impact of uneven MCFA against important swine pathogens. Therefore, the product can be part of the "One Health" approach of the World Health Organization for reducing the risk of Antimicrobial Resistances.

Keywords: MIC-test, Uneven MCFA, Gram-positive bacteria.

EFFECTS OF IMPLEMENTING ANIMAL WELFARE IN PIG HUSBANDRY ON MEAT QUALITY ACROSS FARM SCALES

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Introduction and Objectives

The rapid expansion of large-scale pig production systems in Vietnam has improved housing, nutrition, and biosecurity but has also raised concerns regarding animal welfare under intensive management conditions (Qui et al., 2021; Qui et al., 2025). Long-term stress during the production period is associated with reduced muscle tissue deposition and decreased glycogen concentration in muscle, which negatively affects meat quality (Čobanović et al., 2020; Gvozdanović et al., 2023). This study aimed to evaluate welfare status in finishing pigs and assess associated meat quality traits across farms of different production scales in Vietnam.

Materials and Methods

A cross-sectional survey using the Welfare Quality® framework with 4 principles including good feeding, good housing, good health and appropriate behavior was conducted on 45 pig farms classified as small-, medium-, and large-scale. Additionally, 18 PDLY [(Pietrain x Duroc) x (Landrace x Yorkshire)] pigs were slaughtered, and 36 Longissimus dorsi samples (10th - 15th ribs) were collected for meat quality analysis.

Results and Discussion

Large-scale farms achieved the highest scores for good feeding principle, whereas good health consistently recorded the lowest scores across all production scales ($P < 0.05$). Good housing and appropriate behavior were generally rated at acceptable to enhanced levels. Meat quality analysis showed no significant differences in early post-slaughter pH among farm scales. However, pork from large-scale farms tended to exhibit lighter color, higher drip loss, and greater protein content ($P < 0.01$). Additionally, pigs from large-scale systems showed higher proportions of unsaturated fatty acids and an increased unsaturated fatty acids:saturated fatty acids ratio, indicating a more favorable lipid profile.

Conclusion

Large-scale pig farms in Vietnam showed better feeding- and housing-related welfare and favorable meat quality trends, especially lipid composition. However, limitations in health-related welfare indicators indicate the need for improved management to ensure sustainable production and high-quality pork.

Keywords: Animal welfare, Large-scale farm, Longissimus dorsi, Fatty acid profile, Finishing pigs.

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CROSS-SECTIONAL VIRULENCE GENE EVALUATION AND PROBIOTIC SUSCEPTIBILITY OF SWINE ENTERIC PATHOGENS IN TAIWAN

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Introduction and Objectives

Current diagnostic and treatment approaches often focus on singular pathogens, though coinfections are prevalent. Antimicrobial resistance of pathogens within a coinfection compounds health risks and complicates treatment. Therefore, the study objectives were to (1) quantify enteric pathogen markers across two swine farms of differing health histories in Taiwan, and (2) assess susceptibility of antimicrobial resistant swine pathogens to a multi-strain, health-focused *Bacillus* probiotic.

Materials and Methods

Forty-eight rectal swabs were collected from sows, piglets, and nursery pigs from one historically healthy and one health-challenged farm in Taiwan. Swabs were applied to FTA cards, genomic DNA was extracted, and qPCR was utilized to quantify a panel of toxin and adhesin genes from *E. coli*, *Salmonella*, and *Clostridium* spp. From a swine veterinary collection in Taiwan, 35 *E. coli* and 10 *Salmonella* isolates were tested for antibiotic resistance, hemolysis, and susceptibility to probiotic cell-free fermentate.

Results and Discussion

Virulence genes from multiple pathogens, *Salmonella*, toxigenic *E. coli*, and *C. perfringens*, were detected on both high and low health swine farms in Taiwan, reflecting a similar profile to US swine. On the low health farm, *E. coli* attaching and effacing genes (*eaeA*, *Paa*) were elevated in nursery pigs compared to piglets ($P < 0.05$, Kruskal-Wallis, Dunn's test), and *Paa* showed a similar trend on the high health farm ($P = 0.071$). To complement the gene analysis, swine isolates were tested in a broth microdilution inhibition assay. Thirty-one of 35 *E. coli* and all 10 *Salmonella* isolates were resistant to ≥10 common antibiotics. The *Bacillus* probiotic exhibited an average growth inhibition of 49% against the *E. coli* and 55% against the *Salmonella* isolates, demonstrating potential to inhibit highly resistant pathogens.

Conclusion

Antimicrobial resistant coinfections require comprehensive strategies to combat them. In Taiwan, gene analysis revealed *Salmonella*, *E. coli*, and clostridia coinfections were present on two farms regardless of health history, and veterinary isolate testing underscored the continued challenge of antimicrobial resistance. Importantly, the health-focused probiotic showed potential against highly resistant pathogens, positioning it as a versatile tool to complement holistic swine health programs across the globe.

Keywords: Antimicrobial resistance, Coinfection, *E. coli*, Probiotic, *Salmonella*.

EFFECTS OF PLANT-DERIVED ISOQUINOLINE ALKALOIDS ON STRESS RESPONSE AND PRODUCTIVITY OF SOWS DURING FARROWING AND LACTATION

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Introduction and Objectives

Several challenges in sow production systems negatively affect sow health and litter performance. The progressive restriction and banning of antibiotic use in many countries have increased the need for effective alternative feed additives to maintain productivity. Plant-derived isoquinoline alkaloids (IQ) have been suggested as potential natural additives with stress-modulating and performance-enhancing properties. Therefore, this study aimed to evaluate the effects of combining plant-derived isoquinoline alkaloids (IQ) with chlortetracycline (CTC) on sow productivity and litter performance during farrowing and lactation.

Materials and Methods

A total of 90 sows (2nd - 3rd parity) were assigned to three dietary treatments (n = 30/treatment): control (chlortetracycline; CTC), IQ Low (CTC + IQ at 100 g/t feed), and IQ High (CTC + IQ at 200 g/t feed). Treatments were applied from two weeks pre-farrowing until weaning (21 d postpartum). Measurements included sow performance (body weight, average daily feed intake, body condition score, P2 backfat), serum cortisol and C-reactive protein, mastitis–metritis–agalactia (MMA) score, and litter performance at weaning.

Results and Discussion

Sows in the IQ groups had higher ADFI than the control (6.69 and 6.74 vs. 6.13 kg/d). Body weight and backfat losses during lactation were lower in the IQ groups, and BCS at weaning was higher compared with the control ($P < 0.05$). Sows in the combination of IQ groups exhibited significantly lower serum cortisol and C-reactive protein concentrations than those in the control group ($P < 0.05$), indicating reduced physiological stress and inflammatory status. The reduction of stress maybe influences the improvements of lower mastitis, metritis, and agalactia (MMA) scores ($P < 0.05$) and that leads to having a shorter wean-to-estrus interval in IQ-supplemented sows. In addition, litter performance was enhanced in the IQ groups, as reflected by increased litter weight gain and weaning weight, together with reduced pre-weaning piglet mortality compared with the control group.

Conclusion

Overall, IQ supplementation improved sow health and litter performance. These findings indicate that plant-derived IQ has the potential to support productivity and reproductive efficiency in the era of reduced or eliminated antibiotic use in livestock production.

Keywords: Plant-derived isoquinoline alkaloids, Stress, Inflammation, Sow's productivity.

Acknowledgements: The authors thank Khon Kaen University, Thailand for the support with providing testing facilities.

EVALUATING ANIMAL WELFARE IMPACTS OF NEEDLE-FREE INJECTION WHEN ADMINISTERING IRON DEXTRAN IN NURSING PIGLETS

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Introduction and Objectives

Providing supplemental iron to piglets is essential in commercial swine production with parenteral administration via needle-and-syringe (NS) being the common practice. Several recent studies have documented that the use of needle-free injection devices (NFIDs) in swine not only efficiently deliver injectable medications and biologics, but also optimize animal welfare (Chase et al., 2008; Temple et al., 2020). However, the use of NFID and its benefits on animal welfare during piglet processing is not fully explored. This study aimed to compare retreat behavior and vocalizations in piglet administered iron dextran via NFID or NS.

Materials and Methods

A total of 519 piglets (3.4 days old, 2.3 kg) were randomly assigned to one of two treatment groups: NFID group using the Pulse© 250 (Pulse NeedleFree Systems Inc.,USA); and NS group using a 20G × 1/2" needle and a 3 mL syringe to inject intramuscularly (IM), with the needle changed after each animal. Piglets in both groups were administered 1 mL of 200 mg iron dextran on the left side of the neck. The retreat behavior was assessed individually by a validated ethogram, and the vocalization of each pig was audio recorded. Piglets were eligible only if they remained still without vocalization for at least 3 seconds before the injection.

Results and Discussion

Preliminary results illustrated that the likelihood of showing stronger retreat behavior was higher in the NS group compared to those of the NFID group (OR: 1.47; 95% CI: 1.04–2.04; $P = 0.028$). In addition, the number of vocalizations (per 10 seconds) in NS group was higher than those of NFID group, n = 6.31 and n = 5.32, respectively ($P = 0.006$). Other factors associated with animal welfare indicators will be determined by generalized linear mixed models.

Conclusion

This study showed the use of NFID to administer iron dextran potentially optimize animal welfare during piglet processing.

Keywords: Animal welfare, Drug delivery, Iron dextran, Needle-free injection, Piglet processing.

Acknowledgements: This research is funded by Ontario Pork, Canadian Global Food Animal Residue Avoidance Databank (CgFARAD™) and the Ontario Agri-Food Innovation Alliance, a collaboration between the Government of Ontario and the University of Guelph. The authors also acknowledge the support of staff members in OSRC, and volunteer students.

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LACTOBACILLUS POSTBIOTICS POWER: BOOSTING WEANED PIGLET PERFORMANCE AND GUT HEALTH

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Introduction and Objectives

Postbiotics, defined as preparations of inanimate microorganisms and/or their components that confer a health benefit on the host, have emerged as promising feed additives to enhance gut health. This study aimed to evaluate the effects of dietary *Lactobacillus*-derived postbiotics (GSB) on growth performance and diarrhea incidence in weaned piglets under Escherichia coli (*E. coli*) challenge.

Materials and Methods

Three experiments were conducted. In Experiment 1, 112 weaned piglets (initial BW 6.92 ± 0.82 kg) were assigned to either a negative control (NC) diet or NC supplemented with GSB at 20 g/MT (GSB) for 42 days, with 8 replicates per treatment. In Experiment 2, 525 weaned piglets (initial BW 15.49 ± 1.34 kg) received either NC or NC plus GSB at 20 g/MT for 42 days, with 14 replicates. In Experiment 3, 64 weaned piglets (initial BW 6.55 ± 0.70 kg) were allocated to NC or GSB at 2 kg/MT for 28 days, with 16 replicates. All pigs were challenged with *E. coli* with 5-mL 1 x 10^9 CFU/mL on day 7 or 10. Growth performance and diarrhea scores were recorded throughout each trial. Data were analyzed using JMP (SAS Institute Inc.), with significance at $P < 0.05$.

Results and Discussion

During the challenge period (days 0 - 14) of Experiment 1, piglets receiving GSB showed lower FCR ($P = 0.03$) and lower duration, the scores and incidences of diarrhea ($P < 0.001$) compared to controls. In the challenge period of Experiment 2, GSB supplementation increased ADG ($P < 0.01$), improved FCR ($P < 0.05$), and reduced fecal scores ($P < 0.01$), indicating less severe diarrhea during the challenge period. In Experiment 3, GSB-fed piglets had significantly improved FCR ($P < 0.05$) in the challenge period. Across all studies, GSB supplementation increased ADG by an average of 19.4%, reduced FCR by 11.6%, and lowered fecal scores by 22.5%. The direction of effects was uniform across studies.

Conclusion

The results clearly demonstrate that GSB supplementation effectively enhances growth performance and mitigates post-weaning diarrhea in piglets challenged with *E. coli*.

Keywords: Diarrhea, Growth performance, *Lactobacillus* Postbiotics, Weaned piglets.

EFFECT OF A CALMING BOTANICAL SUPPLEMENTATION ON PIG'S BEHAVIOR AND TAIL BITING

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Introduction and Objectives
Tail biting, as well as tail docking as a prevention measure, represents a significant welfare and health problem in pig farming. Calming botanical extracts can help prevent tail biting outbreaks on farms. This study assessed the impact of a natural solution containing Melissa officinalis and magnesium supplementation on tail biting and behavior in pigs under commercial conditions.

Materials and Methods
After weaning at 28 days, pigs were allocated to either a supplemented (S, n = 103) or a control (C, n = 102) group in identical environments, under commercial conditions. All pig tails were graded once a week from week 7 to week 21. When fresh blood was observed, the supplement (Care Zen) was added to the drinking water (1 L/1000 L) for a 5-day period. In both rooms, one pen was video-recorded at three different periods for 3 consecutive days. The videos were analyzed using the scan sampling method to assess tail biting, resting, exploring, and feeding behaviors. Each scanned hour will be called an observation period (OP). Principal component analysis and hierarchical ascending classification were used to objectively analyze behavioral data and create OP clusters defined by the prevalence of pig behaviors within each. All assessments were carried out by a blinded evaluator.

Results and Discussion
In total, two supplementation periods took place. Tail lesion intensity decreased after the first supplementation in the S group, while it continued to rise in the C group. On camera recordings, tail and ear biting observations were significantly lower for S (Fisher, $P < 0.05$), where pigs also tended to rest more. From video observations, three OP groups were identified based on behavior: Low, Medium, and High activity hours. The C group contained more High activity OP with more aggressive behaviors (Dunn, $P < 0.05$), while the S group included more low-activity OP. Medium activity OP appeared equally in both groups and are mainly linked to feeding times or non-aggressive playful activities.

Conclusion
These results show that even a single supplementation with a standardized botanical product may contribute to reducing tail biting and its severity and induce a calmer atmosphere on farms.

Keywords: Behavior, Botanical supplementation, Melissa officinalis, Tail biting, Welfare.

Acknowledgements: We thank Alexis Nalovic (Epidalis, Vitré, France) for identifying the study farm and for providing technical support throughout the study, allowing the evaluator to remain blinded.

EVALUATION OF DEVI-JEX AS A BEHAVIOUR MODIFIER IN GROWING PIGS: IMPACT ON GROWTH PERFORMANCE, CORTISOL LEVELS, AND EAR LESIONS

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Introduction and Objectives

Pigs are exposed to multiple stressors throughout life. These stressors negatively affect growth performance by reducing feed intake and growth rates, while also compromising welfare through behaviours such as ear, tail, and flank biting. Such behaviours increase disease risk, as open lesions allow pathogen entry. This study aimed to evaluate a feed material, Devi-Jex (Devenish Nutrition Ltd, Belfast), as a behavioural modifier by assessing its effects on growth performance, cortisol concentrations, and ear lesion incidence.

Materials and Methods

312 weaned pigs were allocated to two groups at weaning based on body weight (6.15 ± 0.71 kg). After a two-week adaptation period, pigs were assigned to either a control group, fed a standard weaner diet, or a treatment group, fed the same diet supplemented with 0.3% Devi-Jex for 15 days. Performance parameters including weight and feed intake were recorded. Saliva samples were collected on day 22 to determine cortisol concentrations using an ELISA assay. Ear lesions were scored weekly on a 0 - 3 scale. Data were analysed using ANOVA with Tukey's post hoc test (JMP 18).

Results and Discussion

Pigs receiving Devi-Jex showed a 34 g/day increase in average daily gain compared with controls, resulting in a 1.14 kg greater exit weight. Feed efficiency improved, with similar feed intake between groups (FCR 1.43 vs. 1.48 for Devi-Jex and control, respectively). From week 4, the treatment group exhibited significantly fewer ear lesions, with an average score of 0.8 compared to 1.8 in the control group ($P < 0.001$). This differential was maintained to the end of the trial and is supported by findings from a previous study of reduced aggressive behaviours in pigs supplemented with Devi-Jex (Marchesi, 2021). Cortisol concentrations were 40% lower in pigs fed Devi-Jex (2.22 vs. 3.86 ng/mL; $P < 0.05$), indicating a reduced physiological stress response. The concurrent reductions in cortisol levels and ear lesions suggest lower stress and aggression, likely contributing to the improved growth performance observed.

Conclusion

Supplementation of growing pig diets with Devi-Jex reduced physiological stress and the severity of undesirable behaviours such as ear biting, resulting in improved welfare and growth performance.

Keywords: Behaviour modification, Cortisol, Growth, Stress, Swine.

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EFFICACY OF COCKTAIL HERBS IN INHIBITING PATHOGENIC E. COLI AND *CLOSTRIDIUM PERFRINGENS* TYPE A IN PIGLETS I: AN *IN VITRO* AGAR GEL DIFFUSION TEST

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Introduction and Objectives

Neonatal diarrhea in piglets causes economic losses in pig production, often associated with bacterial pathogens, i.e. *Escherichia coli* and *Clostridium perfringens* (Ngamwongsatit et al., 2016). With increasing concerns over antibiotic resistance (Nguyet et al., 2022), alternative antimicrobial agents like herbal extract are being investigated. This study aimed to evaluate the efficacy of a cocktail herb (Lostop) against *E. coli* and *C. perfringens* type A isolates from diarrheagenic piglets in Thailand by using agar gel diffusion technique.

Materials and Methods

Twenty bacterial isolates (10 *E. coli,* 10 *C. perfringens)* from diarrheagenic piglets were stored at -80°C in the Microbiology Laboratory, Veterinary Diagnostic Center, Faculty of Veterinary Science, Mahidol University. Initially, the agar plate surface is inoculated with 0.5 McFarland standard (10^8 cells/mL) of pathogens by spreading over the entire agar surface. Then, loaded 50 µl and 100 µl of Lostop in each 6mm-well, and placed sterile disc dipped with Lostop on agar plate. The plates were incubated at 37°C under aerobic conditions for Escherichia coli and anaerobic conditions for *Clostridium perfringen* type A (CLSI 2024). The negative control contained PBS and Halquinol disc was used for positive control. The measurement of ZOI diameter in millimeters was performed repeatedly at 16 h after incubation.

Results and Discussion

Lostop showed inhibition zone against all isolates of *E. coli* and *C. perfringen* type A. Halquinol showed inhibition zone against all isolates of *E. coli*, however, it showed inhibition zone against *C. perfringen* type A only 6 out of 10 isolates. Comparing diameter of inhibition zone between Lostop-Drop 100 mL and Halquinol, Lostop showed larger dimeter of inhibition zone than Halquinol against *E. coli* (18.4 vs 15.0 mm). For inhibition zone against *C. perfringen* type A, all dilutions of Lostop showed larger dimeter of inhibition zone than Halquinol (21.4 vs 10.2 mm). The larger ZOI observed, suggesting its higher efficacy for controlling bacterial-induced diarrhea in piglets.

Conclusion

Lostop, a cocktail herb, demonstrated significant inhibitory effects against *E. coli* and *C. perfringens* isolated from diarrheagenic piglets. Further in vivo studies are recommended to assess its therapeutic potential in pig farm.

Keywords: *Escherichia coli*, *Clostridium perfringens*, Herbal extract, Piglet.

Acknowledgements: The authors thank the Maxwell Animal Health and Innovet Corporation Co., Ltd for the supporting the research grant.

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EFFICACY OF COCKTAIL HERBS IN INHIBITING PATHOGENIC *E. COLI* AND *CLOSTRIDIUM PERFRINGENS* TYPE A IN PIGLETS II: ITS REMEDY FOR GUT HEALTH *IN VIVO*

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Introduction and Objectives

Neonatal diarrhea in piglets causes economic losses in pig production, often associated with bacterial pathogens, i.e. *Escherichia coli* and *Clostridium perfringens.* With increasing concerns over antibiotic resistance (Nguyet et al., 2022), alternative antimicrobial agents like herbal extract are being investigated. This study aimed to evaluate the efficacy of a cocktail herb (Lostop) against *E. coli* and *C. perfringens* type A isolates from diarrheagenic piglets in Thailand by testing in pig farm.

Materials and Methods

The experiment started on 4 days of age in which the piglets showed diarrhea. Altogether 300 piglets were divided into 4 groups: Group 1 (control): 75 piglets were orally administered with Enro pump 2 mL/piglet, sid for 3 days (positive control, farm protocol) when the piglet gets sick. Group 2 (Lostop 1mL): 75 piglets were orally administered with Lostop low dose (1 mL/piglet, sid, for 3 days) when the piglet gets sick. Group 3 (Lostop 2mL): 75 piglets were orally administered with Lostop medium dose (2 mL/piglet, sid, for 3 days) when the piglet gets sick. Group 4 (Lostop 3mL): 75 piglets were orally administered with Lostop high dose (3 mL/piglet, sid, for 3 days) when the piglet got sick. Growth performances and preweaning mortality were recorded.

Results and Discussion

Lostop 1 ml showed a superior result in terms of weaning weight at 21 days compared with control (5.53 vs 4.66 kg). Comparing Lostop at different doses, there were no statistically significant differences. However, during the experiment, it was found that the Lostop 3ml was a bit difficult to administer. The pre-weaning mortality rate was found only in control group at 2.7% (2/74). This suggested that Lostop, composite of herbal extract from *Holarrhena antidysenterica*, *Aegle marmelos*, *Plantago ovata*, *Berberis aristate* and *Tinospora cordifolia*, with their properties for astringent, antidiarrhea, anti-inflammation, antibacterial action provided a powerful remedy for gut health in piglets.

Conclusion

Lostop, a cocktail herb, not only demonstrated significant inhibitory effects against *E. coli* and *C. perfringens* isolated from diarrheagenic piglets but also revealed a positive result for the treatment of piglets with diarrhea.

Keywords: *Escherichia coli*, *Clostridium perfringens*, Herbal extract, Piglet.

Acknowledgements: The authors thank the Maxwell Animal Health and Innovet Corporation Co., Ltd for the supporting the research grant.

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LIVESTOCK-ASSOCIATED METHICILLIN-SUSCEPTIBLE *STAPHYLOCOCCUS AUREUS* ST398 AS A DOMINANT RESERVOIR OF ANTIMICROBIAL RESISTANCE IN KOREAN PIG FARMS

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Introduction and Objectives

Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) sequence type 398 (ST398) has long been considered an important reservoir of antimicrobial resistance with significant public health implications worldwide. However, livestock-associated methicillin-susceptible *S. aureus* (LA-MSSA) ST398 has emerged as a major clone in Korean pig farms. To better understand the emergence of LA-MSSA ST398 in Korea, we characterized the genomic features and antimicrobial resistance phenotypes of isolates from pig farms collected between 2021 and 2024.

Materials and Methods

A total of 448 *S. aureus* isolates were genotyped by multilocus sequence typing (MLST), *spa* typing, and staphylococcal cassette chromosome *mec* (SCC*mec*) typing, and whole-genome sequencing was performed to characterize genomic features, including antimicrobial resistance and virulence genes. Antimicrobial resistance phenotypes were assessed using standard susceptibility testing methods.

Results and Discussion

Of the 448 isolates, only nine (2.0%) were identified as MRSA belonging to ST398-SCC*mec* V-*spa* t011, whereas the remaining 439 isolates (98.0%) were classified as MSSA, with ST398 predominating among MSSA (383/439, 87.2%). Importantly, ST398 MSSA strains not only exhibited a significantly broader multidrug resistance (MDR) profile than MRSA strains but also harbored a greater number of antimicrobial resistance genes at the genomic level, including *cfr, fexA, Inu(B), erm(T), aac(6')-aph(2"), aadD, ant(6)-la, Isa(E), dfrG,* and *tet(L)*. Moreover, 13 ST398 MSSA isolates carrying *cfr* (13/20, 65.0%) retained susceptibility to linezolid, attributed to a Q148K mutation (7/13, 53.8%) or 35 bp insertion in promoter region of *cfr* (6/13, 46.2%). Comparative sequence analyses revealed 100% sequence identity among cfr_{Q148K}-carrying plasmids and multiple mobile genetic elements surrounding cfr_{Q148K}, indicating high mobility and inter-host dissemination potential.

Conclusion

Collectively, these findings demonstrate that ST398 MSSA serves as a primary reservoir of multidrug resistance in pig farms at both phenotypic and genomic levels. Our results suggest that surveillance strategies focused on MRSA may substantially underestimate the true antimicrobial resistance burden in pig production systems and highlight the necessity of incorporating MDR MSSA into One Health based antimicrobial resistance monitoring and control programs.

Keywords: Multidrug resistance, Pig farms, ST398 LA-MSSA.

Acknowledgements: This study was supported by Research of Korea Centers for Disease Control and Prevention (Project No. 2021ER220100 and 2024ER220900).

ENHANCING HEALTH CONTROL IN NURSERIES THROUGH SYNDROMIC SURVEILLANCE AND REAL-TIME ANTIBIOTIC USE MONITORING

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Introduction and Objectives

Syndromic surveillance systems enable early detection of health deviations in pig production. Digital tools that standardize clinical data may improve decision-making, particularly during the nursery phase, where disease incidence is high. Porcitrax® is a health-monitoring software that records clinical signs, treatments, antimicrobial use and temporal disease patterns at the batch level. This study aimed to describe the clinical patterns detected in Iberian nursery piglets using this system.

Material and methods

A retrospective analysis was conducted using Porcitrax® datasets from eight consecutive batches of Iberian piglets in the nursery phase. The software provided records on treated animals, age at treatment, syndrome classification, antimicrobial usage (mg/kg treated) and estimated body weight calculated through regression models to assess dosing accuracy. Descriptive epidemiological analysis was used to evaluate temporal clustering of cases, prevalence of clinical categories and patterns of antimicrobial administration. Routine clinical observations and necropsy findings were used to contextualize the digital outputs.

Results and Discussion

The system revealed consistent temporal peaks in enteric disease between days 27 - 36 post-weaning. Enteric syndromes accounted for most clinical events with 43 % of the cases, followed by dermal (12%) and locomotor disorders (7%). The antimicrobial-use module identified dosing deviations, especially in batches with higher enteric morbidity of up to 43% of overdosing in early postweaning piglets. Temporal curves facilitated the recognition of patterns compatible with polyserositis and enzootic pneumonia, later supported by diagnostic findings. Data structure and visualization enabled clear comparison of patterns across batches.

Conclusion

The results demonstrated that Porcitrax® provided consistent, structured data that enhanced the interpretation of health trends in transition-phase piglets. The system supported the early identification of critical periods, deviations in antimicrobial use and recurrent syndromes. Digital surveillance tools of this type appeared to strengthen health monitoring and to guide preventive decisions in commercial pig farms. Further research should assess integration with environmental and production variables to improve predictive capacity.

Keywords: Syndromic surveillance, Health monitoring, Real-time, Nurseries.

ANTIBIOTIC RESISTANCE PROFILE IN BACTERIA ASSOCIATED WITH RESPIRATORY OUTBREAK CASES IN COMMERCIAL PIG FARMS IN MEXICO

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Introduction and Objectives

One of the main health challenges in Mexican swine production is the occurrence of outbreaks of bacterial respiratory diseases, which lead to production losses, encourage the indiscriminate use of antibiotics, and pose a risk to public health (Monger, et al., 2021). The objective of this study was to determine the bacteria present and their antibiotic resistance profile in respiratory disease outbreaks on commercial farms.

Materials and Methods

During Oct 2023 to Oct 2024 were collected tissues of respiratory outbreaks in commercial farms located at different high production regions in México and sent to veterinary diagnostic laboratory to run a general bacteriology test including isolated and subsequently antibiogram test using 11 antibiotics commonly used in a swine practitioner.

Results and Discussion

A total of 44 bacterial isolates were obtained belonging to the following genera *Streptococcus suis* (40%), *Pastereulla multocida* (22%), *Glaesserella parasuis* (16%), *Staphylococcus aureus* (14%), *Trueperella pyogenes* (2%), *Actinobacillus suis* (2%), *Actinobacillus pleuropneumoniae* (2%), *Rothia nasimurium* (2%), according to CDC classification (CDC, 2019) were detected Multi Drug Resist (MDR) 61%, Extensively Drug Resist (XDR) 17%, Pan-resistant (PNR) 11%, specific by phenotypic analysis of bacterial isolates from respiratory outbreaks in pigs shows distinct patterns of resistance to various antibiotics. The results show a high frequency of resistance to tetracycline, tilmicosin, and penicillin G, with values exceeding 40%, like reported by Boeckel et al., 2019 indicating reduced efficacy of these drugs in treating the studied infections. On the other hand, antibiotics such as ceftiofur, fosfomycin, and norfloxacin exhibit higher proportions of susceptibility, exceeding 40% of the isolates, suggesting they remain viable therapeutic options in the current context.

Conclusion

This study shows a profile bacterium in respiratory outbreaks in commercial swine farms, in summary a high prevalence of *Streptococcus suis, Pasteurella multocida,* and *Glaesserella parasuis* was detected. Phenotypic analysis showed that these isolates exhibit high resistance to Tetracyclines, Penicillin G, and Tilmicosin, while Florfenicol, Doxycycline, and Norfloxacin maintain low resistance rates. This suggests an approach to use of certain antibiotics should be reconsidered, and it is recommended to use those with lower resistance to treat these outbreaks.

Keywords: Antibiogram, Antibiotic, Bacteria, Resistance, Respiratory.

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INFLUENCE OF SEASON ON SALIVARY STRESS BIOMARKERS IN TWO INDIGENOUS SPANIHS PIG BREEDS

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Introduction and Objectives

In recent years, various analyses of biomarkers in saliva have been developed to determine stress in pigs (Valros et al., 2022; Tecles et al., 2025). One of the frequent causes of systemic stress is due to climatic stressors such as cold or heat. In this study, the values of different biomarkers in animals raised outdoors were compared, comparing different climatic situations.

Materials and Methods

A total of 183 saliva samples from Chato Murciano (CM, n = 118) and Porco Celta (PC, n = 65) animals were collected using a sponge and Salivette. CM is raised in south-eastern Spain, where the climate is extremely hot in summer, and PC is raised in Galicia, where the climate is cold and Atlantic in winter. In the case of CM, samples were taken in spring (April) and summer (July-August) and in PC in autumn (September) and winter (January-February). Creatine (CREA), amylase (AMIL), creatine kinase (CK), urea, oral proteins (Pr.Or.), adenosine deaminase (ADA), butyrylcholinesterase (BchE), haptoglobin, Ferric Reducing Antioxidant Power (FRAP), Advanced oxidation protein products (AOPP), Chromogranin (CgA), cortisone, and cortisol were determined.

Results and Discussion

In CM, significant differences were found when comparing spring vs. summer samples for CREA (P = 0.005), TEA (P = 0.008), and cortisol (P = 0.015), increased in summer. In PC, in addition to changes in CREA (P = 0.007) and TEA (P = 0.044), AMIL (P = 0.004), Pr.Or. (P = 0.006), BchE (P = 0.004), ADA (P < 0.001), Haptoglobin (P = 0.002), and CgA (P < 0.001) values were significantly increased in winter.

Conclusion

Cold and heat stress can produce changes in different biomarkers in saliva. Cooler climates produce an increase in biomarkers of inflammation such as Pr.Or., Haptoglobin, and the adrenergic response such as CgA that is not found in warmer climates

Keywords: Biomarkers, Climate stress, Chromogranin, Saliva.

Acknowledgements: The authors thank the producers of ASOPORCEL, ACHAMUR and Asociación de Criadores de Cochino Negro Canario.

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POPULATION STRUCTURE AND ANTIMICROBIAL RESISTANCE GENE TRANSFER OF RESPIRATORY *ESCHERICHIA COLI* ISOLATED FROM SWINE IN CHINA

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Introduction and Objectives

Accumulating evidence has demonstrated that ExPEC may cause fatal pneumonia in swine, exerting a severe menace to porcine health (Kong et al., 2017). To enhance the health status and growth performance of swine, a variety of strategies have been implemented for the prophylaxis and therapy of swine colibacillosis, wherein antibiotics stand as the predominant intervention. For Escherichia coli, the evolution and dissemination of AMR are predominantly driven by antibiotic utilization, primarily via selective pressures that elicit the horizontal transfer of antibiotic resistance genes (ARGs) in this bacterium. The present study aims to investigate the transfer of ARGs in respiratory Escherichia coli isolated from swine in China.

Materials and Methods

ExPEC isolates were collected from the lung tissues of pigs exhibiting various clinical signs of respiratory tract infections between 2022 and 2024 pigs suspected of having respiratory tract infections were identified based on clinical manifestations, including lateral recumbency and abdominal breathing. Sequence files of an additional 388 ExPEC genomes isolated from porcine lung tissues were batch-downloaded from the National Center for Biotechnology Information (NCBI, https://www.ncbi.nlm.nih.gov/) using a self-made script.

Results and Discussion

This study analyzed 441 strains of porcine lung-derived ExPEC isolated in China. These strains exhibited high diversity in terms of serotypes and multilocus sequence typing (MLST) profiles, with phylogroups A, B1, and C accounting for a large proportion. A total of 111 ARG subtypes were detected; among them, the prevalence of resistance genes such as sul2 was notably high. Additionally, resistance genes against "last-resort" antibiotics (including carbapenems) were identified. Approximately 77.2% of the ARGs were capable of horizontal transfer, primarily mediated by plasmids. The strains demonstrated strong genomic plasticity and an open pan-genome.

Conclusion

This study analyzed porcine lung-derived ExPEC strains in China, revealing high genomic diversity and prevalent ARGs, including carbapenem antibiotic resistance genes. Most ARGs are horizontally transferable, with plasmids as core carriers. These findings highlight severe AMR risks in Chinese swine farms, providing critical data for global AMR surveillance and targeted control strategies.

Keywords: Antibiotic resistance genes, ExPEC, Horizontal transfer, Mobile genetic elements.

Acknowledgements: The authors thank the Wuhan Kevchunag Biology Technology Co. Ltd for the support with providing testing facilities.

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SEROPREVALENCE AND SEROVAR PATTERNS OF *LEPTOSPIRA* AT THE PIG-HUMAN INTERFACE IN NORTHERN VIETNAM: A ONE HEALTH PERSPECTIVE

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Introduction and Objectives

Leptospirosis is a globally distributed zoonosis transmitted through contact with infected animal urine or contaminated environments. In Vietnam, although human leptospirosis is notifiable, reported cases remain low despite serosurveys indicating substantial exposure in humans and pigs. This study assessed seroprevalence and serovar distribution in livestock farmers and pigs in two northern provinces to characterise exposure at the pig–human interface.

Materials and Methods

A cross-sectional survey was conducted in November 2024 in Lao Cai and Hoa Binh (now Phu Tho) provinces. Serum samples were collected from 305 livestock farmers and 412 sows across 206 pig-keeping households (two pigs per household). Microscopic agglutination tests were performed against 15 serovars, with titres ≥ 1:100 classified as seropositive. Seropositivity was defined as reactivity to at least one serovar. Differences in seroprevalence between species and provinces were assessed using 95% confidence intervals (CIs).

Results and Discussion

Overall seroprevalence was significantly higher in farmers (69.2%, 95% CI: 63.7 - 74.3) than in pigs (37.4%, 95% CI: 32.7 - 42.2). Farmer seroprevalence was similar between Lao Cai (69.9%, 95% CI: 62.0 - 77.1) and Hoa Binh (68.4%, 95% CI: 60.4 - 75.7). Pig seroprevalence was higher in Lao Cai (42.0%, 95% CI: 35.3 - 48.9) than Hoa Binh (32.5%, 95% CI: 26.1 - 39.5), though marginally significant. No significant difference was observed between pig-keeping (67.5%, 95% CI: 60.6 - 73.8) and non-pig-keeping farmers (72.7%, 95% CI: 62.9 - 81.2). Predominant serovars in farmers were Australis (10.8%, 95% CI: 7.6 - 14.9), Pyrogenes (9.5%, 95% CI: 6.5 - 13.4), and Bataviae (8.5%, 95% CI: 5.6 - 12.2); in pigs, Australis (5.1%, 95% CI: 3.2 - 7.7), Saxkoebing (3.9%, 95% CI: 2.2 - 6.2), and Panama (3.6%, 95% CI: 2.1 - 5.9). Serovar-specific positivity differed significantly between species for 10 of 15 serovars. Notably, Autumnalis seropositivity in pigs was substantially higher in Lao Cai (6.1%, 95% CI: 3.3 - 10.3) than Hoa Binh (0.5%, 95% CI: 0.0 - 2.8), suggesting heterogeneous local transmission potentially linked to rodent exposure.

Conclusion

Leptospira exposure was higher in livestock farmers than in pigs, with distinct species- and province-specific serovar patterns. One Health surveillance integrating human, livestock, rodent, and environmental monitoring is needed to elucidate transmission dynamics and inform locally tailored prevention strategies.

Keywords: Leptospira, Zoonosis, Livestock farmers, Pigs, Seroprevalence.

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COMPARATIVE GENOMICS OF *TET(X4)*-CARRYING PLASMID IN *ESCHERICHIA COLI* FROM SWINE AND WASTEWATER IN THAILAND

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Introduction and Objectives

Tigecycline is a last option antibiotic for treating multidrug-resistant Gram-negative bacterial infections (Zhang et al., 2022a). However, the *tet (X)* gene can inhibit tigecycline and confer resistance. Since plasmid-borne tet(X4)-positive *E. coli* was first reported among swine in China in 2019, it has been found in several Asian countries (He et al., 2019; Zhang et al., 2022b). However, Data remains limited in Thailand. Therefore, this study aims to characterize *E. coli tet (X4)*-positive isolates from swine farms and processing environments.

Materials and Methods

A total of 432 *E. coli* isolations originated from human worker feces, pig feces, wastewater, and pig carcasses from a pig farm and a pig slaughterhouse between 2020 and 2023. All isolates were screened with Eosin methylene blue agar containing tigecycline (2mg/ml) confirmed by MALDI-TOF. The minimum inhibitory concentration (MIC) was determined using EUVSEC Sentitre plates and interpreted based on CLSI (2024) and EUCAST (2025) guidelines. DNA was extracted for PCR-based detection of tet(X4), following by whole-genome sequencing. Plasmid structures were compared using BLAST Ring Image Generator.

Results and Discussion

Out of 432 *E. coli* isolates, 12 (2.77%) were tigecycline-positive *E. coli.* These isolates were found in pig carcasses, pig feces and wastewater but not in human samples. All resistant isolates were resistant to gentamicin, cefotaxime, and tetracycline. Six isolates contained *tet(X4)* including one from wastewater, three from pig feces and two from pig carcasses. Genomic analysis revealed plasmid-borne *tet(X4)* was mostly on IncX1 except one hybrid IncFIA(HI1)/IncFIB(K)/IncX1 in wastewater. Two pig-feces IncX1 plasmids (CUPF07 and CUPF08) differed only in bla_{TEM} subtype, indicating a conserved backbone. Pig-carcasses plasmids shared almost identical backbones with reference plasmids pYUXYEH3934-2 and pYUYZPE244-2 from Human and pig feces in China. This suggests a potential dissemination of related tet(X4) plasmid across swine related One Health interface.

Conclusion

This study demonstrates the presence of *tet(X4)*-positive *E. coli* in Thailand's swine production system, mainly located on conserved IncX1 plasmids. Their close relatedness to regional reference plasmids underscores the need for genomic surveillance and strengthened AMR strategies across the pig production continuum within a One Health framework.

Keywords: *Escherichia coli*, Pigs, Plasmids, tet(X4), Whole genome sequencing (WGS).

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ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF *ESHERICHIA COLI* ISOLATED FROM LARGE-SCALE PIG FARMS IN HUNGARY

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Introduction and Objectives

Antimicrobial resistance (AMR) among livestock-associated *Escherichia coli* represents a growing challenge for animal health, food safety, and public health within the One Health framework. Intensive pig production systems, characterized by high antimicrobial usage, may facilitate the emergence and persistence of resistant bacterial populations. The aim of this study was to assess the antimicrobial susceptibility profiles of *E. coli* isolates obtained from large-scale pig farms in Hungary using minimum inhibitory concentration (MIC)-based methods.

Materials and Methods

A total of 203 *E. coli* isolates were recovered from clinically healthy 4-week-old piglets originating from four commercial pig farms. Antimicrobial susceptibility testing was performed by broth microdilution against a panel of veterinary-relevant antimicrobials, including β-lactams, aminoglycosides, tetracyclines, amphenicols, polymyxins, fluoroquinolones, and potentiated sulfonamides.

Results and Discussion

High resistance rates were observed for cefotaxime (88%), amoxicillin (55%), and cefquinome (55%). In contrast, most isolates remained susceptible to marbofloxacin (93%), enrofloxacin (89%), and colistin (74%). Notable resistance was also detected against doxycycline (47%) and neomycin (48%). Multidrug resistance (MDR) phenotypes were identified in as 60.1% of the isolates, indicating sustained selective pressure within intensive pig production systems.

Conclusion

These findings highlight the presence of complex resistance patterns in commensal *E. coli* populations from Hungarian pig farms and emphasize their potential role as reservoirs of antimicrobial resistance. Continuous AMR surveillance and prudent antimicrobial use are essential to mitigate resistance development and to support evidence-based antimicrobial stewardship strategies in swine production, in line with One Health principles.

Keywords: Antimicrobial resistance, *Escherichia coli,* Minimum inhibitory concentration, Prudent antimicrobial use, Swine.

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ISOLATION AND ANTIMICROBIAL RESISTANCE PROFILES OF BACTERIA CAUSING RESPIRATORY DISEASES IN PIGS IN SOUTHERN VIETNAM

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Introduction and Objectives

Porcine respiratory diseases represent a major challenge to pig production worldwide, particularly in intensive farming systems, where bacterial pathogens significantly contribute to disease complexity and therapeutic failure. In Vietnam, information on the prevalence and antimicrobial resistance of key bacterial agents involved in the porcine respiratory disease complex (PRDC) remains limited, especially in the southern region. This study aimed to isolate major bacterial pathogens associated with respiratory diseases in pigs and to evaluate their antimicrobial resistance patterns in Southern Vietnam.

Materials and Methods

A total of 118 clinical samples, including lung tissues and nasal swabs, were collected from pigs exhibiting respiratory symptoms in Ho Chi Minh City and the provinces of Dong Nai, Tay Ninh, and An Giang. Bacterial isolation was performed using selective and enriched culture media, followed by phenotypic identification. Molecular confirmation was conducted using real-time PCR and sequencing for *Actinobacillus pleuropneumoniae* (*APP*), *Streptococcus suis* (*S. suis*), *Glaesserella parasuis* (HPS), and *Pasteurella multocida* (PM). Antimicrobial susceptibility testing was carried out using the disk diffusion method in accordance with CLSI guidelines.

Results and Discussion

Four major bacterial pathogens associated with PRDC were successfully isolated. The detection rates of APP, *S. suis*, HPS, and PM were 16.10% (19/118), 50.00% (59/118), 22.03% (26/118), and 12.71% (15/118), respectively. For all four species, isolation rates from tissue samples were higher than those from nasal swabs. Unlike previous studies that mainly focused on single pathogens, this study simultaneously investigated four bacterial agents within the same clinical samples, providing a more comprehensive insight into PRDC. Notably, co-infection with all four bacteria was detected in two cases. Antimicrobial susceptibility testing revealed that most isolates exhibited high resistance to multiple antibiotics, particularly erythromycin, tetracycline, and amoxicillin. In contrast, higher susceptibility was observed to ceftiofur, doxycycline, enrofloxacin, florfenicol, and gentamicin. All isolates demonstrated multidrug resistance.

Conclusion

This study provides updated epidemiological data on major bacterial pathogens causing porcine respiratory diseases and their antimicrobial resistance profiles in Southern Vietnam. The high prevalence of multidrug-resistant isolates highlights the need for continuous surveillance and prudent antimicrobial use to support effective disease control in pig production systems.

Keywords: Antimicrobial resistance, Co-infection, pigs, Porcine Respiratory Disease Complex.

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HEALTH STATUS OF SOWS: PREVALENCE OF CLINICAL SIGNS AND LESIONS IN FLEMISH FARMS

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Introduction and Objectives

Reproductive performance in pig farms has increased significantly during the past decades. This puts pressure on sow health and welfare, resulting in an increased risk of disease. Measuring the prevalence and severity of clinical signs and lesions can help to monitor sow health and welfare in farms.

Materials and Methods

This field study was conducted in three commercial pig farms (Farm A, B and C) to collect information on clinical signs and lesions in sows. Number of sows, production number and annual sow deaths were 430, 38.50 and 15.03% for Farm A; 350, 37.50 and 7% for Farm B; and 700, 37.09 and 8.80% for Farm C, respectively. The investigated parameters were lesions of the hind claws, udder and vulva, shoulder ulcerations, lameness, diarrhoea and respiratory signs. In each farm, 120 sows were included i.e. 30 sows per production phase (farrowing, weaning, early and late gestation). The prevalences and severity (score 0-3) of these conditions were assessed.

Results and Discussion

The following mean (min.-max.) prevalences were obtained: claw lesions 93.9% (90.0 - 95.8%), udder lesions 29.2% (22.5 - 35.8%), vulva lesions 18.9% (11.7 - 25.8%), shoulder ulcerations 44.7% (35.0 - 54.2%), lameness 39.5% (20.8 - 59.2%), diarrhoea 3.3% (1.7 - 6.7%) and respiratory signs 1.3% (0.0%–4.2%). Udder (63.3%) and vulva lesions (30.0%), and shoulder ulcerations (67.8%) were most prevalent in the farrowing unit, diarrhoea (6.1%) mainly in gestation. Overall, lesions were mild (score 1) or of moderate (score 2) severity.

Conclusion

The prevalences generally corroborate with those found in literature (Heinonen et al., 2013; Nalon et al., 2013), but in the present study, higher prevalences were found for udder lesions (29.2%) and lameness (39.5%). This may be because very mild lesions were also recorded. Additional studies are required to identify causes (e.g. deficiencies in housing and management) and measures to mitigate or prevent these conditions for optimal sow health.

Keywords: Clinical signs, Lesions, Sow health, Welfare.

Acknowledgements: The authors thank all participating farms for their support with providing information and allowing us to investigate these signs and lesions in sows.

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NOVEL TOOLS TO FIGHT RESISTANT PATHOGENIC BACTERIA IN SWINE FARMS

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Introduction and Objectives

Cleaning and disinfection (C&D) protocols are critical for controlling the persistence of pathogenic bacteria, such as *Salmonella*, in pig farms. However, emerging restrictions on hazardous disinfectants like formaldehyde and the resistance of microorganisms have created a need for safer effective alternatives. To address this challenge, the present study evaluated the efficacy of an alternative C&D protocol combining commercial detergents, essential oils, and bacteriophages to reduce total enterobacteria counts, the target bacterium *S. typhimurium* monophasic variant (mST), and enterotoxigenic (ETEC) *Escherichia coli*.

Materials and Methods

Slurry samples were obtained from a pig farm with poor sanitary conditions for testing the C&D protocol on experimental surfaces. The slurry was divided into two experimental groups, one with an inoculum of 106 CFU/ml of mST and the other with an inoculum of 106 CFU/ml of ETEC. The slurry was then spread over the surfaces of an experimental farm, left to dry, and the different products were applied to evaluate their effectiveness in eliminating the target microorganisms at different times. Firstly, the efficacy of three commercial detergents was evaluated. Secondly, the efficacy of two commercial disinfectants and three essential oils was tested. Finally, the efficacy of a bacteriophage cocktail was evaluated. All the tests were conducted in triplicate.

Results and Discussion

The results showed that the basic commercial detergent achieved a complete reduction in total enterobacteria counts. The same result was observed when the three essential oils carvacrol, eugenol and cinnamaldehyde were applied. However, while both commercial disinfectants reduced the concentration of enterobacteria, neither eliminated them completely. The bacteriophage cocktail, on the other hand, achieved a 100% reduction in total enterobacteria and ETEC. However, it should be noted that mST was detected in one of the replicates after the cocktail was applied.

Conclusion

These findings suggest that combining new alternative tools with C & D protocols can effectively eliminate persistent bacteria that may be resistant to conventional disinfectants while remaining safe for animals and the environment. Overall, these alternatives represent a viable way of improving farm hygiene while complying with safety standards.

Keywords: Antimicrobial resistance, Bacteriophages, Cleaning & disinfection, Essential oils, *Salmonella Typhimurium* monophasic variant.

CHALLENGES IN PREVENTING ANIMAL HEALTH ISSUES AND THE ROLE OF FARM-LEVEL DECISION-MAKING

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Introduction and Objectives

Preventive disease control in intensive pig production has become increasingly complex, driven by regulatory pressure to reduce antimicrobial use (AMU) and rising expectations for sustainable production. In newly established, repopulated, or clinically stable herds, the economic value of maintaining high health status may be underestimated, weakening long-term commitment to prevention. This study quantified the consequences of deteriorating preventive health management on animal health and AMU. Additionally, we developed a data-driven, farm-specific approach to assess the epidemiological and production impacts of Streptococcus suis and *Actinobacillus pleuropneumoniae* supporting targeted herd stabilization strategy.

Materials and Methods

A seven-year longitudinal study was conducted on a large-scale farrow-to-finish farm infected with highly pathogenic *S. suis* and *A. pleuropneumoniae* serotypes. Production records, mortality data, AMU, laboratory diagnostics, and slaughterhouse lung lesion scores were systematically collected and analyzed. Preventive interventions included targeted vaccination, strengthened internal biosecurity, management adjustments, and antimicrobial reduction measures. Trends in health, production performance, and AMU were compared across distinct phases: effective disease control, gradual degradation of the preventive system, and disease re-emergence.

Results and Discussion

Following implementation of the targeted control strategy, clinical signs were eliminated. For both pathogens, mortality decreased by up to 90 and 65%, respectively, and AMU was reduced by 98%. During a prolonged period of clinical stability, adherence to preventive measures progressively declined due to management changes and emerging predisposing factors. This deterioration was associated with reduced average daily gain (-60 g/day), poorer herd uniformity, and increased indicators consistent with immune stress. Within 6 months, mean severe and total pleuritis scores increased 8-fold and 4.5-fold, respectively. Delayed corrective action enabled re-emergence of A.pleuropneumoniae, resulting in an estimated production loss of €10 per finisher.

Conclusion

Reducing AMU in pig production should not be pursued as an isolated goal; it must be integrated into a rigorously maintained preventive framework. Our findings highlight the value of detailed, farm-specific analytics for identifying early warning signals and the key determinants of sustained success. Continuous monitoring and robust data collection are essential for timely detection and rapid correction of emerging risks, thereby preserving the long-term gains in animal health and productivity.

Keywords: Antimicrobial reduction, *Streptococcus suis*, *Actinobacillus pleuropneumoniae,* data-driven study, farm-specific approach.

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EVALUATION OF WELFARE FACTORS RELATED TO ROUTE OF ADMINISTRATION OF IRON DEXTRAN IN PIGLETS

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Introduction and Objectives

Injections are a necessary component of swine health management and are routinely administered by automatic-refillable needle-syringe (NS) devices. Needle-free injection devices (NFID) use compressed gas to deliver an injection, removing the use of a needle and offering a sustainable alternative for repeated injections. The current impact of NFID on the welfare of nursing piglets remains limited; this study aims to address this knowledge gap.

Materials and Methods

A total of 206 litters were randomized into three treatment groups for intramuscular iron dextran supplementation: Control (NS with one needle for each piglet, n = 66), Repeated (NS with one needle for the litter, n = 70), and NFID (NFID for the litter, n = 70). Each trial litter contained 10 piglets. Piglets 1 and 10 were restrained at the time of injection to record their vocalizations and behaviour. A critical frequency threshold of 1,000 Hz was used to indicate pain intensity (Weary et al., 1998). Call duration, energy, and rate were also analyzed.

Results and Discussion

A total of 1270 calls were analyzed (Control = 440, NFID = 345, Repeated = 485). Calls above 1,000 Hz were classified as High Frequency (HF) and used to indicate pain intensity (Tallet et al., 2013). Call count data was fit to a negative binomial model to account for overdispersion. Analysis showed the rate of HF vocalizations in piglets treated with NFID was significantly lower compared to Control (IRR = 0.60; 95% CI = 0.40 - 0.91; $P = 0.016$). Repeated needle-use increased the rate of HF calls, although not significantly (IRR = 1.18; 95% CI = 0.80,1.74; $P = 0.41$). Ordinal logistic regression of behaviour scores (0, 1, 2, 3) showed that NFID use significantly reduced the odds of extreme behaviour compared to piglets who received a new needle (OR = 0.38; 95% CI = 0.19 - 0.72; $P = 0.004$).

Conclusion

Our results indicate that NFID use may reduce pain associated with injection procedures in piglets compared to NS. This study highlights the importance of revisiting common animal husbandry procedures as emerging technology develops. Continued research into NFID use in swine is necessary as the industry standard for animal health and evidence-based care continues to improve.

Keywords: Needle-free injection, Iron dextran, Animal welfare, Piglet husbandry.

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COACHING TO REDUCE ANTIBIOTIC USE IN PIG FARMS. FROM INITIAL SKEPTICISM TOWARDS RECOGNIZED ADDED VALUE

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Introduction and Objectives

Despite considerable progress in reducing antibiotic use (AMU) in Belgian pig farming, a substantial number of farms continue to demonstrate AMU levels above benchmarking thresholds ('alarm usage'). Since 2022, these alarm users have received guidance from antibiotic coaches to support AMU reduction. This study aimed to describe the coaching process, explore how herd veterinarians, farmers, and antibiotic coaches experience it, identify key success factors, and formulate recommendations for effective coaching.

Materials and Methods

A qualitative study design was used, combining in-depth interviews with ethnographic observations of on-farm coaching visits. Participants included pig farmers who were currently or previously coached, their veterinarians, and antibiotic coaches. Data were analyzed using inductive thematic analysis.

Results and Discussion

A total of 24 interviews were conducted with 7 coaches, 6 pig farmers, and 7 veterinarians, and 12 coaching visits were observed. Five themes emerged: (1) the goal of antibiotic coaching: promoting sustainable behavioural change by fostering extrinsic and intrinsic motivation; (2) defining the ideal antibiotic coach: a neutral external expert acting as mediator; (3) the essential role of veterinarian collaboration and support; (4) implementing the coaching trajectory, requiring a tailored, collaboratively developed action plan and structured follow-up; (5) participant perspectives on coaching: initial skepticism, distrust, and fear evolving into positive experiences.

Conclusion

Mandatory AMU reduction and the prospect of potential consequences serve as important initial extrinsic motivators, while intrinsic motivation is essential for sustained change. Farmers benefit from solution-based guidance that fosters trust and collaboration among the coach, farmer, and herd veterinarians. Despite initial skepticism, most participants ultimately viewed coaching as a valuable and supportive opportunity.

Keywords: Antibiotic use, Antimicrobial resistance, Antimicrobial stewardship, Coaching, One Health.

PREVALENCE AND CONTROL OPTIMIZATION OF SALMONELLA IN PIG SLAUGHTERHOUSES IN JIANGSU PROVINCE, CHINA

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Introduction and Objectives

Salmonella exists in different stages of pork production, and the slaughter process is a key link to reduce the epidemic of Salmonella in the pork production chain. The purpose of this research is to regularly sample different slaughter links and the environment and slaughter tools to understand the pollution of each link, find the key pollution links, and lay the foundation for later prevention and control.

Materials and Methods

A large-scale semi-automated pig slaughterhouse and a small-scale slaughterhouse in Jiangsu were selected. Salmonella isolation and identification were performed in the laboratory. Whole-genome sequencing (WGS) was conducted for representative strains to analyze phylogenetic relationships. The bactericidal efficacy of disinfectants, including decamethylammonium bromide, was evaluated and on-site application was optimized.

Results and Discussion

This study collected 829 samples in slaughterhouses. The total isolation rate of *Salmonella* was 20.6%. The splitting (28/95, 29.5%) and dressing (22/95, 23.1%) steps exhibited the highest detection rates of Salmonella on carcasses. The key pollution links were floor 9/23 (39.1%), grainer 9/47 (19.1%) and driller 7/40 (17.5%). The dominant serotypes were Salmonella Rissen 73/176 (41.4%) and Salmonella Enteritidis 26/176 (14.8%). The WGS results showed that serious cross-contamination of appliances and environmental samples and carcass wipe samples. The decamethyl ammonium bromide and sodium hypochlorite had the best disinfection effect. Following the implementation of the optimized prevention and control program, the overall contamination level during the slaughtering process decreased by 11.7%.

Conclusion

This study shows that the epidemic trend of Salmonella in different types of pig slaughterhouses is roughly similar, and Salmonella spreads along different slaughter links in the slaughterhouse. According to the pollution dynamics and serotype distribution of Salmonella in the pig slaughterhouse, the key pollution points were determined. In order to reduce public health risks, formulating new prevention and control programs for specific environments is the most effective and economical way to reduce Salmonella.

Keywords: China, Disinfection, Pigs, Prevention and control, *Salmonella*.

ANALYSIS OF RISK PROFILES FOR SALMONELLA EXPOSURE FROM PORK CONSUMPTION IN CHINA: A COMBINED META-ANALYSIS AND QUANTITATIVE MICROBIAL RISK ASSESSMENT MODEL

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Introduction and Objectives

Salmonella can be transmitted through the pork production chain, posing a risk of human infection (Ren et al., 2024). There is a scarcity of research evaluating the exposure risk across different geographic regions and serotypes throughout the entire supply chain. Therefore, this study first conducts a meta-analysis to estimate the prevalence of Salmonella in Chinese pig farms. These estimates are used as inputs for a quantitative microbial risk assessment model for Salmonella in the China pork supply chain.

Materials and Methods

Following the PRISMA guidelines, researchers conducted a systematic review and literature search in June 2025 across PubMed, Web of Science, CNKI, and Wanfang databases. Publications dated from 2000 to 2025 focusing on pig farms in China were included. Data on Salmonella prevalence in pigs and pig feces were extracted. To assess the prevalence of Salmonella, a random-effects model was employed to generate combined estimates. Heterogeneity was evaluated using the I^2 statistic, with values of 25, 50, and 75% considered low, moderate, and high heterogeneity, respectively. The model was run using @RISK software.

Results and Discussion

The model estimated an overall Salmonella prevalence of 8% (95% CI: 5 - 12%) in live pigs and 13% (95% CI: 9 - 19%) in pig feces. The model estimated that annual pork consumption results in approximately 6.53 × 10^6 (95% CI: 7.78 × 104 - 3.78 × 107) cases of salmonellosis. Eastern regions of China had a disproportionately higher incidence of infection. The *Salmonella* 4,[5],12:i:- showed the highest risk of infection from pork consumption. Sensitivity analysis showed that cooking temperature, washing, and chilling were critical control points.

Conclusion

In this study, we initially performed a meta-analysis to determine the prevalence of Salmonella in Chinese pig farms. We constructed a risk assessment model of the pork production chain using a combination of meta-analysis and process parameters derived from the literature. Future work should focus on strengthening prevention and control measures at critical risk points to reduce the risk of Salmonella infection.

Keywords: China, Meta-analysis, Pigs, Quantitative microbial risk assessment, Salmonella.

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EVALUATING HERBAL EXTRACTS AS SUSTAINABLE ALTERNATIVES TO CHLORTETRACYCLINE FOR POST-SURGICAL WOUND CARE IN PIGLETS

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Introduction and Objectives

Routine topical antibiotic use in swine raises antimicrobial resistance (AMR) concerns, necessitating non-antibiotic One Health alternatives (Rippon et al., 2021). This study compared a polyherbal spray (HerbBand® contains polyherbal extract from *Pinus longifolia*, *Eucalyptus* spp., *Cedrus deodara*) against conventional chlortetracycline for wound healing in piglets.

Materials and Methods

Twenty-six piglets (14 - 15 days old) undergoing routine surgery were randomized to herbal treatment (n = 13) or chlortetracycline control (n = 13). Treatments were applied once daily for 7 days. Wounds were scored (0 - 3) for erythema, edema, exudate, dehiscence, and crusting on days 0, 1, 3, and 7 to calculate a composite wound healing score was adapted from previous study (Plavec et al., 2020). Data were analyzed using Mann-Whitney U tests.

Results and Discussion

Clinical outcomes indicated non-inferiority of the herbal formulation. While no differences reached statistical significance ($P < 0.05$), marginal trends at Day 1 favored the herbal group regarding erythema ($P = 0.069$) and exudate ($P = 0.067$). Conversely, controls exhibited persistent discharge. By Day 7, swelling resolution trended faster in the herbal group ($P = 0.075$), consistent with anti-inflammatory efficacy of botanical resins (Bulut et al., 2024). Healing dynamics were comparable between groups. The lack of statistical significance likely reflects limited statistical power due to the small sample size in this pilot study; larger cohorts would be required to definitively confirm these observed advantages.

Conclusion

This pilot study suggests that non-antibiotic polyherbal dressings could support accelerated inflammatory resolution comparable to conventional antibiotics. These multifunctional botanical extracts could offer a sophisticated strategy to enhance animal welfare and antimicrobial stewardship. Integrating such solutions allows the swine industry to proactively address AMR and support One Health initiatives without compromising clinical efficacy.

Keywords: Antimicrobial resistance, Herbal extract, One health, Pig welfare, Wound management.

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TEMPORAL TRENDS IN OVERALL AND REASON-SPECIFIC SOW REMOVAL RATES ON CANADIAN SOW FARMS

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Introduction and Objectives

Sow longevity is a key determinant of productivity, economic efficiency, and welfare, yet sow mortality remains a major issue for the swine industry, data indicating mortality has remained elevated (Paiva et al., 2023). Despite producer and veterinarian concern (Paiva et al., 2023), herd-level Canadian data on mortality and removal reasons remain limited therefore, this retrospective study evaluated sow removals on farms and described reasons for culling, death, and euthanasia and how these data changed over time.

Materials and Methods

Retrospective data from 78 sow farms (2017 - 2024) were extracted from herd-management software, de-identified, and standardized. Removals were classified as culling, euthanasia, or natural death, and annual rates (per 100 sow-years) were calculated. Temporal trends in reason-specific removals were analyzed using univariable negative binomial regression with a log offset for sow-years at risk.

Results and Discussion

Culling predominated as main reason for sow loss (82%), which was driven by productivity reasons. Results showed that productivity culls increased over time with an incidence rate ratio (IRR) = 1.11. Culling rates due to body-condition increased (IRR = 1.14) while culls recorded as unknown decreased (IRR = 0.81) over the study period. Death losses increased for reasons recorded as sudden death (IRR = 1.21) and prolapse (IRR = 1.26). Euthanasia-related deaths were primarily due to lameness and prolapse with both reasons showing an increased trend (lameness IRR = 1.36; prolapse IRR = 1.41). These results align with reports of more locomotor disorders among euthanized sows and supports welfare-oriented removal (Heinonen et al., 2013).

Conclusion

Euthanasia increased over time, mainly for lameness and prolapse, potentially reflecting welfare-based decisions to prevent unnecessary distress. Production records can be a useful tool to investigate reasons for sow removal over time, to monitor shifts in culling, death, and euthanasia categories, and provide evidence to direct management, health, and welfare strategies for improvement in sow longevity.

Keywords: Culling, Euthanasia, Lameness, Sow mortality.

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ALTERED SALIVARY CORTISOL SECRETION IN PIGS WITH CHRONIC DISEASE

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Introduction and Objectives

Chronic disease adversely affects pig health and welfare and is associated with long-term alterations of the hypothalamic–pituitary–adrenal (HPA) axis. Cortisol is widely used as a stress biomarker in pigs; however, its interpretation under chronic disease conditions remains challenging (Sánchez et al., 2022). The objectives of the study were to investigate salivary cortisol concentrations in healthy pigs and in pigs affected by chronic disease under field conditions, and to evaluate potential sex-related differences.

Materials and Methods

Saliva samples were collected from healthy pigs (n = 15) and pigs with chronic disease (n = 17). Diseased animals were naturally occurring in clinical cases rather than experimentally induced models. Chronic disease was defined as the presence of clinical signs (e.g., apathy, inappetence, pain) persisting for ≥ 2 weeks and included locomotor, dermatological, and respiratory disorders. Salivary cortisol concentrations were quantified using a commercial competitive ELISA validated for porcine serum and saliva.

Results and Discussion

Salivary cortisol concentrations were significantly lower in chronically diseased pigs than in healthy pigs (median 1.9 ng/mL, IQR 1.2 - 2.6 vs. 4.3 ng/mL, IQR 3.1 - 5.8; $P < 0.01$), consistent with chronic HPA axis adaptation rather than acute stress. In pigs, prolonged exposure to disease-related stressors induces adaptive changes in HPA axis activity, including reduced cortisol secretion (Sánchez et al., 2022, Ruis et al., 1997).

Among chronically diseased pigs, females (n = 9) exhibited significantly higher salivary cortisol concentrations than males (n = 8) (2.3 ng/mL, IQR 1.6 - 3.0 vs. 1.5 ng/mL, IQR 1.0 - 2.1; $P < 0.05$), whereas no sex-related differences were observed in healthy pigs. Under non-challenging conditions, basal cortisol secretion in pigs is tightly regulated, and sex differences become evident mainly under sustained physiological challenge (Tilbrook et al., 2018).

Conclusion

Salivary cortisol concentrations are reduced in chronically diseased pigs and are influenced by sex in affected animals. These results support the concept of HPA axis adaptation during prolonged disease and indicate that salivary cortisol is a sensitive, non-invasive biomarker for assessing chronic disease-related stress and welfare in pigs.

Keywords: Chronic Disease, Cortisol, Pigs, Saliva, Welfare.

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EFFECTS OF A SUPPLEMENT VIA DRINKING WATER ON INTESTINAL INTEGRITY IN SOWS SUBJECTED TO NATURAL HEAT STRESS

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Introduction and Objectives

Intestinal integrity is one of the body systems affected by environmental heat in pigs (Ortega and Szabó, 2021). However, most research has been conducted on piglets, and there are few studies on breeding sows affected by heat stress. In this study, we investigated how heat affects intestinal integrity and immune activation in the intestines of sows subjected to natural heat stress and the effect of a specific preparation to minimize the effect of heat.

Material and Methods

Twenty-four multiparous sows were assigned to two groups: a control group (CON, n = 12) and a treatment group (XTRA, n = 12) that received a combination of plants extract, vitamin C, and betaine in their drinking water for one week before farrowing and during the third week of lactation. The trial was conducted in central Spain during July 2025. The sows were sampled for fecal material at 0, 1 and 21 days post farrowing. Gene expression was investigated for calprotectin (CAL), occluding (OCL), zonulin (ZON), IFNγ, IFNα, IL1α, IL1β, IL6, IL8, IL10, IL12P35, IL12p40, TNFα and TGFβ, to assess the inflammation, intestinal integrity and immune stimulation of intestine, as previously described (Ramis et al., 2022). A mixed model was used doing MLE calculations, and a related samples comparison.

Results

There was a significant effect of treatment for CALP, TGFβ, and IFNα increased in XTRA ($P < 0.001$) and for OCLD, IL1α and Ilβ; decreased in XTRA ($P < 0.001$). The interaction treatment x sampling moment showed differences for CALP, IFNγ and CLAU ($P < 0.05$). In the related samples analysis, the CON showed that IL1β remained high, IFNα showed no changes and ZON, OCL and CLAU did not improve. The XTRA group showed a decrease for IL1α, IL1β and IL6 (trend), and increase for IFNα, TGFβ, CLAU and OCLD.

Discussion and Conclusion

Analysis using mixed models reveals that the supplement applied via drinking water induces an adaptive intestinal immune response to heat stress, characterized by sustained suppression of proinflammatory cytokines (IL1α, IL1β), activation of regulatory (TGFβ) and antiviral/cellular stress (IFNα) pathways, together with time-dependent remodeling of epithelial barrier components.

Keywords: Heat stress, Betaine, Sow, Intestinal integrity, Immune system.

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CLONAL DIVERSITY AND TRANSMISSION OF FLUOROQUINOLONE-RESISTANT *ESCHERICHIA COLI* ALONG THE PIG PRODUCTION CHAIN IN KOREA

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Introduction and Objectives

Fluoroquinolone-resistant Escherichia coli has emerged as a critical concern in swine production due to its multidrug resistance (MDR) and transmission potential across production systems. However, stage-specific dissemination patterns and clonal relationships remain insufficiently characterized. This study aimed to investigate phenotypic resistance, molecular determinants, and phylogenetic structure of fluoroquinolone-resistant E. coli across pig production stages in Korea.

Materials and Methods

A total of 104 *E. coli* isolates were collected from pigs at five production stages (suckling, weaned, grower, finisher, and sows). Antimicrobial susceptibility testing was performed by disk diffusion according to CLSI guidelines using the following agents: ampicillin, amoxicillin–clavulanic acid, cefazolin, cefoxitin, ceftiofur, ceftazidime, cefepime, gentamicin, streptomycin, kanamycin, oxytetracycline, tetracycline, florfenicol, chloramphenicol, nalidixic acid, ciprofloxacin, sulfisoxazole, and trimethoprim–sulfamethoxazole. Minimum inhibitory concentrations for ciprofloxacin, enrofloxacin, and norfloxacin were determined. Quinolone resistance was assessed by sequencing the quinolone resistance–determining regions of gyrA and parC and detecting plasmid-mediated quinolone resistance (PMQR) genes. Multilocus sequence typing (MLST) and phylogenetic analyses were conducted to assess genetic diversity and infer transmission patterns.

Results and Discussion

FQ resistance prevalence ranged from 28.6 to 66.7% across production stages. All FQ-R isolates exhibited MDR, with resistance to 11–18 antimicrobials. PMQR genes were detected in 37.8% of isolates, predominantly qnrD and qnrS. Chromosomal mutations were identified in 44 of 45 FQ-R isolates, with common substitutions including S83L and D87N in gyrA and S80I and E84A in parC. Double mutations in both genes were frequently associated with high-level resistance (MIC ≥ 256 μg/mL), whereas isolates lacking such combinations showed lower MIC values. Class I integrons were present in 41.2% of isolates, indicating potential for horizontal gene transfer. MLST identified ten sequence types, with ST5229 (41.2%) distributed across multiple stages. Phylogenetic analysis revealed three clades, suggesting both vertical dissemination along the production chain and horizontal genetic exchange.

Conclusion

Clonally related FQ-R *E. coli* is widely distributed across pig production stages, driven by both chromosomal mutations and mobile resistance elements. These findings highlight the need for integrated surveillance and comprehensive antimicrobial stewardship strategies to mitigate high-level fluoroquinolone resistance in swine systems.

Keywords: Antimicrobial resistance, *Escherichia coli*, Fluoroquinolones, Plasmid-mediated quinolone resistance, Production stages.

EVOLUTION AND FARM-RELATED FACTORS ASSOCIATED WITH THE PREVALENCE OF BOAR TAINT IN ENTIRE MALE PIGS: A 10-YEAR STUDY

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Introduction and Objectives

Societal expectations regarding animal welfare led to the prohibition of piglet surgical castration in France in 2022. While producing entire males is a viable alternative, the risk of boar taint (odorous meat) remains a major commercial risk. This study aims to trace the evolution of the boar taint rate over the last decade and to identify and quantify the technical farm factors associated with the prevalence of boar taint at the slaughterhouse.

Materials and Methods

Data from over 20 million entire male pigs slaughtered by the Cooperl cooperative between 2013 and 2023 were analyzed to establish historical trends. Boar taint is assessed by trained human nose method, regularly double checked by chemistry and external audit. To identify risk factors, a detailed analysis was conducted on carcasses from July 2022 to June 2023. This data was cross-referenced with annual farm audits (genetics, feeding, housing) and technical-economic performance indicators (GTE). A binary logistic regression model was used to rank risk factors.

Results and Discussion

The rate of entire male with boar taint significantly decreased by 2.61% over ten years, reaching 1.51% in 2023 ($P < 0.001$). Entire male with boar taint were found to have heavier carcasses (+ 0.350 kg), higher fat content (G3 + 0.3 mm), and were older (+3.9 days) than non-odorous pigs ($P < 0.001$). The multivariate model identified slaughter age as the most significant risk factor (OR = 1.30 (CI 95% [1.15;1.45]), $P < 0.001$). Farms with the lowest prevalence (0.64%) performed better technically (lower Feed Conversion Ratio) and were more likely to use:

Genetics: NUCLEUS lines for both males and females.

Feeding: Liquid feed distribution.

Health: Engagement in "Antibiotic-Free" (PSA) programs. Conversely, the presence of dirty areas (concrete floor) in finishing pens increased the risk.

Conclusion

The prevalence of boar taint has been reduced by more than half in ten years and is now comparable to the rate of congenital defects in castrated herds. Controlling slaughter age, optimizing genetics, and maintaining high technical standards are key to successfully producing entire males without compromising meat quality.

Keywords: Animal welfare, Boar taint, Entire males, Genetics, Farm factors.

SEVERE FEVER WITH THROMBOCYTOPENIA SYNDROME VIRUS AS A ONE HEALTH CONCERN: ZOONOTIC TRANSMISSION, EVIDENCE FROM ANIMAL HOSTS INCLUDING PIGS, AND AN ADENO-ASSOCIATED VIRUS-VECTORED VACCINE APPROACH

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Introduction and Objectives

Severe Fever with Thrombocytopenia Syndrome (SFTS) is an emerging tick-borne zoonotic disease caused by SFTS virus (SFTSV), first reported in China in 2011 (Yu et al., 2011) and subsequently other Asian countries (Chen et al., 2023), with a high fatality rate. SFTSV circulates in a wide range of mammalian hosts, including humans and pigs; in pigs, serological and molecular evidence of SFTSV infection has been reported (Rim et al., 2021), although no clinical cases have been documented. Currently, no licensed vaccine nor therapy is available. Previous studies have demonstrated that Adeno-associated virus (AAV)-mediated expression of individual SFTSV glycoproteins (Gn or Gc) induced immune responses in vivo (Shimoyama et al., 2023). This research aims to develop an AAV-based vaccine platform co-expressing both proteins within a single viral genome.

Materials and Methods

The SFTSV glycoproteins Gn (535 aa) and Gc (538 aa), derived from the M segment of the YG1 strain, were cloned into an AAV vector flanked by inverted terminal repeats (ITRs). The resulting AAV-GnGc construct was packaged into adeno-associated virus serotype 9 (AAV9) via triple transfection of HEK293T cells. Recombinant AAV9-GnGc particles were purified by gradient iodixanol and buffer-exchanged into formulation buffer. Transgene expression was validated in vitro by immunofluorescence assay (IFA) and Western blot (WB).

Results and Discussion

Recombinant AAV9 particles with SFTSV glycoprotein genes were successfully produced. Robust expression of both Gn and Gc proteins was confirmed by WB, while IFA demonstrated their cellular localization. These findings are consistent with previous study highlighting that AAV is an effective vector for transgene expression. In addition, recombinant AAV particles were effectively assembled, exhibited a robust viral titer (1.5 x 1014 vg/ml); *in vivo* evaluation in mouse models is required to assess the immunogenicity of AAV9-GnGc.

Conclusion

SFTSV is an emerging zoonotic pathogen threatening public health, with reported subclinical circulation in pigs posing potential risks to vet and workers with frequent contact. Previous study using AAV9 expressing individual SFTSV glycoproteins (Gn or Gc) have demonstrated preventive potential. In this study, robust *in vitro* expression of AAV9-GnGc supports further evaluation in animal models, highlighting a promising vaccine candidate for mitigating SFTSV burden in high-risk occupational groups.

Keywords: Adeno-associated virus, Glycoproteins, Severe fever with thrombocytopenia syndrome virus.
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DEVELOPMENT OF A GRAPHENE OXIDE-BASED APTASENSOR FOR RAPID DETECTION OF *SALMONELLA ENTERICA*

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Introduction and Objectives

Salmonella enterica is a leading cause of foodborne disease, particularly in pork production, where pigs act as asymptomatic carriers (Saenkankam et al., 2025.). Current detection methods are time-consuming and laboratory-dependent. This study aimed to develop a rapid electrochemical aptasensor targeting the FliC protein of *S. enterica*, using *S.* Typhimurium and *S.* Rissen as representative serovars.

Materials and Methods

A chemically modified 2′F-RNA aptamer was immobilized on a screen-printed graphene electrode (SPGE) modified with graphene oxide-bovine serum albumin (GO-BSA) nanocomposites. Electrochemical responses were measured using differential pulse voltammetry (DPV). The calibration curve was generated by plotting the current change (rI) against the log of bacterial concentration (100 - 108 CFU/mL). Specificity was evaluated against a panel of eight common gut pathogens, including *Bacillus cereus, Escherichia coli, Enterococcus faecalis, Listeria monocytogenes, Pseudomonas aeruginosa, Shigella sonnei,* and *Staphylococcus aureus*.

Results and Discussion

The aptasensor exhibited a linear response described by the equation (rI (μA) = 0.4713 log C + 1.189 (R2 = 0.9634). The calculated limit of detection (LOD) was 4.8 CFU/mL, comparable to the PCR (2 CFU/mL) while shorter assay time (Vinayaka et al., 2019). Specificity tests showed significant signal differentiation ($P < 0.05$) between *Salmonella* targets (> 3.12 μA) and non-target bacteria (range: 0.29 - 1.03 μA). The total assay time was approximately 20 minutes.

Conclusion

This study presents a highly sensitive and specific GO-BSA aptasensor for the rapid screening of *S. enterica*. Its ability to detect common serovars suggests strong potential for food safety surveillance in pork production systems. Future work will focus on validating detection performance in complex matrices.

Keywords: Aptasensor, Food safety, Pork production, Rapid detection, *Salmonella enterica.*

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INTERACTION BETWEEN PRRS STATUS AND "ANTIBIOTIC-FREE" (PSA) PRODUCTION: TECHNICAL RIGOR AS A DRIVER FOR PERFORMANCE

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Introduction and Objectives

The "Antibiotic-Free" (PSA) production model requires a drastic reduction in antimicrobial use, which can be challenging in the presence of endemic diseases. This study compares the performance of four groups of farms based on their PSA engagement (from 42 days of age) and their Porcine Reproductive and Respiratory Syndrome (PRRS) status. The objective is to evaluate whether the technical management required by PSA specifications allows farms to maintain high performance even when facing a PRRS challenge.

Materials and Methods

Technical and economic performance data (GTE) and health indicators (ALEA, health expenses) of 1134 french pig farms, members of Cooperl cooperative, using Nucleus genetic lines, were analyzed across four categories: Standard PRRS-, Standard PRRS+, PSA PRRS-, and PSA PRRS+. All PPRS + farms are vaccinated against PRRS either sows and/or piglets. Key indicators included growth rate (standardized age at 115 kg), mortality (wean-to-finish), and carcass quality (meat percentage and technical value). Statistical significance was assessed using P-values ($P < 0.05$).

Results and Discussion

Surprisingly, the "PSA" group, either PRRS Positive or Negative, achieved the best economic and growth results, with a technical premium of 14.32 and 14.12 ct€/kg and a standardized age of 180 and 179 days. In contrast, "Standard - PRRS Negative" farms had the lowest performance (184.95 days and 13.53 ct€/kg), despite a more favorable health status (PRRS negative status). Productivity: PSA farms had higher numbers of piglets weaned per litter (13.42 vs 13.11) and more kg produced per sow per year (2713 vs 2184, $P < 0.05$). Health: Wean-to-finish losses were significantly lower in PSA farms (6.02 vs $P < 0.01$). Carcass: Lung (3.64 vs 5.96% bad lungs) and nasal (2.62 vs 5.60% bad nose) lesion scores at the slaughterhouse were lower in the "PSA - PRRS Negative" group compared to all other groups suggesting respiratory clinical signs for PRRS + farms or Standard Negative farms.

Conclusion

These results demonstrate a "performance paradox": the absence of PRRS does not compensate for lower technical mastery or systemic antibiotic use. The constraints of the "Antibiotic-Free" specifications appear to act as a lever for technical rigor, allowing farmers to outperform standard herds even in challenged environments.

Keywords: Antibiotic-free, PRRS, Performance, Technical rigor, Pig production.

ESCHERICHIA COLI IN DIARRHEIC PIGLETS: ASSOCIATIONS BETWEEN VIRULENCE FACTORS AND ANTIMICROBIAL RESISTANCE IN BRAZILIAN HERDS

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Introduction and Objectives

Escherichia coli (E. coli) strains harboring specific adhesins and toxins cause enteric disease and represent public health risks. This study aimed to investigate associations between antimicrobial resistance phenotypes and major virulence genes in E. coli isolated from diarrheic piglets in Brazil.

Materials and Methods

Between 2024 and 2025, 537 *E. coli* isolates were screened by PCR for toxin genes (LT, STaP, STb, Stx2e) and adhesin genes (K88 (F4), K99 (F5), F18, F41). Antimicrobial susceptibility testing was performed using disk diffusion test, following CLSI and EUCAST guidelines. Associations were evaluated using Fisher's exact test ($P < 0.05$).

Results and Discussion

Significant associations were observed between virulence determinants and antimicrobial resistance profiles in *E. coli* isolates from diarrheic piglets. Adhesins F18 and F41 were mainly associated with resistance to β-lactams, fluoroquinolones, aminoglycosides, tetracyclines, and sulfonamides, while enterotoxins (STb, STa, LT) and Stx2e were associated with resistance to amoxicillin, sulfamethoxazole/trimethoprim, norfloxacin, tilmicosin, and tiamulin ($P < 0.05$). These findings suggest a potential linkage between virulence and resistance traits, possibly mediated by mobile genetic elements that promote co-selection (Do et al., 2020). However, as antimicrobial usage data were not available, the observed associations may also reflect recent treatment-related selection pressure in diarrheic piglets rather than stable genetic linkage within the bacterial population. Amoxicillin resistance showed significant co-occurrence with multiple antimicrobial classes, including cephalosporins, fluoroquinolones, tetracyclines, aminoglycosides, florfenicol, and sulfonamides, frequently exceeding 60% ($P < 0.05$). Additional associations were observed among fluoroquinolones and between doxycycline and tetracycline. Similar multidrug resistance patterns in porcine *E. coli* have been linked to indiscriminate antimicrobial usage practices, since resistance genes are frequently clustered within mobile genetic elements (Davies & Wales, 2019). Regarding virulence profiles, F18 was frequently associated with other adhesins and toxins, including F41, STb, Stx2e, LT, STa, F4 (K88), and F5 (K99), indicating complex virulence gene combinations ($P < 0.05$) (Renzhammer et al., 2020).

Conclusion

The observed associations between virulence determinants and resistance to critically important antimicrobials in *E. coli* suggest possible co-selection dynamics and underscore the importance of integrated surveillance of virulence and antimicrobial resistance in swine production systems.

Keywords: Antimicrobial resistance, *Escherichia coli*, Piglets, Virulence factors.

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BACTERIAL INHIBITION CAPACITY OF EXTRACTS PEELS FROM AVOCADO (PERSEA AMERICANA) AND POMEGRANATE (PUNICA GRANATUM L.)

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Introduction and Objective

Antimicrobial resistance (AMR) occurs when microorganisms stop responding to treatments, hindering infection control and increasing mortality. This is caused by the inappropriate use of antimicrobials in humans and animals (intensive in agricultural production), which represents a considerable cost to national economies, livestock production, and their health systems, affecting industrial productivity and prolonging hospital stays that require more expensive and intensive care. Currently, the search for alternatives to antibiotic use has focused on the antimicrobial potential of medicinal plant extracts since the peels and seeds have been found to be rich in bioactive substances such as polyphenols and chlorophylls, which are responsible for antioxidant and antimicrobial activity. This is the first step in studying antimicrobial characteristics of two phyto drugs as a treatment option for pigs.

Materials and Methods

A bacterial suspension of *E. coli* and *S. aureus* was prepared in PBS adjusted to a McFarland 1 standard, and then mixed with aquaethanolic extracts of Persea americana and Punica granatum L peel at a concentration of 10 g/L. The mixture was allowed to stand for 15 minutes, after which the Minimum Inhibitory Concentration (MIC) test was performed by titration and drop plating onto BHI agar. Finally, the plates were incubated at 37°C for 24 hours for analysis. The analysis was performed in triplicate.

Results and Discussion

The extracts showed antimicrobial activity against the bacteria studied, with a reduction in bacterial growth (CFU) observed during the first replicate. However, in the second replicate, this inhibitory activity decreased, which could be associated with the possible alteration of phenolic compounds present in the extracts, considering that this replicate was performed one week after the initial one.

Conclusion

The plant extracts exhibit inhibitory activity against bacterial growth; however, their effectiveness decreases over time. This highlights the importance of considering the storage conditions and stability of the extracts when evaluating their antimicrobial potential and their application in future studies, as well as their concentration and diluter. This opens a window to new alternatives for reducing microbial load in different contexts, including the preservation of porcine semen and topical use in swine production management.

Keywords: Ram, Plant Extracts, Bacterial Inhibition, Pig Farming.

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CHARATERIZATION OF *ENTEROCOCCUS FAECALIS* AND *E. FAECIUM* ISOLATES FROM PIGS, SWINE FARM ENVIRONMENTS, AND FARM WORKERS IN SOUTH KOREA

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Introduction and Objectives

Enterococci are gram-positive bacteria that is an opportunity bacteria found in the typical gut flora of both animals and humans as well as in the environment. *Enterococcus faecalis* and *E. faecium* cause a broad spectrum of healthcare-associated infections. Their emergence and spread of antimicrobial resistance (AMR) among livestock are one of the serious public health concerns. This study was carried out to investigate the AMR profiles of *Enterococcus* isolates from healthy pigs in two swine farms during 2024, where are located in a city of Gyeonggi Province, South Korea.

Materials and Methods

Using a standard culture method, enterococcal species were isolated and identified using the bioMérieux VITEK MS system. Antimicrobial susceptibility testing was conducted with 12 antimicrobial disks commercially available.

Results and Discussion

In this study, a total of 334 Enterococcus isolates were obtained from 216 healthy pigs, 128 swine farm environments, and 64 farm workers. Among them, our experimental analyses revealed that 262 E. faecalis and 14 E. faecium strains were isolated with the average isolation rate of 67.6%. Interestingly, E. faecium strains (5.1%) were isolated much less than those of *E. faecalis* (94.9%). Further AMR profiling demonstrated the prevalence of multi-drug-resistant *E. faecalis* strains, especially strains carrying streptomycin-chloramphenicol-tetracycline resistant phenotypes. The highest resistance levels were observed for tetracycline (the resistance ranging from 79.3 ~ 80.5%), followed by streptomycin (the resistance ranging from 44.8 ~ 58.3%), and chloramphenicol (48.8 ~ 56.3%) among the *E. faecalis* strains. No resistance to vancomycin was detected from both *E. faecalis* and *E. faecium* strains in this study.

Conclusion

In swine farming, *E. faecalis* and *E. faecium* are critical indicator bacteria for monitoring antimicrobial resistance (AMR) under the One Health framework. These species act as a reservoir for resistance genes that can be transmitted between animals, humans, and the environment. In this study, we observed high prevalence of MDR *E. faecalis* and *E. faecium* strains. Since the study has been carried out with very limited number of swine farms, the continued monitoring of these species is essential for their source tracking as well as establishing proper interventions in farm managements and/or One Health AMR stewardship.

Keywords: Antimicrobial resistance, Enterococcus faecalis, Enterococcus faecium, One health, Swine farms.

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ASSOCIATION BETWEEN ON-FARM WELFARE INDICATORS AND INTESTINAL BARRIER INTEGRITY IN WEANED PIGLETS

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Introduction and Objectives

Weaning represents a critical period in pig production associated with social, nutritional, and environmental stressors that may compromise intestinal barrier integrity and animal welfare (Guevarra et al 2019; Marçal et al. 2024). Although welfare assessment protocols are widely used in commercial farms, their relationship with gut health biomarkers remains poorly understood. The objective of this study was to evaluate the association between on-farm welfare indicators and intestinal barrier integrity markers in piglets during the post-weaning period.

Materials and Methods

Eight commercial pig farms were included in the study. Fecal samples were collected from 10 piglets per farm (n = 80) at weaning and 15 days post-weaning to evaluate intestinal barrier integrity using inflammatory and epithelial biomarkers. Animal welfare was assessed at farm level using a structured survey that included feed supply, water supply, pen usage, lighting, climatic environment, physical environment, lesions, mortality and culling control, sick animal management, animal mixing, behavioral expression, stereotypes, piglet quality at weaning, post-weaning feeding program, and microbial pressure. Internal consistency of the welfare was validated using Cronbach's alfa. Associations between welfare indicators and intestinal biomarkers were analyzed using Spearman correlation with FDR correction (Benjamini-Hochberg method).

Results and Discussion

Significant correlations were observed between welfare indicators and intestinal biomarkers. Interferon gamma showed a strong positive correlation with animal mixing ($\rho = 0.710$, $P = 0.014$) and staff management ($\rho = 0.693$, $P = 0.018$). A negative correlation was detected between interferon gamma and pen usage ($\rho = -0.712$, $P = 0.014$). Occludin levels were negatively correlated with social behavior expression ($\rho = -0.347$, $P = 0.026$). These findings suggest that management practices influencing social stress and housing conditions may modulate inflammatory responses and epithelial barrier function during the post-weaning transition.

Conclusion

This study demonstrates associations between welfare indicators and intestinal barrier integrity biomarkers in weaned piglets. Integrating welfare assessment tools into herd health monitoring may help identify management practices that support gut health and improve post-weaning adaptation.

Keywords: Animal Welfare, Gut Health, Intestinal Barrier, Piglets, Weaning.

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EFFECTS OF SURGICAL CASTRATION AND PAIN MITIGATION PROTOCOLS ON SHORT-TERM GROWTH IN PIGLETS

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Introduction and Objectives

Surgical castration of piglets is a common husbandry practice associated with acute pain and stress, which impairs animal welfare and may influence short-term performance. While different anaesthesia and analgesia protocols are increasingly used to reduce piglets' pain, it remains unclear how they affect post-procedural growth performance. The aim of this study was to evaluate differences in weight gain among piglets castrated without anaesthesia and analgesia and under different anaesthesia and analgesia protocols. A secondary objective was to distinguish the effects of surgical castration from those of anaesthesia and analgesia alone by including corresponding non-castrated control groups.

Materials and Methods

Six piglets per litter from eight litters per group were included (48 piglets per group). Five control (handling / handling + treatment) and five experimental (castration /castration + treatment) groups were evaluated. Treatments included meloxicam and one of the following methods of anaesthesia: isoflurane inhalation anaesthesia, local anaesthesia with procaine, or general anaesthesia with azaperone and ketamine. A group, castrated without analgesia and anaesthesia was included. Weight was recorded before castration or handling and at 24 and 72 h post procedure. Linear mixed models were used, with average daily gain modelled as a function of treatment group, time interval (0 - 24 h vs. 24 - 72 h), and their interaction. Random effects of litter and piglet nested within litter were included. Statistical significance was assessed using Type III ANOVA with Satterthwaite approximation, and pairwise comparisons were performed using emmeans with Tukey adjustment.

Results and Discussion

No significant differences in weight gain among castrated groups and no group-by-time interaction was found. Only the time interval had a significant effect, with higher gain from 24 - 72 h than from 0 - 24 h. In non-castrated groups, the weight gain did not differ by group, but a significant group-by-interval interaction suggested different time-course patterns. Tukey-adjusted pairwise comparisons within each interval were non-significant.

Conclusion

Short-term weight gain was not significantly affected by the type of anaesthesia or analgesia used during surgical castration. However, weight gain alone does not adequately reflect the multifactorial nature of pain and stress, which should be assessed using additional behavioural and physiological indicators.

Keywords: Anaesthesia, Analgesia, Animal Welfare, Piglet castration, Weight gain.

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ANTIMICROBIAL RESISTANCE AND VIRULENCE GENE ASSOCIATIONS IN *STREPTOCOCCUS SUIS* SEROTYPE 9 FROM BRAZILIAN SWINE FARMS

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Introduction and Objectives

Streptococcus (S.) suis is a major swine pathogen and an important zoonotic agent, with serotype 9 increasingly reported in several production systems worldwide, including Brazil. This study aimed to evaluate the associations between virulence genes and antimicrobial resistance phenotypes in *S. suis* serotype 9 isolates recovered from clinical swine cases in Brazil.

Materials and Methods

Between 2024 and 2025, 74 *S. suis* serotype 9 isolates were collected from 10 Brazilian states. Virulence-associated genes (mrp, strf, ofs, sly, and epf) were detected by PCR, and antimicrobial susceptibility was determined using the disk diffusion method in accordance with CLSI and EUCAST guidelines. Associations between virulence genes and antimicrobial resistance phenotypes were evaluated using Fisher's exact test, with statistical significance set at $P < 0.05$.

Results and Discussion

Among the virulence-associated genes analyzed, epf was the most prevalent (25/74), followed by strf (22/74) and mrp (16/74). A significant positive association was observed between sly and epf ($P < 0.05$), with co-occurrence detected in approximately 14.9% of the strains. No significant associations were detected among mrp, strf, and ofs. As previously reported, the presence of individual virulence-associated genes alone is insufficient to cause disease and must be accompanied by host, management, and coinfection factors (Aradanas et al., 2021). The sly gene was significantly associated with susceptibility to amoxicillin, penicillin, ciprofloxacin, and marbofloxacin ($P < 0.05$), with odds ratios <1, indicating a reduced likelihood of resistance among sly-positive strains. Similarly, the ofs gene showed a negative association with resistance to florfenicol and ceftiofur ($P < 0.05$), suggesting that strains carrying this gene were less frequently resistant to these antimicrobials. Amoxicillin and ceftiofur resistance were strongly linked to multidrug resistance, and consistent co-resistance clusters were observed among fluoroquinolones, tetracyclines, macrolides, and aminoglycosides ($P < 0.05$). This pattern aligns with historical data indicating that multidrug resistance has been widespread in *S. suis* populations in Brazil, likely reflecting sustained antimicrobial selection pressure in swine production systems (Matajira et al., 2020).

Conclusion

Overall, these results reveal contrasting patterns in *S. suis* serotype 9, with limited virulence gene associations but extensive antimicrobial resistance clustering, highlighting concerns about multidrug-resistant strains in Brazilian swine production.

Keywords: Antimicrobial resistance, Pigs, *Streptococcus suis*, Virulence.

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EVALUATION OF THE ANTIBACTERIAL EFFICACY OF COSCINIUM FENESTRATUM, SILVER NANOPARTICLES, AND CHITOSAN AGAINST *STAPHYLOCOCCUS AUREUS* IN VETERINARY MEDICINE

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Introduction and Objectives

Multidrug-resistant (MDR) pathogens increasingly endanger veterinary health, shifting from antibiotics to non-antibiotic biomaterials has become an essential global clinical step, moving beyond theoretical ideas (Ahmed et al., 2024). Promising options include plant-derived phytochemicals, metallic nanoparticles, and natural polymers, each offering distinct strategies to combat bacterial resistance (Shahzadi et al., 2025; Shaik et al., 2024). Here, the antimicrobial effects of Coscinium fenestratum, silver nanoparticles (AgNPs), and chitosan against the reference strain Staphylococcus aureus ATCC 25923 are examined.

Materials and Methods

The antibacterial activity of Coscinium fenestratum [Traditional medicine pharmacy, Vietnam], silver nanoparticles (AgNPs), and chitosan [commercial shrimp shell product, Vietnam] against Staphylococcus aureus ATCC 25923 [Pasteur Institute, HCMC, Vietnam] was assessed using the diffusion method on MHA. The MIC and MBC were determined using the broth dilution method in BHI, with optical density (OD) measured at 620 nm. The inhibition percentage relative to negative controls was calculated as: Inhibition (%) = [1 - (At24 - At0) / (Bt24 - Bt0)] x 100, where At and Bt are the OD values for the treatment and control groups at 0 and 24 hours.

Results and Discussion

Coscinium fenestratum has a moisture content of 9.25 ± 0.88% and a total polyphenol content of 11.56 ± 0.34 mg GAE/g. The chitosan samples surveyed met the standard physical requirements (white powder, shrimp flavor), with a moisture content of 11.87 ± 0.7%, 7% solubility, and a 5-minute dissolution time, yielding 462 mg of chitosan per gram. For antibacterial activity against *Staphylococcus aureus* ATCC 25923, silver nanoparticles (AgNPs) showed the highest effectiveness, with MIC and MBC values of 0.003125 mg/mL and 0.005 mg/mL, respectively. Chitosan followed, with MIC of 1.25 mg/mL and MBC of 12.5 mg/mL. The crude extract of C. fenestratum had an MIC of 12.5 mg/mL and an MBC of 50 mg/mL, indicating that all tested substances exhibited inhibitory activity against the bacteria.

Conclusion

This study emphasizes the significant potential of AgNPs and chitosan-based products in creating antibacterial treatments for animals. Using these materials alongside C. fenestratum supports efforts to reduce reliance on antibiotics in contemporary veterinary practice.

Keywords: AgNPs, Coscinium fenestratum, Chitosan, *Staphylococcus aureus*, MIC & MBC.

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EFFECTS OF DIFFERENT VOLUMES OF A WATER-SOLUBLE AND BIODEGRADABLE NESTING MATERIAL ON BEHAVIOR IN SOWS

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Introduction and Objectives

Providing nesting material supports natural behavior and reduces stress in sows, but optimal quantities for crated systems remain unclear (Monteiro et al., 2023). Conventional materials may obstruct slurry systems when supplied in large amounts (Plush et al., 2021), whereas water-soluble alternatives allow greater provision without management constraints. Based on this, the present study aimed to evaluate how different amounts of a novel water-soluble biopolymer nesting material influence pre-farrowing nest-building behavior in sows.

Materials and Methods

Multiparous sows were assigned to three treatments: no nesting material (CON), 3 kg (BN3), or 15 kg (BN15) of a water-soluble biopolymer provided 24 h before expected farrowing, and behavior was recorded by cameras. Standardized behavioral data were analyzed using PCA to visualize treatment differences, with group separation assessed by confidence ellipses and PERMANOVA based on Bray-Curtis dissimilarity.

Results and Discussion

The first two PCA dimensions explained 71.1% of behavioral variation. BN15 sows were associated with higher nest-building activity, while control sows showed more stereotypies, postural changes, ventral lying, and redirected nest-building to floor. BN3 showed an intermediate profile. PERMANOVA confirmed significant differences between BN3 and BN15 compared with CON ($P < 0.05$), with no differences observed between BN3 and BN15 ($P > 0.10$).

Conclusion

Providing prepartum sows with water-soluble nesting material enhanced nest-building behavior and reduced stress-related behaviors. Supplying at least 3 kg appears effective for improving behavioral welfare in crated sows without compromising slurry systems.

Keywords: Biopolymer nesting, Redirected nesting-building behavior, Stereotypes, Welfare.

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JAPANESE ENCEPHALITIS VIRUS ASSOCIATED WITH REPRODUCTIVE AND NEONATAL DISORDERS IN PIG HERDS IN NORTHERN VIETNAM

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Introduction and Objectives

Japanese encephalitis virus (JEV) is highly endemic in Vietnam, where pigs serve as primary amplifying hosts and infection can lead to reproductive losses. Although seroprevalence in Vietnamese swine is known to be high, field-based evidence linking JEV to reproductive disorders and recent genomic data from clinically affected herds remain limited.

Materials and Methods

This study investigated the clinical, pathological, serological, and molecular characteristics of JEV infection in 11 pig farms in northern Vietnam experiencing acute reproductive abnormalities. Seroprevalence was assessed using a JEV-specific antibody ELISA kit (VDPro®, Median). Tissue samples were tested using RT-PCR targeting the JEV M-E gene, and representative amplicons were sequenced for phylogenetic genotyping. Brain tissues were examined histologically (H&E).

Results and Discussion

Serological testing of adult pigs (n = 300) revealed widespread exposure, with an overall ELISA seroprevalence of 52.7%, highest in sows (75.0%). Tissue samples from fetuses and neonates (n = 57) were examined by RT-PCR, detecting JEV RNA in 28.1% of cases and more frequently in fetal tissues (36.4%). Gross lesions included edema and hydranencephaly, while histopathology showed neuronal degeneration, gliosis, glial nodules, and marked perivascular cuffing consistent with nonsuppurative viral encephalitis. Sequencing of three representative RT-PCR–positive samples identified genotype I viruses clustering with contemporary Asian strains.

Conclusion

These findings indicate that JEV is an important contributor to reproductive and neonatal disease in pig herds in northern Vietnam and underscore the need for strengthened surveillance and reproductive health monitoring within a One Health framework.

Keywords: Japanese encephalitis virus, reproductive disorder, Vietnam.

POSTERS

TOPIC 11: REPRODUCTION TECHNOLOGIES AND LACTATION (RTL)

EVALUATION OF THE EFFICACY OF AN ANTI-MYCOTOXIN AGENT IN MITIGATING THE ADVERSE EFFECTS OF ZEARALENONE IN PREPUBERTAL GILTS

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Introduction and Objectives

Swine are recognized as one of the most susceptible species to the toxic effects of mycotoxins. Zearalenone (ZEN) is of concern due to its estrogenic activity. Sows are especially sensitive to this compound, which can disrupt reproductive physiology, leading to impaired fertility and decreased reproductive efficiency (Wu et al., 2021). This experiment evaluated the efficacy of an anti-mycotoxin agent that included adsorbing material, turmeric (curcumin) extract (500ppm) and milk thistle (silymarin) extract (1500ppm), and yeast-based components, in mitigating the adverse effects of ZEN in prepubertal gilts, acting through adsorption, bioprotection, and postbiotic effects.

Materials and Methods

64 prepubertal gilts with an average body weight of 8.58 kg were included in the 21-day trial. All animals received ad libitum feed and water. The control diet was analyzed in order to ensure the absence of mycotoxins. Animals were assigned to three groups: control, ZEN-exposed (1.2 ppm), and ZEN-exposed (1.2 ppm) with anti-mycotoxin treatment (5 kg/ton). Vulvar volume was recorded every five days, and reproductive tract morphometry was assessed post-slaughter. Statistical analyses were performed using linear mixed-effects and regression models, with individual animals as the experimental unit; significance was set at $P < 0.05$.

Results and Discussion

ZEN exposure induced estrogenic and hypertrophic effects in prepubertal gilts, increasing vulvar volume (+1006.63 cm^3), reproductive tract length (+4.69 cm), and relative tract weight (+0.04 %). The anti-mycotoxin agent significantly alleviated these effects, reducing vulvar volume ($P = 0.0003$) and relative tract weight ($P = 0.0036$); while the decrease in tract length (–2.53 cm) was not statistically significant. Additionally, ZEN caused uterine hypertrophy, increasing endometrium (+176.66 µm), myometrium (+45.55 µm), and total wall thickness (+225.07 µm). The anti-mycotoxin agent attenuated these alterations: - 65.49 µm, -38.08 µm, and -103.90 µm, respectively. Direct comparison between control and ZEN-exposed animals receiving anti-mycotoxin treatment showed complete restoration of macroscopic estrogenic indicators (vulvar swelling, tract length) alongside partial mitigation of microscopic tissue changes.

Conclusion

In summary, ZEN induced pronounced estrogenic alterations in prepubertal gilts, confirming the expected estrogenic activity. The anti-mycotoxin agent at 5kg/ton significantly mitigated these effects, confirming its protective efficacy against ZEN-induced reproductive toxicity.

Keywords: Anti-mycotoxin agent, Prepubertal gilts, Reproductive toxicity, Zearalenone.

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EFFECT OF THE SYNTHETIC PROGESTERONE-LIKE GESTAVET® SYNC ON ESTRUS SYNCHRONIZATION IN PRE-PUBERTAL GILTS

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Introduction and Objectives

Estrus synchronization in prepubertal gilts is critical for optimizing breeding efficiency in commercial swine systems, where uniform reproductive timing enables precise artificial insemination scheduling and improved labour management. Altrenogest, an oral progestin, binds to progesterone receptors in the hypothalamus and pituitary. This suppresses the secretion of FSH and LH and inhibits the hypothalamic–pituitary–gonadal axis until treatment is stopped. Following treatment cessation, a gonadotropin surge triggers estrus and ovulation. The objective of this study was to evaluate the effect of Altrenogest on estrus synchronization in cycling gilts. The study also considered the following variables: the time after treatment withdrawal"and the onset of estrus, estrus concentration in treated females, conception rate, total number of piglets born, and live-born piglets.

Materials and Methods

A prospective, uni-center, block-designed study involving 402 terminal-cross, PIC breed, cycling gilts (mean age: 213 ± 11 days) that had previously exhibited estrus was conducted. The gilts were assigned to a control group (CTL, n = 200; no treatment) or a treatment group (ALT, n = 202; 20 mg altrenogest administered orally once daily at the same time for 18 consecutive days). Estrus was detected daily using a boar, and pregnancy was confirmed by the non-return of estrus and transabdominal ultrasound on days 21 and 35 respectively.

Results and Discussion

No estrus was observed in the ALT group during the 18-day treatment period. The first detection of estrus occurred on day 4 post-treatment, and the last detection occurred on day 9. This resulted in a significantly narrower estrus window (mean interval: 3.7 ± 1.4 days versus 10.4 ± 3.1 days ($P < 0.005$ for ALT and CTL, respectively). There were no significant differences in conception rate, total number of piglets born, or number of live-born piglets between groups ($P = 0.066$, $P = 0.086$, and $P = 0.086$, respectively).

Conclusion

These findings demonstrate that Altrenogest effectively synchronizes estrus in gilts, reduces age dispersion at weaning, and optimizes breeding logistics and resource allocation. These improvements occur without negatively impacting fertility or litter performance under commercial conditions.

Keywords: Altrenogest, Estrus synchronization, Cycling gilts, Reproductive management, Swine.
Acknowledgements: We would like to thank the INGACOT swine company and its entire staff for their assistance with this study.

DETERMINANTS OF STILLBIRTH IN SOWS UNDER TROPICAL CLIMATIC CONDITIONS: INFLUENCES OF FARROWING MONTHS, PARITY, AND LITTER SIZE

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Introduction and Objectives

Stillbirth is a major reproductive issue in hyperprolific sows and is influenced by parity, litter size, and seasonal heat load in tropical regions (Udomchanya *et al*., 2019; Tummaruk *et al*., 2023; Ngo *et al*., 2024). This study evaluated the effects of farrowing months on stillbirth rate, with additional consideration of parity and total piglets born.

Materials and Methods

A total of 10,039 litters from 5,370 Landrace × Yorkshire sows in a northern Thai commercial herd (2023) were retrospectively analyzed following methods described by Akkhaphan et al. (2025). Variables included farrowing month, parity, litter size, stillbirth, and environmental conditions. Sows were grouped by month, parity, and litter-size class. Data were analyzed using SAS 9.4.

Results and Discussion

Overall stillbirth rate was 5.8% and differed by farrowing month ($P = 0.036$), lowest in March (4.6%) and higher in February (6.9%), June (6.5%), and August–November (6.2 - 6.4%), consistent with heat stress impairing farrowing. Stillbirth was lower in parity 2 - 3 (5.4%) than in parity 4 - 6 (6.3%) sows ($P = 0.002$). Litters ≥16 piglets showed higher stillbirth (6.3%) than those with 13 - 15 piglets (5.4%) ($P < 0.001$), reflecting intrauterine crowding.

Conclusion

Stillbirth was influenced by farrowing month, parity, and litter size. Elevated rates during hotter periods, in older sows, and in large litters highlight the roles of thermal load, reduced uterine efficiency, and fetal crowding. Targeted management of heat, parity structure, and litter size may help reduce stillbirth in tropical systems.

Keywords: Heat stress, Parity, Stillbirth, Total born, Tropical environment.

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FACTORS INFLUENCING THE INCIDENCE OF MUMMIFIED FETUSES IN SOWS UNDER TROPICAL CONDITIONS

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Introduction and Objectives

Mummified fetuses represent an important reproductive disorder in pig production, leading to reduced litter size and substantial economic losses (Olanratmanee et al., 2025). Their occurrence is affected by multiple factors, including season, parity, herd, and year (Jaichansukkit et al., 2017). Therefore, this study aimed to evaluate the effects of farrowing month, parity, working hours, and total number of piglets born on the incidence of fetal mummification under tropical climatic conditions.

Materials and Methods

This retrospective study analyzed 10,039 litters from 5,370 Landrace × Yorkshire sows in a commercial herd in central Thailand in 2023, using data collection methods consistent with those of a previous reproductive study (Akkhaphan et al., 2025). Recorded variables included farrowing month, parity, working hours (07:00–17:00 h), and litter characteristics, including the proportion of mummified fetuses per litter. Sows were classified according to farrowing month, parity, working hours, and litter-size category. Statistical analyses were conducted using SAS software (version 9.4).

Results and Discussion

On average, total piglets born and born alive per litter were 13.6 ± 4.0 and 12.0 ± 4.2, respectively. The incidence of mummified fetuses was 6.2% and varied by farrowing month ($P < 0.001$), ranging from 2.9% in August to 10.6% in December. Primiparous sows showed a higher incidence than multiparous sows ($P < 0.001$), consistent with greater susceptibility in gilts (Borges et al., 2005). Litters with ≤ 12 piglets and those farrowed during working hours had higher incidences of mummified fetuses than larger litters and those farrowed during non-working hours ($P < 0.001$).

Conclusion

Under tropical conditions, the incidence of mummified fetuses averaged 6.2% and varied according to farrowing month, parity, litter size, and working hours. Higher incidences were observed in primiparous sows, in litters with ≤ 12 piglets, and during working hours.

Keywords: Herd, Litter size, Mummy, Parity, Reproduction.

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EFFECT OF ORIGINAL XPC™ ULTRA SUPPLEMENTATION DURING ALL GESTATION AND LACTATION ON REPRODUCTIVE PERFORMANCE AND LITTER GROWTH IN MULTIPAROUS SOWS

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Introduction and Objectives

Optimizing sow nutrition during gestation is critical for fetal development, piglet growth and livability. Previous studies have shown yeast-derived postbiotics (SCFP) modulate the maternal and neonatal gut microbiota, enhance offspring intestinal health, and ultimately improve sow reproductive performance (Chang et al. 2024). The present study evaluated the SCFP impact on reproductive performance and piglet growth while sows were fed from early gestation till end of lactation.

Materials and Methods

A total of 364 multiparous sows (Landrace × Large White; average parity 4.5) were allocated to two dietary treatments: a control diet (CON) and a diet supplemented with XPC™ Ultra (1 kg/T feed; SCFP) from early gestation to weaning. Data on litter size total born, born alive, weaned piglets, birth weight and weaning weight were analyzed using a randomized complete block design with parity as fixed effect and sows within treatment as the random effect (PROC MIXED, SAS 9.4). Data were analyzed using the T-test and declared as significant at $P < 0.05$.

Results and Discussion

Sows fed SCFP exhibited significant improvements in total born alive (+1.26 piglets; $P < 0.0001$), litter weight (+3.96 kg; $P < 0.0001$), and average piglet birth weight (+0.19 kg; $P < 0.0001$) compared to CON. At weaning, litter weight increased by 24% (+ 17 kg; $P < 0.0001$), and piglets were heavier (+ 510 g; $P < 0.01$). Pre-weaning mortality decreased by 27% ($P < 0.0001$). It is hypothesized SCFP through microbiota modulation improve the sow energetic status for better placental and fetal nutrition and milk production.

Conclusion

Supplementation of SCFP in early gestation improved sow reproductive performance, reduced mortality, and enhanced piglet growth at weaning. These findings support the inclusion of postbiotics in sow feeding programs to optimize productivity and animal livability.

Keywords: Postbiotics, sow, reproductive performance, mortality, litter growth.

Acknowledgements: The authors thank the Chulalongkorn University, Thailand for the support with providing testing facilities and analyzing the data.

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EFFECTS OF POST-FARROWING PHYTOTHERAPEUTIC TREATMENT ON THE PUERPERIUM AND REPRODUCTIVE PERFORMANCE OF FREE-FARROWING SOWS

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Introduction and Objectives

Phytotherapeutic agents represent a promising alternative to conventional treatments in livestock (Scheuber et al., 2025). Therefore, the objective of this study was to assess the effects of intrauterine administration of a phytotherapeutic preparation on clinical parameters during the puerperium and on reproductive performance in the subsequent litter.

Materials and Methods

A total of 151 sows housed in a free-farrowing system were enrolled in the study. The animals were assigned to one of three groups: a phytotherapy group (300 mL EucaComp® diluted in 0.9% NaCl, n = 49), a placebo group (300 mL 0.9% NaCl, n = 50), and an untreated control group (n = 51). Intrauterine application was carried out once 3 - 12 hours after expulsion of the last piglet using an extended insemination catheter. Fever (Body temperature of ≥ 40°C on the first day post-partum and/or ≥ 39.3 °C on other days), feed intake (Empty through within 1 hour), and vaginal discharge were recorded daily during the first seven days postpartum (Discharge present). Additionally, performance parameters of the current litter (body weight loss of sow (kg), litter and piglet weaning weight (kg)) and reproductive indicators in the subsequent reproductive cycle (total born piglets (n), return-to-oestrus rate (%)) were documented.

Results and Discussion

Reduced feed intake occurred significantly less frequently in the phytotherapy group compared with the placebo and control groups (24 vs. 38 vs. 57%; P = 0.003). The incidence of vaginal discharge was significantly lower in the phytotherapy and control group compared to the placebo group (70 vs. 90 vs. 73%; P = 0.033). No significant differences were observed in the occurrence of fever among groups (34 vs. 38 vs. 35%; P = 0.913). Litter performance parameters and reproductive outcomes in the subsequent cycle did not differ significantly between treatments. A non-significant trend toward a reduced return-to-oestrus rate was observed in the phytotherapy group (6.7 vs. 8.9 vs. 19.5%; P = 0.140).

Conclusion

In conclusion, intrauterine application of EucaComp® significantly improved feed intake without affecting next reproductive performance. Phytotherapeutic treatment may therefore serve as a useful adjunct or alternative to conventional therapeutic approaches.

Keywords: Feed intake, Vaginal discharge, Intrauterine application, Postpartal disorders, Farrowing pen.

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INFLUENCE OF FARROWING ASSISTANCE ON POSTPARTUM UTERINE INVOLUTION IN SOWS MANAGED IN TEMPORARY CONFINEMENT SYSTEMS UNDER TROPICAL CLIMATE

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Introduction and Objectives

Uterine involution restores the uterus to its non-pregnant size and condition, enabling reproductive cycles. Delayed involution can impair fertility and reduce reproductive performance, leading to economic losses in swine production (Björkman et al., 2017). This study investigated the association between farrowing assistance and uterine involution in sows.

Materials and Methods

Ninety Landrace × Yorkshire sows housed in temporary confinement system were assigned to assisted (n = 17) and unassisted (n = 73) groups. Sow and piglet parameters were recorded. Uterine and uterine vessel diameters were measured on days 2 - 14 postpartum and day 21 using transcutaneous ultrasonography with a 5-MHz convex abdominal probe (M9, Mindray®, China), with three cross-sectional measurements averaged per assessment. Linear mixed models were used, with farrowing assistance as a fixed effect and parity and litter size as covariates ($P < 0.05$).

Results and Discussion

Sows receiving farrowing assistance had a longer farrowing duration (322.2 vs. 168.7 min, $P = 0.007$) and a greater total number of piglets born (17.1 vs. 14.3, $P = 0.005$) than unassisted sows, consistent with the higher likelihood of intervention in hyperprolific sows (Wongwaipisitkul et al., 2024). Uterine involution did not differ between groups. Assisted sows showed a reduction in uterine diameter from 31.6 to 13.2 mm (57.3%), while unassisted sows decreased from 29.3 to 12.1 mm (58.1%) between days 2 and 21 postpartum ($P = 0.794$); however, uterine diameter was greater in assisted sows on days 2 ($P = 0.028$), 6($P = 0.049$), 7 ($P = 0.028$), 14 ($P = 0.044$), and 21 postpartum ($P = 0.005$). Uterine vessel diameter declined similarly in assisted (3.9 to 3.0 mm; 23.4%) and unassisted sows (4.1 to 3.0 mm; 25.2%) over the same period ($P = 0.454$), indicating comparable uterine recovery 3 weeks postpartum.

Conclusion

Farrowing assistance was associated with larger uterine diameters, likely due to longer farrowing duration and greater litter size, but it did not affect the rate of uterine involution or vascular regression. Both assisted and unassisted sows returned to normal uterine size within 3 weeks postpartum, indicating that farrowing assistance does not impair uterine recovery in tropical temporary confinement systems.

Keywords: Farrowing assistant, Pig, Postpartum, Uterus, Ultrasound

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UTILISATION OF BRIX CLASSIFICATION OF SOW COLOSTRUM AT FARROWING AS A PREDICTOR OF SOW PRODUCTIVITY

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Introduction and Objectives

Brix measurement of colostrum provides an inexpensive, rapid and accurate estimate of IgG concentration, enabling practical differentiation in colostrum quality (Hasan et al., 2016). Adequate passive immunity is essential for piglet survival, and colostrum is a key determinant of early-life health. Understanding factors associated with variation in colostrum IgG offers insight into broader aspects of sow performance. This study aimed to determine whether the IgG concentration of colostrum, as indicated by its Brix value, is associated with sow productivity traits, specifically the number of piglets born alive and born dead.

Materials and Methods

Colostrum IgG was assessed on-farm using a digital Brix refractometer in 952 multiparous sows from five commercial farms representing a range of genetic lines. 0.3 ml of freshly collected colostrum was analysed immediately after sampling to obtain a Brix percentage value. Productivity records were available for all sows which included the number of piglets born alive/dead. Brix values were classified into four categories: poor (< 20), borderline (20 - 24.9), adequate (25 - 29.9), and very good (≥ 30). For broader interpretation, values were also grouped as optimal (≥ 25) or suboptimal (< 25). Data were analysed using a linear mixed-effects model fitted by REML. Brix category and parity were fixed effects, and farm was included as a random effect.

Results and Discussion

A substantial proportion of sows (36.8 %) produced colostrum classified as suboptimal. These sows tended to have fewer piglets born alive compared with optimal sows (16.43 vs. 17.14; $P = 0.08$). Differences in stillbirth rate were more pronounced: optimal sows had significantly fewer piglets born dead (8.1 %) than suboptimal sows (9.4 %; $P = 0.03$). These results suggest that colostrum quality, beyond its established role in passive immunity, may also reflect underlying maternal performance and physiological status.

Conclusion

Colostrum quality is a key determinant of piglet survival, but this study demonstrates that it also serves as an indicator of sow productivity. The high proportion of sows producing suboptimal colostrum highlights considerable opportunity for improvement. Monitoring herd-level colostrum status and implementing strategies to enhance colostrum quality may support both piglet viability and overall reproductive performance, offering meaningful economic benefits.

Keywords: Colostrum, IgG, Piglets born alive, Sows, Sow Productivity.

Acknowledgements: I would like to acknowledge and thank all colleagues who contributed to the collection, collation and analysis of the data for their dedication, perseverance and sustained effort in producing this dataset.

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OPTIMISING SOW COLOSTRUM QUALITY: A MULTI-FARM EVALUATION OF BRIX CLASSIFICATION IN SOWS SUPPLEMENTED WITH COLFAPIG

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Introduction and Objectives

Colostrum quality in sows is a critical determinant of piglet survival, health, and long-term performance, driven by well-established biological mechanisms. It also serves as a practical indicator of sow productivity reflecting physiological capacity, immune status, nutritional adequacy, and mammary function. Measuring colostrum using a Brix refractometer provides a rapid, inexpensive, and sufficiently accurate estimate of IgG concentration, enabling clear differentiation between high- and low-quality colostrum. This study aimed to quantify the impact of ColfaPig (Devenish Nutrition, Belfast) on colostrum quality using Brix classification.

Materials and Methods

Colostrum IgG content was assessed on-farm using a Brix refractometer before and after ColfaPig supplementation in 1,623 multiparous sows across eight commercial farms in five countries, representing diverse genetic lines. ColfaPig was included in gestation and lactation diets at 1 kg/tonne for at least 12 weeks prior to farrowing. Fresh colostrum samples (0.3 ml) were collected within 0 - 3 hours post-farrowing and analysed immediately. Brix values were categorized as poor (< 20), borderline (20 - 24.9), adequate (25 - 29.9), and very good (≥ 30). For further interpretation, values were grouped as optimal (≥ 25) or suboptimal (< 25). Data were analysed using a linear mixed-effects model fitted by REML, with treatment and parity as fixed effects and farm as a random effect.

Results and Discussion

ColfaPig supplementation significantly increased average Brix values ($P < 0.001$), shifting the mean from borderline (23.5) to adequate (27.3). This improvement corresponded with a substantial rise in the proportion of sows producing optimal colostrum, increasing from 45.6% pre-supplementation to 76.1% post-supplementation ($P < 0.001$). The shift in Brix classification indicates a meaningful enhancement in IgG concentration and overall colostrum quality, suggesting improved immunological support for new born piglets.

Conclusion

ColfaPig supplementation elevated colostrum quality from borderline to adequate and significantly increased the proportion of sows producing optimal colostrum to 76.1%. Enhancing colostrum quality has the potential to improve piglet survival, growth, health, and sow lifetime productivity.

Keywords: Colostrum, IgG, Piglets born alive, Sows, Sow Productivity.
Acknowledgements: I would like to acknowledge and thank all colleagues who contributed to the collection, collation and analysis of the data for their dedication, perseverance and sustained effort in producing this dataset.

INFERTILITY IN A GILT DUE TO THE PRESENCE OF CYSTIC ENDOMETRIAL HYPERPLASIA

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Introduction and Objectives

Cystic endometrial hyperplasia (CEH) is a uterine disorder characterised by an increase in the size and number of endometrial gland cells. It has an endocrinological origin and results from prolonged stimulation by oestrogen and progesterone, leading to increased secretions and reduced myometrial contractility. Cervical closure prevents secretion drainage, causing uterine thickening and cystic gland dilation. This paper reports on the diagnosis and macroscopic and histological findings of CEH in a gilt with repeat breeding.

Material and Methods

After puberty, the gilt was bred on five occasions without achieving pregnancy in any of them. For breeding scheduling, estrus was synchronized in all cases by orally administering 20 mg of altrenogest for 18 consecutive days; after completion of the treatment, a boar was introduced daily to induce the onset of estrus, once standing heat was observed, two semen doses were administered. At 19 months of age, she was euthanized for macroscopic and histological examination of the genital tract. Uterine and cyst samples were paraffin-embedded and sectioned at 4 - 5 µm and stained with haematoxylin–eosin.

Results and Discussion

On macroscopic examination, both ovaries were in the luteal phase, with corpora lutea and small follicles approximately 1 mm in diameter. The uterine horns exhibited marked thickening and elongation. Internally, cystic endometrial hyperplasia was identified, characterized by numerous serous, transparent cysts of varying sizes (3 - 25 mm) that almost completely occupied the uterine lumen. Histological analysis showed that the cyst walls preserved the typical endometrial structure, consisting of superficial columnar epithelium and connective tissue rich in blood vessels and secretory glands. Smooth muscle fibers and a thin perimetrium were also evident. These anatomopathological findings in this CEH case, with extensive endometrial cyst formation, resulted in chronic fertilization failure in the gilt. Ultrasonography is recommended for CEH diagnosis (Moson et al., 2016), based on detection of multiple spherical anechoic structures distributed throughout the uterus.

Conclusion

The persistent occurrence of fertilization failure over time in a gilt has been associated with the presence of CEH at a very advanced stage.

Keywords: Cystic endometrial hyperplasia, Endometritis, Infertility.

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REPRODUCTIVE CONSEQUENCES OF USING A BOAR FROM AN ARTIFICIAL INSEMINATION CENTRE CARRYING THE RECIPROCAL TRANSLOCATION RCP (3;18) (Q14;Q21)

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Introduction and Objectives

Karyotypic alterations can lead to reproductive disorders due to chromosomal imbalances arising in gametes during meiosis. In pigs, the most frequent chromosomal abnormalities are reciprocal translocations (rcp), which consistently result in reduced litter size due to early embryonic mortality and, in some cases, decreased fertility. In the present study, a breeding boar from an artificial insemination centre was identified as a carrier of the rcp(3;18) (q14; q21). The reproductive impact of this chromosomal alteration was assessed by evaluating the fertility and prolificacy of sows inseminated with his semen doses.

Material and Methods

The experiment was conducted on a single commercial farm using hybrid Large White × Landrace sows. Semen doses were obtained from Duroc boars at an artificial insemination center. Each sow received two semen doses during estrus, potentially from different boars. The first insemination was performed at the onset of the standing reflex in the presence of a teaser boar, and the second 24 hours later. The boars' karyotypes were determined by GTL banding analysis in lymphocytes. After identifying a boar carrying a rcp, its reproductive impact was evaluated in sows inseminated during the same experimental period. A total of 315 sows were inseminated with semen from non-carrier boars, whereas 84 sows were inseminated under a scheme including the carrier boar, contributing one of the two semen doses per insemination (50%), no sow was inseminated exclusively with semen from this animal.

Results and Discussión

Cytogenetic analysis identified a boar carrying the rcp(3; 18) (q14; q21). Reproductive performance was assessed using data from artificial inseminations conducted during the period in which the carrier boar was used for breeding. A non-significant reduction of 3.71 percentage points in fertility was observed in sows inseminated with semen doses containing 50% contribution from the carrier boar (78.78% compared with 82.49%). In contrast, prolificacy was significantly reduced by 1.72 piglets per litter in sows whose inseminations involved the carrier boar (8.59 versus 10.86 piglets).

Conclusión

Cytogenetic analysis identified a boar carrying a reciprocal translocation in its karyotype. Boars with such chromosomal abnormalities can lead to substantial production and economic losses; therefore, early identification is essential

Keywords: Reproductive failure, Prolificacy, Fertility, Karyotype, Reciprocal translocation.

THE EFFICACY OF SILVER NANOPARTICLE-SUPPLEMENTED SEMEN TUBE ON THE ANTIMICROBIAL ACTIVITY OF DILUTED BOAR SEMEN DURING PRESERVATION AT 18°C

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Introduction and Objectives

Semen contaminated with bacteria can reduce sperm quality and antimicrobial-resistant bacteria have been increasing (Keeratikunakorn et al, 2024). Silver nanoparticles (AgNPs) have been widely used as an effective antimicrobial agent. AgNPs could inhibit Staphylococcus aureus and no negative effect on sperm quality at 4 mM (Pérez-Duran et al., 2020). New technology, AgNPs are added to polymeric materials, which can slow the release of Ag+ by water diffusion (Kosai et al., 2019). Therefore, the Ag+ can be released slowly for a longer time and concentration of Ag+ is no effect normal cell damage. This study aimed to test the antimicrobial activity of AgNPs-supplemented in the semen tube.

Materials and Methods

Ten fresh boar semen samples were collected and diluted with (A) extender containing gentamicin 250 mg/L; (B) extender without antibiotic; (C) extender without antibiotic and stored in AgNPs50 ppm-supplemented semen tube. Each group's sperm concentration was 3×10^9 spermatozoa/100 mL. The diluted samples were incubated at 18°C until evaluation. After 2, 24, 48, and 72 h of storage, all samples were collected and diluted with normal saline by a tenfold solution. 100 µL per dilution was spread on plate count agar (PCA) and cultured at 37°C. The colonies were counted at 48 hours and calculated into CFU/mL.

Result and discussion

After incubation at 18 °C, bacterial count from semen sample in group B went up to log 2.73 ± 0.15 CFU/mL at 2 h, remained constant at 2 - 24 h and sharply increased to log 3.49 ± 0.29 CFU/mL at 72 h. However, the bacterial count in group C was slightly increased to 2.13 ± 0.33 CFU/mL at 72 h, which bacterial count of group C lower than group B across the experiment. This indicated that AgNPs-supplemented semen tubes can control bacterial growth in diluted boar semen.

Conclusion

AgNPs-supplemented semen tubes showed the potential of bacterial growth inhibition after preservation of diluted semen at 18 °C. From this study, our team can prove that AgNPs can control bacteria in boar semen. Untilnow, using AgNPs in boar semen extender is scarce; we have to study more about the efficiency and toxicity to sperm before using on a commercial farm in the future.

Keywords: Silver nanoparticles, Semen tube, Semen contaminated with bacteria.

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ASSOCIATIONS BETWEEN MATERNAL BLOOD GLUCOSE LEVELS, SOW PERFORMANCE, FARROWING TRAITS, AND PIGLET VITALITY IN FREE-FARROWING SYSTEMS

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Introduction and Objectives

Farrowing is a physiologically demanding process that requires the sow to rapidly mobilize large amounts of energy to support uterine contractions and ensure successful delivery. This study aimed to assess the effect of blood glucose on farrowing kinetics in free farrowing conditions.

Materials and Methods

In 147 sows, feeding time, peripheral glycemia of sows (collected from the ear vein) at the onset and the farrowing process was evaluated including farrowing duration (first piglet-last placenta) and obstetrical intervention (piglet-piglet interval > 60 min; manual extraction of piglets and administration of oxytocin (20 IU)).

Results and Discussion

A mean farrowing duration of 422 ± 130 min and an average of 16.1 ± 3.6 total born piglets were recorded. Blood glucose concentration at the onset of farrowing averaged 4.44 ± 0.63 mmol/L and increased to 4.72 ± 0.79 mmol/L by the end of farrowing. In the general linear model, the interval between the last meal and the onset of farrowing significantly affected farrowing duration ($P = 0.007$). Sows whose last meal was consumed in the morning prior to farrowing exhibited significantly lower blood glucose levels (4.33 mmol/L) compared with sows fed in the evening (4.51 mmol/L; $P = 0.009$); however, they tended to have a shorter farrowing duration (397 vs. 439 min; $P = 0.053$). Obstetrical interventions were required in 50% of the sows. Farrowings involving birth assistance lasted 59 min longer than unassisted farrowings ($P < 0.001$) and tended to be associated with 0.5 more stillborn piglets ($P = 0.054$). Blood glucose concentrations did not differ between sows with or without obstetrical intervention. Older sows (> 4 litters) exhibited lower blood glucose levels at the onset of farrowing and required significantly more birth assistance (62% vs. 37%). Additionally, older sows had a higher number of stillborn piglets compared with younger sows (1.42 vs. 0.78).

Conclusion

Glycaemia had no significant effect on farrowing duration and therefore cannot be used as a predictor of dystocia in sows. However, glycaemic levels were influenced by sow parity and the timing of the last meal prior to farrowing.

Keywords: Glycaemia, Farrowing duration, Parity, Obstetrical intervention, Timepoint of last feeding.

EFFECTS OF THE APPLICATION OF AN ANTI-GNRH VACCINE IN IBERIAN FEMALES FATTENED UNDER FIELD CONDITIONS

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Introduction and Objectives

Immunization against GnRH (gonadotropin-releasing hormone) in Iberian gilts has been reported to provide productive and welfare benefits (Palomo et al., 2012). This study aimed to assess both productive performance and animal welfare in immunocastrated Iberian gilts.

Materials and Methods

Two groups of 50 Iberian gilts were studied: a control batch (C) without treatment and a vaccine batch (V) which received two doses (2 ml) of Vacsincel® (Zoetis, Parsippany NJ, USA) at 27 and 31 weeks of age. Each animal was individually ear-tagged and weighed at 27, 31, 33, 35, 37 and 39 weeks of age, until slaughter at 150 kg live weight. Productive data were recorded, and statistical analyses were performed using R® environment (R Foundation for Statistical Computing, Vienna, Austria), applying mean comparison tests and relevant correlations. Social behavior like mounting, presence of wounds, etc., was evaluated coinciding with the onset of vaccine effect, at 33, 35, and 37 weeks of age. Observations were conducted consistently by the same methodology and personnel. Social behavior was assessed using descriptive exploratory analyses, as the limited number of replications did not allow for classical inferential statistics.

Results and Discussion

Average daily gains (ADG) between consecutive weighings, showed no statistically significant differences. Comparing cumulative ADG between the first weighing and subsequent weighings, from the third onward, either significance or a trend towards significance was observed. This demonstrates that the effect is progressive. Between the first and fifth weighings (first slaughters), statistically significant differences ($P < 0.05$) were found with an improvement of 81.41 g (ADG; C = 0.7447 ± 0.0223 g/day and V = 0.8261 ± 0.0315 g/day). Regarding mortality, a rate of 4% was observed in the C versus 0% in the V, and greater weight dispersion or batch heterogeneity was noted in the C (StandDev C vs V). Behavioral assessments revealed that the V group showed fewer negative social interactions and reduced aggression, reflecting improved welfare

Conclusion

Immunocastration in Iberian gilts may enhance productive performance (statistically proven) and reduce negative social behaviors (not statistically confirmed), supporting improved animal welfare under commercial conditions. Further studies are necessary to confirm this trend.

Keywords: Aggression, Animal welfare, Average daily gain (ADG), Iberian gilts, Immunocastration.
Acknowledgements: The authors thank Juan Pablo Sánchez, Professor at the University of Córdoba, Spain, for his expert advice in statistical data analysis.

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EFFECTS OF PROSTAGLANDIN F2A ON PROLIFERATION, APOPTOSIS AND HORMONE SECRETION OF PORCINE OVARIAN GRANULOSA CELLS *IN VITRO*

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Introduction and Objectives

Exogenous synthetic Prostaglandin F2α (PGF2α) is used for estrus regulation in female livestock. However, its effects on proliferation, apoptosis, and hormone secretion of porcine ovarian granulosa cells (GCs) remain unclear. This study explored the effects and mechanisms of Prostaglandin F2α Tromethamine (PGF2α-T) on porcine GCs' proliferation, apoptosis, and hormone secretion in vitro. The findings may clarify the regulatory mechanisms of porcine follicular development and corpus luteum regression, providing theoretical support for optimizing PGF2α administration protocols in estrus synchronization and parturition synchronization programs.

Materials and Methods

The ovarian tissues were collected from sows weighing approximately 100 kg at a slaughterhouse. GCs were isolated, identified by FSHR, and treated with varying concentrations of PGF2α-T for 24 h. CCK-8, EdU, ELISA and qRT-PCR were used to detect proliferation, apoptosis, hormone levels, and related gene expressions. All experiments were performed with 3 independent biological replicates, each including 3 technical replicates.

Results and Discussion

After treating the cells with PGF2α-T for 24 hours, the proliferation-promoting effect was enhanced as the hormone concentration increased, and the most significant promoting effect was observed at 100 $\mu g \cdot mL^{-1}$ PGF2α-T. It significantly promoted proliferation, accompanied by upregulated mRNA levels of cell cycle-related genes (CCNA1, CCNB2, CCND1, CCNE1, PCNA, IGF1, IGF2) and PI3K/AKT pathway genes (PI3K, AKT, mTOR), which may mediate the pro-proliferative effect via accelerating cell cycle progression and activating the PI3K pathway. In addition, 400 $\mu g \cdot mL^{-1}$ PGF2α-T induced significant apoptosis, with elevated mRNA expressions of apoptosis-related genes (Caspase-3, Caspase-9, Bax/Bcl-2), attributed to upregulated apoptotic gene expression. When GCs were treated with 3 ~1000 $\mu g \cdot mL^{-1}$ PGF2α-T for 24 h, the secretion levels of estrogen and progesterone in the cells were decreased in a dose-dependent manner. Additionally, 100 $\mu g \cdot mL^{-1}$ PGF2α-T significantly inhibited the mRNA expression levels of FSHR and LHR, promoted the mRNA expression level of PTGFR, and significantly suppressed the mRNA expressions of CYP19A1, CYP11A1, and StAR.

Conclusion

Under the tested in vitro conditions, PGF2α-T regulates the proliferation, apoptosis, and hormone secretion of porcine GCs by upregulating cyclins, activating the PI3K/AKT pathway, promoting apoptosis markers, downregulating hormone receptors and steroidogenic genes.

Keywords: Apoptosis, Granulosa cells, Porcine, Proliferation, Prostaglandin F2α Tromethamine.

EFFECTS OF A PLANT-BASED COMPLEMENTARY FEED ON THE PERFORMANCE OF SOWS AND SUCKLING PIGLETS DURING LACTATION

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Introduction and Objectives

Hyperprolificity presents increased risk for sows (longer farrowing, dysgalactia…) which impacts piglet survival and homogeneity at weaning. Physiologically, farrowing and lactation are periods associated with high oxidative stress and inflammatory conditions, favoring the depletion of sows' immune system and therefore performance. To assess the effects of a phytogenic supplementation on sows and their piglets, incorporated in lactation diet.

Materials and Methods

The study was carried out in IFIP (French Institute for Pig and Pork) experimental farm on 72 sows (Large White x Landrace) divided in two groups on their arrival in farrowing house. They were fed the same lactation diet, with phytogenic supplementation SOWEL at 1 kg/T of feed (7 days before farrowing and during lactation) for trial group and without for control group, until piglet weaning at 28 days of age. Colostrum samples (30 - 50 mL) were collected from teats (front and rear) during farrowing. It was filtered through gauze and frozen. Valid samples were sent on dry ice to the third-party laboratory. Total IgG was analyzed using ELISA (Bethyl), with samples diluted to 1/200,000 and measured in triplicate. Farrowing time was recorded (camera) and piglets' survival rate.

Results and Discussion

Phytogenic supplementation during lactation tended to improve sow peripartum parameters and piglet survival under hyperprolific conditions. Sows receiving the supplementation tend to show a shorter farrowing duration (245 vs. 282 min; $P = 0.08$), a lower proportion of farrowing lasting more than 5 h, and spent less time in ventral lying posture during the 24 h post-partum period ($P = 0.06$). Colostrum IgG concentration was significantly higher in the supplemented group (97 vs. 86.5 mg/mL; $P = 0.03$). Piglet survival at 28 days was improved, particularly in light piglets (≤ 1 kg at birth), with a 50% reduction in mortality associated with dehydration and wasting conditions.

Conclusion

Phytogenic supplementation during lactation promotes piglet survival through the sows. These effects are concomitant with an overall improvement of sow peripartum conditions: improved farrowing dynamics, reduced post-partum discomfort and enhanced colostrum immunological quality. Altogether, these findings suggest that the supplementation contributes to a smother farrowing, ultimately supporting piglet viability and improved weaning outcomes.

Keywords: Hyperprolific, Oxidative stress, Phytogenic.

EFFECT OF DIFFERENT GONADOTROPIN FORMULATIONS ON REPRODUCTIVE PERFORMANCE AND OVULATION TIMING IN MULTIPAROUS SOWS

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Introduction and Objectives

Weaning to estrus interval (WEI) variability is a key driver of non-productive days in sow herds. Exogenous gonadotropins such as eCG and eCG+hCG aim to stimulate the onset of estrus and ovulation in prepubertal gilts and weaned sows, contributing to a decrease in NPDs. This study compared two gonadotropin treatments with a saline control to evaluate their effects on reproductive intervals and estrus synchronization in multiparous weaned sows.

Materials and Methods

Multiparous sows of varying parity and body condition (BC score and P2 backfat) were enrolled at weaning and randomly allocated to Control, Gestavet® or PG600® groups, 50 sows per group. Weaning was Day 0, and treatments Gestavet® or PG600® (5 mL/sow; 400 IU eCG + 200 IU hCG) were administered on Day 1 post-weaning. Sows were monitored twice daily for estrus by boar exposure and inseminated following farm AI protocols. Continuous variables (P2, WEI) were analyzed with non-parametric tests (Kruskal-Wallis for P2 and Mann-Whitney for pairwise WEI). Categorical outcomes (pregnancy positive/negative by ultrasound; sectorial probe-3.5 MHz day 24 - 27 post IA) were assessed using chi-square and association coefficients, with $\alpha = 0.05$.

Results and Discussion

Mean P2 backfat was 10.69 mm across groups (Control, Gestavet®, PG600®), with no significant differences ($P = 0.927$, Kruskal-Wallis). Estrus rates reached 90% for both treatments vs. 80% control ($P = 0.236$, chi-square). WEI reduced significantly with Gestavet® (96 ± 14.6 h, $P = 0.014$ vs. control 105±16.9 h) and PG600® (97.1 ± 16.1 h, $P = 0.028$ vs. control), but not between treatments ($P = 0.883$, Mann-Whitney). Pregnancy rates were equivalent (Gestavet®/Control 87%, PG600® 84%; $P = 0.914$, chi-square). These findings align with eCG+hCG literature in multiparous sows: ~9-hour WEI reduction via follicular recruitment without impairing fertility (Knox et al., 2006). Comparable pregnancy rates confirm oocyte/luteal quality. Results support routine use for < 100-hour WEI, minimizing non-productive days

Conclusion

Backfat P2 at weaning was similar among groups, excluding body condition as a confounding factor. Both Gestavet and PG600 reduced WEI by about 9–10 h compared with the untreated control. No significant difference in WEI was detected between the two hormonal treatments, indicating comparable efficacy. Similar fertility across groups suggests that shortening WEI did not impair subsequent reproductive performance.

Keywords: Gonadotropins, Weaning-to-estrus interval, Estrous duration, Reproductive performance.

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THE IMPACT OF A BIOACTIVE MINERAL FEED ADDITIVE ON SOW PRODUCTIVITY UNDER FIELD CONDITIONS IN QUEENSLAND AUSTRALIA

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Introduction and Objectives

A bioactive mineral-based feed additive (BMF), (marketed as Optimize or Proteck geography depending) has been found to increase pigs weaned by 0.7 pigs/litter and improve sows' reproductive performance. The objective of this study was to assess the impact of the BMF on sow productivity under Australian field conditions over a longer period.

Materials and Methods

A long-term longitudinal study was run at 330-sow, farrow to finish farm in Queensland Australia. A total of 81 weeks of data were collected, 18 control (249 farrowings), 16 as a transition (241 farrowings) and 47 weeks (650 farrowings) using BMF at a rate of 2 kg per tonne in both gestation & lactation feed through weeks 19th 2024 to 29th 2025. The farm was run and managed as normal with no changes to management practices or feed made during the evaluation period. Data during the transition period was omitted in the analysis. Sow productivity data (total born (TB), born alive (BA), pigs weaned (PW)) was collected as weekly averages from the farm throughout the period. Data was analysed using JMP statistical discovery 18.2.1.a) A further subset of data was analysed specifically examining the impact of the BMF on sows that farrowed during the summer/ autumn season (December 2024 through May 2025) vs January through May 2024 prior to the start of the feeding of BMF.

Results and Discussions

The average parity was 2.27 ± 6% throughout the period. A rotavirus outbreak was experienced from week 26 of 2024 and eventually controlled by week 43 of 2024. The data from this period was included in the sow productivity analysis. There was a tendency to improve TB per litter (+ 0.44, $P = 0.105$), BA (+ 0.46, $P = 0.062$) and PW (+ 0.51, $P = 0.068$). In the summer/ autumn period TB increased by 0.51 ($P = 0.082$), BA by 0.49 ($P = 0.051$) and PW significantly by 1.21 ($P = 0.001$). Overall pre-weaning mortality dropped from 18.8% to 15.0% ($P = 0.041$) when the rotavirus period was excluded.

Conclusions

This study demonstrates the potential positive impact that supplementing sow diets with the BMF additive has on sow productivity under Australian conditions. Observed response is consistent with previously published studies.

Keywords: Gestation, Lactation, Pigs weaned, Sow Productivity.

ASSESSMENT OF PASSIVE IMMUNITY TRANSFER IN PIGLETS WITH RELEVANCE TO COLOSTRUM MANAGEMENT STRATEGIES

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Introduction and Objectives

Colostrum intake in piglets is important when considering survival, growth and disease resistance (Theil et al., 2014). The study investigated colostrum intake in 10 pig farms by measuring antibodies against PCV-2 or swine erysipelas.

Materials and Methods

Ten Flemish pig farms that agreed to participate were selected. For each farm, blood was collected on two different occasions, each time from 5 sows and 6 piglets/sow (< 7 days old). An ELISA was used on the serum (Biebaut et al., 2021) to test for antibodies against Porcine Circovirus type 2 (PCV-2) or *Erysipelothrix rhusiopathiae* (swine erysipelas). Cut-off values were set at 1070 for PCV-2 and 40 S/P% for *Erysipelothrix rhusiopathiae*; samples at or below these values were considered negative, whereas higher values were considered positive. Colostrum intake was deemed sufficient when the serum antibody ratio of the piglets to that of the mother sow was ≥ 100%. Between the two sampling points, potential risk factors for low colostrum intake were collected using a questionnaire. Based on the results of the questionnaire, farm-specific advice was given to the farmers to optimize colostrum management.

Results and Discussion

The serum antibody ratio (piglets/sow) in the 10 farms ranged from 78 - 212% and 85 - 156% in the first and second sampling point, respectively. On 6 of the 10 pig farms, colostrum intake was sufficient between the sampling points (107 - 212%). On 3 other farms, colostrum intake was insufficient during the first sampling (78 - 94%). In 2 of these farms, they managed to achieve adequate colostrum intake at the second sampling (101% and 104%) by improving feed intake and reducing stress. The third farm did not manage to increase its colostrum intake at the second sampling point (85%), despite the implementation of corrective measures. The colostrum intake in 1 remaining farm was sufficient at the first sampling (131%) but borderline insufficient at the second sampling (99%).

Conclusion

Colostrum intake can be improved by identifying risk factors and proper guiding of pig farmers, though success is not guaranteed. Optimal colostrum management can be achieved by realizing a proper vaccination strategy, optimal drinking water and feed management, and smooth farrowing.

Keywords: Antibodies, Colostrum, Colostrum management, ELISA, Risk factors.

Acknowledgements: The authors thank all participating farms for their support with providing information and allowing us to assess the colostrum intake by the piglets.

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EFFECTS OF GONADOTROPIN TREATMENT ON POST-WEANING ESTRUS IN SECOND-PARITY SOWS: A FIELD CASE STUDY

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Introduction and Objectives

Sow reproductive performance is key for the efficiency of pig farms. The estrus rate within one week after weaning impacts farm profitability. Additionally, anestrus sows may increase culling rates, leading to a high replacement rate and severely impacting the sustainable development of the farm. This study aimed to evaluate the effect of PG600® administration at weaning on post-weaning estrus rate and anestrus incidence in second-parity sows.

Materials and Methods

This case study took place on a commercial farm (386 sows) recently repopulated in Hebei province, China. The herd was PRRS-stable before and during the trial, with no major health issues. After repopulation, a high culling rate due to a high post-weaning anestrus rate (23%) was reported (August 2024 - February 2025). During March 2025, 65 second-parity sows were weaned (historical control group, CG) and their reproductive performance (number of sows exhibiting estrus within 7 days post-weaning (pw), beyond 7 days, and anestrus) recorded. During April, 63 second-parity sows were weaned (test group, TG), treated at weaning day (PG600®) and their reproductive performance recorded. Only sows with a body condition score >1 were enrolled. No significant management, nutritional and environmental measures were implemented between both periods. Data were analyzed by binary logistic regression.

Results and Discussion

The reproductive performance from sows in TG was improved compared to CG. The overall estrus rate was significantly higher in TG (96.82%) compared to CG (76.92%) (OR = 9.15; CI95% [2.00 - 41.92]; $P < 0.05$). The percentage of sows in estrus within 7 days post-weaning was also significantly higher in TG (95.24%) compared to CG (69.23%) (OR = 8.89; CI 95% [2.49- 31.76]; $P < 0.001$). The number of sows in anestrus was significantly reduced in the TG (n = 2) compared to the CG (n = 15) (OR = 0.11; CI 95% [0.02-0.50]; $P < 0.05$).

Conclusion

This preliminary field observation suggests that treating second-parity sows with the tested gonadotropins on the weaning day may significantly increase the overall estrus rate and the estrus rate within 7 days post-weaning compared to a control group. Further research is needed to confirm these preliminary results, including a randomized, side-by-side comparison to avoid confounding risks related to historical comparisons.

Keywords: Anestrus, Estrus rate, Reproductive performance, Wean-to-estrus interval.
Acknowledgements: The authors thank the producer for the field support during the trial.

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EFFECT OF BIOACTIVE MINERAL FEED ADDITIVE ON THE OXIDATIVE STATUS OF SOWS

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Introduction and Objectives

Oxidative stress is a concern in modern swine production and tends to increase together with rising reproductive performance. This study aimed to evaluate the effect of a bioactive mineral feed additive (BMF) (marketed as Optimize or Proteck), on the oxidative status of sows under farm conditions.

Material and Methods

Four independent studies were conducted on commercial farms in the USA (Song et al, 2020), Italy (awaiting publication), Thailand (Elanco data on file) and Spain (Purser et al, 2025), with a total of 2,016 sows. Sows were allocated to either a control group or a treatment group. The treatment group had BMF added at 2 kg/tonne of gestation & lactation feed. Blood samples were collected on day 114 of gestation for analysis (Italy: 145 control, 75 treatment; Spain: 20 control, 19 treatment; Thailand: 39 control, 41 treatment; USA: 15 control, 15 treatment. The biomarkers assessed were Derivatives of Reactive Oxygen Metabolites (d-ROMs) in Italy, glutathione peroxidase (GPX) in Spain, Thailand and the USA, using commercially available kits.

Results and Discussion

In the Italian study, the BMF-fed group showed significantly lower levels of dROMs, indicating a 34% reduction in oxidative damage compared to the control group ($P < 0.0001$). In Spain, while no overall statistical difference was observed in GPX levels, a higher proportion of sows fed BMF (47%) exhibited GPX activity greater than 100 nm/min/mL, compared to 30% in the control group, suggesting an improved antioxidant capacity. In the USA study the BMF group significantly increased GPX levels (47.8 IU/ ml vs 41.7 IU/ mL; $P < 0.05$) and the proportion of sows with < 30 IU/mL tended to reduce from 20% of sows sample to 0% of sows sampled ($P = 0.09$). The study in Thailand found that the levels of GPX increased significantly from 938 nmol/min/ml to 971 nmol/min/mil ($P = 0.0158$).

Conclusions

The results from presented studies indicate that supplementing BMF to sow diets has a positive impact on their oxidative status. The observed reduction in markers of oxidative damage and the suggested improvement in antioxidant enzyme activity demonstrate the additive's potential to mitigate oxidative stress in gestating sows under commercial conditions.

Keywords: Sow, Oxidative Stress, Gestation, Lactation.

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RELATIONSHIP OF BIRTH WEIGHT AND FARROWING KINETICS ON SURVIVAL PROBABILITY IN A COMMERCIAL SWINE FARM

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Introduction and Objectives

Prolonged farrowing in hyperprolific sows increased from 130 min to 396 min, elevating stillbirth rates (Laothong et al., 2024), approximately 10 - 20%. Neonatal mortality occurred in predominantly within the first 48 hours post-farrowing (Schoos et al., 2023). Birth order (BO), birth weight (BW), expulsion interval (EI), and cumulative EI (CEI) are recognized as critical factors of piglet survivability (Laothong et al., 2024). This study aimed to investigate an association of BO, BW, EI, and CEI on farrowing kinetics and perinatal mortality in commercial hyperprolific sows.

Materials and Methods

Data from 250 crossbred sows (Large White × Landrace) with 3,247 piglets were collected. Immediately after birth, time of birth and BW were recorded. BO was ranked sequential of birth within a litter and categorized into four quartiles (Q1 - Q4). CEI was calculated as the cumulative time elapsed from the first piglet birth. Generalized linear mixed models (GLMM) with sow and farrowing batch as random effects were used to evaluate the association of BW, BO, EI, CEI on stillbirth incidence. Survival analysis was used to determine CEI survival probability.

Results and Discussion

As BO increased, EI decreased simultaneously. EI at Q1 vs Q4 showed 19.2 ± 3.1 min and 12.8 ± 2.5 min ($P < 0.05$). Overall stillbirth rate was 10.8%, which increased progressively across BO quartile (Q1-Q4) as 8.2%, 9.5%, 11.4%, and 13.8%, respectively. GLMM demonstrated that BW (OR of being mortal = 0.694 as BW 0.10 kg increased, $P < 0.001$), CEI (OR of being mortal = 1.085 as CEI 10 min longer, $P < 0.001$) significantly affected stillbirth. Survival probability declined progressively with median survival time of 347 min.

Conclusion

Factors such as BO, BW and CEI significantly affected piglet survivability during the parturition. Late-born piglets faced higher mortality than early born piglets. The 347-min median survival time indicates that farrowing supervision should intensify to improve piglet survivability in hyperprolific herds. These findings suggest that targeted assistance for late-born piglets may reduce stillbirth incidence.

Keywords: Birth order, Expulsion interval, Farrowing, Survivability

Acknowledgements: The authors thank Papon Farm for providing research facility.

EFFECT OF ENDOCANNABINOID STIMULATOR TOP-DRESSING ON LACTATING SOW PERFORMANCE AND PIGLET GROWTH

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Introduction and Objectives

Reduced feed intake during lactation can impair sow body condition and limit piglet growth, lowering overall productivity. The endocannabinoid (ECB) system regulates appetite and energy homeostasis, and ECB stimulation may enhance lactation performance. This study evaluated whether top-dressed ECB supplementation improves weaning performance under commercial field conditions.

Materials and Methods

Two field trials were conducted using crossbred Landrace × Yorkshire (LY) sows (total 54 litters: 27 ECB, 27 control). Sows were allocated into ECB and control groups by the farm owner at entry into the farrowing unit, and cross-fostering was performed only within each treatment group. The ECB stimulator (commercial prototype sample; detailed composition not provided by the manufacturer) was top-dressed twice daily at 10 g/day from 7 days pre-farrowing to 7 days post-farrowing, and 20 g/day thereafter until weaning. Measured outcomes included total born, liveborn, piglets at lactation onset, piglets weaned, litter weaning weight, average piglet weaning weight, and pre-weaning mortality. Early weaned piglets were removed temporarily during lactation weeks 1 - 2 when nursing capacity was exceeded, raised on feed, and weaned with their cohort; creep feed intake was not recorded. Early weaned piglets were recorded only as group totals, so counts were assigned to litters with the largest discrepancy between starting and weaned piglets for analysis. In Trial 2, sow feed intake was recorded: ECB (25.5-day lactation) averaged 6.71 kg/day, control (27.2 days) averaged 6.72 kg/day.

Results and Discussion

Across both trials (27 ECB vs 27 control litters), ECB supplementation increased litter weaning weight by + 10.93 kg (ECB 97.30 vs control 86.37 kg; $P = 0.021$; d = 0.64; 95% CI: 2.38–20.21 kg). Average piglet weaning weight was also higher (+ 0.63 kg; ECB 8.76 vs control 8.13 kg; $P = 0.033$; d = 0.60). Numerical improvements were observed in piglets weaned per litter (+0.48) and pre-weaning mortality (−1.53 percentage points). After cross-fostering, no meaningful differences existed between groups in initial litter size or mean birth weight.

Conclusion

ECB-stimulator top-dressing was associated with improved piglet weaning performance, particularly higher litter and piglet weaning weights. Results support the potential utility of ECB modulation in lactating sows; however, further controlled studies with detailed mechanistic and intake measurements are warranted.

Keywords: Endocannabinoid, Feed intake, Lactation, Piglet growth.

Acknowledgements: This study was conducted with the support of Dodram Pig Cooperative Animal Hospital and ACC Co., Ltd.

COMPARISON OF DIFFERENT ALTRENOGEST FORMULATIONS EFFECTS ON ALTRENOGEST CONCENTRATIONS IN PLASMA IN GILTS

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Introduction and Objectives

Altrenogest is a synthetic progesterone, used for synchronizing estrus in gilts and sows. It inhibits estrus by blocking the release of follicle-stimulating hormone (FSH) and luteinizing hormone (LH). Currently it is widely used in Chinese pig industry to establish batch farrowing systems. This study investigates the plasma concentration of altrenogest after administration of different formulations in gilts under commercial conditions.

Materials and Methods

A commercial farm (1000 sows) in Hebei (China) was selected for this purpose. In total, 10 healthy sexually mature gilts (220 days old, 130 kg) were enrolled in this study and divided into: Group A – Regumate Porcine® (MSD Animal Health) administered to gilts (n = 5) for 18 days (oral solution; 20mg/day); Group B – TongYunBao® (Ningbo Second Hormone Factory) administered to gilts (n = 5) for 18 days (1 tablet; 20 mg/day). Gilts were always treated at the same time of the day (7 a.m.) by pouring on the first feed of the day to ensure complete intake. Blood samples were collected from each gilt on Day 0 (1 day before treatment), Day 3, Day 18 and Day 20 (2 days after withdrawal). Sampling took place always at 10 a.m. Altrenogest concentrations in porcine plasma were determined by HPLC-MS. Concentrations between groups were compared by Mann-Whitney U test (Median [CI 95%]).

Results and Discussion

Plasma concentrations of altrenogest were similar between both groups at Day 0 ($P > 0.05$) and Day 3 ($P > 0.05$). On the last day of drug administration (Day 18), the plasma concentration in Group A (14.2 [4.3, 21.7]) was significantly lower than Group B (23.9 [14.2, 50.2]) ($P < 0.05$). On Day 20, plasma concentrations were similar between both groups (A:0.8 [-0.2, 1.8]; B: 0.9 [-1.6, 3.3]; $P > 0.05$). We hypothesize that these lower values are suggestive of a faster activation of the hypothalamus-hypophysis axis leading to a quicker FSH release.

Conclusion

This study demonstrates that plasma altrenogest concentrations in gilts were not different between the oral liquid and tablet formulations of altrenogest on Days 0, 3 and 20. However, on Day 18, altrenogest concentrations in Group A dropped faster than in Group B, which remained higher than the expected range[1].

Keywords: Altrenogest, Estrus, Gilt.

Acknowledgements: The authors thank the producer for the field support during the trial.

POSTBIOTIC SUPPLEMENTATION IMPROVES REPRODUCTIVE PERFORMANCE IN GILTS AND SOWS AND SMALL INTESTINE MORPHOLOGY IN NEWBORNS

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Introduction and Objectives

Selection for hyperprolificity led to increase in incidence of Intrauterine Growth Restriction (IUGR) due to uterine capacity (Hansen et al., 2019). This condition impairs organ development, birthweight and postnatal performance of the piglets. Postbiotics have been demonstrated as a potential supplement for improvement of reproductive performance (Chen et al., 2020), so the aim of this study was to investigate the impact of a concentrated yeast-derived postbiotic (PB) on reproductive parameters of gilts and sows, and organ morphology of the litter.

Materials and Methods

Gilts (n = 141) and sows (n = 242) were randomly selected at GD76 and sorted into two groups: Control diet (C) and supplemented with 30g PB/day/animal until weaning (S). Females were weighted at GD76, GD113, and weaning. Reproductive parameters were recorded at farrowing, and one piglet born with normal birthweight (NBW, 1.6 - 1.9 kg) and one with IUGR (0.7 - 1.0kg) were selected from each gilt/sow, weighed and measured. A subset of n = 8 piglets/group were randomly selected for euthanasia followed by collection of duodenum and colon fragments for histological processing and analysis. Data was analyzed for normality with Shapiro-Wilk and means compared via t-tests (gilts/sows) and ANOVA one-way (piglets), using GraphPad Prism 9.5.0. Results: Mean ± S.E.M.

Results and Discussion

At GD113, S gilts weighed 228.6 ± 1.8 kg, higher than the 220.9 ± 2.2 kg of C gilts ($P < 0.05$). Litter weight in gilts was 21.72 ± 0.46 kg in the S group, higher than the 20.26 ± 0.59 kg of the C group ($P < 0.05$); it represented 11% (S gilts), 8.5% (S sows) of body weight, compared to 9% (C gilts) and 7.6% (C sows) ($P < 0.05$). C sows presented more stillborns (2.05 ± 0.2; S sows: 1.72 ± 0.2, $P < 0.05$). NBW piglets presented higher body weight, biometric measurements, and small and large intestine weight compared to their IUGR littermates ($P < 0.05$), but crown-rump length presented supplementation effect ($P = 0.01$). Colonic crypts were similar between experimental groups ($P > 0.05$), but duodenal villi of NBW_S (81.0 ± 3.0) were wider than the other groups (NBW_C: 76.0 ± 3.0; RIUC_C: 74.0 ± 3.0; IUGR_S: 77.0 ± 3.0) ($P < 0.05$).

Conclusion

Our study corroborates that supplementation with PB can improve reproductive performance and body weight during gestation, especially in gilts, as well as increasing litter weight and piglet survival.

Keywords: Postbiotic, reproductive performance, litter weight, IUGR, birthweight.

Acknowledgements: The authors thank Pôr do Sol farm, where the experiment was conducted; Cargill, for sponsoring the project; and CAPES, CNPq and Fapemig. brazilian financing institutions.

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PRELIMINARY EVALUATION OF TANNIC ACID AS AN ANTIMICROBIAL ADDITIVE IN BOAR SEMEN EXTENDERS

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Introduction and Objectives

Liquid-preserved boar semen is widely used in artificial insemination; however, bacterial contamination during processing and storage remains a major challenge. Bacteriospermia compromises semen quality and fertility, leading to routine antibiotic use (Keeratikunakorn et al., 2025). Concerns regarding antimicrobial resistance have driven the search for alternatives (Farha, 2020). Tannic acid, a plant-derived polyphenolic compound, exhibits broad-spectrum antimicrobial and antioxidant activities (Kaczmarek, 2020). This study aimed to preliminarily evaluate tannic acid as an alternative antimicrobial additive in boar semen extenders during liquid storage.

Materials and Methods

Semen samples were collected from two mature boars using the gloved-hand technique. Only ejaculates with progressive motility more than 70% and sperm concentration more than 100×10^6 spermatozoa/mL were included (Keeratikunakorn et al., 2024). Semen was diluted with Beltsville Thawing Solution (BTS) and divided into six groups: BTS alone, BTS supplemented with antibiotics (gentamicin; 200 µg/mL), and BTS supplemented with tannic acid at 25, 50, 100, or 200 µg/mL. All samples were adjusted to 3×10^9 spermatozoa/100 mL and stored at 18°C. Total bacterial counts were evaluated at 0 and 24 h of storage by spread plate technique.

Results and Discussion

At 0 h, bacterial counts were comparable among all groups. After 24 h of storage, bacterial proliferation markedly increased in the BTS control group without antimicrobial supplementation. In contrast, semen samples supplemented with antibiotics or tannic acid showed reduced bacterial counts. Tannic acid at 100 and 200 µg/mL demonstrated greater antimicrobial efficacy, with bacterial suppression comparable to the antibiotic-treated group. These results are consistent with previous reports on antimicrobial peptides used to control bacteria in liquid-stored boar semen (Keeratikunakorn et al., 2024). Tannic acid exhibits broad-spectrum antimicrobial activity, which may reduce the risk of antimicrobial resistance development.

Conclusion

This preliminary study suggests that tannic acid reduces bacterial growth in liquid-preserved boar semen in a concentration-dependent manner, indicating its potential as an alternative antimicrobial additive, although further studies on semen quality and fertility are required.

Keywords: Tannic acid, Antimicrobial activity, Boar semen, Semen extender, Liquid storage.

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EFFECT OF HORMONAL TREATMENTS AND NUMBER OF ARTIFICIAL INSEMINATIONS ON REPRODUCTIVE PERFORMANCE OF SOWS

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Introduction and Objectives

Optimizing reproductive performance in sows is essential for improving productivity in commercial pig production systems. Hormonal treatments are commonly used to stimulate estrus after weaning, and the number of artificial inseminations (AI) per estrus may influence fertility outcomes. This study evaluated the effects of hormonal treatments and the number of AI doses on post-weaning estrus expression and reproductive performance in sows.

Materials and Methods

The study was conducted at Nucleus Pig Breeding Farm located in Lam Dong province, Vietnam. A total of 120 primiparous and multiparous sows were allocated to six groups (20 sows/group), balanced for parity and backfat thickness at weaning: C2 (2 AI doses, no hormone), C3 (3 AI doses, no hormone), GnRH2 (GnRH + 2 AI), GnRH3 (GnRH + 3 AI), heCG2 (eCG+hCG + 2 AI), and heCG3 (eCG+hCG + 3 AI). Hormones were administered at 24 h after weaning. AIs were performed at 12 h intervals. Estrus response, conception rate at 21 days post-AI, farrowing rate, litter size, and piglet performance were recorded.

Results and Discussion

The overall estrus response within 7 days after weaning was 76.7%. Sows treated with eCG+hCG showed a higher estrus rate (92.5%) than control (65.0%; $P < 0.01$) and GnRH-treated groups (72.5%; $P < 0.05$). The overall conception rate was 90.0% (range 85.0 - 95.0%) and did not differ among treatments ($P = 0.818$). Similarly, farrowing rate averaged 83.3% (range: 80.0 - 90.0%) with no significant differences ($P = 0.945$). hormonal treatment and number of AI doses did not affect total born, selected, or weaned piglets ($P > 0.05$). However, birth weight of selected piglets was higher in the C3 (1.8 kg) compared with other groups (1.5 - 1.6 kg; $P = 0.001$). Piglet birth weight in heCG-treated group (1.5 kg) was slightly lower than in other groups (1.6 kg; $P < 0.05$).

Conclusion

Treatment with eCG+hCG improved post-weaning estrus expression, but did not significantly affect conception rate, farrowing rate, or litter size. Increasing AI frequency did not consistently enhance reproductive performance. Hormonal intervention may therefore be useful for improving estrus response under practical farm conditions.

Keywords: Artificial insemination, Hormonal treatment, Reproductive performance, Sow.

Acknowledgements: The authors would like to acknowledge the Nucleus Pig Breeding Farm and its staff for their valuable assistance in conducting this study.

SEMEN QUALITY OF COLOMBIAN CREOLE BOARS COMPARED WITH COMMERCIAL BREEDS USING CASA AND FLOW CYTOMETRY

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Introduction and Objectives

Genetic-resource conservation programmes for local pig breeds require objective information on male reproductive performance. This study aimed to characterise semen quality in the three officially recognised Colombian Creole breeds (Zungo, Casco de Mula and San Pedreño) and to benchmark their performance against widely used commercial breeds (Duroc, Belgian Landrace and Pietrain).

Materials and Methods

Seven boars per breed (1 - 2 years-old; two ejaculates/boar) from the AGROSAVIA germplasm nuclei (Creole breeds) and an international breed. The sperm-rich fraction was collected by the gloved-hand technique. Ejaculate volume and sperm concentration were recorded, and 100-mL doses containing 3×10^9 sperm were prepared using a commercial extender. Sperm morphology and kinematics were assessed by computer-assisted sperm analysis, while plasma-membrane viability, acrosome integrity and mitochondrial membrane potential (JC-1) were evaluated by flow cytometry. Data were analysed using a linear mixed model with breed as fixed effect and boar as random effect; Tukey-adjusted post-hoc comparisons were applied ($P < 0.05$).

Results and Discussion

Compared with commercial breeds, Creole boars produced lower ejaculate volume (185.5 vs 239.9 mL), sperm concentration (340.5 vs 395.4 $\times 10^6$ sperm/mL), total motility (90.9 vs 95.3%) and progressive motility (63.1 vs 67.2%) ($P < 0.05$). Velocity traits were broadly comparable, but Creole semen showed a lower proportion of morphologically normal sperm (86.1 vs 90.6%) and of viable sperm with intact acrosomes (76.8 vs 87.5%) ($P < 0.05$). Mitochondrial membrane potential did not differ between Creole and commercial breeds. Overall, Creole boars yielded fewer normal and motile sperm per ejaculate (49.3 vs 81.5 $\times 10^9$), translating into an estimated production capacity of approximately 16 - 17 AI doses of 3×10^9 normal and motile sperm, about ten doses fewer than commercial boars. Within Creole breeds, San Pedreño tended to produce larger ejaculates, whereas Zungo exhibited higher sperm quality, resulting in similar totals of normal and motile sperm per ejaculate across Creole breeds.

Conclusion

Colombian Creole boars produce semen that meets common AI quality thresholds, but with reduced output per ejaculate compared with commercial breeds. For conservation-oriented AI programmes, dose planning should prioritise semen quantity constraints rather than major qualitative deficits, and uniform processing recommendations can be applied across the three Creole breeds.

Keywords: Boar, Colombian Creole pigs, CASA, Flow cytometry, Semen quality.

Acknowledgements: We acknowledge AGROSAVIA (Colombian Corporation for Agricultural Research) for access to the germplasm nuclei and technical assistance. This work was supported by the Tolima Government–Administrative Department of Science, Technology and Innovation (COLCIENCIAS call 755) and by the Spanish Ministry of Science (grant RTI2018-101346-B-I00).

ALTRENOGEST: META-ANALYSIS ON REPRODUCTIVE PERFORMANCE IN GILTS AND SOWS

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Introduction and Objectives

Altrenogest is an orally active progestogen used in gilts and sows to suppress estrus and enable reproductive cycle control. The last meta-analysis on this topic was conducted in 2018, and ever since, studies report inconsistent zootechnical outcomes, likely due to methodological limitations, such as small sample sizes. We conducted a meta-analysis of studies published between 2018 - 2025 evaluating the zootechnical effects of altrenogest in swine production.

Materials and Methods

Systematic search was conducted across PubMed, Google Scholar, ScienceDirect, and Web-Of-Science, targeting altrenogest use in swine. Only randomized or controlled trials reporting zootechnical outcomes were included. Random (heterogeneity > 50%) or fixed-effects models were applied using the inverse-variance weighting. Subgroup analyses considered the variable gilt/sow, meta-regression of the effect of dose and duration could not be explored given the lack of variability among the studies. All analyses were performed in R using "metafor" package.

Results and Discussion

Out of the 199 identified articles, nine filed the inclusion criteria; the main reason for exclusion was wrong study objective and absence of a control group. For gilts, altrenogest showed marginal effect on the total piglets born, increase of 0.88 (-0.12; 1.87, 95%CI), $P = 0.08$, a significant increase in the liveborn piglets of 1.35 (0.04; 2.66, 95% CI), $P = 0.04$, and, the pregnancy rate was increased by 14% (8; 20, 95% CI), $P < 0.001$. For primiparous sows, altrenogest increased the total piglets born by 0.89 (0.07; 1.72, 95% CI), $P = 0.03$, but no significant effect was observed for liveborn piglets ($P = 0.60$). No significant effects were found for primiparous and multiparous sows together. Heterogeneity, and publication bias were assessed and any violations were observed (results not shown).

Conclusion

This meta-analysis highlights a distinct difference in response between gilts and sows. Altrenogest was shown to be effective in increasing total piglets born and liveborn piglets in gilts, and total piglets born for primiparous sows. No significant effect was observed in multiparous. However, given the limited number of studies involving primiparous and multiparous, the absence of significance in some outcomes can be a lack of statistical power. Additional investigations will be useful to deeper assess the effects of altrenogest in sows.

Keywords: Altrenogest, Efficacy, Gilts, Meta-analysis, Sows.

EFFECTS OF VIUSID® VET ORAL SOLUTION ON POST-WEANING STRESS AND SUBSEQUENT REPRODUCTIVE PERFORMANCE IN MULTIPAROUS SOWS

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Introduction and Objectives

Post-weaning is a critical transition in sows characterized by activation of the hypothalamic–pituitary–adrenal axis, increased oxidative stress, and temporary reproductive suppression. These changes may prolong the wean-to-estrus interval (WEI) and reduce litter performance. Antioxidant supplementation has been proposed to mitigate stress-related reproductive dysfunction. This study evaluated the effects of VIUSID® Vet Oral Solution on salivary stress biomarkers and reproductive outcomes in multiparous sows.

Materials and Methods

Sixty clinically healthy multiparous sows (parity 2 - 5) were randomly allocated to VIUSID® (5 mL/sow/day) or placebo groups (n = 30/group) from 10 days before weaning through 40 days post-weaning. Saliva samples were collected at -7, 0, 7, and 30 days relative to weaning and stored at -20°C. Salivary cortisol was measured using a competitive ELISA kit. Salivary malondialdehyde (MDA) concentrations were quantified by high-performance liquid chromatography (HPLC) following thiobarbituric acid derivatization with UV detection at 532 nm. Reproductive parameters included WEI, pregnancy rate, farrowing rate, total born, and live born piglets. Data were analyzed using mixed-model ANOVA and Chi-square tests ($p < 0.05$).

Results and Discussion

Treated sows had lower salivary cortisol at day 0 (3.46 ± 0.08 vs 3.77 ± 0.13 ng/mL; $P = 0.043$), day 7 (2.42 ± 0.08 vs 3.24 ± 0.20 ng/mL; $P < 0.001$), and day 30 (2.24 ± 0.06 vs 2.67 ± 0.10 ng/mL; $P < 0.001$) compared to the control group. Salivary MDA concentrations were also lower in treated sows at day 7 (2.43 ± 0.04 vs 2.92 ± 0.10 nmol/mL; $P < 0.001$) and day 30 (2.41 ± 0.03 vs 3.13 ± 0.07 nmol/mL; $P < 0.001$) compared to the control group. Treated sows showed a shorter WEI (4.5 ± 0.3 vs 5.9 ± 0.6 days; $P = 0.045$) and higher total born (16.5 ± 0.2 vs 15.5 ± 0.3; $P = 0.005$) and live born piglets (15.9 ± 0.2 vs 14.7 ± 0.3; $P = 0.005$) compared to the control group. Pregnancy and farrowing rates were numerically higher; findings support oxidative stress and antioxidant benefits (Roca et al., 2015).

Conclusion

Peri-weaning VIUSID® supplementation reduced stress biomarkers and improved key reproductive parameters under commercial conditions.

Keywords: Sow reproduction, Oxidative stress, Cortisol, Wean-to-estrus interval, Litter size.

Acknowledgements: The authors thank the collaborating commercial swine farm for technical support. VIUSID® was provided by Innovet Corporation Co., Ltd.; the sponsor had no role in study design or data interpretation.

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CONTROLLED COOLING ENABLES BOAR SEMEN STORAGE AT 5°C USING MAGAPOR HIGH-PERFORMANCE EXTENDERS

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Introduction and Objectives

Artificial insemination (AI) in the swine industry relies on liquid-stored semen, typically maintained at 15 - 17°C to prevent cold shock. However, lower storage temperatures could reduce bacterial growth and prolong semen shelf life. Controlled cooling strategies may help overcome cold sensitivity in boar sperm. The objective of this study was to evaluate whether boar semen doses can be safely refrigerated to 5°C using high-performance extenders from Magapor S.L. (Spain) under a controlled temperature descent protocol.

Materials and Methods

Semen was collected from 10 boars (one ejaculate per boar; n = 10) and extended with Duragen and Spermax extenders (Magapor S.L.) to 3×10^7 sperm/mL in 80 mL AI doses. Samples were stored at 16°C for 16 h and then transferred to 5°C for up to 6 days. One dose per boar was maintained at 16°C as a control. Sperm quality (total motility, viability, and acrosome integrity) was evaluated on days 1, 3, and 6. Data were analyzed in RStudio using a generalized linear model including Day, Extender, and Condition factors, followed by Tukey's post hoc test (95% significance).

Results and Discussion

Total motility remained above 70% in both control (16°C) and refrigerated (5°C) semen doses throughout the 6-days storage period, with no significant differences between conditions. Sperm viability, assessed by propidium iodide (IP) staining and flow cytometry, remained above 80% in all samples. Acrosome integrity, evaluated using FITC-PNA staining, was consistently higher than 70%. No significant differences were detected between the controlled-cooling protocol to 5°C and the standard storage at 16°C for any of the evaluated sperm quality parameters. Additionally, semen doses extended with both Duragen and Spermax extenders showed comparable results across all the evaluation times.

Conclusion

These results indicate that boar semen doses can be safely refrigerated following a controlled-cooling protocol up to 5°C, after an initial equilibration period at 16°C, if high-performance extenders Duragen or Spermax, from Magapor, are used. This strategy could represent a promising alternative to conventional storage at 16°C, potentially improving semen preservation and reducing bacterial proliferation in artificial insemination systems.

Keywords: Boar semen, Cooled semen, Extenders, Semen preservation, Semen storage.

POSTERS

TOPIC 12: PIG FARMING PRACTICE (PFP)

INVESTIGATING THE IMPACT OF MICROGRANULATION OF TIAMULIN-CONTAINING PREMIXES

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Introduction and Objectives

Product formulation of veterinary premixes largely contributes to the homogeneity of the active compound in the medicated feed and convenience to use. Common powder premixes are simple mixtures of an active ingredient and a carrier. Microgranulation, on the other hand, is an innovative formulation technology ensuring that the active compound is encapsulated in large and equally sized microgranules. The impact of microgranulation of premixes containing 100 mg/g tiamulin hydrogen fumarate and the corresponding medicated feed was investigated.

Materials and Methods

Two formulations: tiamulin microgranulated premix (Vetmulin® - Huvepharma®) and a specific number (n) of tiamulin containing powder premixes.

Premix investigations:

1. Tiamulin particle size distribution by laser diffraction (n = 5)
2. Dust content expressed as mg dust/100 g product (n = 8)
3. Visual evaluation of flowability (n = 1)

Medicated feed investigations:

4. Inclusion level in pig feed (target: 200 ppm) in 10 samples (n = 1)
5. Pelleting stability at 65, 75, 85, 95 and 105°C (n = 2)

Results and Discussion

1. Microgranulation provides larger particles (mean size: +/-500 µm) with a smaller range in particle size distribution. The powder formulations contained much more small particles (<100 µm) which are generally considered to be dust.
2. Lower dust content was determined in the microgranulated premix (6 mg/100 g) compared to the powder formulations (37 to 245 mg/100 g).
3. The microgranulated premix demonstrated superior flowability and reduced wall adhesion resulting in less 'bridge' forming.
4. The coefficient of variation was lower for feed containing microgranulated premix compared to a powder premix; 1.2 and 11.5%, respectively. Mean inclusion levels were 206 and 187 ppm, respectively.
5. Recovery of tiamulin hydrogen fumarate at 65, 75, 85, 95 and 105 °C for Vetmulin® was 100, 99, 100, 98 and 98%, while for the two powder premixes, a recovery of 90 - 90, 89 - 88, 92 - 88, 86 - 85 and 90 - 90% was determined, respectively.

Conclusion

Microgranulation of tiamulin premix (Vetmulin®) results in superior in-feed homogeneity without demixing and facilitates convenience to use compared to powder premixes. Lower dust content and improved flowability minimises the risk of carry-over and cross-contamination. Microgranulation provides better stability in pelleted feed up to 105°C.

Keywords: Homogeneity, Microgranulation, Premix, Tiamulin.

EVALUATING CARDIAC PUNCTURE BLOOD COLLECTION AS A RELIABLE AND BIOSECURE POSTMORTEM DIAGNOSTIC TOOL IN SWINE

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Introduction and Objectives

Successful diagnostic specimen collection from live pigs requires time and skills. Alternative sampling can be conducted using post-mortem specimens for infectious disease outbreak diagnostic investigations that require the absence of blood spillage. Cardiac puncture (CP) blood collection can be easily obtained as an alternative for pathogen detection, as it is a method known anecdotally amongst veterinarians. Therefore, a description of this method from two studies (Kikuti et al., 2024; Melini et al., 2025) is reported to promote awareness of available alternative post-mortem sampling techniques.

Materials and Methods

Blood samples were collected at five Midwestern United States farms in which three were breed-to-wean and two were growing pig farms undergoing a PRRSV outbreak. The age of inclusion and sample size for each study was determined based on the objectives of each of the studies. At each farm, recently dead or humanely euthanized pigs (i.e., < 24 hours) were placed on right lateral recumbency, the punction area was identified in the thorax where the olecranon and intercostal space intersected, and a needle was inserted to collect the blood.

Results and Discussion

A total of 286 CP blood samples were collected originating from 196 suckling and 90 growing pigs. In nine cases, sample collection did not yield enough serum volume for testing, and in four, the RT-PCR reaction was inhibited. Out of the remaining 273 samples, PRRSV was detected in 45% of the samples. Our results highlight the feasibility of obtaining blood samples from recently dead pigs of different ages through CP for viral disease (i.e., PRRSV) diagnosis and surveillance. Due to non-assessed factors nine samples did not yield enough serum for testing even though the specimen did not show evident coagulation. Agreement between CP blood to other collected specimens was as high as 88.89% to superficial inguinal lymph nodes

Conclusion

Blood collection from dead pigs is a viable welfare-friendly alternative for PRRSV detection. After training to collect this specimen, CP is an alternative to obtaining a blood sample for surveillance and diagnosis of pathogens of interest (i.e., PRRSV, ASF, CSF) while minimizing blood spillage and environmental contamination which can increase the risk of pathogen dissemination.

Keywords: Alternative specimen, Cardiac puncture, Porcine reproductive and respiratory syndrome, Post-mortem.

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EFFECTIVENESS OF THE BIOCHECK.UGENT TOOL IN MONITORING AND IMPROVING BIOSECURITY PERFORMANCE IN PIG PRODUCTION

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Introduction and Objectives

The implementation of stringent biosecurity measures along the pig production chain is one of the major solutions to minimize the risk of introduction of pathogens into a farm (external biosecurity) and their spread within the farm (internal biosecurity).

Materials and Methods

In this study, we report on the results of 9 years (2017 - 2025) of biosecurity monitoring in commercial pig farms in Europe. The data were collected through the Biocheck.Ugent tool, a globally recognized quantitative risk-based biosecurity assessment tool.

Results and Discussion

Since the start, the use of the Biocheck.Ugent tool in European pig farms has gradually increased, from 245 records in 2017 to over 5,000 records per year in the most recent years. The total dataset comprises 27,033 observations from 26 different European countries. In 2017, the overall biosecurity score was 64.5, with an external biosecurity score of 69.8 and an internal biosecurity score of 58.7. Between 2017 and 2025, a gradual increase in biosecurity scores was observed. External biosecurity improved by approximately 10%, reaching a score of 76.9, whereas internal biosecurity increased by more than 24%, reaching a score of around 73.0. The overall biosecurity score increased by 16.6% over the last nine years, resulting in an average total score of 75.2%. The size of the database enables more detailed analyses, including assessment of variation between countries and evaluation of specific biosecurity measures. Some caution is warranted when interpreting these results as not all European countries are equally represented and the results are therefore influenced by some overrepresented countries such as Belgium, Finland, Ireland, and Italy. Despite this, the data clearly indicate a substantial improvement in biosecurity. This trend likely cannot be viewed independently from the marked reduction in antimicrobial use in pig production during the same period.

Conclusion

Overall, this study demonstrates a clear and substantial improvement in biosecurity levels in European pig farms over the past nine years, supported by a uniquely large and longitudinal dataset generated using the Biocheck.Ugent scoring tool. The findings highlight the value of continued and expanded biosecurity monitoring and improvement efforts.

Keywords: Biosecurity, pig production, Biocheck.Ugent, Europe, Monitoring.

EVIDENCE OF INEFFECTIVE CLEANING AND DISINFECTION PROCEDURES IN PIG TRANSPORT

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Introduction and Objectives

Transport vehicles can act as mechanical vectors for pathogens in livestock systems. To limit transmission risks, trucks transporting pigs should undergo thorough cleaning and disinfection (C&D) after each journey. This study assesses the effectiveness of C&D performed by truck drivers at a Belgian pig slaughterhouse.

Materials and Methods

Fifteen pig transport vehicles were sampled before and after C&D. Swabs were taken from animal-contact locations, the exterior and the cabin. Total aerobic count (TAC) and gram-negative bacterial count (GNBC) were quantified. After C&D, pooled samples from the animal-contact locations (trailer floor, wall and the interior of the loading bridge) were analysed using 16S rRNA sequencing to evaluate residual bacterial contamination (Spanoghe et al., 2025).

Results and Discussion

C&D reduced TAC on most sampled locations, except in the cabin and on the undercarriage. GNBC decreased in the cabin, on the outside and inside of the loading bridge, on the trailer floor and walls. However, GNBC increased the steering wheel, stair to cabin, foot area of the cabin, wheels and undercarriage. The greatest TAC reduction (2.03 ± 0.98 log CFU/100 cm²) occurred on the trailer floor, resulting in a mean of 4.99 ± 0.66 log CFU/100 cm². The largest GNBC decrease (1.90 ± 0.88 log CFU/100 cm²) was measured inside the loading bridge, resulting in 3.62 ± 0.90 log CFU/100 cm². 16S rRNA sequencing identified 20 dominant bacterial genera, all but one of which were associated with the porcine gut, indicating persistent faecal contamination after C&D.

Conclusion

Despite reducing overall bacterial loads, driver-performed C&D at this Belgian slaughterhouse leaves substantial faecal contamination. These findings indicate that current C&D practices are inadequate to prevent mechanical transmission of bacteria via pig transport vehicles.

Keywords: 16S rRNA sequencing, Bacterial load, Cleaning and disinfection, Gram-negative bacteria, Pig transport.

Acknowledgements: This work was funded by the EU under the Horizon Europe grant 101083923 (BIOSECURE). Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the EU or the European REA. Neither the EU nor the granting authority can be held responsible for them.

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RISK VALUE CHAIN ASSESSMENT OF SWILL FEEDING AND AFRICAN SWINE FEVER TRANSMISSION IN CHINA

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Introduction and Objectives

In August 2018, China reported its first case of African swine fever. In the early stages of the epidemic, investigations found that many pig farms infected with African swine fever had a history of feeding with swill. The study describes the value chain of using swill to feed pigs, analyzes the risk of spreading African swine fever through swill feeding pigs, and briefly evaluates the policy of prohibiting swill feeding pigs.

Materials and Methods

A survey study on swill feeding pigs in Shenyang (in Liaoning, China) was carried out by using risk value chain method. A scenario tree model identifies the risk points associated with the introduction of ASF into the farm. Calculate and compare the economic and social benefits of swill feeding, anaerobic digestion, aerobic composting, and feed conversion. Use cost benefit method and SWOT method to evaluate the policy of prohibiting swill feeding to pigs.

Results and Discussion

The price of each pig and piglet is about 83.87 USD, the cost of vaccine and medication is 11.18 USD, the cost of feed is 48.22 USD, and the sales intermediary fee is 2.79 USD. Pigs can be sold at a price of 1.48 USD per kilogram. Risk analysis shows that swill collectors and vehicles frequently enter and leave the pig farm, without sterilization treatment of kitchen waste, indirect contact transmission by buckets were 3 highest risk factors for ASF pathogens to enter the farm. The main technologies for resource utilization of kitchen waste include anaerobic digestion, aerobic composting, feed conversion, and swill feeding. The average income per ton of treatment were USD 41.69, 10.42, 48.64, and 577.89. The government collects swill in a centralized manner and performs anaerobic digestion on it.

Conclusion

Swill feeding to pigs is the most profitable but risky way of food waste treatment. At present, swill treatment still takes harmlessness as the leading idea and lacks the idea of resource utilization. It can explore a new industrialized swill feeding mode under the condition of controllable risk. Feeding pigs with swill should be prohibited. Or the government can collect and store swill centrally, sterilize it strictly, and then feed it to animals.

Keywords: African swine fever, Swill feeding pigs, Value chain, Risk assessment, Food waste disposal.

Acknowledgements: I would like to express my gratitude to the Food and Agriculture Organization of the United Nations for their funding support for the project, and to the China Animal Health and Epidemiology Center for their collaborative guidance.

EFFECT OF A BACTERIAL BEDDING CONDITIONER APPLICATION DURING LACTATION ON PIGLET HEALTH AND PERFORMANCE

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Introduction and Objectives

Piglet survival and growth during lactation are strongly influenced by farrowing pen hygiene and microbial pressure (Halpin, et al., 2024; Lagoda, 2023). EazyBed Dry (EZB), a bedding conditioner containing beneficial microorganisms, aims to improve the farrowing microenvironment and enhance piglet performance. This study reports results from two trials evaluating the effect of EZB on health parameters, mortality and growth performance during lactation.

Materials and Methods

2 trials were conducted in 2 different farms in France:

-Trial 1: Conducted in a farrow-to-finish farm (2021, 600 sows) where 32 sows were monitored and assigned to 2 different treatments: Positive control (16 sows) and EZB (16 sows). Weaning at 28 days. Bedding protocol: Positive Control (Other bedding conditioner) vs. EZB (1.3 kg/sow over lactation: 100 gr/sow upon entrance in the maternity room, 500 gr/sow during farrowing, 100 gr/sow/day during the first week after farrowing). Parameters measured: piglet weight (weekly) and diarrhea incidence.

-Trial 2: Conducted in 2025 on a collective maternity system with 257 sows, divided into 2 groups: Positive Control (drying powder with no bacterial enrichment, 141 sows) and EZB (116 sows). Protocol included pre-farrowing and post-farrowing applications similar to Trial 1. Parameters measured: Mortality, microbial flora on sow udder 1 day before farrowing, and piglet weight at weaning.

Results and Discussion

-Trial 1: EZB reduced diarrhea incidence compared to control ($P < 0.05$) and tended to improve piglet weight gain over lactation (+440 g/piglet, $P = 0.051$).

-Trial 2: Mortality excluding crushed piglets was significantly lower in EZB pens (14.36 vs. 8.64%, $P < 0.05$). Microbial analyses showed a trend to reduce Enterococcus ($P = 0.09$) counts on sow udder before farrowing. Piglets from treated pens had higher weaning weights and lower variability, reinforcing the positive impact on uniformity and growth performance.

Conclusion

EazyBed Dry application during lactation improves piglet survival, reduces diarrhea incidence, and enhances growth performance while lowering microbial pressure in farrowing pens. These findings support its use as a practical strategy to improve piglet health, welfare and productivity.

Keywords: Conditioner, Lactation, Microorganisms, Piglets, Survival.

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RADAR SIGNAL ANALYSIS FOR MONITORING THE ONSET OF FARROWING IN SOWS WITHIN A FREE-FARROWING SYSTEM

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Introduction and Objectives

Monitoring sows during the pre-farrowing and farrowing periods is critical for optimizing reproductive outcomes for both sows and piglets. Radar technology provides several advantages over traditional cameras, such as resistance to low light, obstructions, and adverse environmental conditions, all while preserving privacy. This study aimed to develop and assess a radar-based algorithm for the early detection of nest-building behavior, which can serve as a reliable predictor of the onset of farrowing.

Materials and Methods

Data was collected using a radar sensor installed above free farrowing pens. In total, 15 farrowing processes were monitored, generating 3D point clouds of sow movements. Velocity data were filtered to exclude external interference and noise, smoothed using a 1-second moving average, and analyzed with a rolling window approach. The algorithm identified elevated activity indicative of nest-building using a dynamic threshold derived from a secondary rolling window. Parameters were optimized per farrowing and tested across others to evaluate generalizability.

Results and Discussion

The sows had a mean parity of 3.60 ± 2.69 and produced an average of 14.00 ± 2.80 liveborn piglets. The mean time to detect the expulsion of the first piglet was 42 minutes and 51 seconds, with a standard deviation of 23 minutes and 47 seconds. The algorithm reliably detected activity changes, demonstrating robust performance even under varying environmental conditions.

Conclusion

The radar-based algorithm shows promise as a reliable tool for early farrowing detection, enabling timely interventions. Its non-invasive nature and resilience to barn conditions make it highly suitable for commercial farming, while also maintaining privacy. However, the small dataset limits generalizability. Expanding the dataset could enable the development of group models, improving prediction accuracy. Integrating radar technology has the potential to enhance operational efficiency and animal welfare in farrowing management.

Keywords: Smart farming, Farrowing monitoring, Farrowing management, First piglet.

INVESTIGATIONS ON INTRADERMAL NEEDLE-FREE INJECTOR AND BOTTLE MOUNT VACCINATOR HYGIENE IN NORTH-WEST-GERMAN PIG FARMS

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Introduction and Objectives

A variety of syringes are used on pig farms, with bottle-mount vaccinators (BMVs) being very popular. These devices are often made of plastic, making them difficult to clean and disinfect. Intradermal vaccination devices are becoming more common. Based on earlier field studies on BMV hygiene, this study investigated the hygiene of an intradermal needle-free injector (INFI) and BMVs in 10 pig farms in north-west Germany.

Materials and Methods

The study was conducted on 10 farms with 250 - 520 sows, all using INFI and at least one BMV. One INFI and one randomly selected BMV per farm were tested. For sampling, a 50cc bottle of demo fluid was attached to the INFI before and after cleaning, and to the cleaned BMV. Six milliliters of solution were injected into sterile tubes and sent to a microbiological laboratory for semi-quantitative germ analysis. MALDI-TOF identification was also performed. Additionally, all samples were tested for ATP levels using an ATP detection handheld device. Semi-quantitative counts and Relative Light Units (RLU) means, and standard deviations were calculated to compare INFI and BMVs. Farms had production rhythms of 1 - 3 weeks, and farmers were aged 30 - 55 years. Devices were cleaned after each use. INFI devices had between 1,531 and 13,808 shots. Device and nose/spike cleanings were ranged from 1 (very good) to 5 (very poor).

Results and Discussion

Mean RLU for INFI was 24 before cleaning and 5.8 after, while BMVs averaged 38.5. Semi-quantitative unspecific germ scores were 11 for INFI before and after cleaning, and 17 for BMVs. Bacterial classification revealed 15 × Cl. perfringens, 11× Staphylococci, 2× Pseudomonas (only in BMVs), and others. Overall, the INFIs tended to be cleaner than BMVs regarding bacterial contamination and ATP content.

Conclusion

The study shows that intradermal needle-free injector devices tend to be cleaner than BMVs on average. This can be an advantage for animal health, vaccination efficacy and disease prevention under field conditions.

Keywords: ATP, Intradermal Needle-Free Injector, BMV, hygiene.

Acknowledgements: The authors thank Biochek BV for the support with providing the ATP detection handheld device and testing materials.

EFFECT OF CALIPER-MEASURED BODY CONDITION AT FIRST SERVICE ON BODY CONDITION DYNAMICS AND LITTER SIZE IN GILTS

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Introduction and Objectives

Gilt development is essential for herd performance, as age, body weight, and body reserves at first service influence reproductive outcomes. Body condition has been assessed using subjective visual methods with low repeatability (Li et al., 2020). The sow caliper provides an objective alternative, although its application in gilts under commercial conditions remains limited (Knauer et al., 2015). This study evaluated the effects of caliper-measured body condition, age, and body weight at first service on gestational body condition dynamics and total number of piglets born (TNB) in the first parity.

Materials and Methods

Data from 166 F1 gilts (Landrace × Yorkshire) from a commercial farm in the coastal region Ecuador (BSh climate) were analyzed. Age, body weight, and body condition assessed by sow caliper at service, 4 weeks post-service, and farrowing were recorded, along with TNB at first parity. Gilts were classified by age (217 - 236 d; 237 - 256 d; 257 - 288 d), body weight (149 - 156 kg; 157 - 164 kg; 165 - 00 kg), and body condition (low [< 12], optimal [12 - 13], high [> - 13]). Generalized linear models were applied to evaluate main effects and interactions on caliper unit changes and TNB ($P < 0.05$).

Results and Discussion

Difference in caliper units between service and farrowing was determined by body condition at service and at 4 weeks post-service ($p<0.001$), as well as by the age–body weight interaction at first service. Gilts with low body condition showed greater gestational increases, whereas those with optimal body condition exhibited more stable trajectories. TNB was influenced by body condition at service; mean TNB for low, optimal, and high body condition were 10.9, 14.9 and 14.7, respectively ($P < 0.001$). Older gilts with optimal or high body condition produced 1.1 - 1.3 additional piglets per litter compared with those with low body condition. These findings indicate that criteria based solely on age or body weight are insufficient and support the use of sow caliper for more precise gilt selection.

Conclusion

Body condition measured by sow caliper at first service is a key determinant of gestational body condition dynamics and litter size in the first parity. Integrating body condition with age and body weight at service improves gilt selection and management, with implications for reproductive efficiency.

Keywords: Body condition, Caliper sow, Gilts, Reproductive performance.

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INEFFECTIVE BOOT HYGIENE PRACTICES IN PIG FARMS

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Introduction and Objectives

Proper boot hygiene is a critical biosecurity measure to prevent infectious disease spread between and within pig farms (Amass et al., 2000; Alarcon et al., 2021), yet the absence of standardized protocols leads to highly variable and often suboptimal implementation. This field study aimed to describe current boot hygiene practices on Belgian pig farms and quantify their effectiveness in reducing microbial contamination.

Materials and Methods

Fifteen pig farms (19 farmers) were visited between July 2024 and December 2025. Farmers performed their routine boot hygiene procedure, with swabs collected from the upper and sole areas of each boot before and after cleaning and/or disinfection to quantify total viable cell counts (TVC) and gram-negative enteric bacterial counts (GNB) as fecal contamination indicators (Hornig et al., 2016).

Results and Discussion

Three farms relied solely on farm-specific boots without cleaning or disinfecting their boots, yielding persistently high GNB levels up to 5.13 log CFU/25 cm². Daily cleaning plus disinfection on five farms and between-round cleaning and disinfection on two farms produced TVC log reductions of 0.32–5.51 log CFU/25 cm², but only one farmer eliminated fecal indicators at all sites. Disinfection without prior cleaning on two farms yielded mixed results with the full GNB reduction on one, while residual indicator bacteria remained present on the other. Cleaning without disinfection on three farms paradoxically increased bacterial counts, indicating contamination redistribution. These findings demonstrate alarming variability and frequent inadequacy of boot hygiene practices, with contaminated boots posing a clear ongoing risk for pathogen transmission between animals and production rounds even when farmers actively implement measures.

Conclusion

Standardized guidelines mandating sequential cleaning followed by disinfection, coupled with training and verification protocols, are urgently needed to mitigate this biosecurity gap. Few studies have evaluated the on-farm effectiveness of boot hygiene practices, and this work underscores the continued need to prioritize and refine these fundamental measures.

Keywords: Biosecurity, Boot hygiene, Hygiene practices, Indirect transmission

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INEFFECTIVE HAND HYGIENE PRACTICES IN PIG FARMS

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Introduction and Objectives

Proper hand hygiene is a simple, yet effective biosecurity measure proven to prevent pathogen transmission on pig and farms, yet data on its on-farm implementation and efficacy remain limited. Pathogens can persist on hands and under fingernails (Amass et al., 2000), facilitating their mechanical spread between farms and within production units during routine activities. This field study aimed to describe current hand hygiene practices among farmers and quantify their effectiveness in reducing microbial contamination.

Materials and Methods

Fifteen pig farms (19 farmers) were visited from July 2024 to December 2025. Farmers performed their routine hand hygiene, with swabs collected before and after washing and/or disinfection: 25 cm² from the dominant hand and the entire non-dominant hand to measure total viable cell counts (TVC) and Gram-negative enteric bacterial counts (GNB) as fecal indicators (Hornig et al., 2016). UV visualization with fluorescent lotion was also applied to assess the effectiveness of hygiene practices.

Results and Discussion

No farmers routinely disinfected their hands. Two used gloves regularly, which reduced TVC and GNB but left residual indicators on at least one new glove per farmer. Hand washing decreased TVC and GNB in all but one case, where counts increased, likely due to contaminated drying towels. Only six of the 19 farmers eliminated GNB from both hands post-washing, with non-dominant hands more often contaminated, highlighting sampling area effects. UV visualization revealed lotion remnants on most hands, particularly nail beds and wrists, confirming incomplete coverage despite routine hygiene practices. These findings expose frequent inadequacy of farmer hand hygiene, often due to omitted disinfection, poor technique, posing ongoing pathogen transmission risks.

Conclusion

Emphasis on basic yet essential biosecurity measures like hand hygiene is critical. Standardized protocols should be refreshed to recommend alcohol-based disinfection lotions, particularly in high-risk zones such as farrowing and quarantine stables, combined with full-coverage washing, disposable drying and training tools like UV visualization for awareness and verification. With few studies evaluating on-farm hand hygiene efficacy, this research underscores the urgent need to prioritize and optimize these core practices.

Keywords: Biosecurity, Hand hygiene, Hygiene practices, Indirect transmission

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VISITOR AND PERSONNEL DOWNTIME RESTRICTIONS AS A BIOSECURITY MEASURE IN PIG PRODUCTION: A REVIEW

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Introduction and Objectives

Downtime, a 24–72 h animal avoidance period between farm visits, originated from early FMDV nasal carriage studies in humans and is now widely recommended in pig production biosecurity guidelines to limit indirect pathogen transmission via personnel and visitors. However, its scientific basis has been questioned, particularly regarding added value over established hygiene measures, while creating practical implications that disrupt regular sector operations for veterinarians and other service providers. The scoping review critically evaluated the effectiveness of downtime as a biosecurity measure to prevent indirect pathogen transmission through personnel and visitors.

Materials and Methods

Following PRISMA-ScR guidelines, PubMed, Web of Science, and Scopus were searched for peer-reviewed studies on: (1) nasal carriage of livestock pathogens in humans post-exposure, (2) downtime as a biosecurity measure, and (3) hygiene interventions targeting mechanical transmission via humans. Selection criteria included production animals, experimental/analytical designs, and relevance to indirect human-mediated transmission. Grey literature and cited references supplemented searches.

Results and Discussion

Fourteen unique studies met inclusion criteria, predominantly in pigs. Nine studies showed short-lived nasal detection of agents like foot-and-mouth disease virus (FMDV), porcine reproductive and respiratory syndrome virus (PRRSV) and Mycoplasma hyopneumoniae, in exposed humans, but viable virus recovery was rare and only one experiment demonstrated possible transmission to naïve animals under artificial conditions. Only two studies directly evaluated downtime (12 - 16 h) (Otake et al., 2002; Pitkin et al., 2010), finding no added protective effect over hygiene measures (hand hygiene, clothing and boot changes, showering). Multiple experiments confirmed that these hygiene measures alone prevented indirect transmission of key porcine pathogens (PRRSV, porcine epidemic diarrhea virus, transmissible gastroenteritis virus, *E. coli*, FMDV). Even in cases where humans might act as biological vectors, downtime (24 - 72 h) is ineffective, as pathogen shedding durations exceed this period. These results reveal a critical evidence-policy gap: downtime lacks proven biological benefit beyond hygiene protocols, yet imposes impractical constraints, potentially fostering false security while diverting focus from verifiable measures.

Conclusion

Given the lack of supporting evidence, policy and farm efforts should prioritize core hygiene measures over downtime enforcement, redirecting resources to practical and verifiable evidence-based biosecurity protocols.

Keywords: Animal avoidance period, Biosecurity, Downtime, Indirect transmission.
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INDIRECT TRANSMISSION OF PATHOGENS VIA ANIMAL TRANSPORT AND ASSOCIATED BIOSECURITY MEASURES: A SYSTEMATIC REVIEW

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Introduction and Objectives
Pig transport vehicles are increasingly recognized as important indirect vectors for pathogen transmission. Contaminated trucks can retain infectious agents, exposing subsequent loads without direct animal contact. Despite widespread implementation of cleaning and disinfection (C & D), persistent contamination continues to be reported. This review aimed to evaluate evidence for indirect pathogen transmission to animals via vehicles and assess the effectiveness of biosecurity measures preventing this risk.

Materials and Methods
A systematic search was conducted on the 13th of June 2025 in Embase, PubMed, Scopus and Web of Science following PRISMA guidelines. Peer-reviewed studies published from 1990 onward and investigating indirect transmission or biosecurity measures in animal transport were included. Sixty-four articles met the criteria, of which 34 focused on pig transport. Studies were categorized by pathogen, study design and evidence level (proven, likely, potential or unlikely).

Results and Discussion
Evidence for indirect transmission via vehicles was strongest for Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), with experimental studies showing infection of naïve pigs after exposure to contaminated model trailers or full-scale trucks, confirming transmission. For other pathogens, environmental swabbing of truck floors and aluminium surfaces, together with bioassay confirmation and increased detection in pigs after transport and lairage, indicates that Porcine Epidemic Diarrhea Virus, *Brachyspira hyodysenteriae* and *Salmonella enterica* can also be introduced via vehicles. African Swine Fever Virus was detected only through qPCR-based environmental sampling and modelling, suggesting a potential risk. Across studies evaluating biosecurity measures, no single C&D protocol consistently eliminated pathogens. Dry cleaning, washing and disinfection each reduced contamination but were insufficient alone. Drying, whether overnight or through thermo-assisted drying and decontamination, eliminated PRRSV under controlled conditions. Field observations showed limited compliance, attributed to insufficient awareness and limited training, and visual inspection proved unreliable, reinforcing the need for standardized, evidence-based C&D guidelines and monitoring.

Conclusion
Although the evidence is limited, studies demonstrate that trucks can act as mechanical vectors for pathogen transmission to pigs. There is no universally effective C&D protocol that performs reliably across diverse field conditions. Strengthening biosecurity implementation, establishing standardized protocols and improving evaluation tools are essential to reduce pathogen spread during transport.

Keywords: Biosecurity measures, Cleaning and disinfection, Indirect transmission, Mechanical vectors, Pig transport.

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EVALUATION OF THE EFFICACY OF A HERBAL EXTRACT SPRAY (HERBBAND®) ON POSTOPERATIVE WOUND HEALING IN PIGS

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Introduction and Objectives

Appropriate postoperative wound management influences infection risk, recovery rate and welfare in pigs. Herbal extracts containing bioactive have been reported to exhibit anti-inflammatory, antioxidant, and wound-healing–promoting properties (Carvalho et al., 2021). In contrast, povidone-iodine has been reported to induce tissue irritation and inhibit the proliferation and migration of fibroblasts and keratinocytes, which may contribute to delayed wound healing. Therefore, this study aimed to compare the efficacy of herbal extract products (HerbBand: Herbal extract from Pinus longifolia, Eucalyptus spp., and Cedrus deodar) and povidone-iodine, a widely used broad-spectrum antimicrobial agent, in promoting postoperative wound healing following hernia surgery in piglets.

Materials and Methods

Sixteen 5-week-old piglets with scrotal or inguinal hernia were randomly divided into two groups (8 pigs per group): a povidone-iodine control group and a herbal extract spray (HerbBand®) treatment group. Treatments were applied daily until wound healing. Outcomes included time to wound dryness, suture removal day, and wound complications. Sutures were scheduled for removal on day 7; otherwise, removal was delayed based on clinical assessment. Data were analyzed using the Mann-Whitney U test ($P < 0.05$).

Results and Discussion

Piglets treated with the herbal extract spray showed significantly faster wound drying than those in the povidone-iodine group (5.00 ± 0.53 vs. 6.88 ± 2.03 days; $P = 0.040$). Sutures were removed by day 7 in all herbal-treated piglets, whereas the povidone-iodine group required longer (8.25 ± 1.28 days; $P = 0.049$). Complications occurred in four treated pigs (discharge, days 4 - 5) and five control pigs (discharge and wound dehiscence, days 3 - 7). These results suggest earlier wound drying and suture removal in the herbal group. Similar anti-inflammatory and wound-healing effects of flavonoid- and tannin-rich extracts in HerbBand® (Pinus and Eucalyptus) have been reported (Criollo-Mendoza et al., 2023).

Conclusion

The results of this study indicate that the herbal extract spray (HerbBand®) was associated with shorter wound drying and suture removal times compared with povidone-iodine.

Keywords: HerbBand, Wound healing, Herbal extract spray, Povidone-iodine, Wound management

Acknowledgements: The authors thank to the Faculty of Veterinary Medicine, Kasetsart University, for support.

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RESOLUTION OF VAGINAL PROLAPSE IN PREGNANT SOWS

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Introduction and Objectives

Mortality in sows has increased during the last decade; in 1993 mortality was 4.3, in 2017, 10% and in 2021, 14%. (Pig health today 2021). Analysis of 418 farms, 1.1 million sows from USA, Canada, Australia and The Philippines, show that from 2012 to 2021 mortality rose from 8.16 to 13.56% (Eckberg et al 2022). Mortality is multifactorial, difficult to identify specific causes. Factors are genetics, diet, diseases, management and facilities, The main causes are sudden death 30.89%, claudication problems 29.1%, prolapses 26.96%, and others 13.05%. Prolapses increased in recent years, occurring mainly peripartum (Supakorn, C, et al, 2017). It is the main cause of increased mortality or elimination and reaches 30%. The farm under study has had an increase in death or elimination of females due to prolapse. Since the farm was closed to entry of replacement females, the goal is to reduce elimination or death of sows from vaginal prolapse.

Material and Methods

The study was conducted on a farm of 9,700 sows, from January 2023 to December 2025. An antepartum record is kept of pregnant sows with vaginal prolapse or candidates for vaginal prolapse. The intervention is performed before taking them to the Farrowing house, if the prolapse occurs while in farrowing house, intervention is still underway. A large stainless-steel needle, plastic webbing, cotton cord and adhesive tape are used. The material is perfectly disinfected. The cord is attached to the needle. Local anesthesia is placed on both sides of the vulva, and cotton cord is inserted making an easy-to-release tie, to allow it to be loosened at the birth of each piglet.

Results and Discussion

From 2023 to 2025, 1,042 sows with peripartum vaginal prolapse were identified, of which 310 were intervened, 628 were eliminated and 106 died. These sows have given birth to 14,033 live piglets that would not have been obtained otherwise. Numerous sows recovered and continued their normal reproductive lives.

Conclusions

The timely intervention to resolve vaginal prolapse allowed recovery of sows that otherwise had to be eliminated, and these sows produced numerous piglets that improved economic results of the farm.

Keywords: Female mortality, Reduction of vaginal Prolapse, Vaginal prolapse.

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SATELLITE SYMPOSIUM





CEVA - SATELLITE SYMPOSIUM 1

Where Vets Meet Economists:
The Economic Benefits of High-Quality Piglets

June 17, 2026, from 12:00 to 13:00

Robert Hoste
Wageningen Social & Economic Research, Netherlands

Biography

Robert Hoste is senior pig production economist at Wageningen Social & Economic Research in the Netherlands. He has 35 years' experience in economic issues on farm and sector level, as well as in supply chain cooperation and international studies. In the institute he is acquiring, leading and performing numerous projects related to pig production, and heading the Sector team on pig production as the institutes' pig sector ambassador.



CEVA - SATELLITE SYMPOSIUM 1

Where Vets Meet Economists:
The Economic Benefits of High-Quality Piglets

June 17, 2026, from 12:00 to 13:00

Dr. Daniel Sperling
Swine and Ruminant Clinic, VETUNI Brno

Biography

Dr. Daniel Sperling, a distinguished swine health expert and Assistant Professor at the University of Veterinary and Pharmaceutical Sciences Brno in the Czech Republic. He holds a DVM, PhD, and a Master's in Vaccinology from the University of Lausanne. With over 15 years of combined experience in academia, field practice, and the animal health industry, including technical and franchise management roles at Ceva Santé Animale, he has contributed extensively to swine disease management, antimicrobial therapy, and diagnostic development across Europe and beyond.

ABSTRACT

The Economic Benefits of High-Quality Piglets

A good start of piglets pays off, but the required focus differs among farms and countries. There is a wide variety among farms, and among countries, in the management of piglets. With highly proliferative sows, management is like top sport, requiring a lot of attention to the sows and piglets, to make them winners. This demands nutritional solutions, housing care, great awareness of workers, and ample data collection and analysis. However, those solutions are often expensive, not the least for labour. So the question is under what conditions it would be wise to focus on top sport, or to prefer a next level sport career for the animals.

In some situations, such as where labour capacity or craftsmanship is limited, farmers are better to sit in the second row of top sporters. We found that many farms in Asian countries lack craftsmanship, not because the theory is not known, but the pressure to perform maximally is simply not present. Mortalities are high, as there is a lack of personal awareness among employees and farmers.

In highly competitive countries, such as in Europe, and meanwhile also among industrialized pig production companies in China, farmers need to outperform others in order to survive the massive competition. Market price pressure urges farmers to be top sporters. In such countries, top genetics are being developed, top nutritional and pharmaceutical products are invented, and labour-limited management procedures are optimized. But even there, an additional piglet born per litter, is not always profitable. It depends on factors such as birth weight, survival rate, ability to give care, nutritional support etc.

In order to optimize farm management, KPIs are needed. Common KPIs focus on zootechnical performance, such as PSY, FCR, ADG. However, it would be helpful to incorporate the economic element in KPIs, as a farmer's goal is economically driven. Economic indicators include the marginal value of zootechnical performance (which KPI is economically more important to focus on). Moreover, indicators such as Value increase per day per present pig, Optimal delivery weight of pigs, or Performance losses, combine zootechnical and economic considerations. An animal-follow-system for optimal management of individual animals during their entire life prevents ruptures in husbandry circumstances or trade-offs among management decisions.
Also risk management is important. Risks are omnipresent, both in economic perspective - prices and margins are volatile, and zootechnical/veterinarian perspective – diseases can cause massive losses.
Finally, a good start of piglets has several positive effects. The zootechnical performance, such as daily gain and feed efficiency, in the rest of the animal's life is positively influenced. This leads to increased profitability. Also the farm management is more convenient, as the process of animal flows is more fluent and predictable. Further, this leads also to happy workers. Moreover, efficient production is also more sustainable. So a good start in a piglet's life pays off in multiple ways.

Iron and Piglet Health: Preventing Deficiency in Modern Pig Production

Iron is an essential component of every cell and tissue in the body. It plays a critical role in oxygen transport and utilization, serves as a key element in various enzymes, and is vital for the proper functioning of the immune system.

Consequently, iron deficiency is the most frequent cause of anemia in swine, with Iron Deficiency Anemia (IDA) being most prevalent in neonatal suckling piglets.

In modern swine production, IDA is a widely recognized clinical condition among fast-growing piglets reared under intensive industrial conditions. It is considered an emerging challenge, attracting significant research interest these days.

This problem is further exacerbated by the large litters of hyper-prolific sows; these litters often show high heterogeneity in birth weights, with a significant percentage of piglets being born already anemic. For instance, during the first week of life, a piglet doubles its body weight from 1.5 to 3 kg, while its plasma volume expands by 30%.

IDA inevitably develops in piglets that do not receive iron supplementation shortly after birth. This is due to several factors: low internal iron reserves at birth, the minimal iron content in sow's milk, the rapid growth rate of newborns, and a lack of access to soil as a natural iron source. To prevent IDA, iron supplementation ideally administered by injection within the first three days of life are a well-established and essential practice.

The objective of this presentation is to provide up-to-date information on the role of iron in piglet development. We will examine how piglet management and supplementation strategies impact efficacy and production performances within the context of current farming practices.



ZOETIS - SATELLITE SYMPOSIUM 1

Raising the Bar in PRRS Management
Immunity, Innovation, and Vaccine Effectiveness
June 17, 2026, from 12:00 to 13:00

Prof. Daniel Linhares
Iowa State University, College of Veterinary Medicine. Ames IA, USA

Biography

Daniel Linhares, DVM, MBA, PhD, is Professor and Director of Graduate Education in the Department of Veterinary Diagnostic and Production Animal Medicine at Iowa State University College of Veterinary Medicine. He also holds the Roy A. Schultz Professorship in Swine Medicine. Dr. Linhares earned his Doctor of Veterinary Medicine degree from the Universidade Federal de Goiás, Brazil, an MBA from Fundação Getúlio Vargas, and a PhD in Veterinary Population Medicine from the University of Minnesota. His research focuses on the development and evaluation of field-based strategies to improve swine health, biosecurity, disease surveillance, and productivity, with particular emphasis on porcine reproductive and respiratory syndrome (PRRS). Dr. Linhares has authored numerous peer-reviewed publications and has received multiple academic honors, including Iowa State University's Early Career and Mid-Career Achievement in Research awards.



ZOETIS - SATELLITE SYMPOSIUM 1

Raising the Bar in PRRS Management
Immunity, Innovation, and Vaccine Effectiveness
June 17th, 2026, from 12:00 to 13:00

Dr. Jose Angulo
Zoetis Inc., USA

Biography

Dr. Jose Angulo is Director Technical Lead, Global Portfolio Marketing – Swine at Zoetis, where he partners with global stakeholders on lifecycle management of the swine portfolio, strategic pipeline development, and execution of global swine health initiatives. With more than 20 years of international experience in veterinary medicine, swine production systems, and animal health industries across multiple regions, Dr. Angulo has established expertise in swine health management, infectious diseases, epidemiology, continuous improvement, and operational excellence. He provides technical leadership and scientific support to global swine teams and key customers worldwide. Dr. Angulo has authored and presented numerous scientific publications and technical papers at international swine conferences and industry meetings. He earned his Doctor of Veterinary Medicine degree in Mexico, a Master of Science in Veterinary Medicine from the University of Minnesota with a focus on PRRS epidemiology, and certifications in Project Management and Lean Six Sigma Black Belt from Villanova University.

ABSTRACT

Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) remain a high-impact disease where the practical challenge is converting diagnostic (Dx) outputs into actionable, comparable metrics for surveillance, benchmarking, and timely on-farm decisions across farms and production systems.

The symposium outlines a practitioner-focused framework to (1) translate Dx results into epidemiologic understanding and (2) apply targeted interventions—including use of PRRS modified-live vaccine (MLV) within integrated control programs—with clear key performance indicators (KPIs) from breeding-herd stability through growing-pig performance.

Materials and Methods (or Main Contents)

Diagnostic-to-metric translation: Dx-test results are organized into clear, farm-ready indicators intended to support surveillance, comparability across time/sites, and faster decision cycles.
Surveillance and KPI framework: A metrics and surveillance approach is applied spanning breeding herd stability and downstream growing-pig performance, defining what "success" looks like operationally and how it should be measured.
Intervention playbooks: Field-tested, targeted interventions are paired to the metric outputs to support confident action, including the strategic use of Fostera PRRS MLV as an immunological tool within integrated programs.

Results and Discussion

The proposed workflow links laboratory outputs to decision-relevant epidemiologic indicators, enabling more consistent surveillance and benchmarking and supporting quicker, more confident responses when PRRS pressure rises. Integrating a KPI-driven surveillance layer with practical intervention strategies (including PRRS MLV use) provides a cohesive management approach that aligns immunological tools, monitoring, and production outcomes in a single operational playbook.

Conclusions and Recommendations

A metric-first PRRS management approach—translating Dx results into comparable indicators, tracking KPIs from breeding to growing phases, and pairing metrics with targeted interventions (including PRRS MLV within integrated programs)—can strengthen monitoring and accelerate timely on-farm action. Future perspectives include continued refinement of standardized indicators for cross-farm benchmarking and broader adoption of concise, practitioner-ready frameworks that unify diagnostics, epidemiology, and intervention decision-making.

Keywords: Diagnostics (Dx), Epidemiologic metrics, PRRS, Surveillance KPIs, PRRS MLV vaccination.



HIPRA - SATELLITE SYMPOSIUM 1

BEYOND GUT HEALTH: STRATEGIES TO UNLOCK PIGLET PERFORMANCE

June 17, 2026 from 12:00 to 13:00

Edgar Manzanilla
Pig Development Department, Animal & Grassland Research and Innovation Centre, Teagasc (Ireland)

Biography

Edgar Manzanilla is a veterinarian and researcher specializing in pig health, production systems, and antimicrobial stewardship. He holds a degree in Veterinary Medicine and PhD from the Universitat Autònoma de Barcelona and is a Diplomate of the European College of Porcine Health and Management (ECPHM).

He is Principal Research Officer / Head of Pig Development in the Pig Development Department at Teagasc, in Ireland. His work focuses on antimicrobial reduction in pig production through improved management practices, nutrition microbiota and immune system interaction, and epidemiology - data analysis.



HIPRA - SATELLITE SYMPOSIUM 1

BEYOND GUT HEALTH: STRATEGIES TO UNLOCK PIGLET PERFORMANCE

June 17, 2026 from 12:00 to 13:00

Emili Barba
HIPRA (Spain)

Biography

Emili Barba is a veterinarian specialized in animal production, holding a PhD from the Universitat Autònoma de Barcelona and postdoctoral experience at the University of Saskatchewan. His expertise focuses on nutrition, gut health, and immune stimulating strategies to enhance productivity and reduce antibiotic use.

He is currently Global Pipeline Manager at HIPRA, leading innovation in swine health by coordinating new product development with R&D teams, field professionals, and international key opinion leaders.

ABSTRACT

Introduction and Objectives

The reduction of antimicrobial use in pig production has become a global priority due to increasing antimicrobial resistance and regulatory pressure. Post-weaning gastrointestinal disorders, particularly those associated with *Escherichia coli,* remain a major challenge, often leading to prophylactic or therapeutic antibiotic use.

This session explores state of the art post weaning strategies, moving beyond traditional "gut health" concepts toward an integrated approach to strengthening gut resilience through nutrition, management, and immunity - guided by the principle that less is more: focusing on essential, evidence based practices that truly work and applying them coherently.

Materials and Methods (or Main Contents)

The main contents are structured around nutrition, management, and immunity because these three pillars collectively determine gut resilience at weaning and largely explain why enteric disorders emerge in the absence of antibiotics.

Nutrition defines the substrates available to not only for pig metabolism but also for gut microbiota, directly influencing pathogen growth. Management determines the level of exposure, stress, and infection pressure faced by piglets at a critical transitional stage. Immunity represents the piglet's ability to cope with inevitable challenges, whether caused by pathogens or production stress, while preserving metabolic function. Addressing all three blocks together allows a shift from reactive, antibiotic-based control toward proactive, system-level prevention, providing a practical and scientifically robust framework for sustainable antimicrobial reduction.

Nutritional Strategies

Evaluation of nutritional interventions, including creep feeding, reduced crude protein diets, and functional feed additives, aimed at limiting substrate availability for pathogenic bacteria.

Management Practices

Assessment of management-related risk factors such as mixing litters, weaning age, stocking density, hygiene, and cleaning protocols, focusing on reducing exposure and infection pressure.

Immune Competence and Host Resilience

Discussion of immune development at weaning, host–pathogen interactions, and the role of immune priming in resilience to enteric challenges, with particular emphasis on the shigatoxin associated diseases, its vascular and functional impacts, its contribution to hidden productivity losses, and the protective value of targeted Shiga toxin–neutralizing strategies.

Results and Discussion

Integrated strategies combining nutrition, management, and immune support are more effective than single interventions.

Qualitative control measures (reducing exposure and stress) are shown to be as critical as quantitative bacterial reduction. Early-life interventions significantly influence post-weaning outcomes, enabling reduced reliance on antimicrobials while maintaining performance and animal welfare.

Conclusions and Recommendations

Antimicrobial reduction requires a holistic, systems-based approach rather than isolated interventions.
Strengthening gut resilience depends on coordinated nutritional, managerial, and immunological strategies.
Future perspectives include precision nutrition, refined management protocols, and resilience-oriented health monitoring to support sustainable, antibiotic-free production.
Preventing Shiga-toxin–associated diseases and vascular damage, mitigates hidden productivity losses, and reinforces herd-level resilience.

Keywords: Antimicrobial reduction, Gut resilience, Immunity, Management practices, Swine production.

CP - SATELLITE SYMPOSIUM 1

Transitioning from Antibiotics to Probiotics in Swine Production: Field Conditions, Omics Monitoring, and Evidence for Real Impact

June 17, 2026, from 12:00 to 13:00



Prof. Nuvee Prapasarakul
Department of Microbiology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand.

Biography

Professor Dr. Nuvee Prapasarakul is a faculty member in the Department of Veterinary Microbiology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand. His research focuses on antimicrobial resistance (AMR), probiotics and postbiotics in livestock production, veterinary microbiology, One Health, and the application of genomics and metagenomics for pathogen surveillance and food safety. He has led and collaborated on multiple national and international research projects related to antimicrobial-resistant bacteria in pigs, probiotic alternatives to antibiotics, and microbiome-based interventions in animal production systems. Dr. Nuvee has extensive experience in veterinary public health, molecular epidemiology, and translational research linking laboratory findings with practical farm applications. He actively contributes as a reviewer and invited speaker for international journals and conferences, particularly in the fields of swine health, probiotics, antimicrobial stewardship, and sustainable livestock production.

ABSTRACT

Introduction and Objectives

The global reduction of antibiotic growth promoters in swine production has accelerated the search for effective probiotic alternatives. However, inconsistent field performance remains a major challenge because probiotic efficacy is highly conditional rather than universal. Recent evidence suggests that probiotic outcomes depend on multiple interacting factors, including strain selection, sanitary conditions, diet composition, pathogen pressure, host microbiota, production stage, formulation, dose, and duration of administration. This article summarizes recent evidence from experimental and commercial pig studies to identify the major determinants of successful probiotic implementation in real farm environments and to provide practical guidance for veterinarians and producers transitioning toward antibiotic-free production systems.

Main Contents

This technical review synthesized findings from peer-reviewed studies and commercial farm investigations published between 2018 and 2026 involving nursery, growing, and finishing pigs. Evidence from controlled pathogen-challenge models, field trials, and microbiome-based studies

was comparatively analyzed to identify the major conditioning factors associated with successful probiotic responses in swine production.

Studies consistently demonstrated that probiotic efficacy is strain-specific. *Bacillus subtilis* DSM 32540 improved average daily gain (ADG) and reduced diarrhea severity in enterotoxigenic *Escherichia coli* (ETEC)-challenged piglets, whereas closely related *Bacillus* strains produced weaker responses. Multi-strain and microencapsulated formulations often enhanced gut morphology, microbial balance, and intestinal health compared with single-strain products. Farm hygiene and diet composition significantly influenced probiotic outcomes. Greater improvements were observed under poor sanitary conditions or high pathogen pressure, in which probiotics reduced inflammatory markers and the incidence of diarrhea. Certain Bacillus-based probiotics also achieved growth performance comparable to that of zinc oxide- and antibiotic-containing diets, supporting their potential as antibiotic alternatives. Baseline gut microbiota and host susceptibility influenced probiotic responsiveness. Weaned piglets showed the greatest benefits due to microbiota instability and immune stress during weaning. In contrast, growing-finishing pigs generally exhibited more modest improvements in feed efficiency and microbiota modulation.

Results and Discussion

The current evidence demonstrates that probiotic efficacy in swine production is conditional rather than universally predictable. Positive responses are more likely when probiotic strains are appropriately matched to the production stage, farm environment, pathogen challenge, and feeding program. Field application requires careful consideration of multiple interacting factors. Strain selection alone is insufficient if environmental hygiene, diet composition, or pathogen pressure are not simultaneously addressed. Similarly, inconsistent outcomes reported in commercial farms may reflect differences in baseline microbiota, management systems, or inappropriate strain selection rather than failure of probiotics themselves. These findings support a precision-based approach to probiotic implementation in pig production systems. Rather than promoting probiotics as universally effective replacements for antibiotics, veterinarians and producers should evaluate farm-specific risk factors and select products supported by strain-level evidence under comparable production conditions.

Conclusions and Recommendations

Probiotic efficacy in swine production is conditional rather than universal. Successful implementation requires matching probiotic strains and formulations to the specific environmental, dietary, microbial, and management conditions of each farm. Field veterinarians and producers should prioritize strain-specific evidence, evaluate farm hygiene and pathogen pressure, and consider the production stage when selecting probiotic products.

Keywords: Antibiotic-Free Production, Antimicrobial Resistance, Gut Microbiota, Probiotics, Swine Production

Acknowledge: The author acknowledges the CE-DMAP, Chulalongkorn University, CPF Co. Ltd. ARDA, Thailand.

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REBER - SATELLITE SYMPOSIUM 2

Outsmarting Swine Respiratory Disease: New Intelligence from the Field to the Lab Bench

June 17, 2026, from 16:45 to 18:00

Dr. Le Thi Ha Thu
Reber Genetics

Biography

Dr. Le Thi Thu Ha is a veterinary scientist with over 25 years of progressive experience spanning research, industry, and entrepreneurship in animal health and livestock management. She holds a Master of Science in Biotechnology from Nong Lam University, Ho Chi Minh City, and is currently a doctoral candidate in Biotechnology at the same institution. Her career includes research positions at the Institute of Agricultural Sciences for Southern Vietnam, technical and laboratory management roles at Bayer Vietnam, and senior technical and marketing management at MSD Animal Health Vietnam, where she received consecutive Technical Manager of the Year awards in 2019 and 2020. Her research expertise focuses on molecular epidemiology, PCR-based diagnostics, and genetic characterization of major swine pathogens including PRRSV, ASF, and PCV2. She currently serves as CEO and Co-Founder of VETLATECH, a One Health consultation enterprise.



REBER - SATELLITE SYMPOSIUM 2

Outsmarting Swine Respiratory Disease: New Intelligence from the Field to the Lab Bench

June 17, 2026, from 16:45 to 18:00

Professor Dr. Sanipa Suradhat, D.V.M., Ph.D.
Faculty of Veterinary Science, Chulalongkorn University
Bangkok, Thailand

Biography

Prof. Sanipa Suradhat is a Professor of Immunology at the Faculty of Veterinary Science, Chulalongkorn University, Bangkok. She earned her Doctor of Veterinary Medicine (D.V.M.) from Chulalongkorn University and a Ph.D. in Veterinary Immunology from the University of Saskatchewan, Canada, in 1999. Her career is defined by significant contributions to veterinary immunology, focusing on the immunobiology of porcine viral diseases, particularly CSFV and PRRSV. Her research emphasizes porcine cellular immunity, regulatory T lymphocytes, and vaccine development. A recognized expert in vaccinology, Prof. Suradhat serves on several national committees and provides expert consultations and lectures to veterinary and biomedical professionals globally, bridging the gap between academic research and international clinical veterinary practice.



REBER - SATELLITE SYMPOSIUM 2

Outsmarting Swine Respiratory Disease: New Intelligence from the Field to the Lab Bench

June 17, 2026, from 16:45 to 18:00

Dr. Frank C.-J. Chang

Biography

Dr. Frank C.-J. Chang obtain his Ph.D. from Life Science and Institute of Genome Science department of Taiwan Yang-Ming Medical University in 2012. He received his postdoctoral training at Molecular Biology Institute of Academia Sinica (Taiwan) and worked as visiting scholar in Frances H. Arnold's laboratory (Nobel Prize in Chemistry winner in 2018), Caltech (USA). Dr. Frank C.-J. Chang has considerable expertise in virology/microbiology, reverse vaccinology and protein engineering for industrial production. His group has successfully developed protein subunit vaccines of swine PRRSV (PRRSQ), PCV2 (CIRCOQ), *Mycoplasma* (MRQ), CSFV E2 and PEDV (PEDQ) in Reber Genetics, furthermore, they also support CDMO/CMO business of novel veterinary Biologicals for other species and companion animal.

ABSTRACT

Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) and porcine circovirus type 2 (PCV2) are the most economically devastating pathogens in global swine production, with co-circulation rates exceeding 80% in commercial operations. Despite widespread vaccination, outbreaks persist, particularly with heterologous PRRSV strains that evade vaccine-induced immunity. Traditional correlates of protection (CoP) have focused on serum antibody titers (virus neutralization and ELISA), yet these metrics fail to predict heterologous protection and do not account for cases in which seronegative animals remain fully protected. Emerging evidence demonstrates that cell-mediated immunity (CMI), particularly IFN-γ-secreting CD4+ and CD8+ T cells, is the primary driver of durable, cross-protective immunity against both pathogens. This presentation aims to: (1) evaluate the limitations of antibody-centric CoP for PRRSV and PCV2 vaccines; (2) present mechanistic evidence that CMI mediates heterologous protection; (3) demonstrate the limitations of current PRRSV and PCV2 vaccines; (4) redefine CoP to include validated T cell metrics such as IFN-γ production, polyfunctional T cell responses, and memory T cell persistence; and (5) explore molecular adjuvant platforms as strategies for inducing robust CMI without immunosuppressive side effects. Further applications include the prevention and control of respiratory intracellular bacterial infections such as swine *Mycoplasma*.

Main Contents

This satellite symposium brings together three expert perspectives to address the evolving challenges of porcine circovirus and respiratory disease management in modern swine production.

Dr. Le presents current molecular epidemiological data from Vietnamese swine herds, highlighting the rising predominance of the PCV2d genotype and underscoring the critical role of continuous surveillance in tracking viral evolution and genotype dynamics as a foundation for effective disease control. Building on this field reality, Dr. Sanipa challenges the conventional antibody-centric view of vaccine protection, demonstrating that both PRRSV and PCV2 immunity rely fundamentally on cell-mediated immunity (CMI); PRRSV evades host defenses through IL-10 overproduction and Treg expansion that delay CMI onset by 4 - 8 weeks, while PCV2-vaccinated seronegative pigs remain fully protected via IFN-γ^+ T cells and $CD8^+$ CTL activity - collectively redefining the correlates of protection (CoP) for both pathogens and calling for next-generation vaccine platforms that simultaneously engage CD4+ Th1, $CD8^+$ CTL, and memory T cell responses. Closing the symposium, Dr. Chang translates these scientific insights into practical solutions, presenting evidence on how the Reber Genetics novel fusion protein platform leverages detoxified bacteria Exotoxin for precision antigen delivery to dendritic cells and macrophages - achieves polyfunctional CTL and Th1 activation, offering a transformative immunotherapy strategy to combat the most devastating respiratory pathogens threatening swine industry productivity worldwide.

Conclusions and Recommendations

This symposium collectively advances our understanding of PCV2 and PRRSV disease dynamics across three critical dimensions: field epidemiology, immune correlates, and vaccine innovation. The demonstrated predominance of PCV2d among circulating field strains in Vietnam from 2024 to 2025 reinforces the indispensable role of continuous molecular surveillance and genotyping in guiding regionally informed disease control strategies. From an immunological standpoint, antibody-based metrics alone are insufficient as standalone correlates of protection for either pathogen; instead, CMI responses, particularly IFN-γ-secreting $CD4^+$ and $CD8^+$ T cells, represent the true mechanistic mediators of cross-protective and durable immunity. Current vaccine limitations must be candidly acknowledged: PRRSV MLV vaccines perpetuate IL-10/Treg-mediated immunosuppression that undermines CMI quality, while conventional PCV2 vaccines focused on antibody induction remain vulnerable to immune escape and genotype drift. To address these gaps, molecular adjuvant platforms offer a scientifically defined and reproducible path toward simultaneous induction of robust CMI and neutralizing antibodies against both pathogens. The symposium therefore recommends that future vaccine development and field evaluation protocols for PRRSV and PCV2 adopt T cell-based metrics, including IFN-γ secretion, $CD4^+$/$CD8^+$ activity, lymphoid tissue integrity, and memory T cell persistence, as standard endpoints alongside conventional serology. In this context, Reber Genetics' PRRSQ and CIRCOQ within fusion protein platform stand as a compelling embodiment of this next-generation vaccine philosophy, demonstrating that precision intracellular antigen delivery, polyfunctional T cell activation, and broad heterologous protection are not merely theoretical ideals, but achievable realities in the ongoing fight against the most economically devastating respiratory diseases in the swine industry.

Keywords: Cell-mediated immunity, Correlates of protection, PCV2d, PRRSV, fusion protein platform.

Acknowledge: The authors gratefully acknowledge Dr. Le and Dr. Sanipa for their invaluable scientific contributions and expertise that formed the foundation of this symposium. Sincere appreciation is also extended to the International Pig Veterinary Society (IPVS) and the organizing committee for their support in facilitating this satellite symposium and providing a platform for advancing swine health science.

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Boehringer Ingelheim - SATELLITE SYMPOSIUM 2
Dynamic Health in Practice: Integrated Control for a Complex Disease Landscape
June 17, 2026, from 16:45 to 18:00

Dr. Oliver Gómez-Duran DVM, PhD, ECPHM
Ingelheim am Rhein, Germany

Biography

Dr. Oliver Gómez-Duran is a veterinarian dedicated to the prevention of swine diseases through management, biosecurity and vaccination. Currently, he is the Leader of the Global Swine Technical team in Global Strategic Marketing at Boehringer Ingelheim Animal Health. In this role, he is providing technical leadership at the interface between Veterinarians in the field, Technical Managers and scientists in Research and Development.



Boehringer Ingelheim - SATELLITE SYMPOSIUM 2
Dynamic Health in Practice: Integrated Control for a Complex Disease Landscape
June 17, 2026, from 16:45 to 18:00

Dr. Joaqiam Segalés
CReSA - Centre de Recerca en Sanitat Animal, Spain

Biography

Joaquim Segalés is a veterinary pathologist at the Veterinary School of the Universitat Autònoma de Barcelona (Spain) and researcher at IRTA-CReSA (Spain). He has been working since 1993 with swine disease research and with zoonotic coronaviruses from 2014 onwards. He has been working mainly with swine viruses, including porcine circoviruses, among others. He is co-author of more than 500 peer-reviewed publications.

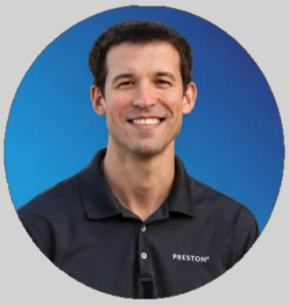


Boehringer Ingelheim - SATELLITE SYMPOSIUM 2
Dynamic Health in Practice: Integrated Control for a Complex Disease Landscape
June 17, 2026, from 16:45 to 18:00

Asst. Prof. Marcelo Almeida
Iowa State University, USA

Biography

Marcelo Almeida received his DVM degree from the University of Brasilia in 2003, a Master's Degree in Preventive Veterinary Medicine by the Federal University of State of Rio Grande do Sul in 2006, and a Ph.D. in Population Sciences in Animal Health from the Iowa State University in 2020. Marcelo has been working with the swine industry for over 20 years with roles in a vertically integrated pork producer, genetic supplier, and pharmaceutical company. Marcelo is currently an assistant professor and food animal diagnostician at the ISU-VDL.



Boehringer Ingelheim - SATELLITE SYMPOSIUM 2
Dynamic Health in Practice: Integrated Control for a Complex Disease Landscape
June 17, 2026, from 16:45 to 18:00

Dr. Joseph Yaros
President of Pipestone Management China Division

Biography

Dr. Joseph Yaros graduated from Cornell University's College of Agriculture and Life Sciences in 2012 with a degree in Animal Science and continued his education at Cornell University's College of Veterinary Medicine, graduating in 2016. Since graduation, Dr. Yaros has spent his career in swine medicine working with Pipestone Veterinary Services. Dr. Yaros has two main responsibilities today: First, since 2017 he has led the management team in China where Pipestone manages 100,000 sows. As a result of the entry of ASF into China in 2019, Dr. Yaros has actively seen and dealt with every major pathogen known in the swine industry. Second, he is the Director of the FarmPro Grow Finish Consulting team, which oversees the health and production of grow/finish pigs throughout

Introduction and Objectives

Modern swine production faces a multifactorial disease landscape, where pathogens interact and amplify health challenges. This symposium, led by Dr. Oliver Duran, but co-presented with global key opinion leaders, explores the integrated control of PCV2, PRRS, and *Lawsonia*, emphasizing holistic herd health and practical solutions. Therefore, the **objective** of this meeting is to highlight the necessity of dynamic, whole-herd approaches and showcase field research and practical experiences that inform best practices for disease management.

Main Contents

1. Whole-Herd Approach to PCV2 Control (by Dr. Joaquim Segales IRTA-CRESA)

This presentation reviews current concepts and practical approaches for the control of porcine circovirus 2-associated diseases (PCV2-ADs) through the implementation of whole herd immunity (WHI). WHI is a population-based strategy aimed at reducing viral transmission, minimizing clinical expression, and improving herd stability by maintaining protective immunity in most animals within the production system. The biological characteristics of PCV2, including its ubiquitous distribution, environmental persistence, and genetic variability, represent some of the challenges for disease control.

Current PCV2 vaccines are considered very effective reducing clinical disease outcome, viremia, and viral shedding, although they do not confer sterilizing immunity. However, different vaccination strategies targeting piglets and breeding stock can be applied, emphasizing the potential benefits of intensified vaccination protocols under conditions of high infectious pressure or complex respiratory disease scenarios. Moreover, mass vaccination strategies represent the possibility of substantially reducing or even eliminating PCV2 circulation within farms. In addition, special attention must be given to the importance of integrating vaccination with biosecurity, management practices, and herd stability measures.

In summary, optimized and herd-adapted immunization programs can substantially enhance PCV2 control and contribute to long-term productive and sanitary stability in swine populations.

2. PRRSV: Central Player in Disease Dynamics (by Dr. Marcelo Almeida ISU)

Porcine reproductive and respiratory syndrome virus (PRRSV) remains one of the most economically impacting pathogens affecting the global swine industry. Beyond its direct impacts on reproductive failure in sows and respiratory disease in pigs of all ages, PRRSV plays a central role in the outcomes of polymicrobial infections in pigs. Its ability to modulate and suppress the host immune system creates conditions that facilitate secondary infection and exacerbate disease severity.

PRRSV infection is characterized by impaired innate and adaptive immune responses, including reduced interferon production, altered macrophage function, and delayed development of protective immunity. These effects increase host susceptibility to a wide range of co-infecting pathogens. Notably, PRRSV has been strongly associated with enhanced severity of porcine respiratory disease complex (PRDC), where interactions with viruses such as swine influenza virus and porcine circovirus type 2 (PCV2), as well as bacteria including *Mycoplasma hyopneumoniae*, *Mycoplasma hyorhinis*, *Streptococcus suis*, and *Pasteurella multocida*, lead to synergistic disease outcomes.

Recent research highlights the variability in PRRSV strains and host responses, further complicating disease dynamics and control strategies. The timing of infection, pathogen combinations, and environmental stressors influence the extent of interaction between PRRSV and other pathogens. Understanding these complex relationships is critical for developing effective integrated disease management approaches.

3. Integrated Disease Control: 3FLEX® + Enterisol® (by Dr. Joseph Yaros, Pipestone)

Porcine Reproductive and Respiratory Syndrome (PRRS), Porcine Circovirus Type 2, *Mycoplasma hyopneumoniae, Lawsonia intracellularis*, and *Salmonella* are 5 primary diseases that the swine industry faces challenges with every day. Boehringer Ingelheim's 3FLEX® program, Enterisol Ileitis® and Salmonella TC® vaccines provide convenient and highly effective vaccination options for all these pathogens. Dr. Yaros will be sharing vaccination routes and case presentations of each of the pathogens to demonstrate efficacy, all while reinforcing safety.

Regarding PRRS, Dr. Yaros will review a case study of a wild type PRRS virus elimination in a complex of 12,000 sows in China via utilization of BI PRRS MLV vaccine. He will also share the safety and data of the Boehringer Ingelheim PRRS MLV vaccine product when utilized in breeding herds. On the topic of Circovirus and *Mycoplasma*, Dr. Yaros will demonstrate strong Circovirus vaccine performance by sharing Pipestone Applied Research trial results of the most effective vaccines of all manufacturers. With *Lawsonia intracellularis*, Dr. Yaros will share the cost benefits of Enterisol Ileitis® vaccination compared to utilizing antibiotics as well as the production impacts before and after application. On the topic of *Salmonella*, Dr. Yaros will review a case where *Salmonella* vaccine was put in place pre-weaning and had significant impacts on the fallout and mortality rates post weaning.

Conclusions and Recommendations

The presentations collectively reinforce the need for holistic, flexible control strategies, leveraging tools like 3FLEX® and Enterisol® Ileitis to simplify execution and deliver consistent results. The foundation built by Ingelvac CircoFLEX® and Ingelvac MycoFLEX®, together with Enterisol® Ileitis and Ingelvac PRRS MLV® has enabled a robust progress in overall disease management. This achievement is exemplified by the global milestone of 5 billion doses of Ingelvac CircoFLEX® delivered, marking a unique partnership between industry and producers and celebrated under the hashtag #withyou5billiontimes.

- ✓ Disease control in swine production must be dynamic and flexible, addressing pathogens from sows to finishers.
- ✓ Integrated vaccination strategies, such as 3FLEX® + Enterisol® Ileitis, simplify management and improve outcomes.
- ✓ Field data confirms that co-infections amplify disease impact, making whole-herd approaches essential.
- ✓ Ongoing innovation and practical experience are key to meeting the complex challenges of modern swine health.

Keywords: Control, Disease, Holistic-approach, PRRS-PCV2/Mhyo-*Lawsonia* solution, Swine.



MSD Animal Health - SATELLITE SYMPOSIUM 2

From Concept to Practice: 30+ Years of Intradermal Vaccination Innovation

June 17, 2026 from 16:45 to 18:00

Dr. Ruud Segers
MSD-Animal Health, Boxmeer, The Netherlands

Biography

Dr Segers obtained a PhD grade at the Veterinary faculty in Utrecht, The Netherlands, in 1991 on molecular studies on Leptospiraceae and since then been employed in R&D at MSD Animal Health. He is now globally responsible for the strategy and development of vaccines for swine and ruminants and leads a group of 90 researchers including 15 PostDocs. This research group has designed and developed more than 30 different veterinary vaccines currently marketed under the Porcilis®, Circumvent®, Bovilis® and Sequivity® brands. The vaccines prevent a variety of viral, bacterial and parasite diseases and contain a variety and combinations of inactivated, recombinant subunit, attenuated live as well as vectored type vaccines which can be administered by intramuscular, intradermal, subcutaneous and/or intranasal route.

Introduction and Objectives

Needle-free intradermal vaccination in swine has evolved from an experimental concept in the early 1990s to a comprehensive platform encompassing multiple vaccine formulations and purpose-built delivery devices. Highlights and scientific-learnings during the more than 30-year history of parallel development of both the Porcilis® vaccine range and IDAL® (IntraDermal Applicator of Liquids) devices will be presented.

Materials and Methods

The IDAL® concept originated during the Pseudorabies virus eradication campaigns of the early 1990s, when the need for hygienic and efficient mass vaccination of swine became apparent. Key questions drove early research: could air-pressure-based needle-free injection be feasible in a handheld, battery-driven format? What vaccine volume and air pressure parameters would ensure consistent intradermal deposition? How would the equipment be cleaned? MRI imaging studies confirmed that IDAL® delivers the standard 0.2 ml vaccine dose as a fine, laterally dispersed cloud within the superficial dermis (extending to approximately 12 mm depth with 18–22 mm lateral spread), in contrast to conventional intramuscular needle injection, which deposits vaccine as a bolus at 12–34 mm depth surrounding deeper structures. Over time the equipment was improved, and four device generations (G0 through G3-2B) have since been introduced into the market, incorporating progressive improvements in ergonomics and reliability. Recently also data

capture, and connectivity with digital farm management solutions have been added. The IDAL® platform is also supported by local training and servicing organizations.

Results and Discussion

Advantages of Intradermal Delivery

Multiple studies have demonstrated key advantages of IDAL® vaccination. Needle wear and tear - a known source of tissue damage and injection site lesions - is eliminated entirely. Behavioral observations confirm reduced stress responses in animals vaccinated intradermally compared to intramuscular injection.

Critically, hygiene studies showed that IDAL® significantly reduces the risk of iatrogenic pathogen transfer between animals: when ASF virus inoculated animals were injected with needles and the same needle then used on naïve sentinels, needle-based injection transferred virus whereas IDAL® did not. The same was also demonstrated for PRRS virus in similar experiments.

Live Vaccines

The first intradermal vaccines developed for IDAL® were live products, including Porcilis® Begonia (Pseudorabies DIVA) and Porcilis® PRRS. Studies confirmed that live viruses survive the air-pressure delivery process and that intradermal administration confers equivalent immunity to intramuscular injection. IDAL® thus offered improved efficiency and hygiene without compromising vaccine efficacy for live formulations.

Inactivated Vaccines and Portfolio Expansion

Extending the platform to inactivated vaccines presented greater challenges, as these formulations require potent adjuvants, in a very small (0.2 ml) volume and must overcome the weaker immunogenicity of killed antigens. A dedicated intradermal formulation was developed for *Mycoplasma hyopneumoniae* (Porcilis® M Hyo ID Once) which demonstrated superior efficacy in a field situation compared to an intramuscular equivalent. Subsequently monovalent intradermal vaccines were also developed for 2 more major swine pathogens: PCV2 (Porcilis® PCV ID), and *Lawsonia intracellularis* (Porcilis® Lawsonia ID). Each product was specifically optimized for intradermal delivery and demonstrated non-inferior or superior efficacy, particularly in the presence of maternally derived antibodies (MDA). Intradermal vaccination showed a notable skewing toward cellular (Th1) immune responses, which may contribute to improved performance in MDA-positive piglets.

Combination Strategies and the Mix & Match Approach

Recognizing that piglets face simultaneous threats from *M. hyopneumoniae*, *Lawsonia*, PRRS, and PCV2, an R&D strategy was developed to enable flexible combination of intradermal vaccines. A double-barrel IDAL® device allows concurrent administration of two vaccines in a single handling event. The "Mix & Match" approach combines lyophilized antigens (e.g., *Lawsonia*) with ready-to-use adjuvanted vaccines, enabling practitioners to deliver multiple antigens - including the recently developed Porcilis® PCV M Hyo ID combination - as single-shot pre-weaning protocols via both intramuscular and intradermal routes.

Conclusions and Recommendations

Over three decades, intradermal vaccination with IDAL® has matured from a novel concept into a validated platform offering improved hygiene, faster vaccination, enhanced performance in MDA-positive animals, favorable Th1-skewed immune responses, improved animal welfare, and a lower ecological footprint. A unique, purpose-designed vaccine portfolio continues to expand, providing swine practitioners with increasingly flexible tools for comprehensive piglet protection before weaning.

Key Words: Animal Welfare, Efficacy, Hygiene, Safety, Vaccination.



KEMIN - SATELLITE SYMPOSIUM 2

ADVANCES IN PRRS MANAGEMENT: NEW RESEARCH TO REDUCE PRODUCTION LOSSES

June 17, 2026 from 16:45 to 18:00

Dr. Chao-Nan Lin
Department Of Veterinary Medicine,
National Pingtung University of Science and Technology, Taiwan

Biography

Dr. Lin holds a Ph.D. from the Graduate Institute of Veterinary Medicine, National Taiwan University, and a veterinary degree from National Chiayi University. Currently, he serves as Distinguished Professor in the Department of Veterinary Medicine at National Pingtung University of Science and Technology (NPUST). He also held the position of Department Chair from August 2022 to July 2025. Dr. Lin began his academic career at NPUST as a Research Assistant and progressed through roles including Research Fellow, Assistant Professor, Associate Professor, and Professor since 2017. With extensive academic and leadership experience, his work focuses on advancing veterinary medicine through research, education, and industry collaboration.

ABSTRACT

Introduction and Objectives

Porcine reproductive and respiratory syndrome (PRRS) remains a major concern for the global swine industry, causing estimated annual economic losses between USD 2.5 and 3 billion. This study assessed the effectiveness of combining Algal beta-Glucan (ABG) with PRRS vaccination in nursery pigs exposed to a highly virulent PRRS virus strain. The objective was to explore the potential for optimizing supportive interventions typically administered alongside the PRRS vaccine.

Materials and Methods (or Main Contents)

4-week-old pigs were randomly assigned to 4 groups. PRRS Modified Live Virus Vaccine was given to T1 and T2 piglets at 4-week-old. The product, ABG is from dried algae containing 50% of β-1,3 glucan provided by Kemin Industries. In groups T1-T3, five pigs were intranasally inoculated with PRRSV strain 108 - 929 (10^3 TCID50/mL), with 1 mL administered into each nasal cavity at 8-week-old.

The remaining five pigs in T1 to T3 were co-habited with inoculated pigs as contact infection.

• T1 (n=10): PRRS vaccination + Algal beta-Glucan (ABG) 200 g/MT;

• T2 (n = 9): PRRS vaccination only;
• T3 (n = 10): PRRSV challenge only (blank: no treatment, no vaccination);
• T4 (n = 3): Negative control (no challenge or treatment).

Results and Discussion

Pigs in the ABG-supplemented group demonstrated superior post-challenge performance. Average daily weight gain after viral challenge was not only maintained but exceeded pre-challenged levels, accompanied by a marked improvement in mortality for T1. These findings indicate that ABG may enhance host resilience to PRRS challenge by mitigating the adverse effects of infection on growth performance and survival, rather than through direct suppression of viral replication. Therefore, ABG shows strong potential as a complementary nutritional strategy to support PRRS vaccination programs under commercial production conditions.

Conclusions and Recommendations

Comparison between the different treated groups versus T3 group, revealed that:

1. The average daily weight gain in T3 group was significantly lowest than treated group T1;
2. The PRRSV load in serum in T3 group was significantly higher than T1 and T2 group;
3. The survival rate of T3 group were significantly lower than T1 and T2 groups.

Taken together, these results provided evidence that PRRSV vaccination plus ABG (200 g/MT) was able to reduce the mortality and PRRSV load in weaned pigs, supporting the possibility of contributing to antibiotic-free pork production.

With a market value of USD 133 per pig, T1 group saved four additional pigs (USD 532) compared with T2 group, yielding an ROI of 222:1. These findings indicate potential biological and economic advantages that may contribute to improved PRRSV control and herd productivity

Keywords: Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), β-glucan supplementation

Acknowledge: Thanks to NPUST, Taiwan for their support with the testing facilities.

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CEVA - SATELLITE SYMPOSIUM 3

Don't underestimate FLU and PRRSV impact on your farm!

June 18, 2026, from 12:00 to 13:00

Dr. Julia Stadler
Clinic for Swine at the Center for Clinical Veterinary Medicine, Ludwig Maximilians University Munich, Munich, Germany

Biography

Dr. med. vet. Julia Stadler is a veterinary specialist in porcine health management and Diplomate of the European College of Porcine Health Management (ECPHM). She is Senior Academic Assistant at the Clinic for Swine, Ludwig-Maximilians-Universität München. Her research focuses on infectious diseases of swine, with particular emphasis on the epidemiology, surveillance, and diagnostics of swine influenza A virus under field conditions. She has contributed extensively to peer-reviewed publications and international research collaborations, addressing disease dynamics and evidence-based control strategies in pig populations. Dr. Stadler is actively involved in European research initiatives, including the European Swine Influenza Network, and serves as Chair of the Credential Committee of the ECPHM. Her work supports the advancement of disease monitoring and sustainable health management in modern swine production systems.

ABSTRACT

Introduction and Objectives

Porcine reproductive and respiratory syndrome virus (PRRSV) and swine influenza A virus (swIAV) are key viral pathogens in modern pig production and major contributors to the porcine respiratory disease complex (PRDC). Beyond their role in respiratory disease, both viruses can negatively affect reproductive performance. PRRSV is a well-recognized primary etiological agent of reproductive failure in swine, whereas the contribution of swIAV is often underestimated, despite field studies demonstrating associations between influenza outbreaks in sow herds and impaired reproductive performance, including increased return-to-estrus, abortions, stillbirths, and reduced farrowing rates. Despite their recognized individual importance, their combined impact under field conditions remains insufficiently characterized, particularly due to diagnostic limitations and complex infection dynamics at herd level.

Main Contents

Swine Influenza A Virus (swIAV)

Swine influenza A virus (swIAV) is widely distributed in pig populations and commonly persists

enzootically within herds. Field observations indicate that virus circulation frequently occurs in clinically inapparent age groups and is characterized by asynchronous infection dynamics and co-circulation of multiple subtypes. These epidemiological features complicate detection under field conditions. Structured sampling approaches were applied, including cross-sectional sampling across age groups. Individual samples (e.g. nasal swabs) were combined with population-based samples (e.g. oral fluids), and molecular and serological methods were used to improve diagnostic sensitivity and support subtype detection.

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV)

PRRSV remains endemic in many production systems despite widespread vaccination. Based on published data, diagnostic approaches have increasingly shifted towards population-based sampling. Processing fluids and oral fluids are widely used for herd-level surveillance due to their efficiency and high sensitivity. Additionally, tongue tips from dead piglets have been described as a practical and sensitive sample type, particularly in breeding herds and low-prevalence scenarios.

Results and Discussion

For swIAV, virus circulation under field conditions showed pronounced heterogeneity across age groups and sample types. Virus detection was not restricted to clinically affected animals, indicating that clinical assessment alone is insufficient to reliably identify swIAV circulation under enzootic conditions. Moreover, different viral subtypes were detected across age groups and, in some cases, across sample matrices within the same herd, indicating complex and spatially heterogeneous circulation patterns. Group-based samples consistently yielded higher detection rates at herd level, whereas individual samples, particularly nasal swabs, remained essential for reliable subtype differentiation. The combined use of both sampling approaches substantially improved the detection and characterization of virus circulation. Pre-analytical factors, including sample stabilization and storage conditions, had a direct impact on RNA stability and diagnostic sensitivity, particularly in group-based samples. These observations are in line with current concepts in PRRSV diagnostics, where population-based sampling approaches have also been established as a sensitive tool for herd-level surveillance.

Conclusions and Recommendations

Reliable diagnostics for swIAV and PRRSV require structured sampling strategies and the combined use of complementary diagnostic methods. Limited or inconsistent sampling leads to underdiagnosis of virus circulation under field conditions. Standardization of sampling, handling, and processing is essential to ensure comparability and reproducibility. Sampling strategies must be aligned with the diagnostic objective. Only the combination of standardized procedures with targeted sampling enables a reliable assessment of virus circulation at herd level.

Keywords: Diagnostic strategies, Epidemiology, PRRSV, Surveillance, Swine influenza A virus.

Acknowledgement: This work was supported by Ceva Santé Animale.

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CAVAC - SATELLITE SYMPOSIUM 3

Outstanding ASF vaccine (MEC-1) aligned with WOAH guideline (No shedding, No transmission, No reversion to virulence)

June 18, 2026 from 12:00 to 13:00

Dr. Jason Lee
President, CAVAC
(Choong Ang Vaccine Laboratories Co., Ltd.)

Biography

Sung-Sik Yoo is Director of the Global Business Division at CAVAC (Choong Ang Vaccine Laboratories), Republic of Korea, and serves as the overall coordinator for the company's African swine fever (ASF) vaccine program. He has extensive experience in veterinary vaccine manufacturing, formulation development, and international business activities for animal health products. His work has included adjuvant technology development and participation in the manufacturing processes of various veterinary vaccines. His professional experience involves vaccines and biologics targeting economically important animal diseases, including African swine fever (ASF), avian influenza, Newcastle disease, and fowl adenovirus infections. He has also participated in multiple national research and development projects related to veterinary vaccines and transboundary animal diseases in Korea.



CAVAC - SATELLITE SYMPOSIUM 3

Outstanding ASF vaccine (MEC-1) aligned with WOAH guideline (No shedding, No transmission, No reversion to virulence)

June 18, 2026 from 12:00 to 13:00

Dr. Sung-sik Yoo
Head of ASF Vaccine Project, CAVAC
(Choong Ang Vaccine Laboratories Co., Ltd.)

Biography

Jason Lee is CEO of CAVAC (Choong Ang Vaccine Laboratories), a leading Korean animal vaccine company specializing in the research, development, and manufacturing of veterinary vaccines. He has extensive experience in the global animal health industry, including previous leadership roles in international animal health companies across Asia and Europe. Since joining CAVAC in 2018, he has contributed to expanding the company's global business strategy, vaccine commercialization, and research collaborations. His recent work has focused on the development of live attenuated African swine fever (ASF) vaccines, including cell adaptation technology, genetic stability evaluation, and field application studies in Korea and Vietnam. He has presented ASF vaccine research at international scientific conferences, including APVS 2023, where his work received the Best Oral Presentation Award.

ABSTRACT

Introduction and Objectives

African swine fever (ASF) continues to spread across Asia and Europe, causing substantial economic losses to the global swine industry. Despite ongoing efforts, the commercial availability of safe and effective ASF vaccines remains limited, particularly for genotype II ASFV strains currently circulating in endemic regions. Live attenuated vaccine (LAV) candidates have demonstrated promising efficacy; however, concerns regarding safety, genetic stability, residual virulence, transmission, and large-scale field applicability remain major regulatory and commercial challenges. SuiShot® ASF-X is a live attenuated ASF vaccine candidate developed from the genotype II ASFV-MEC-01 strain. A series of studies based on the WOAH guideline recommendations for ASF live attenuated vaccines, including safety, genetic stability, dissemination, transmission, and efficacy evaluations, together with commercial farm clinical assessments, were performed to investigate the overall characteristics and field applicability of the vaccine candidate.

Materials and Methods

The ASFV-MEC-01 strain was propagated using a porcine cell-based production system under controlled manufacturing conditions. Multiple production lots were prepared for consistency evaluation.

Safety studies included clinical observation, body temperature monitoring, survival analysis, and adverse reaction assessment. Genetic stability and residual virulence were evaluated through sequential back-passage studies in pigs. Virus dissemination and shedding were examined using blood, tissue, and oral/nasal samples. Protective efficacy was evaluated using virulent genotype II ASFV challenge strains. Clinical signs, mortality, viremia, and pathological lesions were compared between vaccinated and control pigs. Commercial farm evaluations were also conducted to assess field applicability and post-vaccination safety in breeding and growing pigs.

Results and Discussion

Vaccinated animals showed favorable safety profiles without significant clinical abnormalities or severe adverse reactions during the observation period. Sequential passage studies demonstrated maintenance of attenuated characteristics without evidence of reversion to virulence. Genetic characterization confirmed stable deletion profiles across evaluated passages and production batches.

Virus dissemination following vaccination was limited and transient, while horizontal transmission between animals was minimal under the tested conditions. These findings support the biological stability and biosafety profile of the vaccine candidate.

Challenge studies demonstrated significant protection against virulent genotype II ASFV exposure. Vaccinated pigs showed markedly reduced mortality, lower clinical scores, and suppression of severe pathological lesions compared with non-vaccinated controls. Commercial-scale evaluations further demonstrated practical applicability of the vaccine under field conditions.

Vaccinated pigs maintained normal production performance and tolerability, supporting the feasibility of large-scale vaccination programs in endemic regions. Collectively, the results indicate that SuiShot® ASF-X possesses characteristics considered important for future commercialization of ASF live attenuated vaccines, including efficacy, manufacturing scalability, genetic stability, and field applicability.

Conclusions and Recommendations

SuiShot® ASF-X demonstrated favorable safety, genetic stability, and protective efficacy against genotype II ASFV challenge in both experimental and field-associated evaluations. The vaccine candidate also showed promising scalability and consistency for commercial manufacturing applications. The overall findings support the continued development of **SuiShot® ASF-X** as a potential commercial ASF vaccine platform for endemic regions. Further long-term monitoring, expanded field evaluations, and country-specific regulatory studies are recommended to support international registration and commercialization strategies.

Keywords: African swine fever virus, Genotype II, Genetic stability, Live attenuated vaccine, Vaccine safety

Acknowledgement: The authors acknowledge the support and collaboration of Avinext, Chungnam National University, National Wildlife Disease Control Institute, Vietnam Institute of Animal and Veterinary Science, Nong Lam University, and Darby Genetics Vietnam.

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ELANCO - SATELLITE SYMPOSIUM 3

PRRS Control Intelligence: Leveraging Industry Real-World Evidence to Achieve System-Wide Mastery

June 18, 2026, from 12:00 to 13:00

Dr. Cesar Corzo
University of Minnesota, US

Biography

Dr. Cesar Corzo is an Associate Professor and the Allen D. Leman Chair in Swine Health and Productivity at the University of Minnesota's College of Veterinary Medicine and the director of the Morrison Swine Health Monitoring Project (MSHMP), a nationally collaborative initiative funded in part by the Swine Health Information Center (SHIC). Dr. Corzo focuses on the occurrence, transmission dynamics and control of infectious diseases in swine populations. His research integrates real-world production system challenges with epidemiological modeling to develop sustainable strategies for pathogen prevention, control, and elimination.



ELANCO - SATELLITE SYMPOSIUM 3

PRRS Control Intelligence: Leveraging Industry Real-World Evidence to Achieve System-Wide Mastery

June 18, 2026, from 12:00 to 13:00

Dr. Amy Maschhoff
Elanco Swine Innovation & Strategy, US

Biography

Dr. Amy Maschhoff is a veterinary professional at Elanco Animal Health with extensive experience in swine health and production systems. She holds a Doctor of Veterinary Medicine (DVM) degree and has developed a strong focus on infectious disease management, herd health optimization, and applied research in commercial swine operations. Her work integrates scientific evidence with practical field application, supporting veterinarians and producers in improving animal health outcomes and production efficiency. Dr. Maschhoff has contributed to technical training, scientific communications, and cross-functional collaborations within the animal health industry. Her professional interests include vaccine strategies, disease prevention, and sustainable livestock production. Through her role at Elanco, she continues to support innovation and knowledge transfer in global swine health management.

ABSTRACT

TOPIC 1: PRRS in the United States: Current situation and intervention strategies

Introduction

Porcine reproductive and respiratory syndrome (PRRS) continue to be the main swine disease in the United States (U.S.) swine industry. The latest assessment regarding its cost to the industry estimated that the virus generates USD $1.2 billion in annual losses.[4] As the virus completes its fourth decade in the U.S., producers and veterinarians continue to fight back through the implementation of biosecurity, pig flow, vaccines and monitoring. While the industry has learned how to mitigate its impact and prevent viral introductions, there are still unanswered questions.

Current epidemiological situation

Producers and veterinarians have come together to help understand the epidemiology of this virus in the U.S. by sharing their data through the Morrison Swine Health Monitoring Project (MSHMP) (mshmp.umn.edu). The project obtains weekly breeding herd status data from 3.9M sows which has allowed to characterize the virus incidence and prevalence.

Our data indicates that approximately 20% of the breeding herds report a break in any given year with some farms experience more than one break. When assessing what proportion of the breeding herds are weaning PCR positive pigs, 30% of the herds have been weaning virus positive piglets which will then populate growing pig barns in high dense regions which will become a risk to neighboring farms. Fortunately, the industry has been able to maintain 50% of the herds virus free (i.e., seronegative). Interestingly, PRRS outbreaks have followed a cyclical trend over the last 16 years in which the multi-variant PRRS epidemic usually beginning in October-November and ending in March-April. While this pattern is predictable, the industry still does not understand what the triggering factors for such event are but a temporal association between crop harvesting and manure management has been identified but the mechanism has not been elucidated. Through spatial mapping and PRRS classification we have revealed that herds with different PRRS statuses share the same neighborhood which automatically generates risk of infection. Data analysis identified that there are factors such as herd density, herd size (>2,500 sows) and specific years related to increased risk whereas air filtration reduced the risk.[7]

Virus diversity

The co-circulation of multiple variants of PRRS in the U.S. swine industry is contributing to exacerbating the impact of this virus. Work conducted by Paploski et al., (2019) clearly characterized the diversity of this virus in the industry by highlighting the multiple lineages co-circulating.[6] Interestingly, the dominance of specific lineages and sub-lineages shifts every 3 to 5 years approximately with lineage 1 becoming the main one in the industry (VanderWaal et al., 2025). Due to this complex diversity landscape, in 2020 a new virus emerged (i.e., L1C.5 [2]) because of recombination[5]. This newly emerged virus rapidly disseminated through the Midwestern U.S. and served as the ancestor for current variants (i.e., L1C.5.32, L1C.2, L1C.5.35) which are currently generating important outbreaks. Due to this phenomenon, a Variant Under Monitoring (Kikuti et al., 2025) system was established to alert the industry when new viruses emerge.

This system objectively identifies rapidly spreading viruses based on the number of premises being infected and not through the number of sequences generated. Through this metric the industry can better understand the transmissibility of specific variants.

Current intervention strategies to eliminate PRRS from breeding herds

Producers and veterinarians in the U.S. clearly understand the magnitude of the losses generated by this virus. Since the virus causes important welfare concerns and losses, some producers and veterinarians have decided not to have endemically infected populations and have invested resources to develop mechanisms to effectively eliminate the virus by stabilizing infected breeding herds and thus, wean virus free pigs. Weaning a virus free pig will allow pigs to express their genetic potential as the pig can be effectively vaccinated and thus be prepared for challenges downstream. In addition, by weaning virus free pigs, producers will contribute to avoid further spreading viruses.

The industry currently has a comprehensive toolkit to eliminate this virus. The tools that are in such toolkit have been used and validated; these include but are not limited to:

- Pig Flow: Depopulation/repopulation, herd closure, nursery all-in/all-out (AIAO) by site, finisher all-in/all-in (AIAI) by site, AIAO isolation units, and off-site breeding projects.
- Immunity: Modified-live vaccines (MLV), live-virus inoculation (LVI), and killed vaccines (currently under evaluation).
- External Biosecurity: Farm location selection, air filtration, decontamination and drying rooms for supply entry with UV chambers, transport cleaning/disinfection/drying protocols, shower-in/shower-out or Danish entry systems, and mortality management.
- Internal Biosecurity: PRRS-free semen use, McRebel protocols, mortality management (composting vs. rendering), loading/unloading procedures and weaning biosecure piglet management.
- Monitoring: RT-PCR and serology testing, ORF5 and whole-genome sequencing, processing fluids, Family Oral Fluids, Tongue Tip Fluids, serum sampling, and sentinel animals.

The main herd stabilization approach in the U.S. uses a well-designed Herd Closure program that in some cases uses an off-site breeding project. This closure has been extended as the new variants are requiring more closure time with some herds needing 20 to 30 weeks extra to successfully eliminate the virus. In addition to this change in gilt flow, practitioners are using some sort of homogenization of the herd either through MLV or LVI. In some cases, some practitioners use a combination of these and lately, killed vaccines are being assessed. Monitoring of the neonatal population begins three to four months after the outbreak date through the combination of processing fluid, tongue-tip-fluids and due-to-wean pig pooled blood. All these samples are being tested for PRRS via RT-PCR

TOPIC 2: US Experience from the Production Perspective (Vaccine)

The structural evolution of the US swine industry - characterized by 70% consolidation and highly specialized operations - has improved efficiency but complicated disease management.

With approximately 71% of pigs moving locations between weaning and finishing, and over 1.7 million pigs entering Iowa monthly, transport biosecurity and regional viral pressure are critical risk factors.[9] Despite advancements in filtration and biosecurity, the rapid evolution of PRRSV, particularly the emergence of highly pathogenic Lineage L1C variants, necessitates a shift toward data-driven management.[11,12]

That's where recent collaboration and industry goals have come into play. There are several examples of how collaboration amongst diagnostic labs, universities, veterinarians and production systems have started to shape continued lessons learned. Specifically, when concerning diagnostic data, programs like the Swine Disease Reporting System through Iowa State University have allowed for high transparency on RFLP and Lineage trends.[8] These reports aggregate the data across US diagnostic labs together to provide producers with trends. One specific breakdown allows producers to see the trends within seasons and others within PRRS lineages.

Another tool that producers and veterinarians have in the US is the Iowa State University PRRS Outbreak Management Program through the Field Epi team (https://fieldepi.org/pomp). In collaborative original work Linhares, et. al published the basic knowledge the industry has today on PRRS outbreak management regarding time to stability and time to baseline production post a new wild type of outbreak in sow farms (USDA Census of Agriculture. 2017). As a follow up several years later, The Maschhoffs production system utilized that template and partnership to make a tailored approach to monitoring PRRS outbreak management within a specific system for both sow farms and growing sites. Ongoing data collection and standardization on three aspects within sow farms for PRRSV outbreak management included: 1) diagnostic data using weekly processing fluids to categorize PRRSV statuses given response plans of controlling or eliminating PRRSV based on the AASV classification; 2) production data during PRRSV outbreak event (21 weeks before and 52 after) to calculate time-to-stability (TTS, number of weeks to consistently wean negative pigs), time-to-baseline-production (TTBP, number of weeks to achieve baseline of total weekly pig wean), and total losses per 1,000 sows (number of pigs that farm did not wean during the course of the outbreak), metrics that are comparable across breeding herds; and 3) practices and interventions during the outbreak.[13] Subsequently, a similar approach was started for field evaluation of wean to market PRRS practices.

Uniquely, the introduction of Prevacent PRRS made those monitoring tools and resources even more useful for producers and veterinarians when it entered the US market. In additional post approval studies, application of Prevacent PRRS continues to suggest less shedding, improved nursery pig growth performance and safety profile in sow herds without disruptions to sow herd or downstream production metrics.[14,15,16] Ongoing US collaboration between diagnostic labs, universities, veterinarians and producers will help the US industry continue to learn grow and implement the best strategic application of these new solutions for PRRS. Provide background and context of the topic. Highlight its relevance and current challenges.

Keywords: Porcine reproductive and respiratory syndrome, PRRSV epidemiology, Lineage 1C5, PRRS vaccination strategies, Prevacent PRRS.

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VIRBAC - SATELLITE SYMPOSIUM 3
From Treatment to Control: A New Era in *E. coli* F4 & F18 Protection
June 18, 2026, from 12:00 to 13:00

Dr. Edgar Díaz
Commercial Director – Americas, Anitox

Biography

Dr. Edgar Díaz (DVM, MBA) is a swine pathology expert and Commercial Director for Anitox (USA). With over 30 years of experience and 320 published papers, he specializes in the devastating impacts of F4 and F18 pathogens.



VIRBAC - SATELLITE SYMPOSIUM 3
From Treatment to Control: A New Era in *E. coli* F4 & F18 Protection
June 18, 2026, from 12:00 to 13:00

Prof. Ponchalit Assavacheep
Clinic - Chulalongkorn University, Thailand

Biography

Assistant Professor Dr. Pornchalit Assavacheep (DVM, MSc, PhD) is a researcher at Chulalongkorn University, Thailand. His work at the forefront of swine health focuses on herd management, autogenous vaccines, and molecular diagnosis.



VIRBAC - SATELLITE SYMPOSIUM 3
From Treatment to Control: A New Era in *E. coli* F4 & F18 Protection
June 18, 2026, from 12:00 to 13:00

Francisco J. Rodríguez
Global Marketing Manager – Swine Segment, Virbac

Biography

Francisco J. Rodríguez (DVM, MBA) is the Global Marketing Manager for the Swine Segment at Virbac. A vocational veterinarian with 26 years of industry experience across the entire value chain, he currently leads global strategic marketing and the launch of innovative health solutions from Virbac's headquarters in France.

ABSTRACT

Introduction and Objectives

For decades, the global swine industry has primarily reacted to *Escherichia coli* outbreaks through post-clinical treatments[1]. However, in the current "New Era" of production, this reactive approach is no longer sustainable. Infections caused by *E. coli* F4 and F18 strains represent a devastating threat, with mortality rates potentially reaching 30% before clinical signs like diarrhea even manifest[1,2,4]. The objective of this session is to demonstrate the necessity of shifting the paradigm from traditional medication to proactive prevention.

Materials and Methods

This symposium will analyze the 4-step mechanism of infection to understand how these pathogens impact swine health and production. We will examine regional prevalence data, specifically focusing on the 28% prevalence of F18 in Thailand, alongside the challenges faced in US swine production regarding F4 and F18 "culprits". The discussion will detail how current vaccination programs are being implemented to mitigate these risks.

Results and Discussion

Evidence indicates that waiting for clinical symptoms to appear results in significant "Zootechnical Impacts" and high morbidity. Discussion will focus on the transition toward sustainable prevention through advanced health solutions. We will introduce two specific vaccine tools designed to provide robust protection, moving the industry beyond simple disease reaction.

Conclusions and Recommendations

Control must begin before the first clinical sign appears[3]. To ensure long-term sustainability and animal health, it is recommended to adopt a comprehensive control strategy using targeted vaccines5. This turning point in swine health management emphasizes that early prevention is the most effective tool against the economic and welfare impacts of E. coli[5].

Keywords: E. coli F4, E. coli F18, Prevention, Swine health, Vaccination.

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CTC-Bio - SATELLITE SYMPOSIUM 4

Strong Protective Efficacy and Safety of a Live-Attenuated ASF Vaccine (PRO-VAC) in Domestic and International Trials Involving Growing Pigs and Pregnant Sows

June 18, 2026, from 16:45 to 18:00

Dr. Sur, Jung Hyang
Director of R &D, Komipharm International Co., Ltd.,
Republic of Korea

Biography

Dr. Jung-Hyang Sur is a globally recognized veterinary pathologist with over three decades of expertise in infectious disease research. He gained critical experience as a Research and Diagnostic Pathologist at the USDA's Plum Island Animal Disease Center, where he specialized in African Swine Fever (ASF) vaccine development and clinical trials. After 21 years as a Professor of Veterinary Pathology at Konkuk University in Seoul - where he also served as Vice President and President of the Industry-Academy Cooperation Foundation - and authoring over 100 papers in renowned international journals, he now serves as the President of the Korean College of Veterinary Pathologists. Currently, as the Director of the R&D Institute at Komipharm International, Dr. Sur leads global efforts in ASF vaccine development, bridging the gap between high-level academic research and practical solutions for the farming community

ABSTRACT

Background

African Swine Fever (ASF) continues to cause catastrophic losses in global swine production systems, making the development of an effective vaccine to control it an urgent priority. While various vaccine approaches have been attempted, the most consistent protective efficacy reported to date has been achieved using live attenuated virus (LAV) vaccine candidates. Therefore, this study comprehensively evaluated the protective efficacy of the vaccine, viral shedding patterns, reproductive safety including farrowing outcomes in late-gestation sows and passive transfer of maternal antibodies to piglets, using the multi-gene-deleted live-attenuated strain ASF-G-ΔI177L/ΔLVR (PRO-VACTM-ASF) under various simulated infection conditions both domestically and internationally.

Methods and Methods

The study was composed of two main experimental models. Experiment 1 divided 6-week-old pigs into three groups, each containing 12 pigs (4 per experimental model). Each pig received a 1 ml intramuscular injection of 10^3 $TCID_{50}$ ASF-G-ΔI177L/ΔLVR. A positive control group of 2 pigs (n=6) was assigned to each experimental model. The challenge ASFV used for all experimental models was the Korean epidemic strain (ASFV Hwacheon/2020). The first experimental group

(n = 4) underwent three times challenges at 4, 8, and 12 weeks post-vaccination respectively. The remaining models underwent delayed challenges at 8 (n = 4) and 12 (n = 4) weeks post-vaccination. Vaccine efficacy and immune persistence were assessed for each experimental model post-challenge. Experiment 2 replicated a large-scale Philippine field clinical environment by deploying over 200 growing pigs and over 30 pregnant sows. It monitored antibody persistence and viral shedding in growing pigs while precisely analyzing sow farrowing performance and the efficiency of antibody transfer to piglets via colostrum.

Results

Experimental results showed that the vaccinated group in Experiment 1 demonstrated 100% survival and complete clinical protection in both the three-times challenge model and the delayed challenge models, whereas the control group exhibited typical ASF symptoms and died. Experiment 2, a large-scale commercial farm trial, also showed that growing pigs achieved a 93% antibody positivity rate just two weeks post-vaccination and maintained robust antibody levels until market age. Notably, excellent safety was demonstrated, with no vaccine virus shedding observed in whole blood or oral secretions at the time of market age. Furthermore, all pregnant sows farrowed normally, maintaining the stillbirth rate at the control group level (±2%). Maternal antibodies were detected in 100% of the born piglets, and sows also achieved 100% rebreeding success after weaning, confirming no reduction in reproductive performance.

Conclusion

This study demonstrated that the ASF-G-ΔI177L/ΔLVR strain provides sustained and robust immune protection to growing pigs even under the harsh infection conditions of ASF endemic regions. Notably, its high tolerability in late-gestation sows and efficient maternal antibody transfer capability provide key evidence supporting the vaccine's field applicability. Collectively, these data suggest that this attenuated vaccine (PRO-VACTM-ASF) holds significant commercial value as a practical tool capable of dramatically reducing associated mortality and economic losses in ASF-endemic regions like Asia, where sustainable control options

Keywords: African swine fever (ASF), Live attenuated vaccine (LAV), ASF-G-ΔI177L/ΔLVR, Reproductive safety in pregnant sows

Acknowledgement: We thank the National Institute of Wildlife Disease Control and Prevention (NIWDC), the Bureau of Animal Industry (BAI), the Animal Disease Diagnostic and Reference Laboratory (ADDRL), and Nobel Vet International for their collaboration.



BAF - SATELLITE SYMPOSIUM 4

Smart technology solutions for African swine fever (ASF) control and prevention

June 18, 2026, from 16:45 to 18:00

Dr. Nguyen Van Minh
Deputy General Director of BAF Vietnam Agriculture Joint Stock Company and the CEO & Senior Animal Health Consultant at Vet24h Academy

Biography

Dr. Nguyen Van Minh is currently the Deputy General Director of BAF Vietnam Agriculture Joint Stock Company and the CEO & Senior Animal Health Consultant at Vet24h Academy. He served as a lecturer at the Faculty of Veterinary Medicine, Vietnam National University of Agriculture (VNUA) from 2008 to 2017, and has worked as a technical consultant for the International Finance Corporation (IFC). His research and professional expertise focus on optimizing technical and technological solutions in high-tech swine production under the closed Feed - Farm - Food (3F) model and promoting circular economy practices (Pigs raise fields - Fields raise pigs). At BAF Vietnam, Dr. Minh directly oversees the implementation of smart technology ecosystems and advanced biosecurity systems, including international collaborations on smart multi-story swine farming projects. These initiatives are pivotal in achieving BAF's strategic vision of reaching 10 million commercial pigs and 450,000 sows by 2030.

ABSTRACT

Introduction and Objectives

African Swine Fever (ASF) remains one of the most critical challenges facing the global swine industry. The rapid transmission and high mortality rates of the ASF virus (ASFV) have severely disrupted food supply chains and caused immense economic losses. Given the increasingly complex epidemiological pressure, traditional biosecurity measures have revealed significant limitations, particularly their heavy reliance on human compliance and manual operations. To fundamentally address this issue, the livestock industry must transition into a digital era utilizing next-generation technological solutions. The objective of this report is to present and analyze the "Smart Technology" ecosystem currently implemented at BAF Vietnam's mega-projects, specifically high-tech farm models and multi-story pig buildings. The integration of automation, Artificial Intelligence (AI), and "5th Generation" technology platforms aims to establish independent "Biosecurity Islands." This system creates a multi-layered protective barrier that absolutely prevents pathogen intrusion while optimizing land resources and enhancing the management productivity of large-scale herds.

Methods and Methods

Smart technology solutions were deployed and evaluated across BAF Vietnam's international-

standard closed-loop farm systems. The methodology is based on establishing a multi-point risk control mechanism, comprising 10 core technologies divided into 4 main categories:

1. Air Control and Barn Microclimate Technology

- **4-Layer Air Filtration:** Incoming air is treated through a specialized 4-membrane filtration system, meeting standards equivalent to an Intensive Care Unit (ICU). This system maintains positive pressure to prevent the entry of virus-carrying particles from the external environment, achieving a 99.9% filtration rate for viruses and bacteria, specifically effective against ASF and PRRS.
- **Deodorization and Air Disinfection:** Exhaust air is not released directly; instead, it is collected through a smart odor-blocking wall system combined with disinfection modules. This achieves over 95% efficiency in bacterial elimination and odor reduction, ensuring emission standards and community safety.
- **AI Microclimate & Health Monitoring Robots:** Autonomous robots patrol 24/7 within the barns. Equipped with multi-parameter sensors (measuring temperature, humidity, and toxic gases like NH3, H2S) and AI-thermal cameras, these robots automatically detect individuals with abnormal body temperatures or behaviors, triggering real-time health alerts.

2. Movement Control and Physical Biosecurity Technology

- **Smart Shower Systems:** All personnel must pass through an automated shower system before entering the "Biosecurity Island." This system integrates time sensors, automated soap dispensing, and smart interlocking doors to eliminate risks associated with manual procedural errors.
- **Smart Vehicle Disinfection:** Transport vehicles represent the highest risk of infection. Automated disinfection stations utilize 360-degree wide-angle high-pressure nozzles to thoroughly clean the chassis, wheels, and cabin.
- **Thermal Drying and Material Disinfection:** Following washing, vehicles and all incoming materials/tools are processed through a high-temperature drying chamber (above 70°C) combined with UV radiation for a specified duration to completely eradicate surface-bound pathogens.

3. Water Treatment and Spatial Surveillance Technology

- **UF-UV Water Treatment:** Water for both consumption and domestic use is filtered via Ultrafiltration (UF) membranes to remove suspended solids and microorganisms, followed by Ultraviolet (UV) irradiation to disrupt the DNA/RNA structure of ASFV and waterborne pathogens.
- **AI Surveillance Camera Network:** AI-powered cameras are installed at all entry points and intersections between biosecurity zones. The AI performs facial recognition and behavioral analysis, providing instantaneous alerts for personnel wearing incorrect uniforms or violating isolation boundaries.

4. Smart Diagnostics and Early Warning Technology

- **Sound Talk Acoustic Diagnostics:** Highly sensitive microphones installed on barn ceilings utilize Machine Learning to "listen" to and analyze acoustic patterns. The AI recognizes specific coughing patterns in pigs to provide early warnings of respiratory pathologies, often before clinical symptoms become visible.
- **Intelligent Rapid Testing Systems:** Portable genetic amplification devices (e.g., PCR/LAMP) are deployed on-site. These systems feature automated result interpretation, allowing for accurate ASF diagnosis within a short timeframe to facilitate immediate isolation of infected individuals.

Results and Discussion

The synchronized operation of these 10 technologies has established a state of "Proactive Biosecurity," minimizing manual intervention. Practical results at BAF's high-tech farms demonstrate that the 4-layer filtration and smart odor-blocking walls maintain an optimal microclimate with 99.9% sterile air. This significantly reduces respiratory stress and pathogen pressure (ASF, PRRS), leading to improved Feed Conversion Ratios (FCR) and higher survival rates. Furthermore, the integration of AI cameras, patrol robots, and the Sound Talk platform has revolutionized epidemiological management. Management can monitor herd health and personnel compliance 24/7, reducing the time required to detect abnormalities from days to just a few hours. When combined with strict physical barriers (interlocking showers and 360-degree thermal disinfection), cross-contamination risks are virtually eliminated. On-site PCR/LAMP testing provides real-time data, supporting precise isolation decisions during the incubation period.

Conclusions and Recommendations

Smart Technology solutions at BAF Vietnam exemplify the efficacy of digitalization and automation in industrial livestock management. To maintain a safe annual sow growth target of 65,000 and realize the strategic goal of 450,000 sows and 10 million commercial pigs by 2030, the operation of these high-tech "Biosecurity Islands" is essential. This report recommends that large-scale livestock enterprises accelerate digital transformation and invest in integrated IoT, AI, and robotics. This is the definitive path toward controlling ASF, optimizing productivity, and developing a sustainable agricultural sector.

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Cho Kyoung-Oh
Cho Young-Eun
Cho Yun-Chae
Choi Hueng-Sik
Choi Junseok
Choi Minsu
Choi Seung Sub
Choi SunA
Choi Sungwoon
Chompuming Rattaphon
Chorro Miralles Aida
Chote -utai Chitpong
Chou Chih-Hsun
Chou Chung-Hsi
Chou Yi-Fan
Christiansen Groes Michael
Chu Qi Meng
Chu Yi
Chuaychu SH.Boonnithi
Chumsing Wilairat
Chumsing Suksan
Chunta Silva Laura
Chutikan Srisang
Ciprian-Carrasco Abel
Cisse Sekhou
Cital Lorena Lydia
Claerhout Lieven
Classen Dyneah
Claver Miguel
Clavijo Maria Jose
Clive Stephanie
Cobo R. Eduardo
Cociancich Vasilij
Codina Raquel
Coldebella Arlei
Colin Frederic
Collén Nyvall Pi
Colnago Guiseppe
Comtet Loic
Conan Pierre-Yves
Conrady Beate
Consuegra Jessika
Conti De Elisa
Cools An
Córdova-Izquierdo Alejandro
Cornelis Bert
Coronellas Judith
Corrégé Isabelle
Correia Angelica Paula
Cortus Erin
Corzo Agustin Cesar
Cosgrove Andrea
Cossenzo Florentino Galinari Grazielle
Costa de Freitas Eduardo
Costa Roberta Martins Letícia
Cota Valdez David Ángel
Côté Jean-Charles
Cotta Higor
Coulson Thomas
Counotte Michel
Court Stuart
Courtens Laura
Couto Marco
Cox Eric

Crenshaw Joe
Crespo Ruben
Croes Evi
Crommenacker van den Lydie
Crooke Helen
Cru Raul
Cruz Christopher
Cruz Gabriela
Cruz Mauricio Luis
Cu Dinh Tri
Cuc Thi Kim Ngo
Cudal Falconite Roselle
Cudal Roselle
Cuellar Flores Amanda
Cui Jin
Culhane R Marie
Cullen Guillermo
Cuong Phan Van
Cvjetkovic Vojislav
Czanderlová Linda
Czerniecki Marek
da Costa Falcao Heni
Dahlin Lisa
Dahmer Marcio
Dai Guo
Dai Jianghe
Dallago Orlando Giovanne
Dalto Bueno Danyel
Damborg Peter
Dang Anh Viet
Dang Thi Hang
DANG Thi My Dung
Dang Thi Ngoc Anh
Dang-Xuan Sinh
Daniel Gabrielle de Souza Amanda
Daniel Léna
Dao Duy Tung
Dao Hoang Dang
Dao Kien
Dao Thi Mai
Dao Thi Ngan
Dao Tung Duy
Dao Van Kien
Datrianto Sunu Dwi
Dauvier Alexandre
Davalos- Benito Sebastian
Davis Kelly
Daza Carlos
Dazzi Claudia
de Almeida Nielsen Ferdinando
De Barcellos Emílio David
De Bruijn Anne
De Cacqueray Preden
De Conti Elisa
De Conti Rigo Elisa
De Grau Francisco
De Gussem Maarten
De Haro Jorge
De Jonghe Eva
de la Cruz-Vigo Paloma
De La Luna Refugio Jose
De la Luz Armendáriz Jazmín
De La Luz Sanchez Sinai
De La Torre López Renato
De Melo Archangelo Ferreira Cecília
De Mendonça França Monteiro Juliana
De Mergelina Fernando
De Mol Zoë
De Oliveira Ferreira Lucas
De Oliveira Rodrigues Ana Clara
De Paula Gabarro Michelle
De Quadros Alves Fernando
De Roma Carale Verden Mark
De Sousa E Silva Gustavo
De Vos Sven
De Wilde Alice
De-Backer Peggy
Deckert Anne
Decloedt Annelies
Decuadro-Hansen Gustave
Dee Scott
Dee-ampai Wichaya
Deffner Pauline
Defoort Pascal
Dejonckheere Els
Del Pozo Sacristan Ruben
Delahaye Anne-Cécile
Delbene Sebastian
Deleye Lieselot
Delforge Julien
Delgado Ana María
Deluque Adriana

Deng Ming-Chung
Denicourt Martine
Denwood Matt
Depondt Wouter
Deqing Ou
Derscheid J. Rachel
Devriendt Bert
Dewey Cate
Dewolf Bradley
Dewulf Jeroen
Dias Pazinato Clenadro
Diaz Alexandra
Diaz Andres
Diaz Concepcion
Dibarbora Marina
Dijkeman Ronald
D'Inca Romain
Ding Shurong
Dinh Van Nam
Dinh Xuan Phat
Diogo Brito
Dion Kate
Dirain J. Alvin
Direksin Kochakorn
Do Amaral Lopes Armando
Do Duc Luc
Do Duy Tien
Do Hong Thi
DO Huynh Duc Huy
Do Kyung-Hyo
Do Manh Tu
Do Phuc Tue
Do Tan Duong
Do Thi Hue
Do Thi Thuy Dung
Do Tien Duy
Do Van Hieu
Doan Gia Han
Doan Tran Vinh Khanh
Dockx Robrecht
Dodantenna Niranjan
Doden L Heidi
Domingues Francisco
Dongmei Cao
Donnet Fabien
Doolittle Kent
Dos Santos Mariane Fernanda
Doupovec Barbara
Dreval Denys
Du Dai Phong
Du Li-Hwa
Du Mao-Yuan
Duchateau Luc
Due Elizabeth
Dufresn Luc
Dufresne Luc
Dumniem Natchanon
Duong Chi Mai
Duong Minh Nhat
Duong Nguyen Khang
Duong Nhat Nhat
Duong Tan Do
Dupuis Laurent
Durães-Carvalho S. Ricardo
Durrant Izzy
E Silva De Souza Gustavo
Ebner Lia
Echeverria Gabriela
Eckel Bernhard
Eddicks Matthias
Egli Thomas Philipp
Eiamsam-ang Thanaporn
Eising Irene
Ekapongpaisit Thanawat
Ekman Stina
Ellerma Domingo Leonardo
Elvira Mendoza Susana Elisa
Emődi Nikolett
Englebienne Maykin
Engström Fredrik
Enokida Masashi
Enric Vidal Carles Vilalta,
Ensendencia Marjorie Jean
Escobar Jeffery
Escobedo Mariano
Escuder Margarita
Escuder Miguel Joaquín
Espejo Aguilar Amalia
Espigares David
Espinoza Juan
Espín-Palazón Raquel
Esquer Alejandro

Estacio Danielle
Estany-Illa Joan
Esteves Moreira Martins Luís
Eulália Isabela
Ewendt Franz
Fabros Alexander Karl
Fadeev Artem
Fagundes Pereira Deivison
Fajardo Y. Roland
Faksongsakul Niratchaporn
Falcão da Costa Heni
Falconite-Cudal Roselle
Fan Siqi
Fang Jie
Fang Xinyu
Fank Chia Jung Chang
Fano-Gonzalez Eduardo
Farkaš Hunor
Farmer Ryan
Farnir Frederic
Farzan Vahab
Fasina Folorunso Oludayo
Fei Wentao
Feldmann Lori
Felip Maria Ros Jose
Feng Baohai
Feng Bin
Feng Huihui
Feng Tingting
Feng Xiao
Fernandes Carnevalle Rafaella
Fernandes Caroline Jéssica
Fernandes Dominique Saffir
Fernandes Saffir
Fernández Anabel
Fernandez-Colorado Cherry
Fernández-Dueñas Mauricio Demián
Ferraz Maria Eugenia
Ferreira Alves Eduardo
Ferreira Lucas
Ferreira Norberto Alves Felipe
Ferreira Viana Soraia
Ferreira Vitor João
Ferrer Palma Jimwel Bryan Christopher
Ferruzca Alan
Ferruzca Octavio
Fertner Mette
Feurer Carole
Fiechtner Jerome
Filippi Luis Jorge
Filsner Pedro
Fischer Silke
Fittipaldi Nahuel
Fitzsimmons Mark
Fiuza Tatiane Aparecida
Florentino John Ceddrick
Flores Aguiar Gabriela
Flores Salvador
Flores-Montenegro Alejandro
Floros Dimitrios
Földi József
Fong Michelle Wai Cheng
Fong Wai Cheng Michelle
Forero Rafael
Foss Deniss
Fotou Konstantina
França Botta Roberta
Franco-Rodríguez Camilo
Frandoloso Carolina Gabriela
Frandoloso Rafael
Frangopoulos Theophilos
Frayssinet Bastien
Fredholm Merete
Freitas Barbosa Fellipe
Friendship Robert
Frossard Jean-Pierre
Frykberg Lars
Fu Yanan
Fu Zhen
Fuchs Jenny
Ga Eulhae
Gabaldón Toni
Gabinaud Beatrice
Gabler Nicholas
Gagnon A Carl
Gaines L Aaron
Galbraith A Elizabeth
Galdo Novo Sabrina
Galé Ansó María Irene
Galgani Pietro
Galindo Barboza Alberto Jorge
Galindo Hector

Gao Di
Gao Junfeng
Gao Peng
Gao Xiang
Garbossa Augusto Pospissil Cesar
Garcia Andrea
García Camacho Ángelica Lucía
Garcia Hector Jose
García Legaz Simón
Garcia Luis
Garcia-Morales Luis
Garcia-Morante Beatriz
García-Vega Melissa Ana
Garres Frédérique
Garrido Angel
Garza-Moreno Laura
Garziera Tamara
Gatto Renan Honorato Igor
Gauger C Phillip
Gauger Phillip
Gauthier Marie-Lou
Gavidia Cesar
Gaza Von Hartmut
Ge Xinna
Gebhart J. Connie
Gebreyes Wondwossen
Geng Jianxin
Genova Luis Janslller
Gentile Nicla
Genzow Marika
Gerber F Priscilla
Gere Peter
Germiniani Bedendo Laura
Geurts Victor
Ghonaim Ahmed Hamdy
Giacomini Leandro
Giang Phuong Thuy
Giannenas Ilias
Gijsen Emile
Gil Rueda Francisco
Giles Michelle
Gil-Silva Constanza Alix
Gimenez Lirola Luis
Gimenez Luis
Giménez-Lirola G. Luis
Giménez-Lirola Gabriel Luis
Giménez-Lirola Luis
Ginouvès Amandine
Giralt Dolors
Girme Gisela
Gleeson Bernie
Gloaguen Mathieu
Go You-Kyung
Gobbo Federica
Goecke Bakkegård Nicole
Goericke-Pesch Sandra
Goethals Klara
Golinar Oven Irena
Gombos László
Gomes de Almeida Ciriaco Nadia
Gomez Francisco
Gómez Herrera Nidia Luz
Gomez Jeron
Gomez Magtibay Jeron
Gómez-Betancur F. Jair
Gomez-Duran Oliver
Gómez-Fidalgo Ernesto
Gomez-Ramirez Pilar
Gonzalez Davalos Laura
Gonzalez David
Gonzalez Diego
Gonzalez Ornelas Antonio
Gonzalez-Añover Pedro
González-Lozano Miguel
Goodfellow Ian G.
Goossens Tim
Gordsueb Thanchanok
Gottschalk Marcelo
Gougoulias Christos
Goulart Meira Maraísa
Gourgues Figueras Sebastián
Gouva Evangelia
Govaerts Eva
Goyena Elena
Grahofer Alexander
Granados-Servin Yazmin
Greaves Gillian
Greer Amy
Gregersen Maria Patricia
Grigoriadou Katerina
Grommen Ries
Gross Josef

Grosse Kamphake Maike
Grozeva Mariya
Grubješić Goran
Grunewald Febe
Gu Dan
Gu Zhiguang
Guadalupe Nava Aileen
Guan Xiaonan
Guedes M.C. Roberto
Guioguio V. Miguel
Guizzo Antônio João
Guo Baoqing
Guo Haibing
Guo Hui Chen
Guo Huihui
Guo Jingya
Guo Leizhen
Guo Lin
Guo Qian
Guo Xin
Gurgel Wilson
Gurung Parikshya
Gussem De Maarten
Gwo Mao-Chun
H. Osemeke Onyekachukwu
Ha Sanghun
Haach Vanessa
Habineza Gashaka Fidele
Hachemi Mohammed Amine
Haden Cara
Hai Viet Nguyen
Hajdinjak Melita
Hallgren Camilla
Haluwana D. K.
Ham Sehyeong
Hambrecht Ellen
Hamedy Ahmad
Hammer Mark James
Hamon Julie
Han Dandan
Han Jeonghee
Han Jun
Han Seungjae
Han Thi Tuyet Nhung
Han Weiyao
Han Xiangming
Hancock Deana
Hansen Hübertz Birch Lea
Hansen Marie-Louise
Hansen Sally
Hao Fen
Hari Aleksandra
Harms Perry
Harrington D
Harrison Tom
Hascoët Anne-Sophie
Haser Daniela
Hau Thi Anh Hau
Haung Qi
Hayashi Mitsuo Ricardo
Hayashi Shizuka
He Guijin
He Junchang
He Ling
He Qi Gai
He Qiyun
He Xinglin
He Yuanqing
Heeman Filip
Heenemann Kristin
Heiselberg Rudolph Pia
Helsmoortel Charlotte
Henao-Diaz Alexandra
Henry Margaret
Heo Jungmin
Heo Sung-Uk
Hercé Arnaud
Herlt Catherine
Hernández Amaya María José
Hernandez Ignacio Luis
Hernández Jesús
Hernandez Jose Maria
Hernandez Justino
Hernández Maria Jose
Hernández Martín Jonás
Hernandez-Andrade Laura
Hernig Fiorin Luciana
Herrera Andrea
Herrera da Silva Joao Paulo
Herrera Noelia
Hervé Gwendoline
Hervet Caroline

Hettiarachchi Amanda
Heyer Maria Elisabeth Charlotte
Hiang-Chek Ng
Hidalgo Alvaro
Hidalgo Angel Jorge
Hidalgo Emiliano
HIGUERA Angel Miguel
Hinn Kaydance
Hirai Yuka
Hirose Flávio
Hjulsager Kristiane Charlotte
Ho Thieu Khoi
Hoang Van Duong
Hoeltig Doris
Hoffmann Patrick
Hofstetter Ursula
Holcombe Nicole
Holl Elisabeth
Hollis Benjamin
Höltig Doris
Holtkamp Derald
Holtz Adriane
Homwong Nitipong
Hong Toan
Honorato Gatto Renan Igor
Hor Sokpanhapenh
Horn L Nathan
Horst Andreia
Horváth Rita
Hoshino Yukari Roberta
Hosmillo Myra
Hosokawa Masashi
Hosseindoust Abdolreza
Hou Chengcai
Houe Hans
Hourcq Pascal
Hsiao Hui-Ping
Hsieh Cheng-Chu
Hsieh Hui
Hsu Chia-Fu
Hsu Chun-Yi
Hsu Fang-Yu
Hsu Shu-Hua
Hsu Tzu-Hung
Hsueh Chao-Wen (Valen)
Hu Jiameng
Hu Ke
Hu Qunshan
Huang Chao-Wei
Huang Chien-jin
Huang Hongliang
Huang Hsin-Hsuan
Huang I-Hsuan
Huang Qi
Huang Wei-Kai
Huang Wei-Po
Huang Xin-Hui
Huang Xireng
Huang Yu-Liang
Huang Ze
Hübertz Birch Hansen Lea
Huei Bon Chiang
Huerta Fernando Oscar
Huesca Miñon Ernesto
Hui (Yuqi) Angela
Huisman Abe
Hung Chien-Ning
Hung Chung-Shun
Hung Shao-Wen
Hur Jin
Hutter Christoph
Huy Cong Huy
Huy Cong Nguyen
Hwang Ji-Min
Hwang Kyuyeon
Hwang Seong Yun
Ibragimov Emil
Iemura Ryuji
Ikezawa Mitsutaka
Im Changwon
Im Young Bin
Immerseel Van Filip
Imre Nemes
Incze Daniel
Innajak Sukanda
Innama Narathon
Isaravisavakul Sutida
Ishii Koji
Ishikawa Hiromichi
Iskrzak Pawel
Isoda Norikazu
Isusi Caballero Sara

Isusi Sara
Ito Satoshi
Iván Cordón Guillermo Cantero,
Ivanova Desislava
Ivers Daniel
Iveson Thomas
Iwamuro Hisashi
Izzard Lenny
Jacela Jay
Jacobs Cindy
Jacobs Ton
Jacobson Magdalena
Jaescheke Julian
Jahn Laura
Jaima Kwancheewa
Jaime Dario Jairo
Jakobsen Nadia
Jampasa Sakda
Janeczko Krzysztof
Janelt Frauke
Janetanakit Taveesak
Jang Kiyoung
Jang Se Yeon
Jansen Rutger
Janssens Paul Jules Geert
Janssens Thierry
Janvier Emmanuel
Jaramillo Diana
Jaramillo-Jaramillo Ana Sophia
Jardin Agnès
Jayaraman Swami
Jeklova Edita
Jemeršić Lorena
Jensen Elvang Henrik
Jeon Tae-Il
Jeong Chanwoo
Jeong Dae Gwin
Jeong Hyunkyu
Jeong Jiyun
Jeong Jongyeon
Jeong Taekyung
Jerab Gabrielle Julia
Jerzsele Ákos
Jesus Alves Iris
Jheong Weonhwa
Jia Daq
Jia Jiyu
Jiang Xiaohui
Jiang Yiyao
Jiao An Xin
Jiao Xinan
Jimongkolkul Nattanit
Jin Junqi
Jin Qianqian
Jinanan Jittra
Jing Jinzhong
Jing Ran
Jiranart Noppon
Jirawattanapong Pichai
Jitpreuk Kanitta
Jittidecha Jiramate
Jitviriyanon Surapan
Joachim Anja
Johnson Ron
Jong de Matthijs
Jongkaewwattana Anan
Jongprasert Thanakorn
Jordi Argilaguet Liani Coronado,
Jordi Argilaguet Marina Cid
Jørgensen Bøttcher Claus
Jourquin Jan
Jung Seungwon
Juntanupong Boontarika
Jutten Anne Cecile
Kaenson Wenika
Kaeoket Kampon
Kaewchomphunuch Thotsapol
Kaewtapee Chanwit
Kaiser Ørnstrup Marianne
Kamber Taslaman Magda
Kaminsonsakul Tanyanant
Kamnaray Napatsorn
Kan Xi Ze
Kang Eun-Seo
Kang Jung-Ah
Kang Long Xi
Kang Xilong
Kanjanavaikoon Korntip
Kankuntod Somyod
Karamoutsios Achilleas
Karanikolova Mariana
Kareljärvi Peppi

Karembe Hamadi
Kareskoski Maria
Karki Surendra
Karriker Locke
Käser Lea
Kastelic Andrej
Katusime Joshua
Kauffold Johannes
Kawaguchi Nijiho
Ke Ni-Jyun
Kedkovid Roongtham
Keeratikunakorn Krittika
Kelly Jena
Kerdsin Anusak
Kerek Ádám
Kerenyi Katalin
Kesdangsakonwut Sawang
Ketit Sussie
Kettelkamp Erin
Khang An Nguyen
Khang Nguyen Duong
Khanh Tran Vinh Doan
Kharief Sarah
Khongpradit Anchalee
Khophloiklang Vassakorn
KICH DEON JALUSA
Kikuti Mariana
Kim Bumseok
Kim Cheol-Min
Kim Dae-Min
Kim Da-Jeong
Kim Do Soon
Kim Do SoonKim
Kim Do-Kyun
Kim Dong-Yeong
Kim Don-Kyu
Kim Eunseok
Kim Ha Yeon
Kim Hanjun
Kim Hwan-ju
Kim Hyeon-A
Kim Hye-Ryung
Kim Hyeumbum
Kim Hyunil
Kim In Ho
Kim Jae-Hoon
Kim Jaekyeong
Kim Jinsoo
Kim JungHee
Kim Min Ho
Kim Min-Gyu
Kim Se Kye
Kim Si-Eun
Kim So-Hee
Kim Su-Bin
Kim SungIl
Kim Sungjae
Kim Won-Il
Kim Wonjun
Kim Yeon Hee
Kim Yeonji
Kim Yohan
Kim Youngguen
Kim Young-Min
Kinara Elick
Kindlein Liris
King Michael
Kirkwood Roy
Kiros Tadele
Kirwa Elly
Kiss Istvan
Kitamura Tomoya
Kittawornrat Apisit
Klaeui Caitlin
Klein Ulrich
Knudsen Thorup Møller Tine
Knüpfer Hanna
Ko C. Calvin
Ko Seongsik
Ko Young-Seung
Koenders Karien
Kokuho Takehiro
Kolawole Usman Kayode
Kolesnikov Alexander
Komissarov Andrey
Kongcheep Benjawan
Kongpanna Panumas
Konis Taiel
Konsens Hans
Könyves László
Koontanatechanon Anantawat
Kootpetch Prakorn

Koppenol Astrid
Koszegi Marika
Kozuma Tomoyo
Kraitavin Waraporn
Krapež Uroš
Krasaesub Sittipoj
Krasnikov Nikita
Krejci Roman
Kreutz Carlos Luiz
Kristensen Charlotte
Kristensen Sonne Charlotte
Krogh Schak Jesper
Krzysztoń Jarosław
Kuang Yan
Kubo Takashi
Kuhar Urška
Kuhlmann Fernando
Kukkorng Benchawan
Kumar Manoj
Kumpum Watinee
Kunze Marius
Kustán Paliczné Bianka
Kusumoto Masahiro
Kvisgaard Kirstine Lise
Kwan Wei-Fan
Kwofie Ebenezer
Kwon 2 Seongkyun
Kwon Doheon
Kwon Hyeok-Il
L. Baker Amy
Labarque Geoffrey
Labbe Alain
Labrecque Marie-Pier
Lacladere Sylvain
Lacouture Sonia
Lager Kelly
Lagkouvardos Ilias
Lai Po-Yen
Lai Yi-Fang
Lai Zhilai
Lakkanasombat Wirod
Lambert Marie-Ève
Lan Thi Quynh Tran
Langendijk Pieter
Langenhorst Robert
Laohasinnarong Dusit
Lara Puente Horacio Jesús
Larsen Erik Lars
Larsen Inge
Lasierra Maria Teresa
Laub Pereira Ricardo
Laungarichai Hassadin
Laurie Pfleiderer
Lauterbach Nicholas
Lawananon Phawinwit
Lawrence V Bradley
Lawson Steve
Le Dinh Phung
Le Duy Vu
Le Gall Maud
Le H. Ngoc
Le Ha Thu Thi
Le Ha Yen Nhi
Le Hoang Toa
Le Huu Ngoc
Le Lieu Thi
Le Phan Van
Le Phuong Thu Thi
Le Thanh Hien
Le Thi Khanh Dung
Le Thi Lieu
Le Thi Ngoc
Le Thi Thu Ha
Le Thi Thu Phuong
Le Thuc Quyen
Le Thuy Binh Phuong
Le Van Phan
Le Van Tuyen
Le Viet Hai
Le Yen
Ledo Luisa
Lee Dong Ju
Lee Dongkyu
Lee Eun-Gyeong
Lee Gun-Hee
Lee Hu Suk
Lee Jaesuk
Lee Jia Wei
Lee Jia Xin
Lee Jin Kyejin
Lee John Hwa
Lee Jong-Soo

Lee Joo Young
Lee Kyungmoon
Lee Minchul
Lee Min-chul
Lee Sangsik
Lee Se Young
Lee Seongwon
Lee Seoyeong
Lee Shinwoo
Lee Shu-Hwae
Lee Soomin
Lee Su Jin
Lee Sujin
Lee Sungin
Lee Taek Geun
Lee Ting-Yu
Lee Yehyeong
Legaud Jean-Yves
Lehoux Mélanie
Lei Mingkai
Lei Ting
Leijon Mikael
Leite Fernando
Leite Morgana Silva Alline
LEIVAS LEITE LOPES FERNANDO
Lemâle Olga
Lemos de Moraes Mariana
Leneveu Philippe
León Eva
Leonard Mickey
Leonardo Watte Leonardo
Leon-Escalante Gonzalo
Leppkes Viviane
Lertsawat Sirunya
Leveringhaus Elena
Lewandowski Eric
Lewko-Wojtowicz Renata
Leyva Alvaro
Li Benqiang
Li Chaosi
Li Chun-Hsien
Li Cong
Li Ganwu
Li Hang
Li Huaixia
Li Jianbing
Li Jianhai
Li Jing
Li Juan
Li Limin
Li Long
Li Lu
Li Ming
Li Peng
Li Peng fei
Li Pengfei
Li Qirun
Li shang Shuang
Li shen Lin
Li Shubo
Li Shuchun
Li Wentao
Li Xinyao
Li Yafei
Li Yali
Li Yanchao
Li Yi-Chia
Li Ying
Li Zhe
Li Zhen
Lian Wei
Liang Botao
Lianghai Lianghai
Liani Coronado Lola Pailler-García,
Liao Chih-Ming
Liao Nai-Shun
Liao Yi-Chu
Liao Yu-Hui
Licheri Manon
Licheri Matthias
Lillie-Jaschniski Kathrin
Lim Changwon
Lim Ji Hyun
Lim Jong-Woo
Lim Sarah
Lim Yujoon
Lin Chao Nan
Lin Guo
Lin Jin-Seng
Lin Nien-Nong
Lin Wei-Hao
Lin Wei-Ting

Lin Yan
Lin Yunxiong
Linatoc Lubid Marlon
Linh Nguyen Ngoc Dang
Linhares Correia Lima Daniel
Linssen Eric
LIPPKE TESCHE RICARDO
Lippold Martin
Liu Benjin
Liu Chi-Chun
Liu Chun-Wei (David)
Liu Ding Xiang
Liu Hsin-Meng
Liu Huili
liu jia
Liu Junwei
Liu Lihong
Liu Pai
Liu Pingxuan
Liu Qing
Liu Qingyun
Liu Shih-Wei
Liu Sidang
Liu Tianjiao
Liu Wenfeng
LIU Xiaomei
Liu Xing
Liu Xinlei
Liu Yabin
Liu Yang
Liu Yufu
Liu Zhaowen
Liu Zhiguang
Liuiu Jiaqi
Llilianne Ganges Sergio Montaner,
Lllamas Amor Eva
Llorens Anna Maria
Lo Yun-Hwa
Lohman Janković Ivana
Loibl Peter
Lopes Matheus Goés Idael
Lopez Adrian Itzcoatl
Lopez Arturo
Lopez Concepción
López Concepción
Lopez De Jesus Jose
López Espinosa de Jesús Jose
López Rosa
López Sánchez Arturo
López-Andreo María José
Lopez-Figueroa Carlos
Lopez-Lorenzo Gonzalo
Lopez-Moreno Gustavo
Lora Carlos
Lorandi Sara
Lorca-Oró Cristina
Lorenzen Bjørn
Lorenzetti M Arlan
Lorenzo-Rebenaque Laura
Loustaunau Esteban
Lowanitchapat Anchada
Lowary L. Todd
Lozano Bernardo
Lu Cheng
Lu Chia-Hung
Lu L Hang
Lu Ping
Lu Yangyifan
Lu Yue
Luc Minh Kieu
Lückstädt Christian
Ludke Vitor Jorge
Luevano-Adame Jose
Luna Irish Mae
Luna Nereida
Luo Qiong
Luo Yajuan Yajuan Luo
Luong Hung Nam
Luong Tan Phat
Lutz Bérénice
Lutz Julian
Luukkonen Terhi
Lv Yadi
Lv Yaning
Ly Thuyen Quyen
Lyderik Kyed Kimmie
Lynch E Stacey
Lyoo Young S.
Ma Chaozhi
Ma Hailong
Ma Jingjing
MA Junyao

Ma Xiaoyan
MacEachern Samantha
Machado Isadora
Machuca Mariana
Madson Darin
Maele Vande Lien
Maes Dominiek
Mafra Gonçalves Patrícia Júnia
Magalhães Edison
Magalhães Rocha Monique Brenda
Magklaras Georgios
Magtagnob Ermin
Maguregui Ekaitz
Mah ChoewKong
Maher Jackie
Mahmud Md Rayhan
Mai Thi Ngan
Main G Rodger
Main Rodger
Maison Tanavut
Maisonasse Pauline
Majó Natàlia
Makhanon Metta
Makovska Iryna
Makungo Priscilla
Malard Morgane
Maldaner Helena Vitória
Maldonado Coelho Guedes Isabel Maria
Malgarin Carolina
Malik Mateusz
Malladi Sasidhar
Mallaopoma Soriano Ruben
Mallmann Barbara
Maltar Ljupka
Maltret Claire
Manabat Angel Antonio Tomas
Manchego-Sayan Alberto
Manzano Joson Paul Christian
Maprang Roshorm Yaowaluck
Maquering Jan-Bernd
Marcet-Houben F. Marina
Marchesi Marcello
Marchetti Luca
Marco Fuertes Ana
Mariane dos Santos Fernanda
Marin Clara
Marin Flamand Ernesto
Marinez Rebeca Nancy
Markvardsen Mathilde
Marouda Christina
Marquez Rowena
Marr Amy
Marta Muñoz María Jesús Navas,
Martin Briec
Martín Valenzuela Yakelin
Martinez Alarcon Laura
Martinez Alfonso Echavarría Jose
Martínez Andrea
Martínez Bautista Rebeca
Martinez Camilo
Martínez Castañeda Ernesto Francisco
Martinez Echavarría Jose
Martinez Francisco
Martínez Gamba Gustavo Roberto
Martínez Martínez Miryam
Martinez Rebeca Nancy
Martinez Schmiel Enrique Jorge
Martinez Valeria Lilia
Martinez-Hernandez Valeria
Martinez-Lopez Beatriz
Martín-Lluch Mercedes
Martins Coelho Isadora
Martins Costa Roberta Leticia
Martins Marinelli Camila
Mas Boix Oriol
Masching Sabine
Masilungan Rommel
Masujin Kentaro
Mateos Josué
Matias Ferreyra Franco
Matias Novais Debora
Matthijs Thomas
Matti Frida
Maulidi Vera
Mazerolles Philippe
Mazzarollo Bombana Luana
MB Bernat
Mbajiorgu Christian Anayochukwu
McClellan Katlyn
McDonald Wade
McGlone John
McKibben Grace

McLaughlin Angela
McMullen Carrie
McNabb Leanne
Medeiros de Ávila Melo Rafael
Mei Xiaowei
Mejias Pilar
Meksamanasak Nathapong
Melinda Nemes-Terényi
Melini Marcello Claudio
Mellouk Amine
Membrenbe Juver
Méndez Aguilar Miguel Ángel
Méndez-Carranza Johana Kelly
Mendoza-Elvira Susana
Menegat L Alex
Meng Chuang
Mercado Anthony Mark
Merceron Matthieu
Merdy Olivier
Merenda Marianna
Merhi Reimert Mossa
Messier Sylvain
Mesu Pieter
Meyer Denise
Meyns Tom
Meza Garcia Everardo
Mezzina Braga Ana Lígia
Mezzina Lígia Braga Ana
Mgaya Frank Joseph
Mi Thi Tra Bui
Michel Virginie
Miclat-Sonaco S. Ruth
Middelkoop Anouschka
Miguel Escuder Joaquin
Miguel Joaquín
Migura-García Lourdes
Mil-Homens Mafalda
Mil-Homens Pedro Mafalda
Millet Sam
Miolo Angelo Vladimir
Miotto Rovian
Miquel Nofrarias Àlex Cobos,
Miralles Chorro Aida
Miranda Sergio
Mireia Labrador Cecilia García
Miškić Tihana
Miyashita Mali
Miyazaki Ayako
Miyazawa Kohtaro
Mizutani Tetsuya
Mo In Pil
Mo Yupeng
Möddel Anne
Mogollón Darío José
Molina Ramon
Molist Francesc
Molnár János
Molnar-Nagy Viviana
Mondaca-Fernandez Enrique
Mongkolwit Keatipong
Montalvo Noemi
Monteagudo Juan
Montecillo Andrew
Monteiro Rigo Alessandra
Monteiro Saliba Matheus
Montes Citlali
Montes Julia Helena
Monti Gustavo
Montoro-Dasi Laura
Montoya Franco Sebastian
Moon Duhwan
Moon Seong Cheol
Moon Sung-Hyun
MoonJit Pattra
Moradell Luis
Mora-Díaz Juan Carlos
Moraes Chaves Otávio Guilherme
Moraes Daniel
Morais Juan
Morales - Guarin Felipe Juan
Moreno Batlle Bernat
Moreno Fausto
Morgan Mateus
Mori Masafumi
Morris Paul
Morsing Kjelin Malene
Mortensen Preben
Morvan Anne
Mueansree Chananchida
Mueck Sophia
Mugabi Robert
Mulberry Lance

Müller Sabrina
Mun Da Young
Mun JunYoung
Mun Yubin
Munaretto Leonardo
Munguía-Ramírez Berenice
Muñoz Antonio José Antonio
Muñoz-Carrillo Andrés Hernando
Murillo Alberto José
Muro Bracco Donatelli Bruno
Murray Gemma
Musa Mariano
Musskopf Negri Mariah
Mwanga Mike
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Na Woonsung
Nadlučnik Eva
Nagae Ricardo
Nagyházi Balázs
Naikare Hemant
Nakamura Yoshiyuki
Nakano Tenma
Nam Si-Woo
Nam Van Dinh
Nantakhruea Sunaree
Naranjo Rafael
Natàlia Majó Francesc Accensi,
Nathues Heiko
Nava Lisandro
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Navarro Rosa
Navarro-Mamani Dennis
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Nawrot Meaghan
Neaves Matthew
Nechypurenko Oleksii
Negrelli Pilar Melisa
Nelli Kumar Rahul
Nemes Imre
Nemes-Terényi Melinda
Nery Finatto Arthur
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Ng Zi Yao
Ngamwongsatit Natharin
Ngan Kim Nguyen
Nghia Bui Vuong
Nghia Van Nguyen
NGoBa Duy
Ngo Bang Cong
Ngo Hong Phuong
Ngo Quoc Cuong
Ngo Thi Ngoc Tram
Ngo Vo Ky Duyen
Ngoc Dao Hong Tran
Nguyen Anh Phong Van
Nguyen Anh Quynh
Nguyen Ba Tiep
Nguyen Ba Toan
Nguyen Bang
Nguyen Bao Quoc
Nguyen Be Thi Tu
Nguyen Binh Nguyen
Nguyen Chau Nguyet Anh
Nguyen Che Thanh
Nguyen Duc Bang
Nguyen Duc Hung
Nguyen H. K. Vy
Nguyen Ha Thu
Nguyen Hien Thi Thu
Nguyen Ho Minh Thu
Nguyen Hoai Nguyen
Nguyen Hoang Dang
Nguyen Hoang Hai Dang
Nguyen Hoang Thinh
Nguyen Hong Thu Le Suong
Nguyen Huu Trung
Nguyen Huy Hoang
Nguyen Kien Cuong
Nguyen Minh Nam
Nguyen Minh Tan
Nguyen Minh Thi Chau
Nguyen Ngoc Ha Phuong
Nguyen Ngoc Hai
Nguyen Ngoc Minh Thu
Nguyen Nhat Huy
Nguyen Nhu Thi Y
Nguyen Pham Huynh
Nguyen Phuc Van
Nguyen Quang Linh
Nguyen Quoc Hung
Nguyen T. M. Thu
Nguyen Tan Tai

Nguyen Thai Anh
Nguyen Thanh Hai
Nguyen Thanh Nhu
Nguyen Thanh Phong
Nguyen The Viet Hoang
Nguyen Thi Bao Tran
Nguyen Thi Bich Thuong
Nguyen Thi Dieu Thuy
Nguyen Thi Hoa
Nguyen Thi Hong Chien
Nguyen Thi Hong Ngoc
Nguyen Thi Kieu Trinh
Nguyen Thi Lan
Nguyen Thi Lua
Nguyen Thi Mai Linh
Nguyen Thi Mi Mi
Nguyen Thi Minh
Nguyen Thi Ngoc
Nguyen Thi Ngoc Anh
Nguyen Thi Phuong Thuy
Nguyen Thi Quynh Anh
Nguyen Thi Thanh Tinh
Nguyen Thi Thu Hien
Nguyen Thi Thuong
Nguyen Thi Thuy Tien
Nguyen Thi Trang
Nguyen Tran Kieu Anh
Nguyen Trang Thi
Nguyen Trong Tin
Nguyen Trong Tung
Nguyen Tung Trong
Nguyen Van Diep
Nguyen Van Duc
Nguyen Van Hai Vuong
Nguyen Van Nghia
Nguyen Van Nha
Nguyen Van Nhat
Nguyen Van Non
Nguyen Van Phong Anh
Nguyen Van Phuc
Nguyen Van Tho
Nguyen Viet Dung
Nguyen-Viet Hung
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Nicolino Romero Rafael
Niderkvel Victor
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Nielsen Jens Peter
Nielsen Okholm Elisabeth
Nielsen Peter Jens
Nielsen Sandris Dennis
Nienhoff Hendrik
Niepold Jeanette
Nikaido Sae
Nikhomjit Nitikan
Nikolaou Konstantina
Nilubol Dachrit
Nimmansamai Irawin
Ning-Chieh Twu
Niño Ludmila
Nivelle Béke
Nixon Samantha
Niyonsaba Aaron
Nodar Balseiro Lorena
Noelia Herrera
Noguez López Juana Adriana
Noh Dong Hyun
Noh Hyundong
Noh Sanghyun
Nollet Nathalie
Nomura Kosuke
Noréus Kajsa
Numsri Pongsak
Nunes Tiago
Nuñez Zena César
Núñez-Gutiérrez S. Kerlimber
Nuntapaitoon Morakot
Nuntaprasert Athipoo
Nuntawan Na Ayudhya Suparlark
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Nushol Mojca
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O'Brien Caitlin
Ochoa Johanna
Ochoa Stela
Oguttu James Wabwire
Oh Ik Sang
Oh Jin Sik

Oh Su-Hong
Oh Taehwan
Oh Yeonsu
Oh Yusik
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Okones Jeff
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Oliveira Dayanne
Oliveira Isadora
Oliveros Kristel Mae
Oliviero Claudio
Oller Paola
Olvera De La Cruz Omar
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Ooi Peck Toung
Opriessnig Tanja
Orozco Bernal Ignacio
Orozco Nestor
Osemeke Henry Onyekachukwu
Ospina-Chirivi Carlos Juan
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Ozaeta Sofia
Oztas Turkan
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Paller Tomislav
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Palowski Amanda
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Pan Ming Zhi
Pan Shidong
Pan Yu-I
Pan Zhiming
Panek Robert
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Park Rahui
Park Saiam
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Pavan Odair
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Pedersen Steen Ken
Pederson L Kaley
Pedrosa Katia
Pedroti de Quadros Stetahni
Pellenz Jade
Peltoniemi Olli
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Peña Mario
Peña Perea Mauricio
Peng Guiqing
Peng Lu
Peng Tongtong
Peng Zhe
Penndu Daniela
Pennebrink Vanja
Pereira Biar Juliana
Pereira Gomes Ricardo
Pereira Junior Alberto Carlos

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Pérez Gutiérrez Oscar
Perez Lorena
Perez Mauricio
Pérez Navarro Enrique
Perez-Calvo Estefania
Pérez-Núñez Daniel
Perez-Ornelas Ana
Perfumo Carlos
Perrucci Alice
Petric Peter Philipp
Petrovic Stevan
Petrovski Kiro
Petznick Thomas
Pham Chau Giang
Pham Dat Thanh
Pham Duc Toan
Pham Duy Than
Pham Hoang Son Hung
Pham Khac Ninh
Pham Kim Thi Thi
Pham Minh Man
Pham Ngoc Doanh
Pham Thai Binh
Pham Thi Kieu Dung
Pham Thi Kim Thi
Pham Tien
Phan Thi Phuong Thao
Phan Thi Tuong Vi
Phat Luong Tan
Phat Tan Luong
Phatthanakunanan Sakuna
Phitsanuwattana Kritiya
Phoonsap Kamolthip
Phubangdao U-then
Phuengkasem Anawach
Phung Nguyen Hoai Ly
PHUNG Thi Kieu Trang
Phuong Hong Ngo
Phuong Thi Hong To
Phuong Thien Thuong
Phuong Thuy Binh Le
Phupolphan Cherdpong
Picault Sébastien
Pierini Agustina
Pieters Maria
Pillatzki Angela
Pinal Fausto
Pineda Lane
Piñeiro Carlos
Pineyro Pablo
Pinheiro Marques Ana Rita
Platero Luis José
Plaza Angeles
Plichart Gaëtan Vetea
Plourde Lori
Ploypanichcharoen Virakorn
Poakjareon Kanyarat
Podgórska Katarzyna
Poeta Silva Ana Paula
Poeta Silva Paula Ana
Pogranichniy Roman
Pokharel Aashirbad
Polimeni Barbara
Poljak Zvonimir
Poljakovic Robin
Polo Javier
Polo S. Gina
Polyiam Kanokporn
Ponce Mula Sonia
Pons Laurie
Poompramun Chotima
Poor Pegoraro Andre
Poor Pegoraro André
Poppe László
Portela Lobato Inês Zélia
Posedi Janez
Posik Diego
Pospissil Garbossa Augusto Cesar
Post Mariah
Postel Alexander
Pourquier Philippe
Pozzo Dal Ildo
Prada A Jorge
Pradiee Jorgea
Prajapati Meera
Prapasarakul Nuvee
Prapattanakullawong Apichart
Prarat Koscielny Melanie
Prarat Melanie
Prasitphol Boonsarng
Pratt Emily

Preesong Pattaveekan
Pringproa Kidsadagon
Prior Keila
Prpić Jelena
Prucksayoungyuen Worrapon
Pruglo Vladimir
Prüst Herman
Psalla Dimitra
Pulido Cristian
Purser Max
Putarod Matawee
Putz Austin
Pyburn David
Pylypchuk V
Qarih Fahd
Qi Ting
Qian Xu
Qiao Shiyan
Qigai He
Qiu Hualongchuan
Qiu Peng
Qiuhua Longchuan
Qu Xiangyang
Quach Tuyet Anh
Quezada Francisco
Quinn Michaela
Quintana Eduardo
Quintero Victor
Quyen Thuy Nguyen
Rabadán Álvaro
Rabal Martínez Daniel
Rachasapha Suthida
Rademacher Christopher
Radin Cristina Grasiela
Raele de Oliveira Eduardo
Raggio Santiago
Rahman Jamilur Md
Raidan Fernanda
Raines Tracy
Rainha Stephanny
Raj Jog
Rakytianskyi V
Ramaekers Peter
Ramir Fochi Rafaela
Ramirez Mercy
Ramírez Orejel Carlos Juan
Ramirez Zapata Juan Carlos
Ramirez-Aguilar Georgina
Ramírez-Torres María de la Luz
Ramis Guillermo
Ramis-Vidal Guillermo
Ranathunga Lakmal
Raquel Ausejo Marcos
Ratanamongkolmas Apichaya
Rathnapala Pramodya
Rathnasamy Gurugirijha
Rattanadee Arpanuch
Rauh Rolf
Rawal Gaurav
Rebucci Raffaella
Reddi Mounika Bala
Reddy Nandakumar
Reimus Fenja
Reis Chaves Zanetti Aricia
Ren Jinglei
Ren Senhao
Ren Wen
Rendahl Aaron
Rendón Del Águila Uriel
Reneby Amanda
Renoult Christophe
Resende P. Talita
Resende Pilar Talita
Resende-De-Macedo Nubia
Reveles-Félix Saúl
Revilla Manuel
Revilla Yolanda
Reyes Benjamin
Reyes Edith Nydia
Reynoso Yazmin Samantha
Riahi Insaf
Ribeiro Vitoria
Riccobene Paolo
Richards Kirsty
Ricker Nicole
Ricouleau Jean-François
Riehn Katharina
Riera Bastien
Rigo Monteiro Alessandra
Rios Victor Alejandro
Risser Jessica
Ritzmann Mathias

Rivera Benítez José Francisco
Rivera Eduardo
Riveros Andres José
Robbins Rebecca
Rocha Cipriano Gabriel
Rocha Pinto Francisco
Rocher Maliachi Gustavo Daniel
Ródenas Jesús
Rodio Theodoro Thiago
Rodrigues da Costa Maria
Rodrigues Junqueira Daniela
Rodrigues Oliveira Clara Ana
Rodriguez Alberto Jaime
Rodriguez Ampelia
Rodríguez Carmen
Rodriguez Hernán
Rodriguez José Francisco
Rodriguez Maria
Rodríguez Paz Iván
Rodriguez Sierra Eduardo
Rodriguez-Vega Víctor
Rodríguez-Velasco Ana
Roehe Michel Paulo
Roggeman Fien
Rogon Julien
Rojpradit Rangsun
Rolzhäuser Philipp
Romagosa Anna
Romero Aguilar Salvador
Romero Facundo Juan
Rondón-Barragán Iang
Rong Fang
Roorda Wolter
Roques Amélie
Rosas Luis
Rosas Samantha
Roshorm Maprang Yaowaluck
Rossi Leonardo
Rovira Albert
Royo Leandro
Ruampatana Jakavat
Ruangpanit Yuwares
Ruangpet Nongnapas
Rubbo Antonio
Rubico Emil Joseph
Rubico Joseph Emil
Rubin Martina
Rubio-Cervantes Ismael
Ruden Rachel
Rüegg Chantal
Ruenkoed Supranee
Ruiz José Emilio
Ruiz Michelle
Rupasinghe Ruwini
Rus Saša
Ruttkowski Bärbel
Rydal Martin
Rydal Peter Martin
Rykova Sergeevna Valentina
Ryt-Hansen Pia
Ryu Da-Hye
Ryytty Sylvén Kaisa
S. Silva Gustavo
Sá Passoni Ana Paula
Sabadin Jovan
Saendamuen Pathavee
Safiullin Rinat
Sagrera Mònica
Saikaew Narathorn
Saito Atsushi
Saito Shotaro
Sake Hendrik
Salaklang Jatuporn
Saldaña Contreras Flavio
Saliba Monteiro Matheus
Samatiwat Kanokwan
Samson Vivien
San Esteban Christina
Sanchez Adriana
Sanchez Alba
Sánchez Elena María
Sanchez Gregorio
Sanchez Pedro
Sánchez Vargas Alejandro
Sánchez-Betancourt José Ivan
Sánchez-Galán Raúl
Sánchez-Sánchez Raúl
Sandoval Jesús
Sannö Axel
Santa Maria Sofia
Santos Celestrini Machado Geovanna
Santos de Lima Renato

Santos França Luis Giovanni
Santos Regiane
Saornil David
Sara Miguel Jiménez
Sarfati David
Sarmad Muhammad
Sarmiento Rosa
Sarmineto Rosa
Sartori Cintia
Sato Hidetoshi
Sato Paulo Hiroji Jose
Sato Tetsuo
Satsook Phubet Satsook
Saxena Anugrah
Saxena Apoorva
Schaefer Lee Allan
Schatzmayr Dian
Schavetock Bruno
Schlagheck Alexandra
Schmicke Marion
Schmitz Theresa Klara
Schreiner Nadine
Schroeder C Declan
Schroeder Callie
Schroeder Cosmo Declan
Schuh Júnior Inácio
Schulthess Julie
Schulthess Thomas Lukas
Schüpbach Gertraud
Schüpbach-Regula Gertraud
Schuttert Arjan
Schwartz Mark
Schwarzer Uta
Schwertz Claiton
Scollo Annalisa
Scott D Marian
Scott E. Nancy
Scott Marian
Scott Nancy
Seemacharoensri Akaradet
Segalés Joaquim
Segers Ruud
Segura Mariela
Selnihhin Denis
Semitiel Jesus
Seo Dongmin
Seo Hae-Rang
Seo Kwang-Won
Seol Hyein
Serena Soledad
Serod Chinda
Serrano-Garcia Mariana
Seva Alcaraz Juan
Sevastiyanova Milena
Shang Laizhu
Shemelkov Vladimirovich Evgeniy
Shen Hanqin
Shen Sam
Shen Yanbin
Shi Ming
SHI Qinghe
Shi Ying
Shibata Mayu
Shih Jeff
Shimamura Tetsuya
Shin Joann-Gavin
Shin Seongho
Shin Seung Pyo
Shin Yeojin
Shin Yongwoo
Shinkawa Abner
Shrestha Kshitiz
Shrestha Rupesh
Shu Guan
Shukuri Tetsutaro Geraldo
Sia Bang Wen
Sialelli Jean-Noel
Sibbel Richard
Sibeko Nqubeko PS
Sibila Marina
Sidera Pau
Sierra Sara
Sigmarsson Lindberg Haukur
Silathawornwong Suppanat
Silva Almeida Gefferson
Silva de Souza e Gustavo
Silva Junior Roberto Sudário
Silva Mauricio
Silva Neta Speridião Clarice
Silva Poeta Ana Paula
Silva S. Gustavo
Silva Schlindwein Gustavo

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Simmons L Julie
Singthana Worachet
Sinnaeve Marnix
Sipos Roland
Sirimaha Sasithorn
Sirisereewan Chaitawat
Sirisophon Arisara
Sirithanyakul Pisit
Sitthicharoenchai Panchan
Sjölund Marie
Skerbiš Urška
Skoufos Ioannis
Slavec Brigita
Smart Isabel
Smith Chad
Smulders Dennis
Snider Tim
Snoeck Janne
Snow Casondra
Soares Giovanna
Sobko Iryna
Sochanwattey Sochanwattey
Soeckler-Lionetti Christina
Soh Shi Ling
Sokolowski Bartosz
Solà Marc
Soliman Mahmoud
Solis Laura
Son Sona
Son Thanh Toan
Sonálio Karina
Soncin Margherita
Song Daesub
Song Dongcheol
Song Lianghui
Song Min-Kyoung
Song Songlin
Song Tobey
Song Yunfeng
Song Zhiqiang
Sonna Settasart
Sookmanee Kosin
Sootthiluck Kanjanat
Sopin Supasit
Soriano Oscar
Souza Campos S. Fabrício
Souza Hanna Talita Lais
Souza-Neto A Jayme
Spadetto Livia
Spencer L Joel
Sperling Daniel
Spiekermeier Ines
Srimanote Potjanee
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Srisang Chutikarn
Srisawat Chatchawan
Ssu Kuo-Wei
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Steenaert Martijn
Stefan Georgeta
Šteferl Tim
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Steiner Tobias
Stepanova Hana
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Strutzberg-Minder Katrin
Štukelj Marina
Stupar Lucija
Sturza Diego
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Suarez Jose
Suárez Mestas Alberto José
Suarez-Duarte Elizabete Mirtha
Suárez-Mesa Antonio Rafael
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Suda Yuto
Suen Willy
Sueyoshi Masuo
Sugiura Katsuaki
Sugiura Yosuke
Sujka Ewa
Sukmak Manakorn
Sun Dahao
Sun Hua
Sun Jiangcai
Sun Limeng

Sun Lv-Hui
Sun Qinbing
Sun Yu-Ting
Suntisukwattana Roypim
Sunwoo Sun-Young
Supacharuwong Danusorn
Supple Angie
Sur Jung Hyang
Suris Javier
Surmak Andreanna
Suwannathada Pongthorn
Suwimonteerabutr Junpen
Suwor Fareeda
Suwunwong Monticha
Swalla Richard
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Szabó József
Szűr Veronika
Szymankiewicz Krzesimir
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Tactacan Bathan Glenmer
Tactacan Glenmer
Taechavasonyoo Apichaya
Taffarel Ana
Tai Shen Rong
Tajudeen Habeeb
Takami Kyoko
Takano Aruto
Takemae Hitoshi
Takita Tatsuo Gabriel
Tan Chen
Tan Grant Chuan Hao
Tan Justin
Tan Shuming
Tan Tao
Tan Zhigang
Tang Dian
Tang Jiayong
Tang Nick
Tang Pan
Tangen John
Taniguchi Masahiro
Tansarawut Pakamas
Tantawet Siriporn
Tantilertcharoen Rachod
Tantitaveewattana Phakawat
Tantituvanont Angkana
Tao Jie
Tao Pan
Tao Vinh
Tarasiuk Grzegorz
Taris Marion
Tark Dongseob
Tassis Panagiotis
Tasuksai Patchara
Tavai-Tuisalo'o Margret
Taveekaikun Suppachok
Taylor Grace
Tecchio Ari Cicero
Teixeira Angelica
Tellez Alejandra Karent
Tenbrink Krista
Tey David
Thakur Sameer
Thanantong Narut
Thanawongnuwech Roongroje
Thawinphrai Thiwankarn
Thepprechasakul Sakda
Theuns Sebastiaan
Thibault Thomas
Thiery Laurent
Thieu Quang Nguyen
Thinh Phuc Pham
Thu Phoo Pwint Pwint
Thuy Thi Thu Tran
Tian Lang
Tian Liying
Tian Zhongqiang
Tienthai Paisan
Tinh Ha
Tippitak Panida
Tiwari Sarita
Toft Nils
Toledo Manuel
Tollefson Maija
Tomás Jairo
Tong Hao
Tong Ze
Tonita Paul
Torremorell Montserrat
Torrent Joan
Torres Agustin Juan

Torres David
Tort-Miró Carla
Toyokawa Akihiro
Tra Mi Thi Bui
Tra Toan
Tran Danh Son
Tran Hoang Long
Tran Hoang Vu
Tran Hoc
Tran Lam Phuong Anh
Tran Le Bao Anh
Tran Minh Hoang
Tran My Ngoc Linh
Tran Ngoc Le Ngan
Tran Ngoc My Linh
Tran Ngoc Tiep
Tran Pham Nhu Thuan
Tran Pham Tien Thinh
Tran Thi Bao Nguyen
Tran Thi Loi
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CONGRESS ”
INFORMATION





PROGRAM *at a* GLANCE



Pre-congress day - June 15, 2026

15:00-18:00	IPVS Board Meeting and Pre-Congress Activities

Day 1 - June 16, 2026

Time	Congress main Hall - Grand Skylar
09:00 -16:00	Registration
15:15-16:45	PLENARY SESSION 1
	Keynote lectures & Tom Alexander Memorial lecture
16:45-17:45	Opening Ceremony
17:45-18:30	Break
18:30-20:30	Welcome Party

Day 2 - June 17, 2026

Time	Conference Hall 1	Conference Hall 2	Conference Hall 3	Conference Hall 4	
8:30-10:00	**PARALLEL SESSION 1** Nutrition And Gut Microbiota I (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 2** Herd Health Management I (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 3** Aiot In Pig Health And Production (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 4** Virology And Viral Diseases I (Keynote lecture & 4 oral ppts)	
8:30-10:00	Coffee Break & E-Poster Presentation 1				
10:45-11:45	**PARALLEL SESSION 1.2** Nutrition & Gut Microbiota I (4 oral ppts)	**PARALLEL SESSION 2.2** Herd Health Management I (4 oral ppts)	**PARALLEL SESSION 3.2** AIoT in Pig Health & Pro. (Keynote lecture & 2 oral ppts)	**PARALLEL SESSION 4.2** Virology & Viral Diseases I (4 oral ppts)	
12:00-13:00	Luncheon				
	Satellite Symposium 1				
	CEVA	ZOETIS	HIPRA	CP	
13:15-14:45	**PARALLEL SESSION 5.1** Pig Pro. & Sustainability (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 6.1** Bacterial & Parasitic Diseases Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 7.1** Advance. in Imm. & Vacc. I (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 8.1** One Health & Pig Welfare (Keynote lecture & 4 oral ppts)	EXHIBITION AND E-POSTER DISPLAYS
14:45-15:30	Coffee Break & E-Poster Presentation 1				
15:30-16:30	**PARALLEL SESSION 5.2** Pig Prod. & Sustainability (4 oral ppts)	**PARALLEL SESSION 6.2** Bacterial & Parasitic Diseases (4 oral ppts)	**PARALLEL SESSION 7.2** Advance. In Imm. & Vac. I (4 oral ppts)	**PARALLEL SESSION 8.2** One Health & Pig Welfare (4 oral ppts)	
16:45-18:00	**Satellite Symposium 2**				
	REBER	BI	MSD	KEMIN	

Day 3 - June 18, 2026

Time	Conference Hall 1	Conference Hall 2	Conference Hall 3	Conference Hall 4	
8:30-10:00	**PARALLEL SESSION 9.1** Nutrition & Gut Micro. II (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 10.1** Virology & Viral Diseases II (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 11.1** Herd Health Management II (Keynote lecture & 4 oral ppts	**PARALLEL SESSION 12.1** Reprod. Tech. & Lactation (Keynote lecture & 4 oral ppts)	EXHIBITION AND E-POSTER DISPLAYS
10:00-10:45	Coffee Break & E-Poster Presentation 3				
10:45-11:45	**PARALLEL SESSION 9.2** Nutrition & Gut Micro. II (4 oral ppts)	**PARALLEL SESSION 10.2** Virology & Viral Diseases II (4 oral ppts)	**PARALLEL SESSION 11.2** Herd Health Management II (4 oral ppts)	**PARALLEL SESSION 12.2** Repro. Tech. & Lactation (4 oral ppts)	
12:00-13:00	Luncheon				
	Satellite Symposium 3				
	CEVA	CAVAC	ELANCO	VIRBAC	
13:15-14:45	**PARALLEL SESSION 13.1** Emerging Diseases In Swine (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 14.1** Combating African Swine Fever (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 15.1** Advancements in Immunology and Vaccination II (Keynote lecture & 4 oral ppts)	**PARALLEL SESSION 16.1** Pig Farming Practice (Keynote lecture & 4 oral ppts)	
14:45-15:30	Coffee Break & E-Poster Presentation 4				
15:30-16:30	**PARALLEL SESSION 13.2** Emerging Diseases in Swine (Keynote lecture & 2 oral ppts	**PARALLEL SESSION 14.2** Combating African Swine Fever (4 oral ppts)	**PARALLEL SESSION 15.2** Advance. in Imm. & Vac. II (4 oral ppts)	**PARALLEL SESSION 16.2** Pig Farming Practice (4 oral ppts)	
16:45-18:00	Satellite Symposium 4				
	CTC-Bio	BAF			
18:30-22:00	Gala Dinner at Saigon Ballroom – Vinpearl Landmark 81 [With an invitation]				

Day 4 - June 19, 2026

Time	Congress Main Hall - Grand Skylar	
08:30-10:00	PLENARY SESSION 2 Keynote lectures	EXHIBITION AND E-POSTER DISPLAYS
10:00-10:30	Coffee Break	
10:00-10:30	Closing Ceremony Recap video clip Awards [Oral/Poster + Animal Science] Lucky Draws IPVS2028 Promotion Closing speech	

PROGRAM DETAILS



Pre-congress day - June 15, 2026					
15:00-18:00	**IPVS Board Meeting and Pre-Congress Activities**				
Day 1 - June 16, 2026					
Time/Venue	**Congress main Hall - Grand Skylar**				
09:00 -16:00	**Registration**				
15:15-16:00	PLENARY SESSION 1 Chairs: **Assoc Prof. Vo Thi Tra An** **Assoc Prof. Le Thanh Hien**				
	Keynote lecture **A New Paradigm for Biosecurity: Building a Foundation for Long-Term Animal Health and Disease Prevention** **Prof. Derald Holtkamp** *Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, USA*				
16:00-16:45	Tom Alexander Memorial lecture Keynote lecture **From Legacy to Innovation: Applying Mechanism-Based Immunology to PRRSV Control** **Prof. Sanipa Suradhat** *Department of Veterinary Microbiology, Faculty of Veterinary Science, Chulalongkorn University, Thailand*				
16:45-17:45	**Opening Ceremony**				
17:45-18:30	**Break**				
	Ribbon-cutting ceremony of the exhibition at IPVS 2026 **[Main Exhibition Area, IPVS 2026, 5th floor]**				
	Launching of the Poster Area at IPVS 2026 **[Main Poster Area, IPVS 2026, 6th floor]**				
18:30-20:30	**Welcome Party**				
Day 2 - June 17, 2026					
Location	**Conference Hall 1**	**Conference Hall 2**	**Conference Hall 3**	**Conference Hall 4**	**Exhibition and E-poster Displays**
Time/Venue	PARALLEL SESSION 1: NUTRITION AND GUT MICROBIOTA I	PARALLEL SESSION 2: HERD HEALTH MANAGEMENT I	PARALLEL SESSION 3: AIoT IN PIG HEALTH AND PRODUCTION	PARALLEL SESSION 4: VIROLOGY AND VIRAL DISEASES I	
08:30-09:00	**Chairs:** **Assoc. Prof. Nguyen Quang Thieu** **Dr. Hagen Schulz**	**Chairs:** **Dr. Won Hyung Lee** **Dr. John Carr**	**Chairs:** **Asst. Prof. David Rosero** **Assoc Prof. Do Vo Anh Khoa**	**Chairs:** **Prof. Hans Nauwynck** **Assoc. Prof. Nguyen Thanh Lam**	
	Keynote lecture **Functional Nutrition to Drive Productivity** **Dr. Hagen Schulze** *ADM International Sarl, Rolle, Switzerland*	Keynote lecture **Herd Health Management in Pigs: Ten Things to Look at!** **Dr. John Carr** *Melbourne and Adelaide Universities. Howells Veterinary Services, UK*	Keynote lecture **Digital Transformation in Swine Farms: Bridging Innovation and Practical Implementation** **Asst. Prof. David Rosero** *Department of Animal Science, Iowa State University, USA*	Keynote lecture **Porcine Reproductive and Respiratory Syndrome Virus - How to Control this Master of Disguise?** **Prof. Hans Nauwynck** *Faculty of Veterinary Medicine, Laboratory of Virology, Ghent University, Belgium*	
	Oral presentation 1.1	**Oral presentation 2.1**	**Oral presentation 3.1**	**Oral presentation 4.1**	

9:00-9:15	NGM 1.1 (OR-0304) **Milk Fat Globule Membrane (MFGM) Improves Performance of Piglets During the Weaning Phase** *Matthijs De Jong, Astrid Koppenol, Lien Vande Maele, Béke Nivelle, Peter Gere, Peter Ramaekers, Evi Croes*	HHM 1.1 (OR-0523) **Seasonal Effect on the Weaning-To-Estrus Interval in Winter: A Case Report from A Finish Farm** *Stefan Björkman, Alexander Grahofer, Claudio Oliviero*	AIoT 1 (OR-0748) **Harnessing Machine Learning to Identify Predictors of Piglet Survival in Commercial Breeding Herds** *Elly Kirwa, Fernando P. Bortolozzo, Kelly Will, Mafalda Mil-Homens, Gustavo Silva*	VVD 1.1 (OR-0125) **Distribution and Genetic Diversity of Porcine Reproductive and Respiratory Syndrome Viruses in the Russian Federation** *Anton Gennadievich Yuzhakov, Oleg Anatolievich Verkhovsky, Alexei Dmitrievich Zaberezhny, Taras Ivanovich Aliper*	Exhibition and E-poster Displays
9:15-9:30	NGM 1.2 (OR-0329) **Effects of Natural Of 1,25-Dihydroxy Vitamin D3 Glycosides on Inflammation and Reproductive Efficiency in Sows** *Kamolthip Phoonsap, Waraporn Kraitavin, Raffaella Rebucci, Valentino Bontempo, Luca Marchetti*	HHM 1.2 (OR-0730) **Quality Colostrum Profile and Imunoglobulins Transference in Brazilian Swine Production** *Daniela Junqueira Rodrigues, Paulo Eduardo Bennemann, Giovanne Orlando Dallago, Ricardo Mitsuo Hayashi, Camila Marinelli Martins*	AIoT 2 (OR-0102) **Integration of Generative Artificial Intelligence in Veterinary Education: Evaluation of Microsoft Copilot in a Crossover Study** *Heiko Nathues, Jasmin Widmer, Laura Chunta Silva, Alexander Grahofer, Patrick Zanolari, Lucia Unger, Bérénice Lutz, Gertraud Schüpbach*	VVD 1.2 (OR-0555) **Enhancing PRRSV-2 Monitoring and Outbreak Tracing by Adoption of Fine-Scale Classification of Genetic Variants in North America** *Kimberly Vanderwaal Nakarin, Pamornchainavakul, Mariana Kikuti, Jianqiang Zhang, Michael Zeller, Giovani Trevisan, Luc Dufresn, Daniel Linhares, Joao Herrera da Silva, Cesar A Corzo, Tavis K Anderson, Robert Charette*	
9:30-9:45	NGM 1.3 (OR-0961) **Organic Acid and Anionic Diets as Nutritional Strategies to Modulate Urinary PH and AcidBase Balance in Gestating Gilts** *Ana Lígia Braga Mezzina, Matheus Saliba Monteiro, Ana Clara Rodrigues De Oliveira, Fernanda Mariane Dos Santos, Caroline Veloso, Nadia De Almeida Ciriaco Gomes, Jose Echavarría Martinez, Felipe Norberto Alves Ferreira, Clarice Speridião Silva Neta, Alline Morgana Silva Leite, Adriano Bonfim Carregaro, Cesar Augusto Pospissil Garbossa*	HHM 1.3 (OR-0905) **Late Gestation Phase-Feeding Reduces Growth Plate Dysplasia in Neonatal and Weaned Pigs** *Perry Harms, Katlyn McClellan, Carlos Lopez-Figueroa, Mark Weaver, Rebecca Robbins, Eric Weaver*	AIoT 3 (OR-0394) **Establishment of Ten Detection Methods for Pig Pathogens Based on Nanopore Sequencing** *Mengmeng Wang, Longchuan Qiuhua, Senhao Ren, Dongjian Yu, Qianqian Jin, Long Li*	VVD 1.3 (OR-0612) **New Diagnostic Strategies in Porcine Reproductive and Respiratory Syndrome Virus Surveillance in Danish Pig Herds** *Pia Rudolph Heiselberg, Nicole Bakkegård Goecke, Nicolai Weber, Inge Larsen, Lars Erik Larsen, Ken Steen Pedersen*	
9:45-10:00	NGM 1.4 (OR-0725) **Muramidase Supplementation Improves Growth and Gut Functionality of Post-Weaning Piglets** *Lea Hübertz Birch Hansen, Irene ising, Christophe Bostvironnois*	HHM 1.4 (OR-0496) **Maternal Hydroxy-Selenomethionine Supplementation Improves Performance and Immune Competence of Sows and Piglets Under Heat Stress** *Juan Wang, Zhe Peng, Shao-Qing Wang, Hua Sun, Mohammed Amine Hachemi, Denise Cardoso, Barbara Mallmann, Amine Mellouk, Claire Xu, Olga Lemâle, Jessika Consuegra, Lv-Hui Sun*	AIoT 4 (OR-0629) **Deployment of Automated System for Lung Lessions and Pleuritis Evaluation** *Joaquim Roberto Bringas, Miguel Claver, Ewa Sujka, Angel Garrido, Arturo Lopez, Jesus Semitiel, Jorge de Haro*	VVD 1.4 (OR-0303) **Impact of Sample Material and Diagnostic Laboratory on Neonatal Porcine Reproductive and Respiratory Syndrome Virus PCR Monitoring Results** *Karien Koenders, Martijn Steenaert*	
10:00-10:45	**Coffee Break**				
	E-Poster Presentation 1				

	E-Poster Presentation Station 1	E-Poster Presentation Station 2	E-Poster Presentation Station 3	E-Poster Presentation Station 4	
10:02-10:05	17ME1-01-NGM0002 **The Role of Zinc Oxide and Its Physico-Chemical Properties in Enhancing Piglet Health and Growth** *Rita HORVÁTH, Botond Alpar, Alessandra Rigo Monteiro*	17ME2-01-HHM0239 **Identifying Sources of Porcine Reproductive and Respiratory Syndrome Virus Instability in Sow Herds Through Parity-Based Neonatal Monitoring** *Karien Koenders, Elisa De Conti, Daniel Linhares, Martijn Steenaert, Marius Kunze*	17ME3-01-AIoT0295 **Toward Early Detection of Newborn Piglets Using Vocalization Analysis** *Yosuke Sugiura, Tenma Nakano, Tetsuya Shimamura, Yoshiyuki Nakamura, Ayaka Miyazaki*	17ME4-01-VVD0055 **NLRX1 Mediates the Disruption of Intestinal Mucosal Function Caused by Porcine Astrovirus Infection via the ERK/MLCK Pathway** *Jie Tao, Benqiang Li, Jinghua Cheng, Ying Shi, Pan Tang, Huili Liu*	
10:06-10:09	17ME1-02-HHM0039 **Effect of Oral Administration of an Energy Booster at Birth on Piglets Vitality Parameters and Preweaning Performance** *Preden de Cacqueray, Alice De Wilde, Thomas Bureau*	17ME2-02-HHM0247 **Efficacy of Iron Dextran Administered Via Needle-Free Injection Versus Needle-and-Syringe Injection in Nursing Piglets** *Minh Man Pham, Ron Johnson, Maria del Rocio Amezcua, Zvonimir Poljak1, Terri L. O'Sullivan*	17ME3-02-BPD0145 **Case Report: Focus on Cleaning and Disinfection to Tackle Severe Post-Weaning Diarrhea** *Frédéric ACJ Vangroenweghe, Els Dejonckheere*	17ME4-02-VVD0073 **Cereblon Promotes Influenza Virus Replication Through Ampk Ubiquitination** *Thu Ha Nguyen, Dong Ju Lee, Mahmoud Soliman, Myra Hosmillo, Dae-Eun Cheong, Hae-Rang Seo, Don-Kyu Kim, Chul-Seung Park, Hueng-Sik Choi, Tae-Il Jeon, Ian G. Goodfellow, Kyoung-Oh Cho*	
10:10-10:13	17ME1-03-NGM0079 **Dynamics of the Piglet Fecal Microbiome During Lactation with and Without Bacillus Sp. Probiotic Supplementation** *Bang Cong Ngo, Srisang Chutikan, Padet Tummaruk*	17ME2-03-HHM0377 **Porcine Reproductive and Respiratory Syndrome Virus ORF5 Variant Detection Dynamics in the U.S.** *Quyen Thuc Le, Rodger Main, Giovani Trevisan, Daniel Linhares, Guilherme Cezar, Hemant Naikare, Franco Matias Ferreyra, Angela Pillatzki4, Melanie Prarat5, Craig Bowen*	17ME3-03-BPD0028 **Effect of Paromomycin and Enrofloxacin Administration on Intestinal Microbiota Development of Pigs During the First 6 Weeks Post-Weaning** *Lieven Claerhout, Ulrich Klein, Wouter Depondt, Sebastiaan Theuns, Amanda Hettiarachchi*	17ME4-03-VVD0090 **Immunological Evaluation of Non-Interference of a Type 2 Lineage 1 Modified-Live Porcine Reproductive and Respiratory Syndrome Virus Vaccine on the Classical Swine Fever C-Strain Vaccine in Pigs** *Karl Alexander Fabros, Zi Yao Ng, Jay Jacela, Geoffrey Labarque*	**Exhibition and E-poster Displays**
10:14-10:17	17ME1-04-NGM0187 **Replacing Cholecalciferol With 25-Hydroxyvitamin D3 in Pig Diets: Influences on Vitamin D Metabolism and Muscle Development** *Fernanda Mariane dos Santos, Hanna Knüpfer, Franz Ewendt, Estefania Perez-Calvo, Cesar Augusto Pospissil Garbossa, Mirja Rosemarie Wilkens*	17ME2-04-HHM0419 **Evaluation of Long-Acting Ceftiofur for the Prevention and Treatment of Postpartum Disorders in Sows** *Panha Vy, Puchong Waeosri, Tanyanant Kaminsonsakul, Wichian Navasakuljinda, Anchada Lowanitchapat, Kittipat angchokchatchawal, Apichart Prapattanakullawong*	17ME3-04-BPD0580 **Prevalence and Serotype Shift of Porcine Pasteurella Multocida in China (2024-2025): Implications for Disease Prevention and Control** *Zhu Zhan wei*	17ME4-04-VVD0139 **Feasibility of Porcine Enteroids as an Alternative to Cell Culture and Pig Bioassay for Assessing Porcine Deltacoronavirus Viability** *Lu Yen, Juan Carlos Mora-Díaz, Ning-Chieh Twu, Bala Mounika Reddi, Apoorva Saxena, Jesús Horacio Lara Puente, Daniel Gustavo Rocher Maliachi, Ángel David Cota Valdez, Mario Palma Zepeda, Rahul Kumar Nelli, Luis Gimenez Lirola*	
10:18-10:21	17ME1-05-NGM0289 **Fumonisin Management with Enzymatic Biotransformation** *Viviana Molnar-Nagy, Daniel Incze, Zsófia Bata, László Poppe*	17ME2-05-HHM0552 **Impact of Pre-Farrow Ceftifur Sodium on Treatment and Mortality Rate in Piglets** *Paul E Yeske, Casondra Snow, Erin Kettelkamp, Alyssa Betlach*	17ME3-05-BPD0605 **Validation of a New Generation Elisa Test for Antibody Detection for *Mycoplasma Hyopneumoniae*** *Fabien Donnet, Loic Comtet, Angela Bononat, Philippe Pourquier, Rafael Forero, Luis Gimenez-Lirola, Devi Patnayak*	17ME4-05-VVD0151 **The LncRNA HCG4 Regulates the RIG-I-Mediated IFN Production to Facilitate H1N1 Swine Influenza Virus Replication** Jinghua Cheng, Jie Tao, Ying Shi, Huili Liu	

10:22-10:25	17ME1-06-NGM0290 **Alternative to ZnO: Phytobiotics to Prevent Weaning Diarrhea** *Roland Sipos, László Búza, József Földi, Viviana Molnar-Nagy, Alpár Botond, Rita Horváth, László Könyves*	17ME2-06-HHM0700 **Case Report: Reproductive Disorders Caused by Japanese Encephalitis Virus and Parvovirus** *Koji Ishii, Hiromichi Ishikawa*	17ME3-06-BPD0142 **Preventive Vaccination for PWD Due to E. Coli F4 Reduces Antimicrobial Use and Percentage of Runt Piglets at the End of Nursery** *Frédéric ACJ Vangroenweghe, Wolter Roorda*	17ME4-06-VVD0162 **Benefit of INGELVAC PRRS MLV Vaccination on Farm Site 2 in Mexico** *Luis Mauricio Cruz, Fausto Pinal, Rafael Naranjo, Alejandro Esque, Noemi Montalvo, Citlali Montes, Monica Barrios, Miguel Barcenas, Alan Ferruzca, Octavio Ferruzca, Mauricio Perez, Gabriela Cruz*	**Exhibition and E-poster Displays**
10:26-10:29	17ME1-07-NGM0411 **Mitigating Effects of Amulticomponent Mycotoxin Detoxifying Agent Against Combined Dietary Exposure to Multiple Mycotoxins in Pigs** *Panagiotis Tassis, Jog Raj, Goran Grubješić, Marko Vasiljević, Dimitrios Floros, Tobias Steiner, Anawach Phuengkasem*	17ME2-07-HHM0704 **Understanding Sow Mortality in a Midwestern U.S. Herd (2024 - 2025): Insights from Necropsy and Pathophysiology** *Laura Solis, Christopher Rademacher, Gustavo De Sousa e Silva, Daniel Linhares, Marcelo Almeida*	17ME3-07-BPD0652 **Successful Brachyspira Hyodysenteriae Eradication Through a Combined Approach of a Zinc Chelate Treatment and Adapted Management Measures** *Dhithya Venkateswaran, Trong Tung Nguye, Quynh Anh Nguyen, Roypim Suntisukwattana, Waranya Atthaapa, Angkana Tantituvanont, Dachrit Nilubol*	17ME4-07-VVD0228 **Occurrence and Genetic Diversity of Porcine Rotaviruses in Russian Pig Farms** *Nikita Krasnikov, Anton Yuzhakov*	
10:30-10:33	17ME1-08-NGM0472 **Effects of Peat Pellet Provision on Piglet Growth, Health, and Post-Weaning Diarrhea** *Melih Akar, Peppi Kareljärvi, Md Rayhan Mahmud, Olli Peltoniemi, Stefan Björkman, Claudio Oliviero*	17ME2-08-HHM0878 **Longitudinal Monitoring of Porcine Respiratory Disease Complex (PRDC) Associated Pathogens During Fattening and Their Association with Clinical Signs and Lung Lesions at Slaughter** *Julia Stadler, Pauline Deffner, Eliana Abele, Matthias Eddicks, Mathias Ritzmann, Kathrin Lillie-Jaschniski, Nick Vereecke*	17ME3-08-BPD0867 **Comparison of Monovalent and Divalent Copper Sources on In Vitro Antibacterial Activity Against Hemolytic Escherichia Coli** *Alessandra Rigo Monteiro, Marion Taris*	17ME4-08-VVD0236 **Distribution and Diversity of Porcine Circovirus Type 2 and 3 in the Wild Boar Population of Russia** *Valentina Sergeevna Rykova, Yuzhakov Gennadievich Anton*	
10:34-10:37	17ME1-09-NGM0477 **Replacing Added Fat with a Gluconeogenic and Phytogenic Additive in Late Nursery Pig Diets** *Zhigang Tan, Ekaitz Maguregui, Paul William Cardozo*	17ME2-09-NGM0587 **Comparison of Effects of a Phytogenic Supplementation and Zinc Oxide on Performance and Digestive Health of Weaned Piglets** *Corentin Truong, Gaëtan Vetea Plichart, Maria Rodriguez*	17ME3-09-BPD0358 **Evaluation and Application of Tiamulin for the Control of *Mycoplasma Hyopneumoniae*** *Jinglei Ren, Haijun Xiao*	17ME4-09-VVD0243 **Impact of Neonatal Porcine Reproductive and Respiratory Syndrome Virus Status on Farrowing Room Production Performance in Sow Herds in the Netherlands** *Lydie van den Crommenacker, Martijn Steenaert*	
10:38-10:41	17ME1-10-NGM0771 **Longitudinal Characterization of Piglet Fecal Microbiome from Lactation to the End of the Nursery Phase Supranee** *Ruenkoed, Anucha Charoensuk, Phuong Thao Thi Phan, Than Duy Pham, Trong Wisedchanwet, Sukanda Innajak, Fareeda Suwor, Dutrudi Panprommin, Eakapol Wankahart*	17ME2-10-NGM0997 **Dietary Butyrate Glycerides Prevented Growth Retardation and Altered Intestinal Microbiota in Lipopolysaccharid-Challenged Weaned Pigs** *Di Wu, Jose Maria Ros Felip*	17ME3-10-BPD0319 **Successful Mycoplasma Hyopneumoniae Eradication in a Multiplier Herd Using Tracheo-Bronchial Swab Monitoring Combined with Vaccination and Treatment Protocol** *Frédéric Vangroenweghe, Anne Staadegaard-Huijbers*	17ME4-10-VVD0263 **Effects of Porcine Reproductive and Respiratory Syndrome Modified Live Virus Vaccine and Immunostimulant on Oxidative Stress Parameters in Infected Nursery Pigs** *Supasit Sopin, Pakamas Tansarawut, Yonlayong Woonwong, Pichai Jirawattanapong, Narut Thanantong, Wirod Lakkanasombat, Alongkot Boonsoongern*	

	Oral presentation 1.2	**Oral presentation 2.2**		**Oral presentation 4.2**	
	Chairs: **Assoc. Prof. Che Minh Tung** **Dr. Bui Huy Doanh**	**Chairs:** **Dr. Pat Kirwan** **Dr. Won Hyung Lee**	**Dr. Jason YAN** **Assoc. Prof. Le Thanh Hien**	**Chairs:** **Prof. Daesub Song** **Assoc. Prof. Nguyen Thanh Lam**	
10:45-11:00	NGM 1.5 (OR-0826) **Application of Shrimp Peptide in Pig Production: Effects on Feed Intake, Growth Performance, And Health** *Phuong Hong Ngo, To Thi Hong Phuong, Nguyen Kim Ngan, Tran Dao Hong Ngoc, Nguyen Thi Giang Anh, Nguyen Thi Bao Tran*	HHM 1.5 (OR-0563) **Efficiency and Compliance of Vaccination Practices in Brazilian Pig Farms Based on The PigCare AUDVAC Database (2024-2025)** *Amanda Gabrielle De Souza Daniel, Luana Bombana Mazzarollo, Leonardo Rossi, José Luiz Almeida, Maraísa Meira Goulart, Marco Couto, Stephan Von Berg*	10:45-11:15 Keynote lecture **Application and Practice of Multistory Pig Farming: Planning and Configuration Process** *Dr. Jason Yan Beijing Précision Farm Technology LLC, Beijing, China*	VVD 1.5 (OR-0553) **PRRSV-2 Variant-Specific Exposure History and Abortion Outcomes in U.S. Sow Farms** *Julia Bake, Lori Feldmann, Mark Fitzsimmons, Albert Rovira, Kimberly Vanderwaal*	
11:00-11:15	NGM 1.6 (OR-0678) **Effects of Natural Growth Promoter in Diets on The Performance of Growing Pigs** *Nguyen Quang Thieu, To Thi Hong Phuong, Nguyen Kim Ngan, Nguyen An Khang, Nguyen Thuy Quyen, Nguyen Viet Hai*	HHM 1.6 (OR-0493) **Lauric Acid Glyceride Supplementation in Sow Diets Improves Piglet Performance, Litter Uniformity, and Passive Immunity** *Amine Mellouk, Nuria Vieco-Saiz, Virginie Michel, Olga Lemâle, Tom Meyns, Claire Xu, Jessika Consuegra*		VVD 1.6 (OR-0199) **Cross-Protective Efficacy of a Type 2 Lineage 1 Modified-Live Porcine Reproductive and Respiratory Syndrome Virus Vaccine Against the NADC30 Strain** *Karl Alexander Fabros, Zi Yao Ng, Jacqueline Bacon, Geoffrey Labarque*	**Exhibition and E-poster Displays**
11:15-11:30	NGM 1.7 (OR-0623) **Dietary Supplementation with Free MCFA Improves Sow Performance, Colostrum Quality and Offspring Growth** *Yalan Zheng, Yang Liu, Dingguo Wang, Renjie Yao, Johnie Ao, Romain D'Inca, Maartje De Vos, Lianqiang Che*	HHM 1.7 (OR-0594) **The 3D Concept: Data, Diagnostics and Decision. A Deep and Broad-Spectrum View of the Production** *Daniela Junqueira Rodrigues, Ricardo Mitsuo Hayashi, Paulo Eduardo Bennemann, Plinio Barbarino Júnior, Giovanne Orlando Dallago, Inácio Schuh Júnior, Camila Marinelli Martins*	**Oral presentation 3.2** AIoT 5 (OR-0412) **Digital Biosecurity: Enhancing Internal Biosecurity Through Behavior-Based Modification of Workers' Movement Patterns in A Commercial Swine Farm Impacted By PRRSV** *Carlos Piñeiro, Oscar Soriano, Laura Batista, Noelia Herrera, Gonzalo Abad, Diogo Brito, Raquel Andrés*	VVD 1.7 (OR-0753) **Screening and Therapeutic Evaluation of Natural Compounds Against Porcine Reproductive and Respiratory Syndrome Virus** *Tianjiao Liu, Qiongqiong Zhou, Peng Gao, Yongning Zhang, Xinna Ge, Jun Han, Xin Guo, Lei Zhou, Hanchun Yang*	
11:30-11:45	NGM 1.8 (OR-0368): **Etiological Investigation of *Melanosis Coli* in Slaughter Pigs** *Xu Cao, Jun Zhang, Sidang Liu, John Carr*	HHM 1.8 (OR-0784): **Enhancing Biosecurity in Swine Operations: Investigating Wildlife Interactions on Mortality Management Structures of Swine Farms** *Rafael Medeiros De Ávila Melo, Kimberly VanderWaal, Mariana Kikuti, Cesar Corzo, Igor Paploski*	AIoT 6 (OR-0413) **Digital Biosecurity Mobility-Based Facilitates the Detection of Superspreaders Centers and Agents Using Real-Time Network Analysis** *Carlos Piñeiro, Noelia Herrera, Laura Batista, Raquel Andrés, Diogo Brito*	VVD 1.8 (OR-0817) **Comparison of Serological Assays for Porcine Circovirus 2 (PCV2) Antibody Detection Following Experimental and Natural Exposure** *Eduarda Braga, Fernando Leite, Jerome Fiechtner, Tanja Opresnig, Pablo Pineyro*	
12:00-13:00	**Luncheon**				
	Satellite Symposium 1				
	CEVA	**ZOETIS**	**HIPRA**	**CP**	

	Satellite lecture 1 **Where Vets Meet Economists: The Economic Benefits of High-Quality Piglets** **Robert Hoste** *Senior Pig Production Economist, Wageningen University & Research* **Daniel Sperling** *Assistant Professor, Swine and Ruminant Clinic, VETUNI Brno*	Satellite lecture 2 **Raising the Bar in PRRS Management - Immunity, Innovation, and Vaccine Effectiveness** **Asst. Prof. Daniel Linhares** *Swine Medicine, ISU*	Satellite lecture 3 **Beyond Gut Health: Strategies to Unlock Piglet Performance** **Edgar Manzanilla** *Pig Development Department, Animal & Grassland Research and Innovation Centre, Teagasc (Ireland)* *Emili Barba - HIPRA (Spain)*	Satellite lecture 4 **Transitioning from Antibiotics to Probiotics in Swine Production: Field Conditions, Omics Monitoring, and Evidence for Real Impact** **Prof. Nuvee Prapasarakul** *Chulalongkorn University*	
Time/Venue	PARALLEL SESSION 5: PIG PRODUCTION AND SUSTAINABILITY	PARALLEL SESSION 6: BACTERIAL AND PARASITIC DISEASES	PARALLEL SESSION 7: ADVANCEMENTS IN IMMUNOLOGY AND VACCINATION I	PARALLEL SESSION 8: ONE HEALTH, AMR AND PIG WELFARE	
13:15-13:45	**Chairs:** **Dr. Philip Chamberlain** **Assoc Prof. Roy Kirkwood**	**Chairs:** **Dr. Alberto Stephano** **Prof. Roberto Guedes**	**Chairs:** **Prof. Dr. Sanipa Suradhat** **Dr. Dinh Xuan Phat**	**Chairs:** **Assoc Prof. Vo Thi Tra An** **Prof. Daesub Song**	
	Keynote lecture **Managing the Peripartum Prolific Sow for Improved Piglet Production** **Assoc Prof. Roy Kirkwood** *School of Animal and Veterinary Science, University of Adelaide, Australia*	Keynote lecture **Porcine Proliferative Enteropathy: What is New About this Important Disease** **Prof. Roberto Guedes** *Federal University of Minas Gerais, Brazil*	Keynote lecture **The Road Towards a Genetically Stable and Efficacious ASF Vaccine and Its Use in Pregnant Animals in A Field Situation** **Dr. Ruud Segers** *Assoc. Vice President R&D; Head of Global Swine and Ruminants Biologicals R&D MSD Animal Health*	Keynote lecture **Influenza Virus Spillover: Focusing on Viral Changes over the Past 20 years and The Changing Role of Pigs** **Prof. Daesub Song** *College of Veterinary Medicine, Seoul National University, Korea*	**Exhibition and E-poster Displays**
13:45-14:00	**Oral presentation 5.1** PPS 1 (OR-0855) **Associations Among Sows Body Measurements in Different Animal Populations: Data from a Cross-Sectional Study** *Rafaella Fernandes Carnevale, Nathalie Nollet, Cesar Augusto Pospissil Garbossa, An Cools, Geert Paul Jules Janssens, Sam Millet*	**Oral presentation 6.1** BPD 1 (OR-0308) **Enteric Snap-Shot (Oct - Dec 2025): Cross-Sectional Characterization of Enteric Pathogens in Nursery and Fattening Pigs Across Germany, France, and Spain** *Kathrin Lillie-Jaschniksi, David Espigares, Léna, Daniel, Christina Söckler-Lionetti, Sylvain Lacladere, Istvan Kiss*	**Oral presentation 7.1** AIV 1.1 (OR-0387) **Protective Efficacy of an Oil-Adjuvanted Monovalent FMD Vaccine Against Heterologous Challenge in Pigs** *Mark Anthony Mercado, Fahd Qarih, Juan Facundo Romero, Jorge Luis Filippi, Sabrina Beatriz Cardillo, Ana Taffarel, Sabrina Galdo Novo*	**Oral presentation 8.1** OAW 1 (OR-0285) **Three-Year Longitudinal Surveillance of Influenza a Virus at the Human-Swine Interface in Midwest Swine Farms in the United States** *Daniel C. A. Moraes, Ke Hu, Gustavo S. Silva, Daniel C.L. Linhares, Tavis Anderson, Amy L. Baker, Phillip C. Gauger*	
14:00-14:15	PPS 2 (OR-0459) **Use of Fibrates in Gilts with Electronic-Automatic Feeding: Effect on Metabolism** *Guillermo Ramis Vidal, Arturo López Sánchez, Miryam Martínez Martínez, Daniel Rabal Martínez, Aida Miralles Chorro, Gustavo Pappaterra*	BPD 2 (OR-0809) **Half-life of maternal derived antibodies against Actinobacillus pleuropneumoniae Apx-toxins and OmpA protein in a commercial farm** *David Espigares, Marcelo Gottschal, Sonia Lacouture, Guillermo Ramis, Preben Mortensen*	AIV 1.2 (OR-0161) **Exploratory Study of a Novel Live Recombinant Vaccine Against Porcine Epidemic Diarrhea Virus in SPF Piglets** *Jesus Horacio Lara, Mauricio Silva, Francisco Quezada, Juan Agustin Torres, David Sarfati, Bernardo Lozano*	OAW 2 (OR-0904) **Strengthening Smallholder Pig Farm Through the FarmVetCare APP Using One Health Approach with Lab-Supported Diagnostics** *Hien Thi Thu Nguyen, Nam Hung Luong, Hung Quoc Nguyen, Son Danh Tran, Sinh Xuan Dang, Anh Ngoc Bui, Tung Duy Dao, Vuong Nghia Bui, Suk Hu Lee, Hung Viet Nguyen*	

14:15-14:30	PPS 3 (OR-0848) **Methionine Hydroxy Analog Bis-Chelated Copper Compared With Tribasic Copper Chloride In A Reduced-Copper Strategy For Wean-To-Finish Pigs** *Jesus A Acosta Camargo, Jorge A Prada, David Torres, Dexter Amada, Bradley V Lawrence, Marisol Castillo, Deana Hancock*	BPD 3 (OR-0391) **Basolateral Infection of Intestinal Epithelial Cells (IEC-18) by Lawsonia Intracellularis Using an Inverted Transwell Culture Model** *Paula Angelica Correia, Matheus Dias Araújo, Jessica Carolina Reis Barbosa, Renato de Lima Santos, Talita Pilar Resende, Thaynara Parente Carvalho, Mirtha Elizabete Suarez-Duarte, Ricardo Pereira Laub, Roberto M. C. Guedes*	AIV 1.3 (OR-0962) **A Novel Oral Bacillus Subtilis Spore-Based Vaccine Induces Humoral Immune Responses Against Porcine Epidemic Diarrhea Virus in Sows and Confers Lactogenic Immunity to Their Offspring** *Thotsapol Kaewchomphunuch, Kanokporn Polyiam, Namphueng Butkot, Virakorn Ploypanichcharoen, Boontarika Juntanupong, Panida Chanapiwat, Natharin Ngamwongsatit, Yaowaluck Maprang Roshorm, Kampon Kaeoket*	OAW 3 (OR-0861) **Training Community One Health Teams to Prevent Taenia Solium in Rural Rwanda** *Cate Dewey, Carrie McMullen, Joshua Katusime, Venuste Gentil Twagiramungu, Fidele Gashaka Habineza, Vera Maulidi, Anne Deckert*	
14:30-14:45	PPS 4 (OR-0458) **Relationship Between Ketosis and The Body Condition Of Gilts At Farrowing And During Lactation** *Guillermo Ramis Vidal, Arturo López Sánchez, Miryam Martínez Martínez, Daniel Rabal Martínez, Aida Chorro Miralles, Gustavo Pappaterra*	BPD 4 (OR-0709) **Development of Novel Antimicrobial Peptides and Their Engineering into Nanoparticles to Improve Performance** *Shuang Wang, Shuaiyang Wang, Rui Zhou, Qi Huang*	AIV 1.4 (OR-0108) **Oral Immunization with Maize-Expressed PEDV Spike Protein-Derived Antigen Modulates Mucosal Cell-Mediated Immunity and Clinical Outcomes in Weaned Pigs** *Bravo-Parra Marlene, Cauwels Brooklyn1, Wiarda Jayne, García-Vega Ana Melissa, Magtoto Ronaldo, Nelli Rahul Kumar, Mora-Díaz Juan Carlos, Yen Lu, Castillo Ana1, Twu Ning-Chieh, Zhang Danyang, Zhang Yanqi, Buckley Alexandra, Crawford Kimberly, Saltzman Ryan, Escobar Jeffery, Raines Tracy, Sibbel Richard, Hernández Jesus, Giménez-Lirola Luis Gabriel*	OAW 4 (OR-0524) **Correlation of Toxic Element Concentrations with Semen Quality Parameters in Boars: The Role of Tin and Other Heavy Metals** *Stefan Björkman, Terhi Luukkonen, Pilar Gomez-Ramirez, Celine Arzel, Sandra Goericke-Pesch, Maria Kareskoski, Olli Peltoniemi, Melih Akar, Turkan Oztas*	Exhibition and E-poster Displays
14:45-15:30	**Coffee break**				
	E-Poster Presentation 2				
	E-Poster Presentation Station 1	**E-Poster Presentation Station 2**	**E-Poster Presentation Station 3**	**E-Poster Presentation Station 4**	
14:47-14:50	17AE1-01-PPS0035 **Effects of Boar Age and Breed on Semen Production Traits Unchean** *Yamsrikaew, Arisara Sirisophon, Nathaya Young, Morakot Nuntapaitoon*	17AE2-01-BPD0041 **Impact of Nanonisation on Florfenicol Recovery When Used in a Proportioner** *Lieven Claerhout, Wouter Depondt, Ulrich Klein, Sjouke Van Poucke*	17AE3-01-AIV0034 **Heterologous Vaccine Immunogenicity and Efficacy of the Porcine Reproductive and Respiratory Syndrome Virus Modified Live Vaccine - Prevacent PRRS** *James Mark Hammer*	17AE4-01-OAW0072 **Silver Nanoparticles Successfully Controled Antibiotic-Resistance Leptospirosis in a South African Sow Herd** *Thomas Wilhelm Volker, Thomas Günter Bates*	
14:51-14:54	17AE1-02-PPS0049 **Clostridium Butyricum Supplementation in Multiparous Sows Improves Piglet Weight** *Jakavat Ruampatana, Junpen Suwimonteerabutr, Dennis Smulders, Korntip Kanjanavaikoon, Morakot Nuntapaitoon*	17AE2-02-BPD0063 **Return on Investment (Roi) and Impact on Intestinal Score in Pigs Vaccinated with Porcilis Lawsonia Id on a Commercial Farm** *María Elena Sánchez*	17AE3-02-AIV0081 Algae Extract **Supplementation Boosts Humoral Immunity Induced by Attenuated PRRSV-1 Vaccination** *Francisco Rocha Pinto, Frédérick Bussy, Anne Morvan, Pi Nyvall Collén, Luong Tan Phat, Caroline Hervet, Nicolas Bertho, Pauline Maisonasse, Olivier Bourry, Catherine Belloc*	17AE4-02-OAW0185 **Effects of Implementing Animal Welfare in Pig Husbandry on Meat Quality Across Farm Scales** *Anh Ngoc Thi Dang, Duong Tan Do, Thi Kim Thi Pham, Anh Ngoc Thi Dang, Khang Nguyen Duong, Hai Thanh Nguyen*	

14:55-14:58	17AE1-03-PPS0173 **Effects of 10% Butaphosphan and Cyanocobalamin Injection on Day 3 Post Partum to Improve Piglet Productivity in Hyperprolific Sow Farms in Thailand** *Wichaya Dee ampai, Worachet Singthana, Benchawan Kukkorng, Apichaya Ratanamongkolmas*	17AE2-03-BPD0632 **First Isolation of Clostridium Difficile from Diarrheic Neonatal Piglets in Vietnam and Antimicrobial Susceptibility** *Thu T. M. Nguyen, Vy H. K. Nguyen, Ngoc Huu Le, An Thi Tra Vo*	17AE3-03-AIV0099 **Effects on Acute Phase Proteins in Piglets of Two Different PCV-2 and Mycoplasma Hyopneumoniae Vaccination Protocols** *Sebastián Figueras Gourgues, Angeles Plaza, Gisela Girme*	17AE4-03-OAW0196 **Cross-Sectional Virulence Gene Evaluaition and Probiotic Susceptibility of Swine Enteric Pathogens in Taiwan** *Heidi L Doden, Elizabeth A Galbraith, Kaley L Pederson, Sam Shen, Pai Liu, Ming-Tang Chiou, Chao-Nan Lin, Sona Son, Michael King*	**Exhibition and E-poster Displays**
14:59:15:02	17AE1-04-PPS0280 **Effect of Supplementing Sows with a Blend of Micronutrients on Their Hematological Status and Consequences on Their Reproductive Performance** *Ermin Magtagnob, Stela Ochoa, Emmanuel Janvier*	17AE2-04-BPD0031 **Pk/Pd and Clinical Relationships of Tulathromycin for Swine Respiratory Disease (Srd) Treatment** *Lieven Claerhout, Ulrich Klein, Wouter Depondt*	17AE3-04-AIV0365 **Oral Live Ileitis Vaccination Reduces *Lawsonia Intracellularis* Colonisation of the Ileum at Slaughter When Compared to an Injectable Vaccine** *Víctor Rodriguez-Vega, Gisela Girmé, Manuel Toledo, Emilio José Ruiz, Andrea Martínez, Anabel Fernández, Elena Goyena, Simón García Legaz*	17AE4-04-OAW0226 **Effects of Plant-Derived Isoquinoline Alkaloids on Stress Response and Producitivity of Sows During Farrowing and Lactation** *Waraporn Kraitavin, Pongthorn Suwannathada*	
15:03-15:06	17AE1-05-PPS0573 **Impact of Polyphenol-Richfeed Additves on the Performance of Nursery Pigs Under Fluctuating Housing Temperatures** *Chotima Poompramun, Anne Möddel, Bernhard Eckel*	17AE2-05-BPD0271 **Effects of Maternal and Post-Weaning Supplementation of a Bacillus Multi-Strain Probiotc on *Streptococcus Suis* Serotype 9 Colonization in a Challenge Study with Weaned Piglets** *Xiaonan Guan, Lea Hübertz Birch Hansen, Anouschka Middelkoop, Francesc Molist*	17AE3-05-AIV0444 **Compulsory Vaccination Against Porcine Reproductive and Respiratory Syndrome (PRRS): Evaluation of Cost, Coverage and Compliance in Liaoning Province, Northeastern China** *Shubo Li, Wentao Li*	17AE4-05-OAW0265 **Effect of a Calming Botanical Supplementation on Pigs Behavior and Tail Biting** *Claire Maltret, Amélie Roques, Sekhou Cisse, Mohammed el Amine Benarbia*	
15:07-15:10	17AE1-06-OAW0825 **Severe Fever with Thrombocytopenia Syndrome Virus as a One Health Concern: Zoonotic Transmission, Evidence from Animal Hosts Including Pigs, and an Adeno-Associated Virus-Vectored Vaccine Approach** *Vuong Van Hai Nguyen, Hitoshi Takemae, Tetsuya Mizutani*	17AE2-06-BPD0305 **Effect of Oral Live Vaccination Against *Lawsonia Intracellularis* on Production Performance in a Gilt Development Unit in Thailand** *Nontaprecha Bundee, Suthida Rachasapha, Manuschanok Watcharathai, Termsitthi Paphavasit, Kanokwan Samatiwat, Nathaya Young, Juver Membrebe, Rutger Jansen*	17AE3-06-AIV0699 **Evaluation of The Efficacy of an Oil-In-Water Adjuvant in a Foot-And-Mouth Mineralized Virus-Like Particles Vaccine in Pigs** *Regis VIALLE, Sarah Kharief, Juliette Ben Arous, Nicolas Versille, Hui Chen Guo*	17AE4-06-OAW0352 **Livestock-Associated Methicillin-Susceptible Staphylococcus Aureus ST398 As a Dominant Reservoir of Antimicrobial Resistance in Korean Pig Farms** *Ji Hyun Lim, Ji Heon Park, Soomin Lee, Soo-Jin Yang*	

15:11-15:14	17AE1-07-OAW0835 **_Escherichia Coli_ in Diarrheic Piglets: Associations Between Virulence Factors and Antimicrobial Resistance in Brazilian Herds** *Julia Helena Montes, Karina Sonalio, Letícia Roberta Martins Costa, Roberta Botta França, Claiton Schwertz, Leonardo Munaretto, Alessandro Campos*	17AE2-07-BPD0331 **Optimization of the Generation of Porcine _Escherichia Coli_ Fimbrial Adhesins** *Wei-Kai Huang, Hui-Wen Chang*	17AE3-07-AIV0764 **Feed Additive Supplementation Influences Immune Responses Following _Mycoplasma Hyopneumoniae_ Vaccination in Commercial Nursery Pigs** *Li Wang, Xiaoyan Ma, Febe Grunewald, Filip Van Immerseel, Ilias Chantziaras, Milena Sevastiyanova, Christos Gougoulias, Bert Devriendt, Dominiek Maes*	17AE4-07-OAW0547 **Comparative Genomics of Tet(X4)-Carrying Plasmid in _Escherichia Coli_ from Swine and Wastewater in Thailand** *Sokpanhapenh Hor, Nuvee Prapasarakul*	**Exhibition and E-poster Displays**
15:15-15:18	17AE1-08-OAW0909 **Antimicrobial Resistance and Virulence Gene Associations in Streptococcus Suis Serotype 9 from Brazilian Swine Farms** *Karina Sonalio, Julia Helena Montes, Leticia Roberta Martins Costa, Roberta Botta França, Claiton Schwertz, Leonardo Munaretto, Alessandro Campos*	17AE2-08-BPD0044 **Pk/Pd and Clinical Relationships of Pharmasin Water Soluble Granules (Tylosin Tartrate) and Tylovet Premix (Tylosin Phosphate) For the Treatment of Necrotic Enteritis (Ne)** *Lieven Claerhout, Stela Vesselova, Mariana Karanikolova, Ulrich Klein, Wouter Depondt, Suppanat Silathawornwong, Kritiya Phitsanuwattana, Natharin Ngamwongsatit, Kampon Kaeoket*	17AE3-08-AIV0823 **Field Report on "KAICO Powder" in Vietnam: Innovation in Swine Production via Novel Silkworm Technology** *Masahiro Taniguchi*	17AE4-08-OAW0620 **Health Status of Sows: Prevalence of Clinical Signs and Lesions in Flemish Farms** *Febe Grunewald, Margot Andries, Elise Bernaerdt, Dominiek Maes*	
15:19-15:22	17AE1-09-OAW0248 **Evaluating Animal Welfare Impacts of Needle-Free Injection When Administering Iron Dextran in Nursing Piglets** *Minh Man Pham, Ron Johnson, Maria del Rocio Amezcua, Zvonimir Poljak, Terri L. O'Sullivan*	17AE2-09-BPD0427 **Efficacy of a Water-Soluble Phytogenic Feed Additive on The Control of _Lawsonia Intracellularis_ in Fattening Pigs** *Anawach Phuengkasem, Victor Niderkvel, Marko Vasiljević, Tobias Steiner, Panagiotis Tassis*	17AE3-09-BPD1006 **PCR-Based Detection and Prevalence of _Salmonella_ spp., _Helicobacter_ spp., and _Staphylococcus aureus_ in Pig Feces Across Growth Stages in Vietnam** *Quoc Bao Nguyen, Ngan Ngoc Le Tran, Chau Minh Thi Nguyen, Duy Tien Do*	17AE4-09-OAW0687 **Coaching to Reduce Antibiotic Use in Pig Farms from Initial Skepticism Towards Recognized Added Value** *Zoë De Mol, Sibyl Anthierens, Evelien Biebaut, Annelies Decloedt, Jeroen Dewulf*	
15:23-15:26	17AE1-10-NGM0536 **Effects of Gestational Polyphenol Supplementation on Placental Gene Expression in Sows** Juan Pedro Cañete González, Pedro Gonzalez-Añover, María José López-Andreo, Guillermo Ramis-Vidal	17AE2-10-ASF0448 **Precision Eradication of ASF Through Accurate Diagnosis a Successful Field-Outbreak Response** *Zhilai Lai, Jingjing Ma, Junwei Liu, Xiangming Han, Shuaihao Wu, Jiyu Jia, Shuming Tan*	17AE3-10-BPD0938 **First Whole Genome-Level Characterization of _Glaesserella Parasuis_ in the Philippines** *John Ceddrick Florentino, Jimwel Bryan Christopher Palma Ferrer, Irish Mae Luna, Joren Villegas, Wreahlen Cariaso, Zyne Baybay, Andrew Montecillo, Kristel Mae Oliveros, Homer Pantua*	17AE4-10-OAW0225 **Effects of Plant-Derived Isoquinoline Alkaloids on Cortisol and Salmonella Shedding in Transported Pigs** *Waraporn Kraitavin, Valeria Artuso-Ponte, Wondwossen Gebreyes*	
	Oral presentation 5.2	**Oral presentation 6.2**	**Oral presentation 7.2**	**Oral presentation 8.2**	
	Chairs: **Dr. Philip Chamberlain** **Assoc Prof. Nguyen Quang Thieu**	**Chairs:** **Dr. Alberto Stephano** **Dr. Nguyen Ngoc Dinh**	**Chairs:** **Dr. Dinh Xuan Phat** **Dr. Ruud Segers**	**Chairs:** **Dr. Nguyen Viet Hung** **Asst. Prof. Nutthee Am-in**	

15:30-15:45	PPS 5 (OR-0043) **Infrared Thermography: An Ally to Evaluate Pig Growth Efficiency** *Fernanda Raidan, Manuel Revilla, Helomar Barbosa, Patrick Charagu, Allan Lee Schaefer, Hartmut Von Gaza, Abe Huisman*	BPD 5 (OR-0537) **3D Porcine Tracheal Model Reveals *Mycoplasma hyopneumoniae*-Induced Epithelial Damage Beyond Bacterial Culture Status** *Ana Fiorella Castillo-Espinoza, Rahul Kumar Nelli, Juan Carlos Mora-Díaz, Ning-Chieh Twu, Bala Mounika Reddi, Apoorva Saxena, Rolf Rauh, Raquel Espín-Palazón, Clyde Allen Campbell3, Ana Paula Poeta Silva, María José Clavijo, Luis Gabriel Giménez-Lirola*	AIV 1.5 (OR-0751) **Ten Years After Introduction of NADC30-Like Strain in China: A Novel Chimeric Porcine Reproductive and Respiratory Syndrome Vaccine Candidate** *Weixin Wu, Xinyu Fang, Yiyao Jiang, Jiameng Hu, Qiongqiong Zhou, Peng Gao, Yongning Zhang, Xinna Ge, Jun Han, Xin Guo, Lei Zhou, Hanchun Yang*	OAW 5 (OR-0225) **Effects Of Plant-Derived Isoquinoline Alkaloids On Cortisol And Salmonella Shedding In Transported Pigs** *Waraporn Kraitavin, Valeria Artuso-Ponte, Wondwossen Gebreyes*	**Exhibition and E-poster Displays**
15:45-16:00	PPS 6 (OR-0731) **Effects of Immunological Castration on Growth Performance Carcass Quality, and Economic Returns in Fattening Female Pigs** *Trung Huu Nguyen, Khanh Tran Vinh Doan, Tram Thi Ngoc Ngo, Nhat Van Nguyen, Hoang Minh Tran, Hue Thi Vo, Phong Dai Du, Duy Tien Do*	BPD 6 (OR-0473) **A Deep Dive into *Streptococcus suis* Differentiation: From Culture to PCR and Sequencing** *Marius Beumer, Ines Spiekermeier, Amanda Hettiarachchi, Sebastiaan Theuns*	AIV 1.6 (OR-0528) **Cross-Protection Conferred by Intradermal Unistrain PRRS Vaccination Against a Highly Pathogenic Vietnamese PRRSV2 Strain in Pigs** *Tram Thi Ngoc Ngo, Salvador Romero Aguila, To Nga Thi Bui, Lua Thi Nguyen, Linh Ngoc My Tran, Nguyen Hong Thao Vo, Hoa Thi Nguyen, Massimiliano Baratelli, Vinh Tao, Tu Bui, Nhat Minh Duong, Duy Tien Do*	OAW 6 (OR-0388) **Phage Driven Antibiotic Susceptibility Shifts in Multidrug Resistant Extraintestinal Pathogenic *Escherichia Coli*** *Saqib Ali, Pan Tao*	
16:00-16:15	PPS 7 (OR-0930) **Environmental Performance of Pig Manure Bioconversion Using Black Soldier Fly Larvae in Sustainable Pig Production Systems** *Duong Tan Do, Nghia Van Nguyen, Khang Nguyen Duong, Phuong Thuy Binh Le*	BPD 7 (OR-0710) **Development of a Murine Model of *Streptococcus suis*-Induced Arthritis to Screen Therapeutic Drugs** *HuiLin Yang, Yali Li, Tingting Feng, Jing Li, Qi Haung, Rui Zhou*	AIV 1.7 (OR-0443) **T Cell Epitope Content Comparison of a Porcine Reproductive and Respiratory Syndrome Virus Modified Live Vaccine to Four Field Strains** *Lu Peng, Qinyi Zhou, Delan Yang, Weiyao Han, Rui Zhou, Lu Li*	OAW 7 (OR-0389) **Establishment and Application of a Method for Detecting Antibiotic Resistance Genes in Swine Respiratory Pathogens Based on Nanopore Sequencing Technology** *Mengmeng Wang, Qianqian Jin, Senhao Ren, Dongjian Yu, Long Li*	
16:15-16:30	PPS 8 (OR-0172) **Evaluation of Coliprotec F4/F18 for Control of Post-Weaning Diarrhea in an Antibiotic-Free Pig Production System in Thailand** *Sasithorn Sirimaha, Thanawat Ekapongpaisit, Pathavee Saendamuen, U-then Phubangdao, Wichaya Dee-ampai, Worachet Singthana, Chanakarn Wuttikhumpraphan*	BPD 8 (OR-0487) **Bacillus B35 Fermentation Broth Alleviates *Streptococcus suis* Pneumonia Through Bacterostasis, Pulmonary Microbes, and Il-6/Jak/Stat/Apoptosis Pathways** *Pu Pu Yan, Shuang shang Li, Lin shen Li, Qian Guo, Yu lian Wang*	AIV 1.8 (OR-0509) **Holistic Disease Control With 3FLEX: Significant Improvements in Productivity Metrics in A Commercial Pig Farm in Vietnam** *Nguyen Cong Huy*	OAW 8 (OR-0206) **Reducing Antibiotic Use by Targeted Treatment of Diarrhea in Danish Nursery Pigs** *Jens Peter Nielsen, Martin Rydal, Sally Hansen*	
	Satellite Symposium 2				
	REBER	**BI**	**MSD**	**KEMIN**	

16:45-18:00	Satellite Lecture 5 **Predominance of PCV2d among Porcine Circovirus Type 2 Field Strains in Vietnam from 2024 to Now** **Dr. Ha Le Thi Thu**	Satellite lecture 6 **Dynamic Health in Practice: Integrated Control for a Complex Disease Landscape** **Prof. Joaquim Segales** *CReSA - Centre de Recerca en Sanitat Animal, Spain* **Asst. Prof. Marcelo Almeida** *Iowa State University, USA* **Dr. Joseph Yaros** *President of Pipestone Management China Division*	Satellite lecture 7 **From Concept to Practice: 30+ Years of Intradermal Vaccination Innovation** **Dr. Ruud Segers** *Associate Vice President, MSD Animal Health*	Satellite lecture 8 **Pig Production in Transition: Empirical Insights and Novel Approaches to PRRS Mitigation** **Susanne Kirwan** *Intestinal Health Global Technical Service Manager - Kemin Industries, Inc.* **Prof. Lin Chao Nan** *National Pingtung University of Science and Technology (NPUST)*	Exhibition and E-poster Displays
	Satellite lecture 5.1 **Redefining Correlates of Protection in PRRSV and PCV2 Vaccine Development** **Prof. Sanipa Suradhat** *Chulalongkorn University*				
	Satellite lecture 5.2 **Immunotherapy Platform to Combat Major Respiratory Pathogens in Swine** **Dr. Frank C.J. Chang**				

Day 3 - June 18, 2026					
Location	**Conference Hall 1**	**Conference Hall 2**	**Conference Hall 3**	**Conference Hall 4**	Exhibition and E-poster Displays
Time/Venue	PARALLEL SESSION 9: NUTRITION AND GUT MICROBIOTA II	PARALLEL SESSION 10: VIROLOGY AND VIRAL DISEASES II	PARALLEL SESSION 11: HERD HEALTH MANAGEMENT II	PARALLEL SESSION 12: REPRODUCTION TECHNOLOGIES AND LACTATION	
08:30-09:00	**Chairs:** **Dr. Metta Makhanon** **Assoc Prof. Nguyen Huu Van**	**Chairs:** **Prof. Qigai He** **Prof. Jianqiang Zhang**	**Chairs:** **Prof. Jeffrey James Zimmerman** **Prof. Fábio Vannucci**	**Chairs:** **Prof. Fernanda Almeida** **Assoc Prof. Roy Kirkwood**	
	Keynote lecture **Benefits of Functional Feed Additives on Pig Production Beyond the Gut** **Dr. Metta Makhanon** *Animal/ Swine Health Consultant, Thailand*	Keynote lecture **An Update on PEDV Current Status in The USA: Molecular Detection, Genetic Evolution, Prevention and Control** **Prof. Jianqiang Zhang** *Department of Veterinary Diagnostic & Production Animal Medicine, Iowa State University, USA*	Keynote lecture **Interpreting Detection of Multiple Pathogens in Diarrheic Pigs** **Prof. Fábio Vannucci** *Veterinary Diagnostic Laboratory, University of Minnesota, USA*	Keynote lecture **Factors Associated with Colostrum Consumption in Newborn Piglets** **Prof. Padet Tummaruk** *Chulalongkorn University, Thailand*	
9:00-9:15	**Oral presentation 9.1**	**Oral presentation 10.1**	**Oral presentation 11.1**	**Oral presentation 12.1**	
	NGM 2.1 (OR-0449) **Black Intestine in Finisher Pigs: Insights from Gut Microbiome Profiling and Histopathology** *Pakamas Tansarawut, Patcharee Chanachai, Kosin Sookmanee, Pichai Jirawattanapong, Narut Thanantong, Yonlayong Woonwong, Manakorn Sukmak, Alongkot Boonsoongern*	VVD 2.1 (OR-0100) **Intestinal Organoids from Eptesicus Fuscus Support Replication of Select Swine Enteric Coronaviruses: Insights into Bat-Swine Viral Interface** *Ning-Chieh Twu, Juan Carlos Mora-Díaz, Rahul Kumar Nelli, Lu Yen, Apoorva Saxena, Rachel Ruden, Panchan Sitthicharoenchai, Luis Giménez-Lirola*	HHM 2.1 (OR-0519) **Surveillance of Porcine Reproductive and Respiratory Syndrome (PRRS) Using PCR in Vietnam, 2014-2025** *Ninh Khac Pham, Giang Chau Pham, Huy Cong Huy, Tram Thi Ngoc Ngo, Ngoc Thi Hong Nguyen, Tan Minh Nguyen, Vu Hoang Tran, Juver Membrebe, Marius Kunze, Duy Tien Do*	RTL 1 (OR-0216) **Impact of Maternal and Farrowing Parameters on Colostrum Quality in a Free Farrowing System** *Philipp Thomas Egli, Julia Adam, Chantal Rüegg, Gertraud Schüpbach-Regula, Josef Gross, Alexander Grahofer*	

9:15-9:30	NGM 2.2 (OR-0994) **Effects of Phytogenic Supplement on Growth Performance, Nutrient Digestibility, Immune System Biomarkers in Blood, Gut Microbiome and Mucosal Health of Piglets Challenged with E. coli** *Fernando Kuhlmann, Diego Gonzalez, Hans Konsens, Sebastian Delbene, Rosa Navarro, In Ho Kim*	VVD 2.2 (OR-0853) **Market Hog Transportation: A Trailer Study Model for Pathogen Dissemination in the U.S** *Lucas Ferreira, Marie Culhane, Mark Schwartz, Cesar Corzo*	HHM 2.2 (OR-0287) **Quantifying Total Birth-To-Market Losses Per Litter Under Different Sow Farm PRRS Status Scenarios in A Midwest Us Commercial Swine Production System (2022-2025)** *Thinh Tran Pham Tien, Mafalda Pedro Mil-Homens, Derald Holtkamp, Edison Magalhães, Daniel Linhares*	RTL 2 (OR-0224) **Dietary Ammonium Chloride in Late Gestation and Farrowing Duration, Colostrum Production and Piglet Performance** *Thien Dinh Van, Roy Kirkwood, Mariana Caetano, Hue Thi Do, Kiro Petrovski*	Exhibition and E-poster Displays
9:30-9:45	NGM 2.3 (OR-0468) **Effect of Different Inclusion Levels of a Commercial Product in Post-Weaning Diets on The Productive Performance and The Inflammatory and Oxidative Status of Nursery Piglets** *Miryam Martínez Martínez, Daniel Rabal Martínez, Amalia Espejo Aguilar, Antonio Varga, René Bonekamp, Guillermo Ramis Vidal*	VVD 2.3 (OR-0799) **Foot-And-Mouth Disease Virus 3A Antagonizes Innate Immune Signaling by Targeting MAVS and TBK1** *Ashan Subasinghe, Jong-Soo Lee*	HHM 2.3 (OR-0654) **Neonatal Diarrhoea Problems in Asia: Digging into Its Epidemiology, Agents, Load, Age, and Coinfections** *Salvador Romero Aguilar, Joaquín Miguel, Dolors Giralt, Ming Hsun Wu, Wentao Fei, Hyun Dong Noh, Joseph Emil Rubico, Alongkorn Buakhiew*	RTL 3 (OR-0518) **Postpartum Disease in Sows: The Role of Red Blood Counts, Frusctosamine, Uterine Echogenicity and Inflammatory Markers in Predicting Piglet Survival and Uterine Involution** *Stefan Björkman, Roberta Yukari Hoshino, Matheus Saliba Monteiro, Luís Moreira Martins Esteves, Melih Akar, Mateusz Malik, Marianne Ørnstrup Kaiser, Jose Joaquin Cerón, Cesar Augusto Pospissil Garbossa, Rafaella Fernandes Carnevale, Bruno Bracco, Donatelli Muro*	
9:45-10:00	NGM 2.4 (OR-0604) **Effect of Bacillus Subtilis DSM 29784 Supplementation on Post-Weaning Piglets Raised Under Natural Escherichia Coli Pressure** *Tom Meyns, Nuria Vieco-Saiz, Claire Xu, Yi Cao, Yuanqing He, Zhiguang Gu, Jiramate Jittidecha, Wanpuech Parnsen, Anantawat Koontanatechanon, Olga Lemâle, Amine Mellouk, Jessika Consuegra*	VVD 2.4 (OR-0635) **Timing Matters: Modelling the Interplay among Maternally Derived Antibodies, Prevalence of Infection and PCV2 Vaccination in Swine** *Mònica Sagrera, Laura Garza-Moreno, David Espigares, Sébastien Picault, Marina Sibila, Joaquim Segalés*	HHM 2.4 (OR-0802) **Shedding Patterns of Fecal Bacterial and Viral Taxa in Newly Introduced Breeding Gilts** *Xiaoyan Ma, Li Wang, Filip Van Immerseel, Sebastiaan Theuns, Bert Devriendt, Dominiek Maes*	RTL 4 (OR-0080) **Difructose Anhydride III Supplementation in Lactating Sows Reduces Suckling Piglet Mortality and Enhances Body Weight Uniformity of Weaning Piglets** *Bang Cong Ngo, Rachod Tantilertcharoen, Suphot Wattanaphansak, Padet Tummaruk*	
10:00-10:45	**Coffee Break**				
	E-Poster Presentation 3				
	E-Poster Presentation Station 1	**E-Poster Presentation Station 2**	**E-Poster Presentation Station 3**	**E-Poster Presentation Station 4**	
10:02-10:05	18ME1-01-NGM0683 **Effects of Phytogenic Supplementation on Piglets Performance in the Presence of Feed Contaminated with Very High Levels of Mycotoxins** *Corentin Truong, Jean-François Ricouleau, Jean-Louis Blua*	18ME2-01-VVD0264 **Phylogenetic Analysis of Open Reading Frame 5 Sequences of Porcine Reproductive and Respiratory Syndrome Virus in Taiwan Between 2024 and 2025** *Yi-Fang Lai, Yen-Chen Chang, Hui-Wen Chang*	18ME3-01-VVD0465 **Molecular Detection of Atypical Porcine Pestivirus in Free-Ranging Wild Boars in European Russia** *Afshona Anoyatbekova, Darya Zaugolnikova, Anton Yuzhakov*	18ME4-01-RTL0137 **Determinants Of Stillbirth in Sows Under Tropical Climatic Conditions: Influences of Farrowing Months, Parity, and Litter Size** *Nguyen Trong Tran, Dwi Sunu Datrianto, Cong Bang Ngo, Padet Tummaruk*	

10:06-10:09	18ME1-02-NGM0719 **Dietary Co-Exposure to Deoxynivalenol, Zearalenone and Ochratoxin A at EU Guidance Levels Induces Distinct Systemic and Histopathological Changes in Pigs** *Panagiotis Tassis, Christina Marouda, Dimitrios Floros, Arnau Vidal, Dimitra Psalla, Joan Torrent, Christos Gougoulias*	18ME2-02-VVD0092 **Cross-Protective Efficacy of a Type 2 Lineage 1 Modified-Live Porcine Reproductive and Respiratory Syndrome Virus Vaccine Against a Highly Pathogenic Lineage 8 Strain** *Karl Alexander Fabros, Zi Yao Ng, Geoffrey Labarque*	18ME3-02-VVD0479 **Genomic Changes in Vaccine-Like African Swine Fever Virus Field Isolates from Southeast Asia** *Trong Tung Nguyen, Dhithya Venkateswaran, Roypim Suntisukwattana, Anan Jongkaewwattana, Dachrit Nilubol*	18ME4-02-RTL0197 **Factors Influencing the Incidence of Mummified Fetuses in Sows Under Tropical Conditions** *Dwi Sunu Datrianto, Nguyen Trong Tran, Cong Bang Ngo, Padet Tummaruk*	**Exhibition and E-poster Displays**
10:10-10:13	18ME1-03-NGM0733 **Feed Additive Supplementation Reduces Farrowing Duration and Improves Production Performance in Hyperprolific Sows Alongkot Boonsoongnern, Prapassorn** *Boonsoongnern, Narut Thanantong, Yonlayong Woonwoong, Supasit Sopin, Pichai Jirawattanapong, Athiwat Watthanachotchawakit*	18ME2-03-VVD0294 **An Update of Influenza A in Australian Commercial Pigeries** *Stacey Lynch, Kirsty Richards, Bernie Gleeson, Sandy Adsett, Greg Tuckett, Leanne McNabb, Michelle Giles, Toan Hong, Jackie Maher, Matthew Neaves, Frank Wong, David Williams*	18ME3-03-VVD0522 **Lauric Acid Glycerides Modulate Immune Response During Prrsv Infection In Vivo and Ex Vivo** *Olga Lemâle, Amine Mellouk, Tim Goossens, Claire Xu, Jessika Consuegra*	18ME4-03-RTL0218 **Influence of Farrowing Assistance on Postpartum Uterine Involution in Sows Managed in Temporary Confinement Systems under Tropical Climate** *Tip-apa Akkhaphan, Alexander Grahofer, Padet Tummaruk*	
10:14-10:17	18ME1-04-NGM0488 **Gut Microbiota Dynamics and Probiotic Influence During Lactation: Potential Implications to Sow Performance in a European Cohort** *Lea Hübertz Birch Hansen, Maja Weiss, Gisle Vestergaard, Tine Thorup Møller Knudsen, Said El Bohdidi, Dennis Sandris Nielsen*	18ME2-04-VVD0336 **Infection Status of Sows and Piglets from Different Farms of a Chinese Group Company Following Routine PCV2 Vaccination** *Yunxiong Lin, Jun Zhang, Frank Zhao, Frederic COLIN, Philippe Mazerolles*	18ME3-04-VVD0601 **Surveillance Of Swine Pathogens in Northern Vietnam in 2025** *Minh Thi Nguyen, Son Nguyen Vu*	18ME4-04-RTL0400 **The Efficacy of Silver Nanoparticle-Supplemented Semen Tube on the Antimicrobial Activity of Diluted Boar Semen During Preservation at 18oC** *Boontarika Juntanupong, Panida Chanapiwat, Natharin Ngamwongsatit, Supa Wirasat, Kampon Kaeoket*	
10:18-10:21	18ME1-05-NGM0796 **Effects of Combination of Organosulfur and Copper-Exchanged Clay in Diets to Replace Antibiotic Growth Promoter on Performance of Pigs** *Nguyen Minh Anh, Le Thanh Vu, Dang Nguyen Ngoc Linh, Ly Nguyen Hoai Phung, Doan Tran Vinh Khanh, Nguyen Quang Thieu*	18ME2-05-VVD0367 **Environmental PRRSV Surveillance in Sow Herds: An Innovative Monitoring Alternative** *Víctor Rodriguez-Vega, Gisela Girmé, José Antonio Antonio Muñoz, Jairo Tomás, Gonzalo Lopez-Lorenzo*	18ME3-05-VVD0608 **Risk Factors Associated with Introduction of Wild-Type Prrsv into Growing Pigs in The Midwestern Us** *Jose Angulo, My Yang, Albert Rovira, Aaron Rendahl, Montserrat Torremorell*	18ME4-05-RTL0619 **Assessment of Passive Immunity Transfer in Piglets with Relevance to Colostrum Management Strategies** *Febe Grunewald, Eva Govaerts, Caroline Bonckaert, Dominiek Maes*	
10:22-10:25	18ME1-06-NGM0816 **Vitamin Optimization Mitigates the Impact of Short-Term Heat Stress on Pig Growth Performance** *Estefania Perez-Calvo, Wen Ren, Jingcheng Zhang, Zhenzhen Wang, Shikui Wang, Jose Maria Hernandez*	18ME2-06-VVD0371 **Generation and Investigation of Ectodomains of Betaarterivirus Suid 2 Minor Envelope Glycoproteins and the CD163 Cellular Receptor Protein** *Chao-Chun Chang, Hui-Wen Chang*	18ME3-06-VVD0638 **Whole-Genome Sequence Analysis of Vaccine-Like Porcine Reproductive and Respiratory Syndrome Virus 2 Strains in a Clinical Outbreak on q Pig Farm in the Philippines** *Jimwel Bryan Christopher Palma Ferrer, Zyne Baybay, Andrew Montecillo, Ruffa Maze Balmes, Wreahlen Cariaso, Jeron Gomez, Alfred Agustin, Karl Alexander Fabros, Roselle Falconite-Cudal, Homer Pantua*	18ME4-06-RTL0650 **Effect of Bioactive Mineral Feed Additive on the Oxidative Status of Sows** *Ewa Sujka, Max Purser*	

10:26-10:29	18ME1-07-NGM0944 **Comparative Analysis of Enzyme - Zearalenone Interactions to Identify Detoxification Strategies** *Nikolett Emődi, Zsófia Bata, Kinga Nyíri, Beáta G. Vértessy*	18ME2-07-VVD0385 **Alternative Sample Matrices for the Detection of Antibodies Against Classical Swine Fever Virus** *Denise Meyer, Sandra Blome, Lia Ebner, Paul Becher*	18ME3-07-VVD0736 **Strain-Dependent Virulence and Intestinal Microbiota Dynamics of Porcine and Bovine Rotavirus A in Neonatal Balb/C Mice** *Ahmed Hamdy Ghonaim, Wentao Li, Qigai He*	18ME4-07-RTL0691 **Preliminary Evaluation of Tannic Acid as an Antimicrobial Additive in Boar Semen Extenders** *Krittika Keeratikunakorn, Panida Chanapiwat, Kampon Kaeoket*	**Exhibition and E-poster Displays**
10:30-10:33	18ME1-08-NGM0993 **Effect of Neonatal Supplementation of Hypertonic Solution on Piglets Performance from Birth to 45 Days Post-Weaning** *Supranee Ruenkoed, Keatipong Mongkolwit, Phong Anh Van Nguyen, Tan Zhigang, Sergio Miranda, Paul W Cardozo*	18ME2-08-VVD0395 **Maternal Antibodies Shape Hepatitis E Virus Infection Dynamics in Pigs: Insights into Age-Dependent Susceptibility** *Xiaoyan Xiong, Gustavo Monti, Xing Liu, Xin Yin, Wim Van der Poel*	18ME3-08-VVD0797 **The Cd46 Receptor Does This Pathogens Magnet Restrict the Risk for a Pestiviral Host Switch?** *Elena Leveringhaus, Robin Poljakovic, Paul Becher, Alexander Postel*	18ME4-08-RTL0585 **Effects of a Plant-Based Complementary Feed on The Performance of Sows and Suckling Piglets During Lactation** *Corentin Truong, Anne-Cécile Delahaye, Sylviane Boulot*	
10:34-10:37	18ME1-09-NGM1009 **Effects of Lauric and Capric Acids on Gut Microbiota, Microbial Fermentation, and Nutrient Digestibility in Pigs from the Mekong Delta Under in Vitro Conditions** *Man Minh Chau, Thi Cong Vo, Anh Hau Thi Hau, Huy Nhat Nguyen, Bao Anh Le Tran, Tri Dinh Cu, Nam Phuong Hoang Vo, Tai Tan Nguyen, Phuong Thuy Thi Nguyen, Han Gia Doan, Khoi Thieu Ho*	18ME2-09-VVD0414 **Isolation and Biological Characteristics Study of Porcine Reproductive and Respiratory Syndrome Virus GZ2022 Strain** *Xinmei Yang, Wentao Li, Qigai He*	18ME3-09-VVD0879 **Seroprevalence of Influenza Viruses in Swine Populations** *Ching-Ping Tsai*	18ME4-09-BPD0399 **Seasonal Comparison and Analysis of Lung Lesion Scoring in Slaughtered Pigs from a Chinese Company** *Xu Cao, Jun Zhang, Frederic COLIN, Philippe Mazerolles*	
10:38-10:41	18ME1-10-NGM0019 **Deoxynivalenol and Enniatins Affect Growth Performance and Gut Health in Piglets: The Beneficial Effect of an Algoclay-Based Detoxifier** *Leandro Royo, Morgane Malard, Matthieu Merceron, Francesc Molist, Regiane Santos*	18ME2-10-VVD0455 **Potential Mechanisms of Immune Modulation by African Swine Fever Virus CD2V Via Protein Translocation** *Hui-Ping Hsiao, Yu-Ting Sun, Chia-Yu Chang*	18ME3-10-VVD0890 **Vaccination With a PRRS Modified Live Vaccine to Piglets Less than One Week of Age Provides Protection to a Rosalia PRRSV Challenge** *Kimberly Ann Vonnahme, Marc Buxeda, Deb Amodie, Marta Cabana, Niels Wuyts, Monica Balasch*	18ME4-10-BPD0061 **PK/PD and Clinical Relationships of Apramycin Premix Administered to Pigs for the Treatment of Enteric Infections Caused by Escherichia Coli** *Lieven Claerhout, Mariana Karanikolova, Ulrich Klein, Wouter Depondt, Shotaro Saito, Masahiro Kusumoto*	
	Oral presentation 9.2	**Oral presentation 10.2**	**Oral presentation 11.2**	**Oral presentation 12.2**	
	Chairs: **Dr. Metta Makhanon** **Assoc Prof. Nguyen Quang Linh**	**Chairs:** **Assoc Prof. Le Van Phan** **Assoc Prof. Nguyen Thanh Lam**	**Chairs:** **Prof. Fernanda Almeida** **Prof. Nguyen Trong Ngu**	**Chairs:** **Prof. Padet Tummaruk** **Assoc Prof. Do Duc Luc**	
10:45-11:00	NGM 2.5 (OR-0684) **Efficacy of A Microencapsulated Essential Oil Complex in Controlling Swine Dysentery in Fattening Pigs** *Zhigang Tan, Ekaitz Maguregui, Paul W Cardozo*	VVD 2.5 (OR-0201) **Circulation of Japanese Encephalitis Virus in Swine Herds of Viet Nam** *Hai Nguyen Ngoc*	HHM 2.5 (OR-0924) **Feasibility and Application of Tongue Tip Sampling for Influenza A Virus Surveillance in Pigs from Weaning Through Nursery Phase** *Mark Schwartz, Maria Pieters, Kaydance Hinn, Maija Tollefson, Montserrat Torremorell*	RTL 5 (OR-0375) **Effect of Dietary Phytogenic Additives on Serum Cytokine Concentrations of Lactating Sows** *Caroline Veloso, Matheus Saliba Monteiro, Fernanda Mariane dos Santos, Ana Lígia Braga Mezzina, Ana Clara Rodrigues de Oliveira, Jose Alfonso Echavarria Martinez, Nadia de Almeida Ciriaco Gomes, Cesar Augusto Pospissil Garbossa*	

11:00-11:15	NGM 2.6 (OR-0211) **A Novel Dietary Dairy Bioactive (FXP) Enhances Post-Weaning Enteric Health in Nursery Pigs** *Nathan L Horn, Adrienne L Woodward, Joel L Spencer, Hang L Lu, Julie L Simmons, Kolapo L Ajuwon, Arun L Bhunia, Aaron L Gaines*	VVD 2.6 (OR-0923) **Isolation and Characterization of Swine Influenza Viruses Harboring PDM/09-Derived Internal Genes in South Korea in 2023** *Yeojin Shin, Minjoo Yeom, Shinwoo Lee, Hyunil Kim, Seongho Shin, Eunseo Bae, Woonsung Na, Daesub Song*	HHM 2.6 (OR-0540) **Sample and Pooling Strategies for Early Detection of PRRS Virus in Boars Studs** *Jose Luevano, Jose Suarez, Alexandra Diaz, Ampelia Rodriguez, Concepcion Diaz, Andres Diaz*	RTL 6 (OR-0831) **The Plant Solanum Glaucophyllum Reduces Farrowing Duration and Increases Early Piglet Survival** *Kathrin Bühler, Milena Sevastiyanova, Katia Pedrosa, Ana Paula Pavaneli, Eduardo Raele de Oliveira*	
11:15-11:30	NGM 2.7 (OR-0622) **Postbiotics and Phytogenics Reduced Diarrhea by Enhancing Intestinal Barrier and Modulating Immune Profile When Incorporated from Weaned Diets** *Xiaomei Liu, Guanhong Yue, Junyao Ma, Junjun Wang, Dandan Han, Maud Le Gall, Qinghe Shi, Ping Lu, Zhanqiao Yu*	VVD 2.7 (OR-0881) **African Swine Fever in Wild Boar in Catalonia, Spain: Experience of An Ongoing Outbreak** *Xavier F. Aguilar, Osvaldo Fonseca-Rodríguez, Lola Pailler-García, Liani Coronado, Carles Vilalta, Enric Vidal, Àlex Cobos, Miquel Nofrarias, Marina Cid, Jordi Argilaguet, Guillermo Cantero, Iván Cordón, Carlos Sánchez, Albert Sanz, Mercè Soler, Núria Ribas, Francesc Accensi, Natàlia Majó, Joaquim Segalés*	HHM 2.7 (OR-0189) **Study to Search for Associations Between Biosecurity Measures and PRRS Status of Sow Herds in The Netherlands** *Herman Prüst, Martijn Steenaert, Arjan Schuttert, Filip Heeman, Emile Gijsen*	RTL 7 (OR-0627) **Reproductive Performance of Replacement Gilts After Estrus Synchronization with Different Altrenogest Formulations** *Sacristan, Xinlei Liu, Di Gao, Ruben Del Pozo Sacristan*	
11:30-11:45	NGM 2.8 (OR-0516) **Effect of Dietary Antioxidant Supplementation with a Natural Source of Superoxide Dismutase on Oxidative Stress Biomarkers and Performance in Post-Weaning Piglets Under Heat Stress Challenge** *David Saornil, Laia Blavi, Astrid Koppenol, José Joaquín Cerón*	VVD 2.8 (OR-0750) **Evaluating Non-S Indel and S Indel Porcine Epidemic Diarrhea Virus Differential Real-Time RT-PCR Assays Targeting Spike Gene and Assessing Detection Frequency of The Two Virus Strains in The United States** *Jinnan Xiao, Hao Tong, Abigail Briley, Phillip Gauger, Jianqiang Zhang*	HHM 2.8 (OR-0675) **Containment of a PRRSV Outbreak in A Boar Stud Through Rapid Biosecurity and Management Interventions** *Anna Romagosa, Eduardo Rodriguez Sierra, Xavier Barrera*	RTL 8 (OR-0595) **Investigation of Whether Repeated PGF2 Treatment Induces Dependence in Porcine Ovarian Granulosa Cells In Vitro** *Fen Hao, Bei Bei Zhou, Meng Qi Chu, Hong Mei Zhu*	**Exhibition and E-poster Displays**
12:00-13:00	**Luncheon**				
	Satellite Symposium 3				
	CEVA	**CAVAC**	**ELANCO**	**VIRBAC**	
	Satellite lecture 9 **Don't underestimate Flu and PRRS impact on your farm** **Julia Stadler** *Senior Academic Assistant, Ludwig-Maximilians Universität München*	Satellite lecture 10 **Outstanding ASF vaccine (MEC-1) aligned with WOAH guideline (No shedding, No transmission, No reversion to virulence)** **Dr. Sungsik Yu** *Head of ASF Vaccine Project, CAVAC (Choong Ang Vaccine Laboratories Co., Ltd.)* **Dr. Jason Lee** *President, CAVAC (Choong Ang Vaccine Laboratories Co., Ltd.)*	Satellite lecture 11 **PRRS Control Intelligence: Leveraging Industry Real-World Evidence to Achieve System-Wide Mastery** **Prof. Cesar Corzo** *University of Minnesota's College of Veterinary Medicine, USA* **Dr. Amey Maschhoff** *Senior Advisor, Elanco Swine Innovation & Strategy*	Satellite lecture 12 **From Treatment to Control: A New Era in E. coli F4 & F18 Protection** **Dr. Francisco José Rodríguez Calvente** *Global Marketing Manager, Swine Segment – Virbac* **Dr. Pornchalit Assavacheep** *Assistant Professor, Department of Internal Medicine, Chulalongkorn University* **Dr. Edgar Diaz Estrada** *Commercial Director for Anitox in the Americas Region and collaborator of Diaz Consulting Group*	
Time/Venue	PARALLEL SESSION 13: EMERGING DISEASES IN SWINE	PARALLEL SESSION 14: COMBATING AFRICAN SWINE FEVER	PARALLEL SESSION 15: ADVANCEMENTS IN IMMUNOLOGY AND VACCINATION II	PARALLEL SESSION 16: PIG FARMING PRACTICE	

	Chairs: **Prof. Hanchun Yang** **Prof. Joaquim Segales**	**Chairs:** **Dr. Aruna Ambagala** **Prof. Roongroje Thanawongnuwech**	**Chairs:** **Prof. Sanipa Suradhat** **Prof. Chanhee Chae**	**Chairs:** **Prof. Derald Holtkamp** **Asst. Prof. Pariwat Poolperm**	
13:15-13:45	Keynote lecture **Old Enemies to New Challenges: The Changing Landscape of Swine** **Prof. Joaquim Segales** *Departament de Sanitat i Anatomia Animals, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB); Unitat mixta d'investigació IRTA-UAB en Sanitat Animal, CReSA*	Keynote lecture **ASF Lessons Learned: Regional Coordination & Sustainable Solutions** **Prof. Roongroje Thanawongnuwech** *Chulalongkorn University, Thailand*	Keynote lecture **Interaction and Vaccination of PCV2, PRRSV, and Mycoplasmas** **Prof. Chanhee Chae** *Seoul National University, Korea*	Keynote lecture **Health and Production Management in Pig Farm** **Asst. Prof. Pariwat Poolperm** *Swine health and production consultant* *Professional Training and Consultant Co., Ltd*	
	Oral presentation 13.1	**Oral presentation 14.1**	**Oral presentation 15.1**	**Oral presentation 16.1**	
13:45-14:00	EDS 1 (OR-0221) **Emergence of Getah Virus in Hubei Province (China), in 2024** *Wentao Li*	ASF 1 (OR-0959) **Global Distribution and Genetic Classification of African Swine Fever Virus** *Tien Pham*	AIV 2.1 (OR-0763) **Development, Immunological Characterization, And Evaluation of The Clinical Efficacy of Vaccines Based on Actinobacillus suis** *Rafael Vale, João Antônio Guizzo, Claudia Dazzi, Stetahni Pedroti de Quadros, Laura Germiniani Bedendo, Luiz Carlos Kreutz, Gabriela Alves, Adriane Holtz, Sandra Barioni, Rafael Frandoloso*	PFP 1 (OR-0786) **Evaluation of Deployable Fan Coverings for Biocontainment of Airborne Particles Associated with Swine Viral Transmission** *Erin Kettelkamp, Callie Schroeder, Paul Yeske, Alyssa Betlach*	**Exhibition and E-poster Displays**
14:00-14:15	EDS 2 (OR-0378) **Pathogen Dynamics in The U.S. Swine Industry: A Macroepidemiological Perspective** *Quyen Thuc Le, Rodger Main, Giovani Trevisan, Daniel Linhares, Guilherme Cezar, Hemant Naikare, Franco Matias Ferreyra, Angela Pillatzki, Melanie Prarat, Craig Bowen*	ASF 2 (OR-0220) **Pathological Characteristics of The Emerging Recombinant African Swine Fever Virus Genotypes I And II in Vietnam** *Phan Van Le, Dung Viet Nguyen, Hoang The Viet Nguyen, Ambagala Aruna, Hee Yeon Kim*	AIV 2.2 (OR-0875) **Local and Systemic T Cell Responses Induced by *Mycoplasma hyopneumoniae* Vaccination Associate with Protection in Pigs** *Xiaoyan Ma, Li Wang, Filip Van Immerseel, Ilias Chantziaras, Oliver Gomez-Duran, Marika Genzow, Bert Devriendt, Dominiek Maes*	PFP 2 (OR-0611) **Assessment of Personal Protective Equipment (PPE) Usage by Truck Drivers During Market Hog Unloading at a Us Harvest Facility** *Lucas Ferreira, Samina Chatila, Marie Culhane, Mark Schwartz, Cesar Corzo*	
14:15-14:30	EDS 3 (OR-0892) **A Survey of Critical Control Points of Truck Washes Operated in The United States and Canada** *Kate Dion, Emiliano Hidalgo, Perry Harms, Derald Holtkamp, Rebecca Robbins*	ASF 3 (OR-0103) **Evaluation of Immunogenicity and Reproductive Safety of An ASF Live-Attenuated Vaccine in Growing Pigs and Pregnant Sows During Commercial Use** *Seung Pyo Shin, Keun Seung Ahn, Seung Sub Choi, Do SoonKim Kim, Aaron Niyonsaba, Su Jin Lee, Xinghua Zheng, Sun A Choi, Seong Cheol Moon, Jung Hyang Sur*	AIV 2.3 (OR-0058) **Reduction of Pneumonia and Clinical Protection Against PCV2 and Mycoplasma hyopneumoniae After Vaccination with A Bivalent Combo Vaccine in A Chinese Commercial Farm in Liaoning Province A Case Report** *Fujie Zhu, Jiwen Ou, Di Gao, Ruben Del Pozo Sacristan*	PFP 3 (OR-0757) **Survey of The Current Status of Biosecurity in Selected Pig Farms in Vietnam Using the Pighealth Security-X Software** *Anh Thi Ngoc Dang, Han Nguyen Ngoc Vu, Thuan Pham Nhu Tran, David Tey, Stuart Court, Justin Tan, Tinh Thi Thanh Nguyen, Nguyen Hoai Nguyen, Duong Tan Do, Tram Thi Ngoc Ngo, Duy Tien Do*	

14:30-14:45	EDS 4 (OR-0505) **PRRSV Variants Under Monitoring (Vum): An Initiative for Proactive Near Real-Time Surveillance** *Mariana Kikuti, Nakarin Pamornchainavakul, Igor A. D. Paploski, Kimberly VanderWaal, Cesar Corzo*	ASF 4 (OR-0897) **Evaluation of The Persistence of AVAC ASF Live Vaccine Virus in Pigs Post-Vaccination** *Diep Van Nguyen, Duc Van Nguyen, Dang Xuan Vu, Ngoc Thi Nguyen, Tiep Ngoc Tran, Doanh Ngoc Pham*	AIV 2.4 (OR-0370) **Immunogenicity and Efficacy of A Mycoplasma hyopneumoniae / Porcine Circovirus Type 2 Combination Vaccine Against Experimental *Mycoplasma hyopneumoniae* Infection in Pigs** *Li Wang, Dominiek Maes, Filip Van Immerseel, Ilias Chantziaras, Karina Sonálio, Ana Panneitz, Xiaoyan Ma, Roman Krejci, Bert Devriendt*	PFP 4 (OR-0591) **Assessing Behavioral Readiness for Biosecurity Adoption Among Vietnamese Pig Farmers Using the Adkar Methodology** *Jeroen Dewulf, Nele Caekebeke, Ngo Thi Kim Cuc, Paula BarryWalsh*
14:45-15:30	**Coffee Break**			
	E-Poster Presentation 4			
	E-Poster Presentation Station 1	**E-Poster Presentation Station 2**	**E-Poster Presentation Station 3**	**E-Poster Presentation Station 4**
14:47-14:50	18AE1-01-EDS0616 **Pathogenicity of Clostridium Perfringens Type A Alpha-Toxin and Immunoprotection Analysis of a Non-Toxic Mutant** *Jiaying Zhao, Zhen Li, Yunfeng Song*	18AE2-01-ASF0104 **Durability of Protective Immunity Induced By an ASF-G-I177I/LVRVaccine: Efficacy and Safety in a Two-Consecutive-Challenge Model and in a Delayed Primary Challenge at 3 Months Post-Vaccination** *Su Jin Lee, Yeonji Kim, Xinghua Zheng, Se Young Lee, Sun A Choi, Seung Pyo Shin, Wonjun Kim, Seong Cheol Moon, Weonhwa Jheong, Jung Hyang Sur*	18AE3-01-VVD0891 **A Modified Live PRRS Vaccine Administered at Processing in Maternally Derived Antibody Positive Piglets and Challenged with a High Pathogen PRRSV Strain** *Kimberly Vonnahme, Debbie Amodie, David Pyburn, Richard Swalla*	18AE4-01-PFP0042 **Investigating the Impact of Microgranulation of Tiamulin-Containing Premixes** *Lieven Claerhout, Ulrich Klein, Wouter Depondt*
14:51-14:54	18AE1-02-BPD0577 **In Silico Design of a Universal Multi-Epitope Vaccine Candidate Targeting Conserved Antigens of Streptococcus Suis** *Muhammad Sarmad, Ba Xiaoliang*	18AE2-02-ASF0349 **Naturally Occurring African Swine Fever Cases Following Live-Attenuated Vaccination at a Commercial Pig Farm** *Aaron Niyonsaba, Sujin Lee, Do Soon Kim, SunA Choi, Seung Pyo Shin, Seong Cheol Moon, Jung Hyang Sur*	18AE3-02-VVD0926 **Evaluation of an Intranasal Vaccination Strategy Followed by a Challenge with the Thailand PRRSV-2 Strain During the Nursery Phase** **Apichart** *Prapattanakullawong, Tanyanant Kaminsonsakul, Anchada Lowanitchapat, Wichian Navasakuljinda, Pichai Jirawattanapong, Yonlayong Woonwong, Narut Thanantong, Alongkot Boonsoongnern, Thiwankarn Thawinphrai, Waranya Atthaaapa, Roypim Suntisukwattana, Dachrit Nilubol*	18AE4-02-PFP0714 **Ineffective Boot Hygiene Practices in Pig Farms** *Julia Gabrielle Jerab, Evelien Biebaut, Ilias Chantziaras, Filip van Immerseel, Jeroen Dewulf*
14:55-14:58	18AE1-03-BPD0143 **Successful *Brachyspira Hyodysenteriae* Eradication Through a Combined Approach of a Zinc Chelate Treatment and Adapted Management Measures** *Frédéric ACJ Vangroenweghe*	18AE2-03-ASF0432 **Evaluation of Safety, Immunogenicity, and Protective Efficacy of an Orally Administered African Swine Fever Vaccine Candidate ASF-G-Δ177IΔLVR** *Yeonji Kim, Wonjun Kim, Sun A Choi, Su Jin Lee, Seong Cheol Moon, Keun Seung Ahn, Xinghua Zheng, Se Young Lee, Yongwoo Shin, Jung Hyang Sur, Weonhwa Jheong*	18AE3-03-VVD0964 **Detection, Isolation and Determination of Genetic Characteristics of Pig Circovirus Type 2 From Pigs Associated with Debilitating Syndrome in Vietnam** *Tu Manh Do*	18AE4-03-PFP0169 **Effectiveness of the Biocheck.Ugent Tool in Monitoring and Improving Biosecurity Performance in Pig Production** *Jeroen Dewulf, Evelien Biebaut, Nele Caekebeke*

Exhibition and E-poster Displays

14:59:15:02	18AE1-04-BPD0384 **Efficacy of Whole-Herd Oral Vaccination in Controlling *Lawsonia Intracellularis* in a Previously Infected Sow Herd: A Thai Field Study** *Alongkot Boonsoongnern, Prapassorn Boonsoongnern, Narut Thanantong, Yonlayong Woonwoong, Manakorn Sukmak, Arisara Sirisophon, Nontaprecha Bundee, Pichai Jirawattanapong*	18AE2-04-ASF0782 **Possibilities for the Reduction of African Swine Fever Virus in Feed Through Bioactive Plant Substances** *Chotima Poompramun, Elisabeth Holl, Van Phan Le*	18AE3-04-VVD0975 **Global Spatiotemporal and Genetic Distribution of Porcine Reproductive and Respiratory Syndrome Virus Type 2** *Dung Tran Cao*	18AE4-04-PFP0435 **Risk Value Chain Assessment of Swill Feeding and African Swine Fever Transmission in China** *Shubo Li, Wentao Li*	**Exhibition and E-poster Displays**
15:03-15:06	18AE1-05-BPD0147 **Vaccination With a Live Avirulent *E. Coli* Vaccine Resulted in Improved Production Performance Combined with a Significant Reduction in Antimicrobial Use** *Frédéric ACJ Vangroenweghe, Thomas Matthijs, Marnix Sinnaeve*	18AE2-05-ASF0805 **Surveillance and Biosecurity Measures for Maintening an ASF-Free Breeding Farm in China** *Julie Hamon, Estelle Vanbergue, Arnaud Hercé, Arnaud Buchet, Charlie Cador, Trang Thi Kieu Phung*	18AE3-05-VVD0983 **T Cell Epitope Comparison Score (EPICC) for Porcine Circovirus Type 2 Sequences from China, 2016 to 2025** *Jose Angulo, Deniss Foss, Qing Lan Wei, Kewen Wang, ChoewKong Mah, Alvaro Aldaz*	18AE4-05-PFP0902 **Evaluation of the Efficacy of a Herbal Extract Spray (Herbband) on Postoperative Wound Healing in Pigs** *Narut Thanantong, Alongkot Boonsoongern, Pichai Jirawattanapong, Panida Tippitak, Settasart sonna, Yonlayong Woonwong*	
15:07-15:10	18AE1-06-BPD0315 **Preventive Vaccination for PWD Due To *E. Coli* F4 Optimizes Production with a Reduction of Mortality and Antimicrobial Use During the Post-Weaning Period** *Frédéric ACJ Vangroenweghe, Izzy Durrant, Gillian Bryson, Thomas Iveson*	18AE2-06-ASF0822 **Pathological Study of The First Outbreak with African Swine Fever Virus in Taiwan, 2025** *Fang-Yu Hsu, Yen-Wen Chen, Kuo-Jung Tsai, Jen-Chieh Chang, Ming-Chung Deng, Chia-Huei Yang, I-Hsuan Huang, Yi-Chu Chiu, Nien-Nong Lin, Li-Hwa Du, Yu-Liang Huang*	18AE3-06-VVD1007 **Rapid and Extraction-Free Detection of African Swine Fever Virus Using a Lamp Assay 1** *Tu Be Thi Nguyen, Y Nhu Thi Nguyen, Duy Tien Do, Quoc Bao Nguyen*	18AE4-06-PFP0716 **Visitor and Personnel Downtime Restrictions as a Biosecurity Measure in Pig Production: A Review** *Julia Gabrielle Jerab, Evelien Biebaut, Anna Catharina Berge, Ilias Chantziaras, Jeroen Dewulf*	
15:11-15:14	18AE1-07-BPD0466 **Using Gastrointestinal Fluids from Weaned Piglets to Assess the Antibacterial Activity of Glycerides of Lauric Acid Against *Streptococcus Suis*** *Olga Lemâle, Tom Meyns, Amine Mellouk, Nuria Vieco-Saiz, Claire Xu, Jessika Consuegra*	18AE2-07-ASF0921 **Development of an Indirect ELISA for the Detection of Antibodies Against the African Swine Fever Virus Using Three Recombinant P30, P54, and P72 Antigens** *Orawan Boodde, Wilairat Chumsing, Pattra MoonJit, Visanu Boonyawiwat, Alongkot Boonsoongnern, Pichai Jirawattanapong, Yonlayong Woonwong, Manakorn Sukmak, Worawidh Wajjwalku*	18AE3-07-VVD0737 **Genetic Diversity Depending on PRRSV Infection Status in Pig Herds in Vietnam from 2023 to 2025** *Hai Ngoc Nguyen*	18AE4-07-VVD0681 **Integrating Algae Beta Glucan with PRRS Vaccination a Strategy for Enhanced Survival in Nursery Pigs** *Wei-Ting Lin, Chao Nan Lin, Vannie Wan, Apichaya Taechavasonyoo, Gurugirijha Rathnasamy, Suart Court*	
15:15-15:18	18AE1-08-BPD0168 **Effect of Yeast Beta-Glucans in Mitigating the Negative Impact of *Lawsonia Interacellularis* in Experimentally Challenged Pigs or Pigs Exposed to Natural Infection** *Tadele Kiros, Olivier Merdy2, Julie Schulthess*	18AE2-08-ASF0945 **Evaluation of Prosidium: A Novel Peroxypropionic Acid-Based Solution for the Mitigation of African Swine Fever Virus (ASFv) in Feed** *Agnes Thng, Grant Chuan Hao Tan, Tobey Song, Jatuporn Salaklang, Kin Ken Chew, Yee Ting Wong, Hari Chirakkal*	18AE3-08-VVD0436 **Field Evaluation of a Combined PRRSV, PCV2 and Mycoplasma Hyopneumoniae Vaccine (3Flex) in Thai Swine Production** *Nontaprecha Bundee, Termsitthi Paphavasit, Kanokwan Samatiwat, Nathaya Young, Juver Membrebe, Carmen Alonso*	18AE4-08-BPD0900 **Molecular Epidemiology of Streptococcus Suis in Belgian and Dutch Pig Farms** *Andre Pegoraro Poor, Bruno Bracco Donatelli Muro, Lieselot Deleye, János Molnár, Maykin Englebienne, Maarten de Gussem*	

15:19-15:22	18AE1-09-BPD0507 **Prevalence of *Lawsonia Intracellularis* in Vietnamese Swine Farms and a Counteractive Dietary Intervention with Essential Oils** *Anawach Phuengkasem, Jittra Jinanan, Supranee Ruenkoed, Anh Phong Van Nguyen, Dat Thanh Pham, Marko Vasiljević, Tobias Steiner, Duy Tien Do, Panagiotis Tassis*	18AE2-09-ASF0974 **Preliminary Evaluation of the Safety and Immunogenicity of AVAC ASF LIVE Vaccine in Breeding Pigs** *Diep Van Nguyen, Ngoc Thi Nguyen, Duc Van Nguyen, Dang Xuan Vu, Tiep Ngoc Tran, Tham Thi Bui, Linh Thi Vu, Tue Phuc Do, Doanh Ngoc Pham*	18AE3-09-VVD0430 **Conformational Epitope Mapping of the E2 Glycoprotein in Classical Swine Fever Virus, Bovine Viral Diarrhea Virus, and Border Disease Virus** *Xin-Hui Huang, Helen Crooke, Denise Meyer, Yu-Liang Huang, Chun-Hsien Li, Ngoc Ha Phuong Nguyen, Chia-Yi Chang*	18AE4-09-BPD0386 **Phylogenetic Analysis of The Transferrin Binding Protein B of Glaesserella Parasuis in Taiwan** *Lo Jung Chen, Hui Wen Chang*	**Exhibition and E-poster Displays**
15:23-15:26	18AE1-10-BPD0544 **Organotypic 3D Tracheal Model Resembles Non-Pathogenic Responses to Mycoplasma Flocculare and *Mycoplasma Hyopneumoniae* Strain J** *Ana Fiorella Castillo-Espinoza, Rahul Kumar Nelli, Juan Carlos Mora-Díaz, Rolf Rauh, Bala Mounika Reddi, Apoorva Saxena, Ning-Chieh Twu, Calvin C. Ko, Rachel J. Derscheid, Luis Gabriel Giménez-Lirola*	18AE2-10-ASF0447 **Diagnosis and Prevention of an African Swine Fever Gene-Deleted Strain Outbreak** *Zhilai Lai, Jingjing Ma, Junwei Liu, Shuming Tan, Xiangming Han, Dahao Sun, Qinbing Sun, Jinhua Pan, Shuaihao Wu, Jiyu Jia, Junfeng Gao*	18AE3-10-VVD0806 **Bridging Continents: A Comparative Genomic Evolution of the African Swine Fever Virus Genotype II Between Bulgaria and Vietnam** *Miroslava Valerieva Zdravkova, Desislava Ivanova*	18AE4-10-BPD0457 **Temporal Evaluation of Halquinol Susceptibility in Swine Enteric Pathogens in Thailand, 2019-2024** *Yonlayong Woonwong, Alongkot Boonsoongern, Pichai Jirawattanapong, Manakorn Sukmak, Somyod Kankuntod, Suksan Chumsing, Monticha Suwunwong, Narut Thanantong, Wichaya Dee-ampai, Apichaya Ratanamongkolmas*	
		Oral presentation 14.2	**Oral presentation 15.2**	**Oral presentation 16.2**	
	Chairs: **Prof. Hanchun Yang** **Dr. Hongyao Lin**	**Chairs:** **Assoc. Prof. Do Tien Duy** **Dr. Aruna Ambagala**	**Chairs:** **Dr. Pat Kirwan** **Dr. Francois Van Niekerk**	**Chairs:** **Prof. Nguyen Trong Ngu** **Assoc. Prof. Duong Thanh Hai**	
15:30-15:45	15:30-16:00 Keynote lecture **Mapping Out One Health Initiatives in Southeast Asia** **Dr. Flavie Goutard** *French Agricultural Research Centre for International Development, France*	ASF 5 (OR-0361) **Safety Concerns and Recombination Risks Associated with Genotype—Unmatched Live Attenuated African Swine Fever Vaccines** *Tomoya Kitamura, Kentaro Masujin, Mitsutaka Ikezawa, Takehiro Kokuho*	AIV 2.5 (OR-0597) **In Vitro Antigenicity Profiling Predicts Broad In Vivo Protection Induced by SAFESUI Glasser One, The Fisrt Single-Dose Inactivated Glaesserella parasuis Vaccine** *Rafael Frandoloso, João Antônio Guizzo, Heni Falcão da Costa, Flávio Hirose, Ferdinando Nielsen de Almeida, Igor Renan Honorato Gatto*	PFP 5 (OR-0976) **Colostrum Composition in Relation to Farrowing Dynamics and Reproductive Performance of Sows** *Laura Jahn, Lea Käser, Rupert Bruckmaier, Alexander Grahofer*	
15:45-16:00		ASF 6 (OR-0440) **Subtle Genetic Shifts of African Swine Fever Virus Among Vietnamese Domestic Swine Following Live-Attenuated Vaccines Commercialization** *Thanh Che Nguyen, Phakawat Tantitaveewattana, Nakarin Pamornchainavakul, Hai Ngoc Nguyen, Duy Tien Do, Roongtham Kedkovid, Roongroje Thanawongnuwech*	AIV 2.6 (OR-0713) **Development and Evaluation of Two Nanoparticle Vaccines Against *Streptococcus suis*** *Huaixia Li, Yongqing Zhang, Huixia Zhan, Tingting Feng, Xiao Feng, Zijian Zou, Rui Zhou, Qi Huang*	PFP 6 (OR-0383) **Improving Piglet Weaning Outcomes Through Precision Creep-Feeding Management** *Alongkot Boonsoongnern, Prapassorn Boonsoongnern, Pichai Jirawattanapong, Narut Thanantong, Yonlayong Woonwoong*	

16:00-16:15	**Oral presentation 13.2** EDS 5 (OR-0076) **Effect of Repeated Sampling on Time-To-Detection in Active Participatory Surveillance for Transboundary Pathogens** *Berenice Munguia-Ramirez, Paul Morris, Giovani Trevisan, Gustavo Silva, Danyang Zhang, Chong Wang, Rodger Main, Jeffrey Zimmerman*	ASF 7 (OR-0431) **African Swine Fever (ASF) Control and Repopulation Strategies in Malaysia: Effectiveness of Cleaning and Disinfection Protocols** *Shi Ling Soh, Michelle Wai Cheng Fong, Peck Toung Ooi*	AIV 2.7 (OR-0886) **Evaluation of Streptococcus suis IgM Protease as A Cross Protective Vaccine Antigen: Distribution, Genotyping and Efficacy in Swine Challenge Models** *Ruud Segers, Ries Grommen, Sasha Badbanchi, Thea van Kasteren-Westerneng, Luis Garcia-Morales, Sjors van der Lans, Ton Jacobs*	PFP 7 (OR-0916) **Knowledge, Attitudes, and Practices Toward Transboundary Animal and Emerging Zoonotic Diseases Among Pig Farmers in Northern Vietnam** *Nam Hung Luong, Hien Thi Thu Nguyen, Hung Quoc Nguyen, Son Danh Tran, Sinh Xuan Dang, Tung Duy Dao, Vuong Nghia Bui, Hu Suk Lee, Hung Viet Nguyen*	Exhibition and E-poster Displays
16:15-16:30	EDS 6 (OR-0293) **A Commercial Japanese Encephalitis Pig Vaccine Protects Against the Australian Genotype IV Virus** *Caitlin O'Brien, Willy Suen, Lenny Izzard, Kelly Davis, Grace Taylor, Antonio Rubbo, Elise Browne, Stacey E Lynch, David T Williams*	ASF 8 (OR-0539) **Evolution and Adaptation of Biosecurity Measures for Large-Scale Swine Farms Under African Swine Fever in China** *Zhen Yang, Wenzhe Wang, Kangning Zhao*	AIV 2.8 (OR-0033) **An Emerging Tool to Estimate Immunogenicity: T Cell Epitope Content Comparison of a Porcine Reproductive and Respiratory Syndrome Virus Modified Live Vaccine to Four Field Strains** *James Mark Hammer*	PFP 8 (OR-0756) **Effect of an activated zinc oxide to replace pharmacological zinc oxide in piglets to control post-weaning diarrhea** *Charlotte Maria Elisabeth Heyer, Isabela Eulália, Luiz Vitagliano, Odair Pavan, Lucio Araujo*	
16:45-18:00	**Satellite Symposium 4** **CTC-Bio** Satellite lecture 13 **Strong Protective Efficacy and Safety of a Live-Attenuated ASF Vaccine (PRO-VAC) in Domestic and International Trials Involving Growing Pigs and Pregnant Sows** **Prof. Jung Hyang Sur** *Director of R &D, Komipharm International Co., Ltd.*	**BAF** Satellite lecture 14 **Smart Technology Solutions for African Swine Fever (ASF) Control and Prevention** **Nguyen Van Minh** *Deputy General Director BAF*			
18:30-22:00	**Gala Dinner**				

Day 4 - June 19, 2026		
Time/Venue	**Congress Main Hall - Grand Skylar**	Exhibition and E-poster Displays
08:30-09:15	PLENARY SESSION 2 Chairs: Prof. Roongroje Thanawongnuwech Prof. Cesar Corzo	
	Keynote lecture **Active Surveillance Based on Environmental Sampling: Opportunities and Challenges** **Prof. Jeffrey James Zimmerman** *Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, USA*	
09:15-10:00	**Keynote lecture** **Understanding the Epidemiology of Swine Diseases Through Voluntary Programs** **Prof. Cesar Corzo** *Department of Veterinary Population Medicine (VPM), College of Veterinary Medicine, University of Minnesota, USA*	
10:00-10:30	**Coffee Break and E-Poster Displays**	
10:30-11:30	**Closing Ceremony**	
	Recap video clip	
	Awards [Oral/Poster + Animal Science]	
	Lucky Draws	
	IPVS2028 Promotion: IPVS2028 Promotion: IPVS2028 Bid Presentation by Spain at the General Assembly	
	Closing speech	

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PCV2 whole herd approach: the foundation of a successful production
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PRRSV: A Central Player & Its Interactions With Other Diseases
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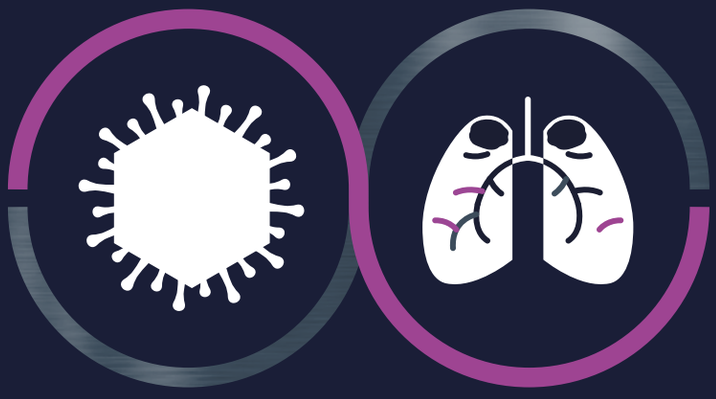
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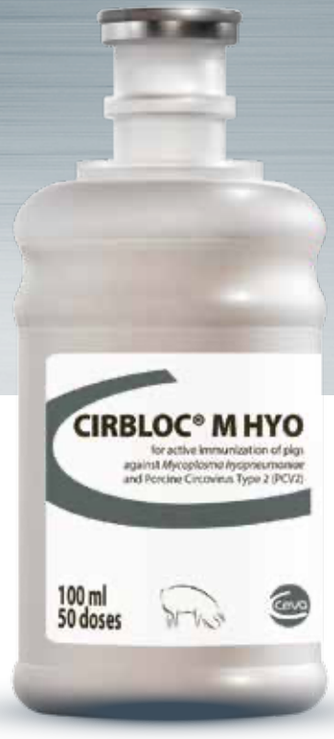


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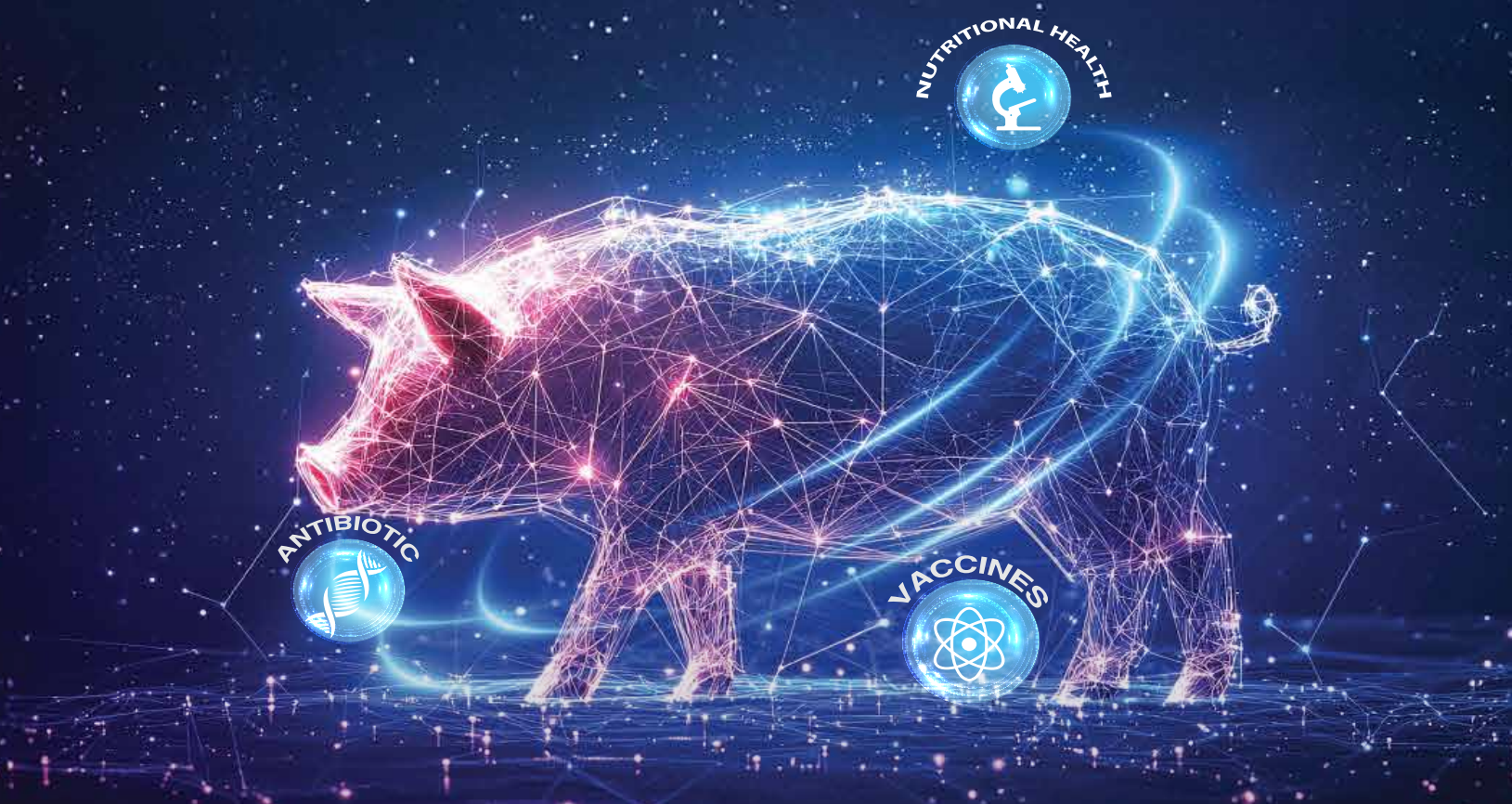
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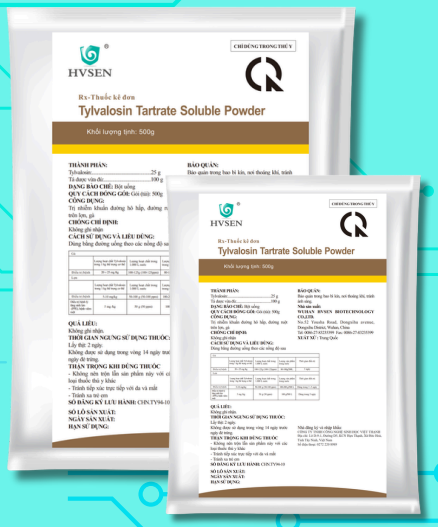








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