# 2025 Allen D. Leman Swine Conference Research Abstracts and Proceedings

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## Table of Contents – Proceedings

# Methionine hydroxy analogue bis-chelated Zn, Cu and Mn supplementation reduces inflammation in E. coli F18 challenged pigs and enhances feed efficiency under commercial conditions compared with inorganic trace mineral sources.

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## Introduction

Trace minerals are essential for numerous physiological functions, including immune development and modulation, and intestinal integrity. Enhancing nutrient delivery through highly-available, bis-chelated mineral sources may support better health and performance outcomes. These studies evaluated the effects of methionine hydroxy analogue bis-chelated (MHAC) Zn, Cu, and Mn compared with inorganic forms in F18 E. coli challenged pigs and pigs in commercial production conditions.

## Materials and Methods

Exp. 1: Fifty-four barrows (initial BW=5.30 kg) were allocated to three treatments (n=6 pens/treatment): (1) pharmacological Zn oxide with Cu and Mn in sulfate form (P-ZnO; 1,800, 125, and 40 mg/kg for Zn, Cu and Mn, respectively); (2) MHAC; and (3) sulfate trace minerals (SULF). The MHAC and SULF treatments contained Zn, Cu, and Mn at 100, 125, and 40 mg/kg, respectively. After a 9-day acclimation period, E. coli F18 (~$1.0 \times 10^9$ CFU/pig) was orally inoculated. On d -13 post-inoculation, two pigs/pen (n=12) were euthanized for jejunal tissue sampling.

Exp. 2: A total of 364 pigs (initial BW=5.76 kg) were allotted to 28 pens (n=14) comparing MHAC and SULF for 40 days in a commercial facility.

Exp. 3: A total of 1,152 pigs (initial BW=5.59 kg) were assigned to 48 pens (n=24) comparing MHAC with modified oxides (MOXI: particle-modified Zn, cuprous oxide, and manganese oxide) for 35 days in a commercial facility.

In Exp. 2 and Exp. 3, Zn, Cu, and Mn were supplemented at 100, 130, and 40 mg/kg from days 0–14, and 100, 80, and 40 mg/kg thereafter. Data were analyzed using PROC MIXED (SAS v9.4).

## Results

In Exp. 1, pigs fed MHAC had lower jejunal mucosal expression of proinflammatory cytokines compared with SULF (NFKB-P50: 0.31 vs 1.31, P=0.067; TNF-α: 0.21 vs 5.04, P=0.012; IL-8: 0.54 vs 1.61, P=0.069). The P-ZnO group was intermediate (1.16, 1.12, and 0.93, respectively). No treatment differences were observed in claudin and zona occludens-1 mRNA expression . P-ZnO had greater villus height compared with SULF (437 vs 336µm; P=0.007). Also, MHAC-fed pigs tended to have greater villus height than SULF (394 vs 336 µm; P=0.107). No difference in villus height between P-ZnO and MHAC was observed. There were no differences among treatments in crypt depth. Villus height: crypt depth ratio tended to be higher for P-ZnO versus SULF (2.25 vs 1.90; P=0.072), with MHAC intermediate (2.10).

In Exp. 2, MHAC improved feed conversion ratio (FCR) 5.2 points over 40 days compared with SULF (1.422 vs 1.474; P=0.068). For Exp. 3, MHAC-pigs had 3.5 points lower FCR (1.376 vs 1.411; P=0.020) compared with pigs fed MOXI.

Conclusions

Supplementation with MHAC bis-chelated minerals reduced inflammatory responses following E. coli F18 challenge and improved villus morphology. MHAC improved feed efficiency compared with sulfate and modified oxide sources under commercial conditions, demonstrating the importance of MHAC bis-chelated minerals as a nutritional strategy for enhancing overall pig health and performance.

**Herd level risk factors associated with influenza A genetic diversity in piglets at weaning**

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Introduction

Influenza A virus (IAV) is a major pathogen in swine herds causing significant economic losses to producers. Emergence of new influenza viruses is common in part due to the segmented nature of the virus genome, the co-circulation of distinct viral strains and the frequent introductions of novel strains particularly those of human origin which can result in new reassortant viruses. Although IAV diversity has been well documented, there is limited information on how farm management practices influence the diversity of IAV. In this study, we evaluated the association between herd-level management practices and the genetic diversity of IAV in weaning piglets.

Methods

We used a whole-genome sequence approach on IAV-positive nasal swabs collected from weaning piglets obtained from 14 Midwestern swine farms (Nirmala et al., 2021). Each gene segment of the influenza virus was classified based on its origin (or lineage). A genotype was defined as the constellation of distinct lineages detected across the whole IAV genome. If a segment could not be sequenced, a genotype included the "not sequenced (N/S)" denomination for that segment. To quantify diversity of IAV at the herd level we used the Shannon diversity index which takes into consideration the number of unique genotypes (richness) and the evenness of the genotypes. Information on production management practices was obtained for each herd using a structured survey and included information on IAV vaccination, farm ventilation, gilt origin, gilt housing, porcine reproductive and respiratory syndrome (PRRS) status, and herd size. A linear regression analysis was carried out with the Shannon diversity index as outcome variable, and management practices obtained from the survey as predictors. Model fit was assessed using adjusted $R^2$, and the contribution of each variable was evaluated using ANOVA.

Results

The Shannon diversity index varied across herds, with herds exhibiting both higher genotype richness (having more genotypes) and higher evenness (genotypes being more evenly distributed). The final regression model showed a strong association between genotype diversity and specific management practices (adjusted $R^2 = 0.7377$). Timing of vaccination was the most influential factor ($F = 67.7$, $p < 0.001$) with herds using mass or pre-farrow vaccination having significantly lower genotype diversity compared to farms that did not vaccinate. Gilt housing also affects genotype diversity with gilts using all-in/all-out procedures at the room or barn level also having reduced diversity compared to continuous flow. Herds with mechanical ventilation ($F = 6.4$, $p = 0.012$) and those sourcing gilts from within the same production system ($F = 23.4$, $p < 0.001$) had lower diversity than herds with mixed ventilation or external gilt sources. In contrast, recent PRRS virus introduction ($F = 69.8$, $p < 0.001$), and larger herd size ($F = 7.7$, $p = 0.006$) were associated with increased IAV diversity.

Conclusions

This study provides field-based evidence that herd-level management practices can influence the genetic diversity of IAV in pig populations. Practices such as vaccination, gilt management and co-infection with other diseases appear to shape the evolutionary landscape of IAV by modulating opportunities for co-infection and reassortment. Integrating IAV surveillance with specific management practices may be essential to design effective IAV control strategies in pigs.

**The Effect of HumiSynTM IFC4 in Nursery Pigs on Growth Performance and Mortality in PRRSv Challenged Pigs**

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The objective of this study was to evaluate the effects of a proprietary blend of a humic acid substance and short chain fatty acids (HumiSyn™ IFC4) supplemented through the feed on growth performance and mortality in nursery pigs. A total of 840 pigs (PIC 800 × Line 3; ~21 days of age; ~12.5 lb BW) were enrolled in a 42-day randomized complete block design trial conducted at a commercial research facility with pen as the experimental unit. Blocks were randomly allotted by weight and sex. Pigs were allocated to one of two treatments, each consisting of 20 replicate pens with 21 mixed-sex pigs per pen. The HumiSyn™ IFC4 group (HUM) received the additive at 4 lb/ton in Phase 1 (days 0–9) and 2 lb/ton in Phases 2 and 3 (days 9-20 and 20-42, respectively), while the control group (CON) received none. All pigs were fed a standard three-phase nursery diet program ad libitum that was formulated to meet or exceed requirements as recommended by NRC (2012). Pigs tested positive for PRRSv during phases 2 and 3.

Pen weights and feed disappearance were recorded by phases to calculate performance metrics including average daily gain (ADG), average daily feed intake (ADFI), and feed/gain (F/G). Mortality and injectable treatment rates were also monitored. Statistical analysis was conducted using a linear mixed model R v 4.3.2 with treatment as a fixed effect and block as a random effect.

Supplementation with HumiSyn™ IFC4 significantly improved growth performance during early nursery phases. In Phase 1, HUM had greater ADG (0.462 vs. 0.425 lb; P = 0.02) and ADFI (0.413 vs. 0.393 lb; P = 0.04), and tended to have improved feed efficiency (F/G = 0.897 vs. 0.934; P = 0.07) compared to CON. In Phase 2, HUM improved ADG (0.859 vs. 0.784 lb; P = 0.001), ADFI (1.044 vs. 0.994 lb; P = 0.03), and F/G (1.216 vs. 1.270; P = 0.001). No significant differences were observed in Phase 3. Over the entire 42-day study period, HUM improved ADG (1.065 vs. 1.033 lb; P = 0.05) and F/G (1.297 vs. 1.310; P = 0.07), though ADFI was not significantly different. Pen gain and body weight transferred per pig placed were significantly greater for HUM (928.8 vs. 888.9 lb; P = 0.02 and 56.6 vs. 54.7 lb; P = 0.02, respectively).

Total mortality (1.0% vs. 2.6%; P = 0.04) and the percentage of pigs requiring treatment (4.3% vs. 8.6%; P = 0.05) was significantly lower in HUM compared to CON. While this is a low mortality by industry standards, even modest reductions in mortality and treatments can significantly improve producers' profitability.

This study demonstrates that supplementing pigs with HumiSyn™ IFC4 in the feed during the nursery program can significantly reduce mortality and improve growth performance, even in the presence of a PRRSv challenge. These results are similar to prior studies on humic substance1,2.

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**Improving piglet production by optimizing phosphorus and calcium absorption in sows and piglets**

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Phosphorus (P) is a key metabolite for the productivity of sows, piglets and hogs. Its cost as a nutrient has been increasing, mostly due to the new demand for this mineral for the batteries of electric vehicles. A novelty molecule has been developed, a polyol of a long chain fatty acid, which optimizes the absorption of phosphorus and calcium (Ca). The application of the molecule, as well as its formulation matrix were validated for sows and piglets. Sows (51) were distributed into three groups, a positive control group (PC), with the recommended levels of Av.P and Ca, using DCP; a negative control group (NC), with 0.08% less Av.P and 0.08% Ca in the diet, and a third group (GM), which received the same diet as the negative control group, but enriched with the molecule (400g/ton GrowMater©). Treatments were maintained from the 76th day of gestation until weaning (gestation and lactation diets), at 24 days of lactation. No differences in performance were seen in the sows, regarding body weight and score. Feed consumption was slightly higher for the treated sows. NC sows weaned significantly lighter piglets (6.364kg), whereas the treated sows weaned significantly heavier piglets (7.100kg), even higher than PC sows (6.433kg). After weaning, 540 piglets were divided into six groups, according to the treatment of the dam and with or without the molecule, 1kg/ton on top. Four phases were formulated, all with the recommended level of Av.P and Ca. Overall, piglets weaned by the NC mothers performed worse than the other groups. The best results were seen in the treated group of piglets, weaned by the GM mothers. Weight at the end of the first phase was highest for the treated pigs weaned by the GM mothers, at 7.849kg, followed by the untreated piglets of GM mothers, 7.592kg. The lightest piglets were those from the NC mothers, at 7.257kg (treated) and 7.007kg (untreated piglets). Those from the PC mothers had intermediate results, at 7.570kg for treated and 7.506 kg for untreated piglets. At the end of the post-weaning period, feeding phase 4, although there were no significant differences, piglets weaned by GM females were the heaviest, at 20.865 kg and 20.742 kg for treated and untreated piglets respectively, whereas the lightest were those from untreated from NC mothers, 19.480 kg. It can be concluded that the usage of the molecule in the diet of breeding females allows the reduction of 0.08% of Av.P and 0.08% Ca, with no change in the performance of the females, but with an increased performance of the piglets, significantly heavier at weaning. Treating the females also positively affected the piglets after weaning, allowing a better performance than those weaned by untreated sows. Finally, piglets receiving 1kg of the product per ton, on top, reached the highest weight at the end of the post-weaning period, nearly 1 kg more than the control group, with an expressive return over the cost of the inclusion of the product.

**Novelty molecule optimizes absorption and utilization of phosphorus and calcium in growing and finishing pigs**

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Phosphorus (P) is a key metabolite for the productivity of swine. The amount of available P can determine performance, after the initial feeding phases. Its cost has been increasing, mostly due to the new industrial demands. A novelty molecule has been developed, a polyol of a long chain fatty acid, which optimizes the absorption of phosphorus and calcium (Ca). The effects of the molecule, as well as its formulation matrix, were validated for growing and finishing swine. In the first trial, four different diets were formulated in order to create a scale of available P, at 0.28%, 0.32%, 0.36% and 0.40% Av.P.. A fifth diet was also produced, with 0.28% Av.P., to which the molecule was added, at the rate of 1 kg per ton (GrowPork©). Each diet was a treatment, with 5 pens of 10 females and 5 pens of 10 castrate males each, totaling 500 animals. The performance (average weight gain ADG, body weight BW) of the treated animals (0.28% Pd + polyol) (87,02 kg BW, 1,039 g/d ADG) was similar to that of the animals with the highest level of Pd (0.40%) (88.58 kg BW, 1,065 g/d ADG), and significantly lower than those with 0.36% Pd (90.52kg BW, 1,106 g/d ADG), the optimal level. It is known that excessive amounts of Av.P will reduce the performance of growing pigs (Arouca et al. 2010). In the finishing phase, considering this result, the inclusion of the emulsifier was reduced to 250g/ton. Treated animals had a final performance (139,78 kg BW) similar to those with the optimal level of 0.36% (140,03 kg BW), recovering from the loss in the growth phase, with a significantly better average daily weight gain (1,139 g/d ADG) than the other treatments (1,110 g/d ADG). In order to validate a matrix of Av.P and Ca, a second round was performed. Growing pigs (144) were distributed among three treatments. A control group, with 0.36% Av.P in the diet; one treated group, with 0.28% Av.P in the diet, 500 g per ton of the product in the growing phase and 250 g in the finishing phase; and a second treated group, with same P levels, but with 400 g of the product in both phases. Calcium was also reduced by 0.08% in the treated diets. At slaughter, metacarpi were collected, and strength and ash content of the bones were measured. The performance of all three groups was the same, with no significant differences in any of the parameters (on average ADG 1,045 g/d, BW 131,95 kg, FCR 2.37). There was also no significant difference in the resistance of the bones, but the control group showed a significantly lower level (62,32%) of bone ashes versus the two treated diets (65.06%, 64.25%). It can be concluded that the use of this molecule positively affects the absorption and utilization of Ca and P in growing and finishing swine and allows a reduction of 0.08% of Av.P and Ca, contributing for the economic results of the activity as well as its sustainability.

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**Participatory Network Modeling of Live Pig and Pork Product Trade in the Caribbean**

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African swine fever (ASF) introduction is a major, persistent threat to the US and Caribbean, largely from ongoing outbreaks in the Dominican Republic (DR) and Haiti. Because trade and movement data are limited and affected by regional geopolitical and administrative complexities, our understanding of ASF transmission risk in the Caribbean has significant gaps. In participatory epidemiology, stakeholders are directly involved in understanding and solving health issues that impact them. These methods are highly useful for identifying and characterizing disease risks, especially in settings where data are limited. Here, we aimed to characterize inter-island connectivity of live pig and pork product trade in the Caribbean using participatory modeling and social network analysis, ultimately to understand the potential risk of ASF spread regionally if an introduction were to occur outside of Hispaniola. Using import and export trade data from United Nations (UN) Comtrade from 2022-2024, two separate preliminary directed networks were created for movements of live pigs and pork products among 30 Caribbean countries and territories. Countries and territories served as nodes, and edges represented the directional flow of live pigs or pork. The networks were printed onto large-scale maps for the participatory modeling exercise. Participatory modeling was then conducted with 15 veterinary and agricultural officers from 10 Caribbean countries and territories, including the DR, as part of a broader workshop on ASF preparedness held at Ross University School of Veterinary Medicine, St. Kitts, in June 2025. Participants were divided into two groups and asked to annotate the network maps using their knowledge of formal and informal trade routes. Moderators also took notes on the discussion to capture additional context for the reported routes. These participatory inputs were merged with existing data to generate updated networks. Network-level and node-level properties were quantified, such as degree, betweenness, closeness, and community structure. Overall, the participants added many missing informal connections, which are otherwise not formally reported but are highly important for disease spread. The pork trade network was substantially larger and more interconnected than the live pig movement network. The DR, Trinidad and Tobago, Jamaica, and Barbados were highly central within the pork trade network with high out-degree, betweenness, and eigenvector centrality. In contrast, the live pig network had fewer connections, with many countries with low degree of 1 or 2, reflecting the limited movement of live pigs in the Caribbean. The pork trade network also exhibited stronger community structure, with four distinct communities approximating densely connected trading blocs. While these results may be limited because participants from all Caribbean countries and territories were not present, they provide detailed and important

information about the potential spread of ASF through the movements of live pigs and pork, which is otherwise not available. In particular, ongoing formal and informal pork trade from the DR was identified. This work demonstrates the strength of utilizing participatory methods and local expert input when policy decisions must be made regardless of data scarcity, and ultimately supports ASF preparedness within the region and for the US.

**PRRSV-associated abortion risk by parity and lineage-specific exposure history on sow farms using live virus inoculation**

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For the past ~30 years, PRRSV control has relied, in part, on immunological interventions aimed at inducing protective immunity. Several methods are in use today, modified live vaccines (MLVs), live virus inoculation (LVI), and inactivated vaccines (e.g. subunit or whole virus). LVI has been favored by some practitioners as it uses a farm-resident virus to generate "homologous" immunity within their herd, assuming that this offers better protection than the heterologous protection generated using MLVs. In this study, we systematically investigated PRRSV outbreak dynamics in four sow farms that use LVI as their primary PRRSV immunological control strategy. During clinical outbreaks of PRRSV-2 on the farms, we assessed the impact of exposure history on the odds of aborting for different parity groups to determine which factors of exposure—such as cumulative exposure or virus homology with previous exposures—impact the odds of aborting.

A US swine production management company that utilized LVI for PRRSV control shared data from sow farms under management from 2018 through 2024. Production data, including abortion counts with associated parity information, ORF5 sequences from PRRSV outbreaks, LVI inoculum sequences and administration schedule, and herd inventory with parity structure, were shared. Weekly abortion counts were used to identify clinical PRRSV outbreaks though applying exponentially weighted moving average (EWMA) analysis. We tabulated the number of outbreaks that were attributed to one of three outbreak types based on the causative virus : 1) a new variant and sub-lineage, 2) a new variant from a farm-resident sub-lineage-i.e., gilts/sows had been previously exposed to a virus of the same sub-lineage, or 3) a farm-resident variant (suggestive of a re-break). From there the abortion data were stratified by parity group: parity 0 (gilts), parity 1-2, parity 3-4, and parity 5+.

For each abortion outbreak on each farm, the odds of abortion were modeled using a mixed-effects logistic regression model. The number of sows aborting for each age group was reported (n_abort/n_total). The fixed-effect predictors included parity group, cumulative viral exposures for that group, the ORF5 amino acid distance from current virus to that group's most recent exposure virus. The abortion outbreak category (as defined above) was also included to assess whether previous exposure history to the same variant or the same lineage reduced the outbreak's clinical impacts (as measured by abortions). To account for farm-level variability, farm was included as a random effect.

This model helps clarify how cumulative exposure, especially of higher parity sows, versus recent exposure of homologous vs non-homologous viruses in lower parity sows shape abortion risk for different parity groups on sow farms. This information will help inform future immunological intervention strategies and efforts for different age groups on sow farms.

**Assessing the role of gilt-related risk factors for PRRSV time-to-stability**

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Introduction

Porcine reproductive and respiratory syndrome (PRRS) continues to cause significant economic and pig production losses. Despite elimination efforts, PRRSV outbreaks and elimination failures continue to occur and the ability to eliminate the virus from herds has been recently perceived by veterinarians to be more challenging at times. In support of this, Linhares et al. (2022) showed that the median time-to-stability (TTS) for herds undergoing a herd-closure within the past decade was 36 weeks, approximately ten weeks longer than previously observed. Age at the time of PRRSV exposure may influence how long pigs remain infected and their ability to transmit the virus. Previous research has shown that younger pigs exhibit longer periods of viremia and higher viral loads in pulmonary macrophages compared to older pigs. These findings have prompted questions in the field regarding the role of gilt age at introduction and exposure in the success of PRRSV elimination efforts. Therefore, objectives of this study were to evaluate the infection dynamics post-LVI of different gilt ages at introduction, and to evaluate the effect of gilt age on the probability of producing PRRSV-negative litters.

Materials and Methods

An observational study was conducted on a commercial 2,500-head category 1A PRRS infected sow farm. The enrolled farm had an on-site gilt isolation area and allowed for the entry of various aged gilts at the start of closure. Two-to six-month-old gilt cohorts were longitudinally sampled throughout the closure, starting at the initial LVI event. Oral fluids (n=4) were collected from each gilt age cohort at approximately 1, 3, 7, 11, and 16 weeks post-LVI. Tonsil-oral scrubbing (TOSc) samples were collected from 15 randomly selected gilts and longitudinally sampled at 30 and 90 days of gestation and prior to farrowing. Aggregated processing fluids were collected weekly from gilt and P2+ litters throughout the closure. Samples were tested for the presence of PRRSV genetic material via RT-PCR. Differences in time-to-PRRSV-negative post-LVI based on gilt age were evaluated using a Kaplan-Meier survival analysis and Cox Proportional Hazard Regression model. Descriptive analysis was conducted from the TOSc and processing fluid data to assess the effect of gilt age on producing PRRSV-negative litter.

Results and Conclusions

A significant difference in the time it took different gilt age groups to test negative for PRRSV post-LVI was observed ($p = 0.035$). Notably, 4-month-old gilts were more likely to clear the virus sooner than 2-month-old gilts, with a hazard ratio of 7.03 ($p = 0.022$). Despite these differences in infection duration, no numerical differences were observed in the rate of PRRSV-negative litters produced across gilt age groups. These findings suggest that younger gilts may require a longer cooling-off period post-exposure but do not appear to negatively impact litter status.

In conclusion, the age of gilts at the time of PRRSV exposure influences how quickly they clear the infection, though it may not impact litter status at farrowing. Further research across multiple farms and PRRSV strains is warranted to validate and expand upon these findings.

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**Evaluation of needle teeth resection on piglet performance and piglet and sow injuries**

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Pigs are born with 8 sharp pairs of teeth – four canines and four incisors. (J.B. Brookes & I. J. Lean). These teeth are referred to as needle teeth and are commonly used to fight for teats. The fighting can cause facial scarring and injury among littermates, and damage to the sow's underline. The most common way to combat this is to clip or resect the needle teeth. The practice of clipping needle teeth can be viewed as painful and unnecessary and requires additional care by farm crews. The objective of this study was to evaluate the impacts of clipping needle teeth on pre-weaning mortality, piglet growth rates, piglet facial scaring, and sow underline lesions. Data were collected on 85 sows who were randomly assigned to treatments within parity blocks (n=42 teeth not clipped; and n=43 teeth clipped). The average parity for this trial was 3.1, ranging from 1-6. Cross fostering took place within 24 hours after birth and was performed within treatment. The number of piglets over teat count and started was not different between treatments, and on average sows were loaded to teat count with an average of 14 pigs per sow. Facial and udder lesions were scored on days seven, 14, and 21 before weaning, and conducted by designated personnel to ensure consistency. Lesion scores were classified into four categories: none, low – superficial scratches not penetrating the full derma thickness, moderate – superficial scratches with some deeper wounds, and severe – deep and large wounds or lacerations or signs of infection. Birth weights and weaning weights were collected to calculate average daily gain (ADG), and all death loss recorded. All data were analyzed using SAS (version 9.4). Piglets whose teeth were intact had heavier weaning weights ($P=0.02$), and increased ADG ($P=0.03$) compared to the piglets with teeth clipped. Regarding facial and udder lesions on day 7, there was a significant ($P<0.01$) increase in lesions from the litters with intact teeth compared to those with teeth clipped, specifically in the moderate to severe categories. On day 21 (at weaning) a similar pattern was observed for the teeth not clipped treatment with a greater amount ($P<0.05$) of piglets and sow underlines classified in the moderate to severe categories. Pre-weaning mortality averaged 17.9% for piglets with intact teeth and 15.7% for those with clipped teeth; however, this difference was not statistically significant ($P > 0.05$). Despite this, the teeth-clipped group weaned one additional pig per litter on average, a significant increase ($P < 0.05$). When evaluating specific causes of death there was a numerical increase in injury trauma and joint infection from the teeth not clipped treatment. In this trial teeth clipping resulted in decreased lesions in piglets and sow underlines, a numerical reduction in pre-wean mortality, but also decreased growth performance in piglets. These results indicate that producers may need to investigate when it is best to use the practice of teeth clipping to maintain the longevity of sow underlines and reduce facial scaring in piglets.

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**Thermal imaging technology in swine production: Guidelines for application and use**

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Background and problem

Thermal imaging is a noninvasive tool increasingly used in the swine industry to monitor animal health, welfare, and productivity. During my summer internship, I employed thermal imaging to assess colostrum intake in piglets. Results showed no significant correlation between piglet surface temperature and colostrum intake, body weight, or immunocrit levels. This experience revealed that thermal infrared imaging was less accurate than anticipated for this application. Reflecting on these findings, I recognized a gap in the literature: a lack of concise, practical resources on the effective use of thermal imaging in swine. To address this, I conducted a comprehensive literature review and developed best practice guidelines based on scientific evidence and firsthand experience. These guidelines aim to help veterinarians and researchers use thermal imaging technology more effectively in commercial swine settings.

Approach

A literature review was conducted using databases, such as PubMed and ResearchGate. The search included keywords like “thermal imaging” and “swine production.” Fifteen peer-reviewed articles were selected based on relevance, technological principles, applications, and limitations. Key findings were synthesized to develop practical recommendations for use in commercial settings.

Findings

Five critical areas were identified to improve the accuracy and consistency of thermal imaging in swine:

Equipment selection and calibration:Various thermal cameras are available, ranging from mobile device attachments (e.g., FLIR One) to high-resolution radiometric models (e.g., FLIR A320, Fluke TI32). A resolution of ≥160×120 pixels is critical, with >640×480 pixels being ideal for detecting small thermal differences. An emissive setting of 0.98 is recommended for pig skin.

Animal handling and positioning:Images should be captured when the piglet is stationary and away from heat sources. A fixed distance of 30 cm from the camera improves consistency. It is recommended to capture the images while the animal is resting to avoid temperature fluctuations caused by activity.

Targeted anatomical location:The eye and back of the ear are preferred imaging sites due to minimal hair and reduced contamination risk, offering more reliable temperature readings than the flank or abdomen.

Environmental control:Environmental conditions, such as temperature, humidity, airflow, sunlight, and nearby heat sources can affect accuracy and should be documented. Imaging should occur at consistent times, especially for longitudinal studies, to limit external variation.

Data accuracy and validation:Consistently using one anatomical site is acceptable, but multiple sites improve reliability. Cross-validating with internal temperature (e.g., rectal readings) enhances data integrity. For biosecurity, camera protection via plastic bags may be needed, but caution inferences, as it may affect thermal readings through altered heat transmission or reflection.

**NATURALLY AVIRULENT LIVE VACCINE FORMULATED WITH THE G16X STRAIN AGAINST A FIELD CHALLENGE WITH A HIGHLY PATHOGENIC PRRSV L1B (1-37-2) VARIANT IN A WEAN-TO-FINISH SITE.**

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Introduction

The objective of this study was to assess the efficacy of a naturally avirulent live vaccine (containing the G16X PRRS strain) against a field challenge with wild PRRSV on a farm located in a high-pressure infection area, in a wean-to-finish (WTF) site. The productive performance of animals vaccinated with G16X was compared with historical records of previous groups vaccinated with a commercial modified live vaccine (MLV).

Materials and Methods

The study was conducted in a PRRSV-positive WTF farm, which receives 28-day-old weaned piglets originated from a serologically and virologically PRRSV negative Site 1. Prior to this field study, the pigs used to be vaccinated with an MLV PRRS vaccine, presenting regularly clinical signs, and increased mortality between 11 to 14 weeks of age (WOA) and detrimental effects on daily weight gain (DWG) and feed conversion (FC).

8,444 piglets were vaccinated with the G16X vaccine intranasally (IN) at arrival at 4 WOA, dividing them in two groups, and housed in two different units separated by 2.7 km. Group 1 (G1) included 4,956 piglets housed in unit "A" and Group 2 (G2) included 3,488 piglets housed in unit "B". Upon arrival to site 2, prior to vaccination, quantitative PCR (qPCR) and ELISA (IDEXX PRRS X3 Ab) tests for PRRSV were performed, and twenty tagged pigs were longitudinally monitored at 6, 8, 12 and 15 WOA, by ELISA and qPCR tests. During the trial production parameters were recorded and analyzed statistically using GraphPad Prism software (version 10.4.1).

Results and Discussion

In the G16X vaccinated groups (G1 and G2), the vaccine strain replicated efficiently, as confirmed in blood samples by qPCR, and ORF5 sequencing in silico as L5A (1-6-2), matching with the vaccine virus strain.

In group G1, at 12 WOA, qPCR test detected the presence of a PRRSV genetically heterologous to the vaccine, classified as L1B (1-37-2), meaning a natural field exposure, although, no relevant clinical signs were observed in the infected animals. In the sampling carried out at 15 WOA, 95% of the pigs tested negative by qPCR, and the positive ones had low genetic loads (High CTs values) suggesting control of field infection and protection. In group G2, no natural field PRRSV challenge was detected.

In the comparison between group G1 and G2, mortality didn´t differ significantly between groups, according to the chi-square test ($\chi^2 = 1.72$, $p = 0.19$), despite the natural challenge in group G1, neither other production parameters were affected, meaning protection of the animals.

The comparison between G16X groups with five previous historical groups housed in the same facilities, that were vaccinated with a commercial PRRS MLV vaccine, results showed statistic improvements in mortality, DWG and FC in the G16X vaccinated groups, using Welch's t test.

Conclusions

The G16X vaccine protected the pigs against a field challenge with a highly virulent PRRSV strain L1B (1-37-2), and when compared with the historical MLV vaccinated groups, results showed significant lower mortality (p= 0.0437), higher productive efficiency measured by DWG (p= 0.0045) and better FC (p= 0.0372).

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**Organotypic 3D tracheal model enables earlier detection of viable Mycoplasma hyopneumoniae compared to bacterial culture: A pilot study using tracheal swabs of known status**

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Introduction

Mycoplasma hyopneumoniae (Mhp) is a slow-growing bacterium that targets porcine airway epithelial ciliated cells1. Although bacterial culture remains the reference method for determining Mhp viability, it is labor-intensive, slow, and often compromised by overgrowth of contaminated mycoplasmas2. In a previous study, we demonstrated that porcine-derived airway epithelial cells cultured in the air-liquid interface (ALI-PRECs) support Mhp infection, enabling the characterization of pathogen-induced cytopathic effect (CPE), ciliostasis, and host gene modulation3. In this pilot study, we assessed the susceptibility of the ALI-PREC model compared to conventional bacterial culture using tracheal swabs (TS) of known Mhp infectious status.

Methods

Tracheas from three-weeks-old, high-health pigs (n=3) were used to isolate PRECs. Cells were seeded onto collagen-coated transwells and differentiated under ALI conditions for 4 weeks. Differentiated ALI-PRECs were inoculated with TS from Mhp-positive and Mhp-negative pigs, as well as controls (107 CCU/mL of Mhp strain 232 and a negative TS). All inocula were tested by Mhp qPCR (Tetracore Inc.) and bacterial culture at time of inoculation. After a 2-h incubation at 37°C and 5% CO2, inocula were removed, and ALI-PRECs were monitored over 72 h post-inoculation (hpi). CPE and ciliary motility were evaluated every 24 h, and cells were analyzed by immunofluorescence (IFA) for Mhp P46 and tight junction protein ZO-1. At 72 hpi, cells and basolateral subnatants were collected for qPCR and culture.

Results. No CPE was observed in ALI-PRECs inoculated with Mhp-positive TS by 24 hpi, whereas Mhp 232-inoculated cultures showed progressive ciliary loss. qPCR detected Mhp DNA in Mhp-positive TS (Cq: 18.7) and Mhp 232 (Cq: 17.3). Viable Mhp was recovered from culture at 9 days post-inoculation (dpi) for Mhp 232 and at 18 dpi for TS samples. At 72 hpi, Cq values in ALI-PRECs inoculated with Mhp-positive TS ranged from 28.8 to 31.8; viable bacteria were recovered from 1 of 3 replicates as early as 12 dpi. Mhp P46 protein was detected in ALI-PRECs inoculated with either Mhp-positive TS or Mhp 232, and ZO-1 disruption was evident in both groups. Mhp DNA was detected in the basolateral medium in 1 of 3 Mhp-positive TS cultures. Negative controls remained negative.

Conclusions

ALI-PRECs offer a host-relevant model for evaluating Mhp viability from clinical tracheal swabs, shortening detection time compared to direct bacterial culture. These findings support its potential for diagnostic workflows and align with previous reported differences in host susceptibility to Mhp infection.

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**Deeper look into Caretaker Biosecurity**

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In recent years, the Swine Health Information Center (SHIC) has identified caretaker motivation related to compliance with biosecurity behaviors as a priority needing to be better understood. The current research was built on previous SHIC-funded study (submitted to Lemans Conference 2024, submitted for publication) that utilized a quantitative methodology to explore the motivations and barriers to caretakers consistently performing biosecurity control measures, utilizing a framework from the Theory of Planned Behavior and the Job Demands/Resources Model of Burnout. This initial study identified key drivers of motivation (Attitude was strongest, Social Norms were not significant. Additionally, that researcher initially identified the job resources which exert the greatest positive influence (Supervisor Support & Job Control) and least positive influence (Rewards) on motivation, and also the job demands determined to be most strongly acting as barriers which can prevent biosecurity compliance (Physical Workload & Demanding Contact with Animals). Notably, results seem to suggest that supervisors do not play a role in motivating caretakers through Social Norms, despite providing support.

This current exploratory study follows up those quantitative findings with an in-depth interview methodology focused on collecting additional information related to Physical Workload, Demanding Contact with Animals, Supervisor Support, Job Control and Rewards. The research team partnered with several companies of different sizes (in different locations within the United States) to conduct interviews with caretakers to gain further information and insight into the aforementioned five areas of work found to be most influential to the caretaker experience in relation to biosecurity compliance. Analyses of the qualitative data collected utilize natural language processing and linguistic/semantic analyses utilizing coding and programs in R/Python. This allows researchers to conduct in-depth analysis and build a deep understanding of the responses and information provided by caretakers during the interviews.

The purpose of the semantic/content analyses is to identify key themes and topics in the participant's responses and also to determine the positive and negative aspects of the information that they share. While analyses are ongoing, initial findings suggest that trust and anticipation of issues are important to success in the role of caretakers, rewards are not as salient/present (but have positive connotation), and that money and resources are areas that negatively impact caretaker experience and ability to successfully complete their work. More in-depth results will be shared at the conference and in the subsequent reports and publications.

Additionally, the researchers can relate that qualitative information back to previous findings and those in a survey that were administered prior to the interviews. This information will improve understanding of the issues facing caretakers and provide insight on how to address those issues to improve biosecurity compliance in the swine industry (and wean-to-harvest facilities, in particular). Ultimately, these findings allow the research team to utilize its expertise to communicate where targeted interventions would be most efficient and appropriate.

**Pradalex treatment of secondary bacterial infections of clinical PRRSV lineage 1C in nursery pigs**

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Introduction

The emergence of porcine reproductive and respiratory syndrome virus (PRRSV) strain 1-4-4 lineage 1C has been a significant cause of severe outbreaks in pig production since 2020. This strain, notable for its rapid transmission and high mortality rates, often partners with secondary bacterial infections such as Streptococcus suis (S. suis) and Glaesserella parasuis (G. parasuis), worsening the health impacts on nursery pigs. Previous in-vitro studies established the potential efficacy of Pradalex (pradofloxacin), a fluoroquinolone antimicrobial, toward these bacterial pathogens (Risser J, et al.). This case demonstrated the therapeutic effects of Pradalex in managing complex infections in nursery pigs, focusing on the reduction of mortality and improvement of health parameters.

Methods

A large-scale swine operation experienced nursery mortality rate of 20-35%. The operation, weaning approximately 2,000 pigs weekly into off-site nurseries, sought intervention to curb these devastating mortality rates. Diagnostic methods included PCR confirmation of PRRS viremia and bacterial culture from necropsied tissues to establish S. suis (serotype 2) and G. parasuis (serovar 5) infections. Following sensitivity testing, Pradalex was selected for its efficacy against these pathogens. The medication was administered once intramuscularly at a dosage of 7.5 mg/kg body weight to pigs (approximately 5-6 weeks old) exhibiting clinical symptoms. This treatment was coupled with enhanced biosecurity protocols, such as segregated pig flows and strict sanitation measures, to prevent further spread of PRRSV.

Results

Two weeks post-intervention treated groups exhibited a dramatic reduction in mortality rates from the historic 20-35% to less than 7%. Post-treatment necropsy findings showed a reduced secondary bacterial presence with less noticeable lung and serosal gross pathology lesions. The average daily weight gain (ADG) improved by 15-20%, attributed to reduced chronic illness burdens. While PRRS viremia continued as anticipated, its clinical manifestations were significantly tempered by the intervention. As expected, Pradalex demonstrated safety with no observable injection-site or other adverse reactions.

Discussion and Conclusion

Pradalex demonstrated substantial efficacy in mitigating the impacts of secondary bacterial infections concurrent with PRRSV, thereby reducing the overall mortality significantly below the levels typical in severe PRRSV cases. The core of this success lies in Pradalex's broad-spectrum bactericidal activity, effectively breaking the cycle of bacterial amplification that exacerbates PRRSV symptoms. However, the persistence of PRRS infection highlights the need for long-term strategies integrating improved biosecurity and management adjustments. This case outcome suggests that proper implementation of Pradalex can offer a robust defense mechanism against multi-pathogen threats, and a pivotal strategy in mitigating mortality and enhancing growth performance in PRRSV associated bacterial outbreaks in nursery pigs.

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**Antiviral Activity of EO9 against PRRSV and the ASFV Algal Surrogate Virus**

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Essential oils are natural products extracted from aromatic plants. These oils have been utilized for centuries as seasoning, fragrance and herbal remedies. Essential oils have been increasingly studied over the last few decades with numerous studies demonstrating their antibacterial, antifungal and antiviral properties (1). Ralco Nutrition Inc. works to provide essential oil-based products for use in agriculture against pathogens that can cause harm to animal health and lead to economic losses. Two important pathogens include ASFV and PRRSV. ASFV is a double stranded DNA virus containing an icosahedral capsid and viral envelope. The virus belongs to the Asfarviridae family and is classified into Group I of the Baltimore classification (2). Infection by ASFV causes a disease in swine known as African swine fever (ASF), which includes clinical signs of hemorrhagic fever leading to high rates of mortality in infected populations (3). PRRSV is a single-stranded RNA virus containing an icosahedral capsid and viral envelope that belongs to the family Arteriviridae. PRRSV is classified into Group IV of the Baltimore classification (4). Infection causes a disease of the same namesake with clinical symptoms of respiratory distress and reproductive failure in sows leading to large economic losses (4).Ralco's essential oil product, EO9, has shown promising results as a potential antiviral strategy against ASFV and PRRSV in-vitro (5). For this project, EhV was used during the exposure experiments as a surrogate for ASFV due to high similarity in the structure and stability of the two viruses as both viruses are members of the clade known as nucleocytoplasmic large DNA viruses (NCLDVs) (6,7). The mention of "viable" virus particles denotes the concentration of particles that contain a complete and intact viral envelope/structure that may therefore still lead to infection and subsequent disease (7). The viability dye administered before nucleic acid extraction and qPCR amplification is membrane-impermeable. Therefore, the dye can only enter "non-viable" particles with damaged or incompetent structures, and the binding of the dye to the viral RNA/DNA will inhibit the RNA/DNA from amplifying during PCR or RT-PCR (7). Our research shows virucidal activity of EO9 at a concentration of 0.1% v/v with ≥4 logarithmic reductions of viable virus particles observed after exposure and incubation of PRRSV and EhV virus stocks with the oil. The logarithmic reduction in concentration of viable virus particles makes EO9 a promising candidate for further studies to understand the mechanism by which the oil causes such a reduction in viable virus.

**Novel Biosafe and Scalable Detection of Influenza A (H5N1, H3N2, H1N1) for Veterinary and One Health Applications**

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Introduction

Influenza A remains a global health concern due to its rapid transmission and significant morbidity. Timely, accurate, and biosafe diagnostic methods are essential for effective public health responses (Velayudhan, 2022; Uyeki, 2019; Merckx, 2017). However, U.S. regulations require influenza diagnostic samples to be processed under BSL-2 or BSL-3 conditions, limiting accessibility and delaying One Health research.

This study evaluates an integrated workflow for influenza detection outside BSL-3 facilities, combining PrimeStore® Molecular Transport Medium (MTM) — an FDA-cleared inactivation transport medium— with an automated nucleic acid extraction platform and a specialized RT-qPCR detection system. By inactivating and stabilizing viral material at the point of collection, the workflow reduces biosafety requirements, facilitating safer sample handling. We hypothesize that this workflow will maintain diagnostic accuracy while improving biosafety and accessibility.

Methods

Field samples were tested: H5N1 in dairy milk and pooled poultry oropharyngeal swabs, and H3N2/H1N1 in swine oral fluids. Samples were collected in PrimeStore® MTM (Longhorn Vaccines and Diagnostics) for inactivation and processed in a BSL-2 lab. RNA was purified using the Maxwell® RSC Pathogen Total Nucleic Acid Kit on the Maxwell® RSC 48 Instrument and detected using GoTaq® Endure RT-qPCR System with publicly available primer and probe sequences or GoTaq® Enviro Wastewater Flu A, Flu B, SC2 System (Promega). Results were compared to standard-of-care assays, and the use of positive and negative controls ensured contamination-free results.

Results

The workflow demonstrated ease-of-use, reproducibility, and strong performance outside BSL-3 facilities. Detection of a positive or negative sample matched standard PCR results with no false positives detected. Reproducible results across multiple replicates confirmed the reliability of the workflow.

Conclusion

This workflow offers a biosafe, scalable, and accurate alternative for influenza detection. It expands diagnostic capabilities for clinical, veterinary, and field surveillance applications. Future work should address regulatory approval, cost-effectiveness, and validation across diverse settings.

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**Optimizing pooling strategies for PRRSV surveillance: RT-PCR detection limits for PRRSV1 and PRRSV2**

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Introduction

A Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) monitoring program is key to its control1,3,4. Serum from due-to-wean pigs tested in pools is the recommended method by the American Association of Swine Veterinarians (AASV) for breeding herd monitoring and PRRSV status classification1. Therefore, this study aimed to evaluate the detection limit of RT-PCR by pooling PRRSV (PRRSV1 and PRRSV2)-positive serums with different levels of viremia and evaluate the dilution effect of pooling on initial Cycle threshold (Ct) values.

Material and methods

A total of 47 of PRRSV-1 and 33 PRRSV-2 positive samples were categorized into the following Ct range groups: 18-25, 25-30, 30-35, and 35-38. Samples were serial diluted simulating 5, 10, 30, 60 and 120 pools.

Viral RNA extraction and quantification was performed following the manufacturer's instructions kit (MagMAX™ CORE Nucleic Acid Purification Kit and VetMAX™ PRRSV EU & NA 3.0 Kit). Only samples ≤ 38 were considered positive for this study.

Sensitivity was estimated for each Ct group at each dilution range. Furthermore, a linear mixed model was calculated to estimate the increase in Ct values by each dilution. All dilutions were transformed into base 10 logarithms scale. Data analysis was performed using R software (version 4.4.1, R Core Team).

Results

Samples with Ct<30 maintained a 100% sensitivity in all the dilution groups, excepting one sample that tested false negative in the 25-30 Ct group at 1:120 dilution for PRRSV2. On the other hand, samples with initial Ct>30 had a decrease in sensitivity whilst increasing the pool size in both PRRSV1 and PRRSV2. Difference between species were probably explained for the number of samples used in that group.

The linear mixed model equation for each species was calculated:

- PRRSV1: Ct= 24.6483+3.2784·log 10 (Dilution)
- PRRSV2: Ct= 25.88497+3.73059·log 10 (Dilution)

Discussion & Conclusion

Understanding the effect of pooling on RT-PCR PRRSV positive samples is key to implement an effective surveillance strategy, especially in low prevalence scenarios1. Results from this study confirm that; pooling at least 5 serums has either no effect on sensitivity on serums with Ct values below 30, or a moderate effect on Ct values over 30 for both PRRSV species. This sensitivity results are consistent with previous studies2,3. This indicate that the sensitivity of pooled samples depends on the viral load of the

positive sample. Considering new highly pathogen strain scenarios in some countries/regions, where infection with PRRSV results in a high viral load in serum, pooling can be a valid strategy to reduce cost and still detect the early onset of the disease. Based on our model, the maximum number of dilution possible before overcoming the 38 Ct threshold varied depending on the initial Ct value. Thus, considering the worst-case scenario defined as a single positive sample with a Ct value of 35 the maximum allowable dilution for PRRSV-1 and PRRSV-2 would be 1:8 and 1:6, respectively. Pooling serum samples compensates the loss of individual sensitivity with the benefit of a larger sample size allowing to monitor more animals at reduced costs

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**Assessment of serum pooling strategies for African Swine Fever detection via qPCR**

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Introduction

African swine fever (ASF) is a hemorrhagic disease that affects all members of the Suidae family. The current situation of the ASF represents the major threat to the global swine industry, as there is no vaccine or treatment and the complex epidemiology of the disease the implementation of a correct early-stage viral detection surveillance is needed to take actions2,3.

Materials and Methods

Positive serum samples were obtained from ASF experimental studies in a BSL3 facility and were diluted with qPCR ASF negative serum samples. The pooling and dilution effects were assessed. Positive samples were categorized into the following Ct range groups: <30 Ct and >30 Ct values. Regarding sensitivity, only samples with < 37 Ct were considered positive.

For virus detection, viral nucleic acid was extracted using a commercial kit, IndiMag Pathogen Kit (Indical Bioscience), following manufacturer instruction. Subsequently, qPCR was performed according to the in-house TaqMan qPCR assay for detection and quantification of ASF virus (ASFV) protein kinase gene protocol (IT-A4-EPCR 252), with results recorded as Ct values.

A linear mixed model was calculated to estimate the increase in Ct values by each dilution. All dilutions (1:3, 1:5, 1:10) were transformed into base 10 logarithms scale (1.48, 0.70, 1.00, respectively).

Results

Serum samples with Ct value < 30 maintained 100% (95% CI:63-100) sensitivity across all pooling levels. In the group with Ct values > 30, sensitivity decreases from 77.8% (95% CI:40-97) in pools of 3 to a minimum of 55.6% (95% CI:21-86) in pools of 5 and 10 serum samples.

The lineal mixed model equation allows to calculate the maximum number of dilutions before reaching the Ct limit of 37. Therefore, when the Cts from the initial sample are below 33, it can be pooled up to 10 times.

Discussion & Conclusions

These results indicate that sensitivity is not compromised when pooling up to 10 serum samples during high viremias. Furthermore, are consistent with other studies1, where positive serum samples were diluted with negative serum samples. This approach could be particularly useful in high dense swine production areas, in which the efficient collection processing, and analysis of samples are critical components to speed up the diagnostics in order to take actions and decisions towards elimination3.

ASF primary viremia can be identified as early as 8 h post-infection and secondary viremia between 15th and 24th hours post infection2. Therefore, the dilution effect will be higher at the beginning or at the end

of the viraemia period when low viral load is present (Ct > 35)2. On the other hand, pooling serum by 10 could potentially reduce the diagnostic delays in the lab by 76% compared to individual testing 3. Nevertheless, a more conservative strategy in terms of loss of sensitivity and cost would be a pooling ratio 1:32.

In conclusion, pooling can be a valuable strategy to reduce laboratory bottlenecks during large outbreaks. As it may compromise diagnostic sensitivity, it is recommended to adapt the pool size dynamically according to the outbreak phase and the laboratory workload.

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**Association between reproductive resilience to PRRS infection in natural outbreaks and growth and feed efficiency traits in Large White sows**

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Results from numerous studies provide evidence of genetic variation in response to disease, indicating that disease resilience can be improved via genetic selection. In general, genetic improvement is facilitated by collecting data on purebred animals under disease-free conditions, but the genetic relationship between traits recorded at this level, with disease resilience, is not well-understood. Therefore, the main objective of this study was to evaluate the genetic relationship between reproductive and production traits measured under Porcine Reproductive Respiratory Syndrome (PRRS)-free conditions with reproductive performance at the commercial level before, during, and after a PRRS outbreak.

A total of 53,377 farrowing records, collected from 16,674 purebred Large White sows, were used for this study. Data collected in five commercial multiplication farms (located in the United States and Spain), including phenotypic measurements recorded before, during, and after a PRRS outbreak. Pedigree information was available for each individual, and genomic information was available for 483 sires and for a subset of sows (N = 3,518) at 23,301 genetic markers. Estimated breeding values (EBVs) for reproductive traits (number of piglets born alive, number of mummified piglets, number of stillborn piglets, total number of piglets born dead, and number of piglets weaned) and production traits (test daily gain, youth daily gain, lifetime daily gain, feed intake variation, and total feed intake) were available for each sow from Topigs Norsvin's routine genomic evaluation pipeline, which are (in general) estimated using data collected under PRRS-free conditions. EBVs for these same reproductive traits were also estimated using the commercial data available for each outbreak phase (i.e. before, during, and after the PRRS outbreak). Animal models were used to estimate separate EBVs for each reproductive trait, for each phase, and Pearson correlations were calculated: 1) between EBVs for reproductive traits from routine genomic evaluation with EBVs for reproductive traits for each phase; and 2) between EBVs for production traits from routine genomic evaluation with EBVs for reproductive traits for each phase. Only EBVs with an accuracy above 0.30 were considered in the correlation analyses.

Correlations between EBVs for reproductive traits from routine evaluation with EBVs for reproductive traits estimated using the commercial data ranged from -0.08 to 0.72, -0.05 to 0.59, and -0.14 to 0.67 for traits measured before, during, and after the PRRS break, respectively. Correlations between EBVs for production traits from routine evaluation with EBVs for reproductive traits estimated using the commercial data ranged from -0.16 to 0.12, -0.31 to 0.16, and -0.22 to 0.11 for traits measured before, during, and after the PRRS break, respectively.

In conclusion, results from this study indicate that collecting reproductive performance data during PRRS challenge is critical, if maximizing reproductive performance during a PRRS break is part of the breeding goal. Results also revealed a weak genetic relationship between EBVs for production traits from routine genomic evaluation with EBVs for reproductive performance during a PRRS break, which does not support

the popular theory that intensive selection pressure for increased growth and feed efficiency under non-challenged conditions has increased sensitivity to disease challenge.

**Piglets per sow per year and its association with disease outbreaks between January 2022 and March 2025 in Latin American countries**

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[1]PIC

Introduction

Infectious disease outbreaks are known to be the main disruptor of KPI in the swine industry (Mil-Homens et al. 2025). Additionally, the number of piglets per sow per year (PSY) is the main KPI in sow farms. However, the adjusted effect of disease outbreaks on PSY and other KPI in the field is not totally understood. Hence, the objective of this study was to estimate the adjusted association between PSY and disease outbreaks using production records.

Methods

Production records from 85 farms located in Latin America (Bolivia, Chile, Colombia, Ecuador, Perú, Costa Rica, Guatemala, México, and Panama) were used for this study. First, an standardized monthly PSY was estimated (PSY = (total weaned piglets per month / average sow Inventory) × (365.25 / days in the month)). Then an Exponential Weighted Moving average (EWMA) of FR and preweaning mortality (PWM) was calculated to classify farms with or without a disease outbreak. Values crossing the estimated control limit derived from the EWMA baseline were considered and outbreak (Baker et al. 2025). Outbreak 1 (OB1): Abrupt decrease in the FR and Outbreak 2 (OB2): abrupt increase in the preweaning mortality rate. We estimated monthly outbreak incidence and the average number of outbreaks per farm during the study period. Finally, we estimated the association between PSY and disease outbreak at the crude and adjusted level by other KPI of the sow farm.

Results

Eighty-five farms with a total of 331,904 sows and an average of 3905 sows per fam in 2025 (range 227 to 14818 per farm) were used for this study. There were in total 81 outbreaks with decreased farrowing rate (OB1) and increased preweaning mortality (OB2); seven with only OB1; and six with only OB2. The monthly incidence rate of disease outbreak ranged from 2.4% to 18.8%. In average each farm had 3.6 outbreaks during the study period (minimum of 1 and maximum of 8 within 39 months). While there was no difference in TB or LV between farms with or without OB2, the average TB and LB was lower in farms with OB1 compared to farms without OB1 ($p<0.05$). There was a 2.4 PSY difference between farms with or without OB1($p<0.001$) and 3.6 PSY difference between farm with or without OB2 ($p<0.001$).There was no evidence of confounding between FR and PWM over PSY. Finally, we found that there were 5.1 less PSY in farms with OB1 and OB2 compared to farms without OB1 and OB2, and 1.9 more PSY per unit increment in TB after adjusting by OB1 and OB2 ($p<0.001$).

Conclusions

Performance records are a powerful tool to estimate the impact of disease outbreaks when used properly. Preventing disease outbreaks can improve PSY and decrease production variability overtime.

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**Lifestyle, occupational exposures and self-reported health conditions among Midwestern swine workers: A cross-sectional survey**

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Introduction: Understanding health outcomes in swine workers requires a multifactorial characterization of their exposures both at home and on the farm.

Methods: As part of the swine worker microbiome study, we conducted a 20-minutes phone survey with 107 questions to gather information on demographics, health status, and occupational and non-occupational exposures among a convenience sample of swine workers in the Midwest. Forty-nine workers from four farms in Minnesota (n=29), two in Iowa (n=14) and one in South Dakota (n=6) were enrolled based on the following eligibility criteria: employment on the farm ≥ 3 months; age between 18 and 60 years old; and no history of incarceration, hospitalization, or use of antibiotics, immunizations or immunosuppressants in the past 3 months.

Results: Among 49 respondents, 84% (31/49) were Spanish speakers, 65% (32/49) were male and the average age was 35.5 years (range: 22 – 59). Additionally, 63% (31/49) had a college degree and 6% (3/49) held a graduate degree.

The three most common self-reported respiratory conditions among workers were allergies or sinus problems (12%, 6/49), cough or sore throat (12%, 6/49), and infection of eye, ear, nose or throat (10%, 5/49). In addition, the three most commonly self-reported skin conditions were eczema (6%, 3/49), skin rashes (6%, 3/49), and skin allergies to latex or nitrile gloves (6%, 3/49). Workers also reported the following food or drug allergies: lactose intolerance (6%, 3/49), allergy to penicillin (6%, 3/49), and allergy to metamizole (2%, 1/49).

In the context of non-occupational exposures, the average swine worker household consisted of 2 adults (range: 1 – 6) and 1 child (range: 0 – 6), 45% (22/49) lived with another person who worked with animals, and 43% (21/49) had daily contact with other animals, mainly dog and cat pets. Also, 16% (8/49) were smokers (averaging 46 cigarettes per week) and 13% (6/49) were taking medication for a chronic disease.

Among occupational exposures, the average lifetime occupational exposure to swine was 9 years (range: 3 months – 35 years). On their current jobs, workers physically handled an average of 605 pigs over 6 hours per day. The three most frequent job tasks on the farm were: performing euthanasia (94%, 46/49), housekeeping task in non-pig areas (93%, 45/49), and examining, diagnosing or treating swine (90%, 44/49). The three less common tasks were: working with piglets ≤ 3 days old (61%, 30/49), obtaining swine bodily samples (55%, 27/49), and performing administrative/office work (39%, 19/49). Regarding personal protective equipment (PPE) use, 77% (37/49) always use disposable gloves, 22% (11/49) always wear either safety glasses or goggles, and 10% (5/49) always use a face mask of any kind. In addition, 100% (49/49) adhered to a showering-in and -out protocol and, on average, washed their hands 6 times per day while on the farm.

Conclusions: This study summarizes a broad set of exposures, highlighting the need to consider additional factors when assessing health outcomes in swine farm workers.

**Genotypic and virologic characterization of PRRSV escape variants derived from cell-to-cell transmission under neutralizing antibody pressure**

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Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) remains a significant threat to swine health, causing over $1.2 billion in annual losses in the U.S. The virus typically spreads from cell-to-cell during an infection cycle in the swine host by extracellular budding and egress from an infected cell. Consequently this method of spread is amenable to interaction with neutralizing antibodies due to its dependence on interaction with host CD163 receptor. However, intercellular nanotubules and exosomes have been shown to enable cell-to-cell spread, which are independent of the CD163 receptor and inaccessible to neutralizing antibodies, enabling the virus to persist and evade host immunity. These inter-cellular mechanisms may contribute to the limited efficacy of current vaccines and undermine gene-editing approaches, such as CD163 knockout pigs, to control PRRS. The goal of this study was to identify and characterize PRRSV variants that can efficiently utilize nanotubules for cell-to-cell transmission to escape serum neutralization and to uncover the genetic mutations responsible for this phenotype.

Methods

To block extracellular viral transmission, MARC-145 cells were first infected with PRRSV isolate NC-174 at a low multiplicity of infection (MOI) and then treated with 10 µM GW4869, an exosome biogenesis inhibitor and a high titer neutralizing antibody specific to the isolate. To validate the effect of GW4869 on viral replication both extracellular and intracellular virus yields were quantified using an RT-qPCR. In addition, exosomes were isolated from infected MARC-145 cells by ultracentrifugation and analyzed by Western blotting using anti-Alix antibodies to confirm successful inhibition of exosome release.

To select viral variants capable of cell-to-cell transmission, a trans-well system was employed. Cells in the upper chamber were infected with NC-174, while uninfected MARC-145 cells served as sentinels in the lower chamber. Both chambers were treated with GW4869 and high titer NAbs to prevent extracellular viral spread. After 96 hours, lower chamber cells were immunostained for PRRSV nucleocapsid protein to verify absence of extracellular virus infection. Cells in the upper chamber were collected for sequencing to identify viral amino acid mutations associated with enhanced cell-to-cell transmission. In parallel, second set of upper chamber cells were immunostained for the PRRSV nucleocapsid protein to evaluate plaque number and size.

To compare spread patterns, selected variants and input virus were each used to infect MARC-145 cells at a low MOI in the presence of NAbs and GW4869. After 24 hours, cells were fixed and stained for F-actin and PRRSV nucleocapsid protein to visualize nanotube-associated viral distribution.

Results and Conclusions

PCR results indicate GW4869 has no effect on viral adsorption and replication, while exosome release from MARC-145 cells were significantly inhibited by GW2869 treatment. Besides, larger plague size is observed in the group treated with NAbs compared to normal pig serum. Studies are underway to identify

viral variants by sequencing and to assess the presence of viral proteins within nanotubes with neutralizing antibody treatment. This work will provide critical insights into viral adaptation, with implications for understanding viral persistence, developing vaccine designs and gene-editing strategies that are applied to PRRSV control efforts.

**Evaluation of formaldehyde when complete feed was inoculated with porcine epidemic diarrhea virus, porcine reproductive and respiratory syndrome virus, and Seneca Valley virus 1**

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Introduction

Chemical mitigants have been found to decrease virus concentrations in feed. Continued research is needed to identify the appropriate inclusion levels and application time for different viruses in this matrix. Therefore, the objective was to evaluate different inclusion levels of formaldehyde when applied either pre- or post-inoculation of porcine epidemic diarrhea virus (PEDV), porcine reproductive and respiratory syndrome virus (PRRSV) and Seneca Valley virus 1 (SVV1) to complete feed.

Methods

The experiment was designed in a 2×2 factorial with a formaldehyde-based product (Termin-8, Anitox Corp. Lawrenceville, GA) applied either before virus inoculation (pre-inoculation) or after inoculation (post-inoculation) at either a 2 or 3 kg/MT. On d0, samples of swine feed were weighed in 50 g aliquots and added to 500 mL bottles. Chemical mitigants were applied to the pre-inoculation samples at their respective inclusion levels and 50 µL each of 1×107 TCID50/mL PEDV, 1×108 TCID50/mL PRRSV, and 1×108 TCID50/mL SVV1 were added to the post-inoculation samples. All bottles were shaken and allowed to sit at room temperature for 24 hours. On d1, virus was added to the pre-inoculation samples and chemical mitigants were added to the post-inoculation bottles. Half of the samples were immediately processed (0 hr) and the other half were incubated at room temperature for an additional 24 hours (24 hr). Samples were processed and aliquots were analyzed via triplex PCR at Kansas State University Veterinary Diagnostic Laboratory. Cycle threshold and proportion PCR positive were analyzed using SAS GLIMMIX v 9.4 (SAS, Inc., Cary, NC) with each virus individually.

Results

An application time × inclusion level interaction was observed for PEDV at 0 hr and SVV1 and PEDV at 24 hr in feed, where less viral RNA ($P < 0.05$) was detected in the post-inoculation samples at either inclusion level as compared to the positive controls. An application time effect was noticed where less RNA was detected in the post-inoculation samples at 0 hr ($P < 0.05$) compared to the pre-inoculation samples and the control, and at 24 hr, both the pre- and post-inoculation samples had less detectable RNA ($P < 0.05$) than the control. Both the 2 and 3 kg/MT had less detectable PEDV, PRRSV, and SVV1 RNA ($P < 0.05$) than the control at 24 h. The quantity of detectable RNA detectable RNA decreased ($P < 0.05$) as the incubation time increased.

Conclusions: Formaldehyde can reduce detectable RNA immediately in contaminated swine feed, with greater decreases observed as mitigant contact time continues.

**Groundwater surveillance of swine pathogens from private wells supplying swine farms in Iowa**

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Introduction

Groundwater from private wells is a poorly understood biosecurity risk for pathogen transmission on swine farms. Water is one of the largest daily inputs on swine farms by volume and is not routinely tested or disinfected before consumption by animals [1-2]. However, pathogens on the landscape, such as bacteria, viruses, and protozoa from swine manure, can reach groundwater and contaminate wells, presenting a potential route for disease transmission and increase biosecurity risks [1-5]. In laboratory studies, porcine reproductive and respiratory syndrome virus (PRRSV) has been demonstrated to percolate and successfully be recovered via virus isolation from Minnesota soils [6], as well as to survive up to 11 days in various water sources [7]. Porcine circovirus 2 (PCV2) has been detected in groundwater, and tile drains [8-9]. Swine fecal indicator bacteria have also been identified in groundwater sources, indicating a potential manure-to-groundwater pathway exists [10-12].

The objective of this study was to survey private wells supplying Iowa swine farms using dead-end ultrafiltration with subsequent quantitative polymerase chain reaction (qPCR) to detect endemic swine pathogens and swine manure markers.

Methods

Private wells supplying 40 unique commercial swine farms in Iowa were sampled in the spring (n=20) and fall (n=20) of 2024. Enrolled farms included growing pig operations (n=36), breeding farms (n=3), and one nursery. Farm inventories ranged from 1200 – 5900 head with an average of 3200 head. Negative control samples were collected in the field for each field sample, which were tested for all organisms if the corresponding field sample tested positive for any organism. Samples were analyzed for 10 microbial gene targets using quantitative polymerase chain reaction. Organisms included porcine reproductive and respiratory syndrome virus genotype 2 (PRRSV-2), porcine epidemic diarrhea virus (PEDV), porcine circovirus 2 (PCV2), rotavirus C, swine influenza A virus (IAV-S), Cryptosporidium spp., Salmonella spp., enteropathogenic E. coli, and two swine manure markers (pig Bacteroides).

Results

Endemic swine pathogens and manure markers were detected in spring (7 of 20 samples) and fall (3 of 20 samples). Swine manure markers were detected most frequently (7 of 40 samples). Other detections included Cryptosporidium spp. and PCV2 (≤ 3 samples each); five samples contained two or more detected organisms. Tested control samples were negative for all organisms, except for one control sample that tested positive for PCV2 but no other organisms were detected.

Conclusions

Results demonstrate that manureborne microorganisms, including swine pathogens, can contaminate private well water used for pig production. Findings indicate that groundwater may be a potential biosecurity risk for swine farms. Further study of waterborne pathogen transmission on swine farms may help inform water biosecurity practices in the swine industry.

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**Traditional genetic selection for enhanced disease resilience substantially reduces progeny losses post-PRRS challenge**

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[1]Topigs Norsvin

Previous research conducted by our group provides evidence of substantial natural, genetic variation in response to a multifactorial PRRS challenge. This was demonstrated both across and within genetic lines, as significant differences in growth rate and mortality between sire lines, and among sire families, respectively. Results of genetic analyses also show that growth rate and mortality under challenge are heritable, meaning that genetic selection for improved resilience to multifactorial PRRS challenge is possible. The efficacy of this approach has been validated following exposure to the 1-7-4 and 1-4-4 PRRSV strains. The objective of this study was to evaluate the efficacy of this selection strategy following inoculation with yet another (highly pathogenic) PRRSV strain circulating in the USA.

Topigs Norsvin Landrace x Large White (TN70) females were mated to either a synthetic (TN Tempo) or Duroc (TN Duroc) line to produce the pigs used for this study. Boars were selected based on estimated genetic merit for disease resilience, using genotypic and phenotypic data collected from previous PRRS challenge trials. Approximately 2 weeks post-insemination, the sow farm broke with PRRSV 1-4-4 L1C. Piglets (N = 2,924), which were PRRS+ at weaning, were placed in a commercial research facility, consisting of approximately equal numbers of high resilience (HR) or low resilience (LR) TN Tempo- and TN Duroc-sired pigs. Pigs were penned by line and resilience group, and tissue was collected for genotyping at 25K genetic markers. At ~51 days of age, each pig was individually inoculated with 2 x 105 TCID50 of the 1-8-4 L1H PRRSV isolate. Body weight, mortality, and treatment data were recorded from 0 days post-inoculation (dpi) through marketing. Traits were analyzed using SAS, where line, resilience group, line*resilience group, sex, and room were fitted as fixed effects. Growth rate and number of treatments were analyzed as continuous traits and mortality as a binary variable.

Overall mortality rate from 0 dpi to market was 28%. Throughout the study, pigs tested positive for PRRSV, influenza, Streptococcus suis, Mycoplasma hyorhinis, and Pasteurella multocida, among other pathogens. Overall, HR TN Tempo-sired pigs were considered most resilient, demonstrating the lowest mortality rate and highest growth rate post-challenge. Results for the main effect of resilience group show that HR-sired pigs grew 0.04 lbs/day faster than LR-sired pigs from 0 to 42 dpi (P = 0.03), but no significant difference was detected between groups from 43 dpi to market (P = 0.12). The HR-sired pigs also had 6% lower mortality rate (P = 0.0002) and required 0.1 fewer treatments (P = 0.007) than LR-sired pigs.

Results from previous studies conducted by our group show that selection for reduced mortality under challenge validates across genetic lines, challenge models, and following inoculation with either or both PRRSV 1-7-4 and 1-4-4. Results from this study show that this selection strategy also validates following inoculation with the 1-8-4 PRRSV strain. These findings reveal that selecting sires based on existing, natural genetic variation in disease resilience can substantially reduce progeny losses following multifactorial challenge with a highly pathogenic PRRSV strain.

**Biosecurity in Motion: A descriptive study of market hog truck driver interaction with the harvest plant during the unloading process**

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Introduction

Truck drivers play a critical yet underexamined role in animal transportation. Daily, a market hog truck driver may visit the same or multiple farms to load pigs and haul them to one or several harvest plants, thereby creating a potential risk for infectious disease transmission to farms. There is no data on driver practices and behaviors during the market hog unloading process at the plant. Therefore, this study aimed to characterize biosecurity procedures employed by market hog truck drivers.

Methods

Data were collected biweekly at a Midwestern U.S. harvest facility, interviewing 15 drivers per visit. Drivers were surveyed on (Personnel-Protective-Equipment) PPE, trailer sanitation, loads hauled per day, destination after unloading, and documenting whether drivers needed help from plant personnel during unloading.

Results

A total of 123 truck drivers had been interviewed between November-2024 and June-2025, totaling 240 surveys with some drivers being interviewed 1 or 14 times. Drivers reported hauling one (45%), two (45.4%), or three (9.6%) pig loads per day. In 17.5% of the interviews, drivers confirmed transporting both pigs and cattle using the same trailer.

When loading pigs at the farm, 54.2% of drivers only stepped on the trailer, while 45.8% stepped on both the trailer and chute-barn. At the plant, unloading pigs was completed in 19 minutes on average. PPE used varied with 91.6% of the drivers wearing rubber boots, 4.2% leather boots and 4,2% were wearing other types of footwear. Among them, 8.4% and 7.9% wore disposable plastic or shoe covers over their footwear, respectively. Fabric coveralls were worn by 57.7% of the drivers, while 13.4% used disposable coveralls. The remaining 28.9% did not wear any type of coverall. Among those, 19% wore regular clothing (shirt and pants), 5% wore chaps over pants, and 4.9% wore other garments. Fabric work gloves or latex gloves were used by 86.1% and 7.2% of them, respectively. A total of 6.7% of the drivers used no gloves. When 97 drivers were asked why they chose their PPE, 14 (14.4%) mentioned biosecurity, 83 (85.6%) mentioned comfort or avoiding getting dirty or becoming malodourous.

Drivers unloaded pigs without plant personnel help in 54.6% of the cases. However, in 20.4%, 22.9%, and 2% of cases, 1, 2, or 3 plant employees entered the trailer to assist with unloading, respectively. Non-ambulatory (12,9%), dead (17,9%), or both types of pigs (3,75%) were observed during unloading.

Half (50.4%) of the drivers had their trailer washed with cold water before loading pigs, 17.9% did not wash, 14.6% washed, disinfected, and allowed it to dry, 11.7% washed and disinfected but did not let the trailer dry, 4.2% used hot water, and 0.8% washed, disinfected, and baked the trailer while 0,4% didn't know if the trailer was washed.

Conclusion

The results of this study reveal several current risk factors that pose a threat to the industry, including PPE use, trailer sanitation, and farm-level biosecurity breaches. Further studies are needed to better understand interactions between truck drivers and harvest facilities.

**Strengthening Puerto Rico's African Swine Fever Response Plan with the Use of a Tabletop Exercise**

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Introduction

African Swine Fever (ASF) was detected for the first time in the Dominican Republic and Haiti in September of 2021 after 40 years. In response to the increased regional threat, the United States Department of Agriculture (USDA) designated Puerto Rico (PR) as an ASF protection zone. This designation requires the implementation of enhanced biosecurity and preparedness measures. To strengthen the preparedness and improve the coordination of response efforts across the swine industry, tabletop simulation exercises (TTX) provide a valuable opportunity for local, state and federal stakeholders to evaluate the existing plans, identify gaps, and practice critical decision-making under a realistic scenario. The objective of this study was to develop a TTX to assess swine industry stakeholder preparedness during a potential ASF outbreak in PR.

Methods

A 1.5-day TTX was conducted in San Juan, PR in June of 2025. Recruitment occurred through professional connections between the investigators and collaborators at the USDA and the Puerto Rico Department of Agriculture. The TTX utilized a facilitated discussion format, engaging participants from federal and local levels, including producers. The hypothetical scenario involved an ASF suspicion in a commercial swine site, and was divided into three modules: 1) Disease Notification, Confirmation, and Immediate Needs; 2) Epidemiological Investigation, Depopulation, Disposal, and Decontamination; and 3) Continuity of Business. Four trained evaluators from outside Puerto Rico observed the discussions and collected data regarding participants' knowledge and perceptions of roles and responsibilities. Feedback surveys were collected from participants, using Likert scales to capture agreement levels for different statements and open-ended responses.

Results

A total of twenty-six people attended the exercise. Of the completed feedback surveys (n=15), nine respondents reported holding federal roles, three held state roles, two held academic positions at universities, and one was involved in swine production. When asked how prepared for an ASF outbreak response participants felt Puerto Rico was on a scale from 0 (not at all) to 5 (extremely), the average answer before the exercise was a 2.64. In contrast, the average response was a 3.43 after the exercise. The majority of participants agreed the workshop was helpful in furthering PR's ASF planning efforts with an average response of 4.71 on the same scale. Evaluations showed strength areas for preparedness included laboratory capabilities, timeline for investigation activities, and technical federal Emergency Management Response System expertise, while areas for improvement included details and training on the Incident Command System, logistics on depopulation and disposal options, and producer readiness for permitting and indemnity.

Conclusion

In conclusion, discussions from the TTX provided an opportunity for identifying critical gaps in the ASF response plan and strengthening stakeholder coordination. Additional data analysis of evaluation criteria will continue, and ongoing education efforts will be crucial to ensure an effective response to ASF.

**Validation of a new generation ELISA test for antibody detection of antibodies against Mycoplasma hyopneumoniae**

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Introduction

Mycoplasma hyopneumoniae, the etiological agent of enzootic pneumonia, remains a major contributor to economic losses in swine production worldwide due to impaired growth performance, increased feed conversion ratios, and heightened susceptibility to secondary infections. Effective control strategies—including vaccination, antimicrobial protocols, and eradication programs—depend on accurate serological monitoring. However, variability in the performance of currently available assays often limits diagnostic confidence. To address these challenges, IDvet has developed the ID Screen® Mycoplasma hyopneumoniae competitive ELISA, which incorporates a highly specific monoclonal antibody directed against a conserved epitope of the P65 protein of M. hyopneumoniae, designed to enhance both sensitivity and specificity.

Materials and Methods

Diagnostic specificity was assessed using serum samples from breeding herds confirmed to be free of M. hyopneumoniae exposure by established serological methods.

Analytical specificity was evaluated using sera obtained from Iowa State University, originating from pigs experimentally inoculated with Mycoplasma flocculare, Mycoplasma hyorhinis, or Mycoplasma hyosynoviae; samples were collected at 0 and 56 days post-inoculation. This evaluation was done in the Iowa State University VDL.

Diagnostic sensitivity was determined using serial samples from eight pigs experimentally infected with M. hyopneumoniae, collected at multiple time points from day 0 to day 56 post-inoculation. Comparative analysis was performed using the IDEXX indirect ELISA targeting M. hyopneumoniae antibodies. This evaluation was done in the Iowa State University VDL.

In other independent study performed by Univeristy of Minnesota VDL, they analyzed the results of samples from various diagnostic cases that were false reactors in the IDEXX ELISA kit. These samples (n=152) were from a period of ten months, came from mycoplasma negative populations and were further tested by ID Vet ELISA. They also tested samples from a farm with vaccinated and acutely infected animals to determine sensitivity of both tests.

Results

All samples from M. hyopneumoniae-free herds and pigs inoculated with other Mycoplasma species tested negative, demonstrating both high diagnostic and analytical specificity. In terms of sensitivity, the ID Screen® ELISA detected seroconversion earlier than the comparator assay, identifying antibody presence between days 17 and 49 post-inoculation, while the IDEXX indirect ELISA detected seroconversion between days 24 and 49.

The University of Minnesota comparison shows that ID Screen® Mycoplasma hyopneumoniae competitive ELISA kit was more sensitive (68%) and specific (95.39%) with this set of samples. This data was presented by Devi Patnayak in the AAVLD 2024.

Conclusion

The ID Screen® Mycoplasma hyopneumoniae competitive ELISA demonstrated superior diagnostic performance compared to the IDEXX indirect ELISA, particularly in early detection of seroconversion. These findings support its utility as a reliable tool for accurate herd monitoring and improved decision-making in the control of enzootic pneumonia in swine populations.

**Serological potency and clinical efficacy of multivalent vaccines in pigs experimentally challenged with H1huN2 Influenza virus**

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Introduction

Porcine respiratory diseases are multifactorial conditions, collectively known as the porcine respiratory disease complex (PRDC), representing one of the leading causes of morbidity and mortality, with significant economic impact on swine herd production. Among the pathogens involved, the influenza A virus (IAV) stands out due to its high genetic and antigenic variability. In Brazil, the high diversity of circulating subtypes, which include H1N1 (human-like or pandemic), H1N2 and H3N2, and the limited cross-protection provided by monovalent vaccines hamper disease control efforts (CIACCI-ZANELLA et al., 2015; TOCHETTO et al., 2023). The present study aimed to evaluate the immunogenicity and clinical efficacy of two novel multivalent vaccine formulations against influenza subtypes, focusing on protection against an experimental challenge with the H1huN2 strain.

Methods

A total of 48 clinically healthy piglets (21 days old), free of antibodies to IAV, were randomly allocated into four homogeneous groups (n = 12). The piglets received intramuscular immunizations as follows: Group 1 (Vaccine A; trivalent), Group 2 (Vaccine B; trivalent), Group 3 (Vaccine C; commercial monovalent), and Group 4 (Placebo). Vaccination was performed on Day 0 (D0) and boosted on D14. On D30, all piglets were challenged intratracheally with the H1huN2 influenza virus strain (AFK 242/21). Half of the animals from each group were euthanized on D37 for pathological evaluation, while the remaining were assessed until D43. Vaccine efficacy was evaluated through: (i) monitoring clinical signs; (ii) evaluating the serological response (hemagglutination inhibition assay – IH) against H1pdmN1pdm, H1huN2, and H3N2 on D0, D14, D30, D37, and D43; (iii) detecting viral shedding (nasal swabs and quantitative real-time reverse transcription PCR - RT-qPCR); and (iv) measuring viral load in lung tissues at necropsy.

Results

Both multivalent vaccines (A and B) elicited robust antibody responses against all tested subtypes, with significantly higher titers at D30 compared to D14 ($p < 0.05$). Vaccine B induced the highest HI titers, particularly against H3N2. In contrast, Vaccine C (commercial monovalent) induced a serological response solely against H1pdmN1pdm. Nasal viral shedding was detected only in Vaccine C and placebo groups. Lung viral presence was confirmed in 100% of placebo and 50% of Vaccine C piglets at D37, while no viral genome was detected in lungs from pigs vaccinated with A or B. Pulmonary lesion scores were significantly lower in A (0.08) and B (0.15) groups compared to Vaccine C (7.41) and placebo (15.26) ($p < 0.05$). By D43, no viral RNA was detectable in lung tissues of any group.

Conclusions

The novel multivalent vaccines evaluated demonstrated superior immunogenicity and clinical efficacy compared to the commercial monovalent vaccine, effectively preventing viral shedding and pulmonary lesions following H1huN2 challenge. These findings highlight the potential of multivalent formulations in improving influenza control strategies in swine populations.

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**EpiCC-Guided Vaccine Candidate Selection Improves T-cell Epitope Coverage Against Circulating European Swine Influenza A Virus Strains**

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Introduction

Swine influenza A virus (sIAV) poses significant economic challenges to the global swine industry. Vaccine efficacy is often limited by antigenic mismatches between commercial vaccine strains and circulating field isolates. Current vaccine selection approaches primarily rely on serological and phylogenetic analyses, which may not fully capture the complexity of T-cell-mediated immune responses. T-cell Epitope Content Comparison (EpiCC) is a computational approach that evaluates the shared putative T-cell epitope content between vaccine strains and field isolates and provides quantitative metrics for assessing vaccine candidates. Here, we conducted an analysis of European sIAV strains and compared their T-cell epitope profiles with those of existing commercial vaccines. Within this dataset, we identified superior vaccine candidates based on epitope coverage and EpiCC scores.

Methods

We conducted a comparative analysis of the hemagglutination (HA) sequences of European sIAV strains. This analysis included the strains discussed by Henritzi (2020), as well as other more recently identified European sIAV strains. First, we used the PigMatrix algorithm to identify T-cell epitopes within each HA sequence. Next, we employed EpiCC to evaluate the relationship between predicted T-cell epitopes in the HA protein sequences of field isolates with those in one monovalent and one trivalent commercial European sIAV vaccine. EpiCC generates a score for each vaccine-isolate comparison and determines the coverage of T-cell epitopes. After assessing the two commercial vaccines for their shared T-cell epitope content with the field isolates, we evaluated each isolate included in this study as a potential vaccine candidate. Our goal was to identify potential vaccine candidates that could provide improved protection, as measured by EpiCC.

Results

Overall, mean T-cell epitope coverage of the commercial vaccines ranged from 43% to 66% when comparing the vaccine strains with field isolates of the same HA classification. Interestingly, the cluster containing confirmed H1pdm isolates showed a distinct pattern of two subclusters, which was reflected in our EpiCC scores and T-cell epitope coverage. When evaluating the existing dataset for isolates qualifying as vaccine candidates based on EpiCC scores and T-cell epitope coverage, we identified several isolates which showed greater EpiCC scores and T-cell epitope coverage, from which we further selected the best to evaluate as vaccine candidate using EpiCC. Compared to the trivalent and monovalent vaccines, T-cell epitope coverage increased by 6% and 8%, respectively. However, on a strain-by-strain basis, greater differences could be observed. Maximum T-cell epitope coverage was 91% (+22%) and 86% (+10%) for the newly identified vaccine candidates, compared to 69% and 76% for the commercial vaccines.

Conclusions

Our findings demonstrate the value of EpiCC as a tool for evaluating vaccines. EpiCC successfully identified multiple field isolates as promising vaccine candidates that exhibit superior T-cell epitope coverage compared to commercial formulations. It is important to note that our analysis was limited to a small panel of isolates, suggesting that broader screening may reveal candidates with even greater immunological potential. Together, these results establish EpiCC as a valuable in silico tool for vaccine design and emphasize the critical importance of systematic, multi-parameter evaluation in vaccine candidate selection.

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**The impact of diet and commingling on the fecal resistome of production pigs exposed to metaphylactic antibiotics: a randomized controlled trial in a commercial flow**

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Introduction

This study aims to evaluate whether dietary fiber and/or commingling can be used to mitigate the development and persistence of antimicrobial resistance genes (ARGs) within the fecal microbiome after metaphylactic antibiotic use in production pigs.

Methods

A total of 84 litters from two rooms within a single sow farm were included in this 2x2 factorial design randomized controlled trial. Treatment allocation was performed randomly at the litter level. From each litter, up to ten piglets were randomly selected and enrolled into the study as they were born within an hour to no more than 24 hours after birth (N=833 piglets across 84 litters). At enrollment, each piglet was tagged with a unique ID, weighed, and given a single dose of Excede (ceftiofur, 100 mg/mL, 0.5 mL intramuscularly; Zoetis Animal Health). Immediately after processing (i.e., 2-5 days post-birth [dpb]), the first factor treatment was initiated, wherein enrolled litters were either kept within a single farrowing pen with their sow and littermates (“CONV”) or they were allowed to commingle and move freely across multiple pens and suckle from multiple sows (“MSCC” for multisuckle, common creep). On days 17–18 dpb, all enrolled piglets received Baytril (enrofloxacin, 100 mg/mL, 0.35 mL intramuscularly; Elanco US Inc) immediately prior to the introduction of pre-weaning creep feed, which was the second study factor in the 2x2 design. Creep feed was either standard feed/low fiber (LF) or supplemented with potato starch/high-fiber (HF), depending on the pre-allocated treatment group. At 23–24 dpb, all piglets were weaned and moved to the nursery facility, where they were weighed upon arrival. Piglets were rectally sampled with sterile swabs at 0–12 h post-birth (hpb), daily until 2–4 dpb, and at key production stages: MSCC treatment (5–6 dpb), 8, 11, 14 dpb, Baytril injection and creep feed initiation (17–18 dpb), one and three days later, one day before moving to the nursery facility (22–23 dpb), and at 4, and 7 days post-weaning (dpw). Final samples were collected one day before marketing (149–151 dpb). Swabs were stored at –80°C in sterile Whirl-Pak bags. Total DNA was extracted and pooled by sow/litter and sampling timepoint. A total of 1,197 DNA samples were submitted for metagenomic library preparation and sequencing. The resulting sequencing data were processed using the AMRplusplus bioinformatic pipeline to identify ARGs in each sample. Resistome profiles were then compared by treatment group and time point.

Results

We observed a significant interaction between commingling and diet on average daily gain (ADG) at the end of the nursery period (P=0.04), with the MSCC-HF group showing higher ADG than the other groups. The average piglet mortality rate was 15% and varied numerically between treatment groups. Across all samples, we identified 513 unique ARGs, 136 AMR mechanisms, and 46 classes. The resistome–microbiome profile exhibited temporal changes, showing a high resistome count early in life and a subsequent decline as pigs aged, with the lowest counts observed prior to market across all treatment groups. Significant differences in fecal resistome composition were observed between the CONV and MSCC groups, with a group-by-time point interaction prior to the second metaphylactic antibiotic exposure and creep-feed allocation (PERMANOVA, $R^2 \leq 5\%$, $P = 0.001$). Following creep-feed initiation and one day prior to weaning, both treatment (i.e., MSCC and CONV, with high-fiber and low-fiber combinations) and sampling point were associated with differences in resistome composition (PERMANOVA, $P < 0.01$), and a significant treatment-by-time point interaction effect on the resistome composition was observed during the post-weaning/nursery period (PERMANOVA, $R^2 = 3\%$, $P = 0.024$). One day prior to market/final sampling, the resistome count was lower in the MSCC group fed with high-fiber creep feed compared to all other groups, although this difference was not statistically significant. However, overall resistome composition varied significantly by treatment group (PERMANOVA, $R^2 = 6\%$, $P = 0.012$).

Conclusions

We expect that our results will provide insight into whether commingling and creep diet can be used as potential interventions to minimize AMR spread and persistence within microbial communities after metaphylactic antibiotic exposures, while supporting overall performance in production pig population.

## RETROSPECTIVE ANALYSIS OF SWINE INFLUENZA LABORATORY RESULTS IN MEXICO (2019-2025)

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Introduction

Influenza is a viral disease with high impact on human, animal and swine health and closely monitored by The World Health Organization (WHO) under the "One Health" approach, thus, its surveillance is essential for understanding the dynamics of viral circulation and development of effective vaccines and control strategies. This retrospective analysis examines laboratory results obtained in years 2019 to 2025, with the aim of identifying the frequency and trends of swine influenza viruses (SIV) infections in Mexico.

Materials and Methods

To perform this study the results of 5,303 PCR-SIV tests, 774 molecular SIV characterizations, 743 virus isolates, and 1,119 ELISA tests of samples submitted to Diagnósticos Clínicos Veterinarios (DCV), between January 2019 and February 2025, from pig farms located in different states in Mexico, such as Chiapas, Mexico City, Guanajuato, Jalisco, Morelos, Puebla, Sonora, Veracruz, and Yucatán, were included.

Results and Discussions

PCR-SIV testing showed 87% of negative samples and 13% with positive results. Maybe the low positive results are due to erroneous sampling in the field, inadequate conservation or transportation methods, which suggest that proper training of farm personnel is needed.

Viral sequencing showed that SIV subtype H3N2 was found in a higher frequency during years 2019 (50%), 2020 (41.2%) and 2021 (50.8%), meanwhile for subtype H1N1 a higher frequency was observed in years 2022 (52.7%) and 2023 (52.9%). Finally, subtype H1N2 had a higher frequency detection in years 2024 (70.7%), and in the first two months of 2025 (90.9%), showing important variations in virus subtype/variant dynamics, maybe due to swine industry practices, like movement of live animals, products, byproducts or others.

The cumulative seropositive cases by month/year, detected by competitive ELISA, showed a higher number of positive cases during the winter months, being the peak in February, followed by a drop in positive cases during summer and a new increase in seropositive samples in August and September, meaning typical seasonal influenza behavior.

The country's regional SIV isolates distribution was 53% in the Northwest (Sonora), 24% in the West (Jalisco) and 15% in Southeast (Chiapas), which corelates with intensive swine production areas. The remaining isolates were randomly distributed in the country.

Finally, the positive SIV isolates according to type of sample were 70% from lung samples and 30% from nasal swabs. In this sense, lung samples offered the greatest likelihood of isolation, while in the field, nasal swabs are the most practical and economical samples to be collected.

Conclusions

Significant variations in SIV subtype/variants frequency were observed during time, highlighting the need for accurate viral identification and sequencing, especially crucial for the infection dynamics and development of effective vaccines that match with field viruses to enhance control strategies. The appropriate choice of sample type and sampling timing are essential to increase the reliability of the results. Well distributed sampling, accompanied by an analysis of timing and location of cases, allows early detection and rapid response to SI outbreaks. This retrospective analysis highlights the importance of having a well-planned national SIV surveillance.

**Measuring the effect of Ralstonia picketti growth in boar semen**

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Introduction

Ralstonia pickettii is a gram negative, aerobic bacteria that is commonly found in contaminated water. Compared to historical numbers, Ralstonia has appeared with increased frequency in water samples from boar studs and may appear in associated semen samples.3 R. pickettii is an opportunistic pathogen affecting the immunocompromised and was associated, along with Achromobacter xylosoxidans, with a case of endometritis in sows undergoing a PRRSv break.2 Previous work has described that R. pickettii has no effect on sperm motility and is highly susceptible to antibiotics present in semen extenders.1 Due to concern regarding the frequency of Ralstonia growth in both water and semen samples, the effect of Ralstonia growth on semen with and without antibiotics was tested.

Materials and Methods

R.pickettii was cultured from field samples. A serial dilution was performed to determine the approximate CFU/ml of the sample. 4.7 ml of extender was mixed with 0.3 ml of semen to achieve a 1:16 dilution. The semen was collected in the following manner: The standard 3 glove technique was utilized to obtain a free catch collection and the penis tip cleansed prior to the collection of 2-3 ml of semen. Samples were cooled to room temperature and controls were cultured on a blood agar plate. Each sample was analyzed on Day 0-3 for motility and acrosome integrity.

Study 1 utilized antibiotic free extender and compared a negative control to samples containing 100, 1,000, 10,000, and 100,000 CFU/ml. There was a significant decrease in acrosome integrity in semen samples starting at 10,000 CFU/ml. Study 2 compared a negative control to samples containing 1,000, 2,500, 5,000, 7,500, and 10,000 CFU/ml. Acrosome integrity decreased significantly at 5,000 CFU/ml and higher, with failing acrosome scores starting at 7,500 CFU/ml. No significant difference in semen motility was found in either study.

Study 3 utilized extender with antibiotics. Ralstonia was mixed into extender and allowed 1 hour after mixing to simulate the time from mixing extender to adding semen in a boar stud. A control was compared to samples containing 5,000, 10,000, 100,000, 1,000,000 and 10,000,000 CFU/ml. Notably each control grew a single Ralstonia colony and a corresponding water sample from the stud had Ralstonia growth. No significant difference in motility was found between the groups, but acrosome integrity was significantly lower in groups starting at 10,000 CFU/ml and higher, with failing acrosome scores starting at 100,000 CFU/ml. The experiment was repeated with 5,000, 10,000, 50,000, 100,000 , and 500,000 CFU/ml. In this study acrosomes were significantly lower than the control group starting at 10, 000 CFU/ml and higher, with failing scores starting at 50,000 CFU/ml.

Discussion

Ralstonia growth appears to have a negative effect on semen acrosome integrity at growth levels above 5,000 CFU/ml with failing acrosome scores beginning at 7,500 CFU/ml without antibiotics and at 10,000

CFU/ml with failing acrosome scores at 50,000 CFU/ml with antibiotics. This demonstrates the importance of routine bacterial testing of both water and semen samples in boar studs.

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**Unseen Burdens: Environmental Pollution and Wildlife Threats from Endemic ASF in the Philippines**

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Introduction

The African Swine Fever (ASF) outbreak, which emerged in Southeast Asia following China in 2019, has devastated the Philippine swine industry for over five years. Its seasonal outbreak trend has led to the disease becoming endemic and difficult to eradicate. While primarily affecting animal health, ASF also causes significant socioeconomic, public health, and notably, environmental problems. This study specifically aimed to explore these broader impacts using qualitative methodology, with a focus on environmental concerns, to strengthen the nation's ASF response through a One-Health approach.

Methods

In November 2024, a stakeholder mapping exercise was held in Batangas, Philippines. Forty veterinary experts participated in a roundtable discussion to pinpoint key environmental impacts of ASF. They were divided into six teams based on their work regions. They then used a pre-developed questionnaire to create a consensus-based report, rating the severity (low, moderate, severe, or extreme) of impacts across six different environmental domains by location. Subsequently, online semi-structured focus group interviews (FGIs) were conducted in April 2025 with a subgroup of these experts across the main islands of Luzon, Mindanao, and Visayas. Audio transcripts were manually transcribed, and a thematic analysis approach was used to identify common themes and island-specific insights.

Results

The veterinarians reported numerous complex challenges in controlling the environmental impact of ASF. The stakeholder mapping exercise highlighted severe to extreme environmental concerns. These primarily included wastewater from pig farms (containing dead animals and waste) and the threat to wildlife, such as wild boars. Follow-up online FGIs revealed three main themes regarding ASF control. First, farmer behavior is a major hurdle; most farmers don't follow critical biosecurity measures because they see them as too expensive, cling to traditional practices, and feel ASF is unavoidable. This non-compliance fuels disease spread and worsens environmental pollution. Second, government efforts are hampered by insufficient funding, staff shortages, political interference, and a lack of essential baseline data. Finally, operational challenges include communication barriers with diverse farmer populations, difficult access to mountainous farms, and unclear local administrative boundaries, all of which hinder effective control zone establishment.

From an environmental standpoint, improper pig carcass disposal causes significant water and soil pollution and generates noxious odors. Concerns also emerged regarding the misuse of disinfectants and

polluted water sources, which appear linked to ASF recurrence. Wild boars were also identified as posing a transmission risk. Although the Environmental Management Bureau was mentioned as a relevant government agency, current policies appear insufficient to prevent improper pig carcass disposal effectively.

Conclusions

Future ASF research must quantify its broader impacts, integrating animal, public, and environmental health. Effective mitigation critically depends on strong collaboration, especially with the Environmental Management Bureau and the Department of Environment and Natural Resources, as highlighted by stakeholder mapping.

**Death risk factor analysis based on production data**

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Introduction

Sow mortality has been increasing in recent years, posing significant challenges to commercial pig production. It not only affects animal welfare and farm productivity but also leads to substantial economic losses. Previous studies have identified risk factors such as high parity, seasonal effects, and farrowing-related complications. However, limited research has quantified mortality risk at different reproductive stages in Spain. This study aimed to examine sow mortality patterns and identify associated risk factors.

Methods

Individual sow records from January 2019 to December 2024 were collected from 16 Spanish farms selected for consistent sow death classification. Gilts removed before the first service were excluded. Incidence rates were estimated using two-level Poisson regression models (GLIMMIX procedure) with an offset, applied separately to two risk periods: insemination to farrowing and farrowing to the next insemination. Herd-level variables, including the gilt replacement strategy, were modeled as fixed effects. Pearson's correlations were used to assess associations between herd-level mortality and indicators such as herd size and pigs weaned per sow per year (PWSY). At the parity level, univariate models were run with sow-level covariates. Additionally, three matched case-control studies compared reproductive and lifetime performance between deceased sows and matched controls.

Results

Across the 16 farms, 55.59% of sow deaths occurred before farrowing and 44.41% after. Mortality peaked during late gestation (days 105–118) and during the first- and fourth-weeks post-farrowing. Among farm-level factors, internal gilt replacement was associated with post-farrowing mortality. At the sow level, service frequency and parity played important roles. Before farrowing, sows with parity ≥3 and those that received only a single service exhibited a higher mortality incidence. After farrowing, increased mortality was observed in parity 1 sows and those with repeat breeding. Seasonal effects were evident, with the highest mortality rates found in sows bred in spring and farrowing in summer. Matched case-control analysis revealed that parity 0 sows had a younger age at first service, and deceased sows had shorter gestational length, fewer piglets born, born alive, and a higher incidence of stillbirth fetuses at their last litter. Comparing the lifetime performance, dead sows had younger gilt age at first service, fewer parity at removal, higher average number of piglets born, born alive, born still and born mummified per parity, but they had fewer weaned piglets and nonproductive days.

Conclusions

This study highlights farrowing, especially late gestation and the first week postpartum, as the most critical window for sow survival, warranting greater attention to peripartum care. Internal gilt replacement and increased mortality risk in parity 1 sows after farrowing emerged as key risk factors. Repeat services before farrowing may signal underlying reproductive or health issues that increase postpartum mortality

risk. Seasonal vulnerability around summer farrowing underscores the need for environmental mitigation strategies. Case-control comparisons suggest that sows that died tended to show suboptimal performance in their last litter and lifetime productivity, despite producing more piglets per parity. These patterns emphasize the value of integrating early reproductive indicators into long-term sow management and culling decisions.

**Comparing feed efficiency and water disappearance in immunocastrated and physically castrated barrows in a US customer setting**

Micah Jansen[1], Deb Amodie[1], Richard Swalla[1], Kimberly Vonnahme[1]

[1]Zoetis

Improvest® [IMV; gonadotropin releasing factor (GnRF) analog-diphtheria toxoid conjugate] is an anti-GnRF product for immunological castration. It has been approved by several countries and the U.S. Food and Drug Administration to control boar taint, and many studies have demonstrated an increased growth performance and carcass quality, as well as improved animal welfare compared to physical castration of male pigs. Improvest management is achieved by injecting pigs twice, with at least a 4-week interval, during the grow-finish phase. Water intake, measured as water disappearance, has been reported to be 14% less in immunocastrated (IC) vs physically castrated (PC) barrows. The hypothesis for the current study is that the wean to finish feed efficiency would be improved and water disappearance would be reduced in IC vs PC barrows in a commercial setting in the Midwest of the US. Males were either physically castrated (PC) less than 7 days post farrowing or left intact for immunocastration (IC). At weaning, PC and IC barrows were separated and placed in pens randomized within the wean-to-finish site (i.e., 7 pens/treatment). Weights, feed disappearance, and water disappearance per pen were recorded at weaning (day 0) and every 7 to 28 days until day 139 when all pigs were marketed. The IMV doses were administered on day 70 and 112 of the study to IC barrows. Data were analyzed with a generalized linear mixed model approach for repeated measurements (with day as the repeated measure) and single time point variables. There was no difference in initial body weight (P=0.175), but by the end of the study, IC barrows were 5.8 lbs heavier (P =0.017) than PC barrows (322.3 vs 316.5 ±1.7 lb). Average daily gain increased in IC vs PC barrows after the second IMV dose so that there was a 1.8% increase (P=0.025) in IC vs PC barrows (2.23 vs 2.19 ±0.01 lb/day). Average daily feed intake was lower (P≤0.05) prior to the second IMV dose, so that overall ADFI was 7.7% lower (P<0.01) in IC vs PC barrows (4.66 vs 5.02 ±0.04 lb/day). Wean-to-finish feed efficiency was improved by 10% in IC vs PC barrows (2.09 vs 2.30 ±0.02). Daily water disappearance was decreased (P≤0.05) from day 23 through day 114, and similar between days 114 to 139. Total daily water disappearance was decreased by 12.6% (P<0.01) in IC vs PC barrows (1.11 vs 1.25 ±0.02 gallons). We accept our hypothesis that IMV administration in barrows would improve feed efficiency and decrease water usage.

**PigmentRx: A practical method for assessing medicator accuracy**

Molly Jones

North Carolina State University

Water medicators are a critical tool used for vaccine and treatment delivery in modern pork production. These products, though vital to pig health, are often expensive and contribute significantly to the cost of raising pigs. Despite their importance, medicators are seldom evaluated for accuracy, leaving ample opportunity for failure. Variability in dosing can lead to suboptimal health outcomes, economic loss, and risk of antimicrobial resistance. A broader study of medicator accuracy suggests that an in-barn method of evaluating dosing inconsistencies is warranted. PigmentRx is an accessible, field-ready colorimetric tool designed to serve as a practical solution for assessing medicator dosing accuracy at the level of the water nipple. It enables producers, veterinarians, or production staff to quickly evaluate medicator accuracy, troubleshoot inconsistencies, and make decisions without specialized equipment.

To develop the tool, stock solution was prepared using 1 gallon of water and 1 Reload Pack® DT 1x. In addition, clean water samples were collected and mixed from 13 swine farms to account for variation between farms and improve practical application. Nine dilutions were created from the stock solution and clean farm water: 1:80, 1:100, 1:128, 1:160, 1:200, 1:300, 1:400, 1:500, and 1:1000. A spectrophotometer was used to analyze each of these by measuring full spectrum wavelength and absorbance values. To turn this lab-based data into a visually intuitive tool, ColorLab(1) (Python-based program, Ratcliff Group, Univ of AZ) was used to convert each dataset into a standardized PNG color file. These were compiled to form the PigmentRx colorimetric scale. The resulting scale is a visual representation of the expected color of each dilution when the stock solution is correctly prepared.

This tool is meant to be paired with a simple protocol that uses materials commonly used on farms. The protocol involves mixing a stock solution at a precise ratio of 1 gallon of water to 1 Reload Pack® DT 1x and running it through a medicator at a rate of 1:128. After a set amount of time (~1-4 hours), samples are collected across the barn and compared to the scale to estimate the relative dilution of each sample. This process aids in detecting dosing inaccuracies, measuring time required for medication to reach specific areas, and assessing intra- or inter-barn variation.

PigmentRx is designed to encourage field-based problem solving by bridging the gap between lab-based measurements and barn-level practicality. This tool is a practical step forward in ensuring antibiotic judiciousness and promoting high-quality medication practices. Its simplicity, proven accuracy, cost-effectiveness, and use of readily available materials make it well-suited for widespread adoption on commercial swine farms.

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**Comparison of PCV2d antibody response generated by different commercial PCV2 vaccines**

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[1]Boehringer Ingelheim Animal Health USA Inc.

Introduction

Porcine circovirus type 2 (PCV2) is an endemic virus to swine populations worldwide which has a high mutation and evolution rate (1,2). Genotype shifts have occurred in the United States and globally. Today, the most prevalent genotype is PCV2d (1,2). Although cross protection among genotypes has been demonstrated, a main reason for the emergence of PCV2d has been suggested to be due to limitations of the immunity conferred to PCV2d by PCV2a based vaccines which may lead to a selection pressure toward PCV2d (1,2). With the introduction of a novel commercial vaccine in the United States which contains both PCV2a and PCV2d antigens, this study had the objective of comparing the immune response conferred by this vaccine and other commercial vaccines on the market to the PCV2d genotype to evaluate the hypothesis that homology would confer a significantly greater immune response.

Methods

A randomized, controlled, blinded study was conducted with four different treatment groups each containing 15 pigs included in the study post weaning at approximately 21 days of age. Pigs were obtained from a high health status PCV2 naïve herd and assigned to treatment randomly after blocking for the effects of litter. Treatments were: T01) Non-vaccinated control; T02) Vaccinated with CircoFLEX® AD; T03) Vaccinated with Circumvent® PCV G2; T04) Vaccinated with Fostera® Gold PCV. Pigs received their respective vaccine treatment on day 0, and blood was collected on day 28 to assess their humoral response. Serum samples were sent to Kansas Veterinary Diagnostic Laboratory for quantitative PCV2d IFA assay to measure antibody levels. The quantitative titer results were log2 transformed for statistical analysis. Serum samples were also evaluated for PCV2 viremia by PCR. All pigs were co-housed throughout the trial.

Results

Evaluation of the PCV2d specific antibody response revealed significant differences between treatment groups. Pigs in T02 had a median PCV2d antibody titer of 10.39 (95% CI 9.66-11.12), being significantly superior to those in T03 and T04 which had median titers of 8.26 (95% CI 7.53-8.98) and 8.06 (95% CI 7.33-8.78), respectively ($p<0.0001$). As cross protection among genotypes is known to occur, not surprisingly all vaccinated groups (T02-T04) developed significantly greater antibody responses to PCV2d compared to controls (T01) which had a median titer of 4.32 (95% CI 3.59-5.05) ($p<0.0001$). No pigs developed viremia during the trial.

Discussion and Conclusions

In this controlled study, pigs immunized with CircoFLEX® AD had a significantly greater antibody response toward PCV2d as compared to those vaccinated with Circumvent® PCV G2 and Fostera® Gold PCV. The latter two vaccines do not contain a PCV2d antigen. These findings support the recent study by Kroeger et al., 2025 (3) on the impact of homology versus heterology toward PCV2a and PCV2d genotypes and the importance of a vaccine to contain a protective PCV2d antigen to maximize immunity to PCV2.

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**Efficacy of a novel vaccine containing both PCV2a and PCV2d antigens**

Troy Kaiser[1], Alyssa Jarrett[1], Summer Escoe[1], Mark Hinds[1], Fernando Leite[1]

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Introduction

Porcine circovirus type 2 (PCV2) is a DNA virus with a high evolution rate which has been categorized into at least eight different genotypes: PCV2a-h (1,2). PCV2d has become an emerging and predominant genotype in the United Sates and globally (2,3,4). A reason for the rise in the prevalence of PCV2d has been suggested to be the widespread use of PCV2a based vaccines, which despite providing some cross protection, may exert a lower level of protection towards PCV2d thereby leading to an immune selection pressure favoring this genotype (2,4). In the US, PCV2a is still a relevant genotype representing the second most common after PCV2d (3). This study evaluated the efficacy of CircoFLEX® AD, the first and only commercial vaccine to contain both PCV2a and PCV2d antigens designed to confer broader and more complete PCV2 protection.

Methods

Two separate blinded, vaccination-challenge studies were conducted using cesarean-derived, colostrum-deprived pigs vaccinated at 15 days of age. For each study, pigs were blocked by litter and randomized to treatment group. On D0, pigs were intramuscularly administered either a 1-mL dose of placebo or CircoFLEX® AD (a novel commercial vaccine containing PCV2a and PCV2d antigens). Four weeks after vaccination (D29), pigs were challenged with a 2-mL dose (1 mL intramuscular and 1 mL intranasal) of virulent PCV2: first study with 4.78 log10TCID50/mL PCV2a and second study with 4.63 log10TCID50/mL PCV2d. Blood samples were collected prior to challenge and twice weekly during the three-week challenge phase for the evaluation of viremia by qPCR. Tonsil, tracheobronchial lymph node, mesenteric lymph node, and external iliac lymph node samples were collected for histopathology and PCV2 immunohistochemistry (IHC) evaluation. A pig was considered positive for lymphoid depletion lesions if these were observed in any of the four tissues and was considered positive for colonization if any of the four tissues had PCV2 detected by IHC.

Results

Vaccination significantly reduced the number of pigs with the presence of lymphoid depletion from 86% for PCV2a and 96% for PCV2d to 21% for PCV2a and 4% for PCV2d ($P<0.0001$). Likewise, vaccination also significantly reduced lymphoid colonization from 86% for PCV2a and 100% for PCV2d to 21% for PCV2a and 11% for PCV2d ($P<0.0001$). Viremia was significantly decreased ($P<0.0001$) for each timepoint post-challenge for both challenge viruses in vaccinates compared to non-vaccinates.

Conclusion

Vaccination with CircoFLEX® AD significantly protected pigs against PCV2a and PCV2d with genotype specific antigens, providing a high level of protection against lymphoid depletion, colonization, and viremia.

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**Evaluation of Transportation GPS Technology to Assess Biosecurity Route and Downtime Procedure Compliance**

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Introduction

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) and Porcine Epidemic Diarrhea Virus (PEDV) continue to present major challenges to the U.S. swine industry, with outbreaks reported year-round. In April 2025, the Swine Disease Reporting System recorded the highest PRRSV positivity rate since 2018, with grow-finish sites being most affected[1]. Holtkamp et al. (2022) linked increased site activity to a greater likelihood of disease outbreaks[2]. Previous work indicates that excluding human movement from assessments can underestimate outbreak risk[3]. These findings highlight the risk of indirect disease transmission via vehicles, personnel, and other fomites. Despite detailed biosecurity protocols, compliance with practices (e.g., vehicle routing, downtime) remains insufficiently monitored due to limited real-time data and alerting. Digital platforms such as Farm Health Guardian (FHG) may offer a potential solution via automation of movement traceability and downtime enforcement. This study evaluated the effectiveness of GPS-based technology in enhancing visibility and improving compliance with transportation-related biosecurity protocols.

Materials and Methods

An observational study was conducted within the wean-to-finish segment of an integrated swine production system. The FHG platform was integrated with the company's GPS tracking system to monitor real-time vehicle movement and biosecurity compliance. Feed trucks and fleet vehicles (e.g., vehicles, maintenance trucks) were monitored. Geofences were established around each production site to record vehicle entries and exits throughout the study period. Site health statuses were updated weekly and synchronized with the FHG platform to apply appropriate movement restrictions. Sites with more than one pig health status during the trial were excluded to preserve the integrity of biosecurity flow evaluations. The study was carried out in two periods: Period 1 (7 weeks) served as a baseline, in which initial geofences and biosecurity criteria were monitored and refined; and Period 2 (8 weeks) involved monitoring vehicular events and biosecurity alerts and aligning operational biosecurity expectations. Activity level data was collected before and after FHG implementation, as well as following refinements to technology adaptation. Key evaluation areas included downtime compliance and adherence to biosecurity pyramid protocols by vehicle type. Biosecurity breach alerts were categorized by type and production phase to identify high-risk patterns. Data was descriptively analyzed.

Results and Conclusions

Implementing the FHG platform improved visibility of transportation-related biosecurity compliance, though several refinements were required to optimize data accuracy. Geofences required review and adjustments to ensure accurate site boundaries, while GPS coordinates were verified to reduce false breach alerts. Timely updates of site health statuses were essential for accurate classification of movements. Following these improvements, median weekly feed truck breaches declined from 81 to 12.5,

while fleet vehicle breaches declined from 88 to 11 between periods 1 and 2. Breach counts were numerically similar across different biosecurity health statuses. FHG also enabled the generation of example outbreak reports, supporting traceability by modeling exposure timelines and identifying high-risk contacts. Study findings demonstrated that real-time, GPS-based monitoring can enhance transport and vehicle biosecurity compliance and increase awareness of breach risk. Widespread adoption of such technology may strengthen adherence to protocols and support more effective disease prevention and response strategies within swine production systems.

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**USDA Updates Algorithm Supporting the National Surveillance Plan for Influenza A Virus (IAV) in Swine**

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Proactive and adaptable pathogen surveillance is critical for mitigating threats to animal agriculture and public well-being. The United States Department of Agriculture (USDA) Animal Plant Health Inspection Service (APHIS) continuously reviews and updates its disease surveillance programs to ensure efforts meet program objectives and to incorporate relevant new technologies and diagnostics. Following a recent evaluation, APHIS incorporated several updates to modernize and expand our long-standing National Surveillance Plan for Influenza A Virus (IAV) in Swine (established in 2009; formerly known as National Surveillance Plan for Swine Influenza Virus in Pigs). From inception, this plan has relied on a voluntary and anonymous sample submission process utilizing the National Animal Health Laboratory Network (NAHLN). Updates aim to increase the number of eligible samples entering the diagnostic stream and to reduce submission barriers by expanding sample types, removing the requirement for reported influenza-like illness (ILI), and leveraging existing data to increase the PCR cycle threshold cutoff for eligible samples. The revised algorithm will promote the inclusion of a larger representation of viruses. This program will continue to track the dominant groups of IAV circulating in swine in the United States, facilitate analyses that track spatial and temporal patterns in genetic diversity, and provide a repository of virus isolates for characterization and additional study. Beyond the testing algorithm, new guidance will also improve the reimbursement and submission processes. APHIS is now providing funding for IAV PCR, along with either virus isolation or whole genome sequencing for all influenza A real-time PCR positive sample submissions. Collectively, these updates are anticipated to significantly enhance representativeness, phylodynamic analyses, and the availability of isolates from the surveillance plan for characterization and further study. APHIS will continue to publish quarterly reports summarizing epidemiological trends and representative strains available in the repository, and will perform routine evaluations to monitor submission rate, cost, and the quality of the data being collected. This work supports the swine industry and the APHIS Veterinary Services' mission to protect the health of the United States swine herd. Given the plan's capacity to detect viruses with zoonotic potential, such as novel viruses introduced to pigs from non-swine hosts, it will also continue to promote public health initiatives, awareness, and partnerships.

**Post-weaning supplementation with the nutritional supplement Furst Strike Direct™ improved wean-finish performance in a large-scale system comparison - Part. 2**

W. Kwon[1], G. Hartsook[1], P. Aparachita[1], K. Soltwedel[1], R. Fischer[1], F. Sandberg[1]

[1]Furst-McNess Company

Furst Strike Direct™ (FSD) is an innovative water-soluble technology that provides the pig with monoglycerides, natural extracts, flavorings and emulsifiers to support early feed and water intake. FSD is delivered through a proprietary delivery system that allows for high levels of longer chain monoglycerides to be provided through drinking water to support overall health and critical gut development for life-time performance. Previous report using more than 49,000 pigs has shown that supplementation of FSD via drinking water at nursery placement improved life-time feed efficiency and minimized load-to-load variation with the numerical improvement of full value pigs (Kwon et al., 2024). However, it was only the first half of the entire trial, thus the trial continued to evaluate the effects of post-weaning supplementation of FSD in a large-scale production system and eventually completed the second half of the trial by utilizing additional 31,414 pigs. Therefore, the objective of this trial was to evaluate the effects of FSD supplementation through drinking water for 7-10 consecutive days at placement on the wean-finish performance and specifically increase percentage of full value pigs to market in a commercial setting. The trial included 80,809 weanling pigs (initial BW: approximately 12.5 lbs.) from 31 different barns in a large-scale production system that were randomly assigned to 2 water treatments (Control vs. FSD) in a paired barn-to-barn setup under the same management. The FSD treatment was the application of FSD at 1 x 16 oz bottle per 5 gallons of stock solution, metered at 1:128 into drinking water from placement to 7-10 days post-weaning depending on the time to fill the site (average pig days on FSD = 7 days). Performance data was collected through a recording system and analyzed using the GLM procedure in Minitab Statistical software with Fisher's t-test determining differences between the treatments. After the formal outlier testing by Grubb's analysis, 2 barns (1 from Control and 1 from FSD) were detected and eliminated from the final data. Since the system markets pigs on a fixed weight basis, there was no difference in final BW of pigs at market between Control and FSD treatment. FSD supplementation tended ($P = 0.06$) to improve Full Value ADG, and it significantly improved Full Value feed conversion ratio (FCR) by 3% (2.63 vs 2.71; $P < 0.01$). The improvement in ADG and FCR was driven in large part by the significant improvement in Full Value Sold % (92.2% vs 88.7%, $P = 0.02$) for the FSD treatment which also resulted in significantly lower mortality of 3.3%p ($P = 0.02$). The numerical improvement in load-to-load variation (CV) and the numerical reduction in cull pigs would be supportive evidence of improved uniformity of pigs when FSD supplemented. Collectively, this trial confirmed again that FSD supplementation in the nursery period is significant in supporting life-time performance and profitability of pigs.

**Safety assessment of dietary supplementation of FeedARMOR™ as a novel feed mitigant in nursery pigs**

W. Kwon[1], G. Hartsook[1], P. Aparachita[1], K. Soltwedel[1], R. Fischer[1], F. Sandberg[1]

[1]Furst-McNess Company

When considering whole farm biosecurity, using a feed mitigant for feed biosecurity is a significant tool to reduce the probability of entry of pathogens onto the farm. FeedARMOR™ is a novel feed mitigation that is designed to provide a) efficacy as a mitigant, b) safety to mill staff and feed milling equipment, c) safety to animals, d) sustenance of animal performance, and e) cost-efficiency for producers. Among the benefits of using FeedARMOR™, the most fundamental is safe to use for animals and no negative impact on animal performance while using it in the feed formulation. Therefore, the objective of this trial was to evaluate the safety of dietary FeedARMOR™ supplementation for up to 15 lb/ton of completed feed in nursery pigs by measuring growth performance especially feed intake. A total of 1,152 weaned pigs (13.7 ± 0.3 lb) were randomly assigned to 4 dietary treatments: 1) Control, 2) Control + 5 lb/ton of FeedARMOR™, 3) Control + 10 lb/ton of FeedARMOR™, and 4) Control + 15 lb/ton of FeedARMOR™. There were 24 pigs (mixed sex) per pen and 12 replicate pens per treatment. Nursery diets during the 42-day experiment consisted of a 3-phase feeding program: N1 (d 0-7), N2 (d 7-21), and N3 (d 21-42) and FeedARMOR™ was included only in N1 and N2. Nursery pigs were weighed at d 0, d 7, d 21, and d 42, and daily feed intake per pen recorded through the automatic feeding system for calculation of feed efficiency. Data were analyzed in R using linear mixed models with Treatment as a fixed effect. Along with the performance data, pH of FeedARMOR™ (pH = 3.5) was also measured and compared with pH of other competitors (pH of Product A = 2.1; pH of Product B = 3.2) in the market to ensure the safety of handling FeedARMOR™ and its non-corrosiveness toward any metal equipment. Pigs fed FeedARMOR™ regardless of different inclusion level during N1 had increased (Treatment, P = 0.003) feed intake by 20% compared to control. However, feeding 5 lb/ton FeedARMOR™ increased (Treatment, P = 0.001) feed conversion ratio (FCR) compared to control and feeding 10 lb/ton FeedARMOR™. During N2, the experimental barn tested positive by culture and PCR for F18 enterotoxigenic Escherichia coli. Increased scouring was reported in all pens. During the health challenge, there was a linear reduction (P = 0.030) in total removals in N2 from 3.2% to 1.06%. Furthermore, feeding 10 lb/ton FeedARMOR™ tended to reduce (Treatment, P = 0.056) injectable treatment compared to control during N2. In conclusion, this safety trial confirmed that FeedARMOR™ supplementation did not impact negatively on growth performance especially on feed intake. Rather, using FeedARMOR™ was beneficial in pigs' survivability during the enteric health challenge in nursery period.

**NUVIO, a Signal-Level Microbiome feed product for Reducing Post-weaning Dysbiosis in piglets.**

Alain Labbe

MicroSintesis Inc

Introduction

Weaning dysbiosis remains a critical challenge in pig production, adversely affecting piglet health and performance. It is driven by microbiome disruption during the transition from sow's milk to solid feed, compounded by environmental stressors such as separation, transportation, and handling. NUVIO Swine is a novel, signal-level microbiome feed product designed to reduce the impact of dysbiosis by attenuating bacterial quorum sensing. This approach "quiets" pathogenic bacteria, thereby reducing their virulence and interaction with the host. To evaluate the efficacy of NUVIO under commercial conditions, a field trial was conducted in collaboration with a nursery facility in Quebec, Canada. The objective was to assess NUVIO's ability to mitigate post-weaning dysbiosis and support piglet health and performance in real-world production environments.

Methods

The study consisted of two side-by-side trials in separate rooms of a nursery barn, each housing approximately 700 piglets. One group received NUVIO Swine through the drinking water at 24 mg/kg body weight via a dedicated medicator system; the control group received no supplementation. Piglets, including both barrows and gilts, were sourced from a single PRRS-negative farrowing unit and placed at 3–4 weeks of age. They were randomly assigned to pens of 34 animals. A subset of 90 piglets (45 per group) was ear-tagged and weighed on days 0 and 9 post-placement to assess early growth. Diarrhea was evaluated daily for 10 days in four pens per treatment group using a 5-point fecal scoring system and estimated incidence percentage. Mortality and need for individual medical treatments were also tracked throughout the study.

Results

NUVIO supplementation led to a significant reduction in diarrhea incidence across both trials ($p = 0.0075$ and 0.0032), indicating improved gut health and resilience to dysbiosis. Fecal score analysis showed a statistically significant improvement in one trial ($p = 0.0025$) and a numerical trend in the other, further supporting NUVIO's beneficial role in managing enteric health. Weight gain outcomes were variable due to small sample sizes, with one study showing a 0.51 kg gain at day 44, while the other showed a 0.07 kg loss, averaging a net gain of 0.22 kg. This suggests a positive performance trend linked to improved microbiome function. Additionally, mortality was numerically reduced in both trials, with an average decrease of 0.55% compared to control groups.

Conclusions

The field trials demonstrated that NUVIO Swine effectively reduces the impact of weaning dysbiosis, primarily evidenced by decreased diarrhea incidence and improved fecal scores. These results suggest the establishment of a more stable and resilient gut microbiome in supplemented piglets. Although early weight gain differences were not statistically significant, the average performance trends and reduced mortality indicate potential long-term benefits. These findings align with previous clinical data (1) and

support the inclusion of NUVIO as a practical tool for enhancing early piglet health and managing weaning-associated challenges in commercial production systems.

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**Demonstrating the safety of PRRSGard®, a lineage 1 modified-live PRRSV vaccine**

Nicholas Lauterbach[1], Jeff Okones[1]

[1]Pharmgate Animal Health

Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) continues to challenge swine veterinarians and producers, with production losses reaching an estimated $1.2 billion from 2016 to 2020. PRRSGard® is a lineage 1, PRRSV modified live vaccine (MLV) that has demonstrated efficacy in the face of heterologous PRRSV challenges, while having limited impact on growth and average daily gain post-vaccination. Three independent evaluations were conducted to further demonstrate the safety of PRRSGard in commercial growing pigs. The objective of this project was to summarize the findings of these evaluations and reinforce the safety of PRRSGard in commercial growing pigs.

Methods

Three separate safety studies were conducted using PRRSGard in newly weaned, commercial pigs in Iowa and North Carolina. The pigs enrolled averaged 21 days of age at the time of vaccination.

931 pigs were vaccinated with a full-dose of PRRSGard, given intramuscularly on the same side of the neck. Pigs were vaccinated on day 0, shortly after placement into the nursery or wean to finish site. The pigs enrolled were of various genetics, health status and were of mixed gender.

Each pig that was vaccinated was individually examined for adverse events, such as vomiting, convulsions, or other signs of anaphylactic shock, as well as swelling at the injection site by the farm's attending veterinarian. The attending veterinarian observed each pig immediately following vaccination on day 0, 48-72 hours post-vaccination, seven days post-vaccination, and 21 days post-vaccination. If there was swelling at the injection site, it was given a score based on size and severity, as described by the attending veterinarian. General observations and health checks were done daily by the farm's caretaker.

Results

No adverse events were reported by the attending veterinarians immediately after vaccination with PRRSGard on Day 0 or at any of the three other observation timepoints. 48-72 hours after vaccination, swelling at the injection site was reported in 1.7% of the pigs vaccinated. The average score of the injection site, in pigs identified with swelling, was 1.0. Seven days after vaccination, swelling at the injection site was reported in 3.3% of the pigs vaccinated, with an average score of 0.7. 21 days after vaccination, swelling at the injection site was reported in 0.75% of the pigs vaccinated, with an average score of 1.0.

Discussion

PRRSV MLV remains a relevant tool to reduce the impact of lateral PRRSV pressure. Previous trials have demonstrated PRRSGard is an efficacious option for PRRSV protection, that has limited impact on pig growth post-vaccination. This summary highlights the safety of PRRSGard and, along with previous trial work, reinforces PRRSGard as an option for PRRSV MLV in commercial growing pigs.

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**Evaluating PRRSGard in growing pigs against a PRRSV 1-4-4 RFLP challenge with suspected maternal immunity**

Nicholas Lauterbach[1], Jeff Okones[1], Gustavo Silva[2], Darin Madson[3], Hans Rotto[3]

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Introduction

In swine dense areas, PRRSV modified live vaccine (MLV) is routinely administered to breeding and growing pig herds. With the current usage of PRRSV MLV in breeding herds, understanding the potential role of maternal immunity on PRRSV MLV usage in growing pigs is important. PRRSGard® is a lineage 1, PRRSV MLV that has demonstrated efficacy in the face of heterologous PRRSV challenges. The objective of this trial was to evaluate the efficacy of PRRSGard in growing pigs against an experimental challenge with a PRRSV 1-4-4 RFLP isolate in the face of suspected maternal immunity.

Materials and methods

Pigs originated from a sow farm that had recently performed a mass vaccination with Prevacent® roughly 60 days prior to the start of the trial. One hundred sixty-four, three-week-old pigs were placed into a two-barn nursery site. At placement (Day 0; D0), the pigs received PRRSGard (n=71), Prevacent (n=72), or saline (n=21), which acted as non-vaccinated controls. From D0 to D35, Prevacent vaccinated pigs were housed in one airspace, while the PRRSGard and non-vaccinated pigs were housed in separate pens within the second airspace. On D35, pigs were moved into the same airspace, distributed by treatment group within pens, and challenged with 2 mL of PRRSV 1-4-4 isolate.

The trial concluded on D49, when remaining pigs were euthanized and lung lesion scoring was conducted. Individual pig weights were collected on D0, D35, and D49. Twenty pigs from each treatment group were sequentially bled weekly, from D0 through D49. Regression models were built to assess statistical differences and post-hoc comparisons to identify differences between treatment groups.

Results

On D0, 58% of all serum samples were positive on PRRSV ELISA testing. 0% were positive on PRRSV PCR testing. Non-vaccinated pigs housed in the same airspace as PRRSGard vaccinated pigs remained negative on PRRSV PCR testing through D35.

On D49, PRRSGard vaccinated pigs were heavier (48.68 pounds) than non-vaccinated pigs (43.50 pounds) and Prevacent vaccinated pigs (48.29 pounds). PRRSGard vaccinated pigs (0.28 pounds/day) had a significantly higher average daily gain (ADG) after the PRRSV challenge (D35 – 49) when compared to the non-vaccinated pigs (-0.03 pounds/day). PRRSGard vaccinated pigs had numeric advantages over Prevacent vaccinated pigs in end weight (0.39) overall ADG (0.0074), and livability after the PRRSV challenge (3.91%).

Discussion

PRRSGard vaccinated pigs saw improvements on average end weight (p=0.04), ADG after the PRRSV challenge (p=0.03), and overall ADG (p=0.08) compared to the non-vaccinated pigs. PRRSGard vaccinated pigs had numeric advantages over Prevacent vaccinated pigs on average end weight, overall ADG, and livability after the PRRSV challenge.

PRRSGard is a viable option when evaluating PRRSV MLV to protect growing pigs against lateral PRRSV 1-4-4 challenges. Additional work with larger sample sizes is needed to evaluate the potentially significant benefits of using a heterologous PRRSV MLV in growing pigs when compared to the PRRSV MLV being used in sow herds, as seen in this trial.

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**Piglet Weights and Variation Relationship to Total Born in High Productivity Sows**

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Introduction

Greater litter size increases concerns about birth weight and intrauterine growth restriction. Individual piglet weight data from high producing sows is lacking. Individual pigs are not routinely weighted at birth nor weaning. Benchmark piglet weight data could provide valuable insights into typical variation and opportunities for improvements in production practices and nutrition of the sow and offspring.

Materials and Methods

Data from 891 farrowing records from sows followed from parity 1 through 3 were used. Total born (TB) impact on offspring weights and variation was evaluated. Sows were Topigs TN70 females. Data was analyzed using the Descriptive Statistics function of the Data Analysis Toolkit within Excel. Data were analyzed for individual TB categories from <6 pigs to 22 pigs per litter. Data from litters with 8 and 9 pigs/litter was combined as was data from 7 and 6 pigs/litter. The remaining data was classified as less than 6 (<6) pigs/litter. At 24 hours after farrowing, pigs were cross fostered to 14.8 + 0.9 pigs/litter. Pigs were individually scored at birth for physical signs of intrauterine growth restriction (IUGR) with the percentage of pigs with no signs of IUGR calculated. The percentage of pigs less than 1 kg was also determined.

Results

As litter size increased, TB individual pig weight declined from 1,927 g/pig at <6 TB to 1,203 g/pig at 22 TB. Liveborn (LB) average pig weight was negatively related to TB declining from 1801 g/pig at <6 TB to 1182 g/pig at 22 TB . Average piglet LB weight range across litters within a TB category decreased as TB increased. The min/max weight range was 2,331 g/pig at <6 TB compared to 907 g/pig at 22 TB. The LB range decrease with increasing TB occurred due to the minimum LB weight increasing as TB increased more than the maximum LB weight decreased as TB increased. The coefficient of variation (CV%) of individual pig LB weight declined with increasing TB. The percentage of pigs within a litter without signs of IUGR averaged 85.7% + 20.9 and did not appear to be influenced by initial TB. However, percentage of pigs weighing <1kg ranged from 1.1% at <6 pigs/litter to 24.1% at 22 pigs/litter and did appear to increase with increasing TB. Sows weaned 14.0 + 1.3 pigs per litter with no difference based on original number TB. Preweaning mortality after cross-fostering was lowest at <6 TB (2.7%) and increased with increasing TB to 8.2% at 22 TB despite suckling similar numbers of piglets. Individual piglet weaning weight averaged 8.7 + 1.1 kg at 30-d of age with no apparent impact of original TB. Additionally, weaning weight CV% and range were not impacted by initial TB.

Conclusions

These results confirm the negative relationship between TB and piglet birth weight. Increasing TB resulted in more pigs <1 kg but did not impact physical IUGR features. Total born did not influence milk production as measured by weight.

**At what times do growing-finishing pigs typically eat? An example from pigs raised under minimal environmental control**

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Understanding feeding behavior in pigs is valuable for improving nutritional strategies and overall farm efficiency. Electronic feeding stations (ESF) can accurately record individual feed intake and feeding behavior. However, their use requires significant investment and has been limited mainly to feed intake registration of purebred animals in highly controlled nucleus farms. In contrast, this study aimed to investigate the feeding behavior of crossbred growing-finishing pigs raised under minimal environmental control. Data were collected from a commercial Brazilian farm with no artificial lighting at night, open-sided barns and natural ventilation, where temperature ranges from 0 °C to 32 °C throughout the year, on average. As is typical in Brazilian systems, temperature regulation was limited to opening and closing blinds during extreme heat or cold, with no additional environmental control. A total of 219,147 feeder visits from 216 pigs (Duroc x F1 sows) were recorded using Nedap ESF systems equipped with radio-frequency identification technology. We analyzed daily feed intake, number of feeder visits, and duration per visit across four age periods: P1 (70–90 days), P2 (91–111 days), P3 (112–132 days), and P4 (133–153 days). The pigs were tested in four separate batches, each spaced 28 days apart between November 2024 and February 2025 (spring-summer). They were fed a corn-soybean-based diet ad libitum and housed in 18 pens (12 pigs per pen, evenly split by sex). Data analysis was conducted in R using linear regression models (lm and lsmeans). Fixed effects included sex, batch, pen, and the hour the feeder visit began. All effects were significant ($P < 0.001$), except for batch across all traits and sex for feeding duration. Across all periods, females had lower feed intake and fewer visits than males. Average daily feed intake increased from 1,839 g (P1) to 2,493 g (P2), 3,095 g (P3), and slightly declined to 3,026 g (P4). The number of daily visits was relatively stable, ranging from 11.76 (P1) to 13.09 (P3). However, time spent feeding decreased with age, from 76.11 minutes/day in P1 to 60 minutes/day in P4. Throughout all periods, all traits followed a consistent daily pattern, with two distinct activity peaks at approximately 8 a.m. and 5 p.m., becoming more pronounced in P3 and P4. Pigs were most active between 5 a.m. and 7 p.m., during which 80% of feeding events occurred, although a slight dip in activity was observed between 10 a.m. and 1 p.m. These results show that pigs under minimal environmental control display strong diurnal feeding patterns with little nighttime feeding. Substantial deviations from the patterns described in this study could signal health or welfare issues. These results help identify the key periods to focus on feed delivery to optimize feed intake when ad libitum feeding is not applied. Overall, the findings provide valuable insight into feeding behavior in commercial conditions and support the development of tailored nutritional strategies, in addition to providing signals of health and welfare issues in pig farms.

**Foreign farm employees (TN-visa workers) in the U.S. Swine Industry: strategies to increase retention and their potential**

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The U.S. swine industry has been increasingly dependent on foreign professionals joining the workforce through the Trade NAFTA (TN) visa program due to ongoing labor shortages. There is little data on these workers' job satisfaction, language skills, perceived stress, and training or benefit requirements, despite the increased utilization of this labor. The goal of this study was to produce evidence-based skills, literacy and training needs of TN-visa workers to guide retention strategies and support their long-term contributions to the swine industry.

A research team from the University of Missouri, The Ohio State University, North Carolina State University, and the University of Minnesota created and administered a bilingual survey in Spanish and English. Seven themes were covered in the survey, which was directed at TN-visa workers in six of the top states that produce pork: (1) farm information; (2) demographics; (3) cultural and professional background; (4) career goals; (5) training opportunities; (6) job benefits and working conditions; and (7) retention drivers. A total of 261 responses were collected from 15 states, mostly from in-person interviews (81%) and the remainder from online sources.

The responses revealed five levels of job satisfaction: "very unsatisfied" (5.0%), "somewhat unsatisfied" (6.9%), "neither satisfied nor unsatisfied" (15.3%), "somewhat satisfied" (41.0%), and "very satisfied" (31.8%). Over 70% of the people who answered said they were "somewhat satisfied" or "very satisfied" with their jobs, which means that most people are happy with their jobs. On the other hand, less than 12% said they were dissatisfied. People who were dissatisfied referred to issues with coworkers, unfair treatment at work, not getting enough training, and bad management. Meanwhile, about 45% of the survey respondents reported feeling somewhat or very stressed. The most common reasons were bad management, too much work, and trouble with communication.

When TN-visa workers were asked to self-assess their English literary, 85% of them were most comfortable speaking Spanish, and only five percent said they were fluent in English. Most respondents said their English was basic or intermediate, and nearly 80% thought other farm workers could only understand some of what they said.

The respondents indicated that improving skills for workforce development was a priority, with 70% of TN-visa workers expressing a strong interest in developing skills to work with pigs, which was identified as the top priority; the same percentage was closely followed by training in employee management, self-care and wellness, and conflict management, each rated as "very important" by over 65% of respondents. Over 60% of workers rated managing personal finances as "very important," despite it being slightly lower.

This study looks at all the TN-visa workers in the swine industry and offers suggestions for how they can keep their jobs. Some ways to improve U.S. swine farms for workers include offering bilingual training,

providing culturally aware supervision, and training their supervisors in employee management; these measures can help workers get along and increase profits in the long run.

**PRRS virus Detection in Boar Studs: Impact of Sample Type and Pool Size Using RT-PCR**

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Introduction

Monitoring of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in boar studs is essential to prevent viral transmission through semen to sow farms (1). The selection of appropriate sample types and diagnostic methods is critical for early viral detection. Serum and blood swab samples are commonly used (2) for PCR; however, pooling strategies may compromise diagnostic sensitivity due to dilution effects.

Methods

This study aimed to evaluate the influence of sample type and dilution ratio on PRRSV detection by RT-PCR using known positive samples and three commercial kits. A total of 20 PRRS positive samples (9 serum and 11 swabs) were categorized by viral load (high: Ct <30, low: 30–34, and suspect >34). Samples were pooled with negative samples at dilution ratios of 1:5, 1:10, and 1:15 and then three commercial RT-PCR kits were used. Swabs were test in triplicates for a total of 120 RT-PCR reactions across the entire study. Results were compared in RStudio (v4.2.3) and differences found were considered significant when the p value for Kruskal-Wallis test and Dunn's post hoc comparisons was lower than 0.05.

Results

No significant differences were observed between sample type within each category. However, significant differences were found between PCR kits ($p < 0.015$) and between dilution ratios at 1:15 ($p < 0.001$). Higher dilution levels were associated with increased Ct values and reduced detection sensitivity, particularly in samples within the suspect category. While sample type had minimal impact on PRRSV detection, both dilution ratio and PCR kit selection significantly influenced diagnostic sensitivity. To ensure early detection — specially at very early stages of viremia —pooling beyond 1:10 is not recommended. The use of pooled samples of 10 represents a cost-effective and technically viable strategy for the monitoring PRRS virus, provided that validated diagnostic kits with adequate sensitivity are used. Additionally, the use of blood swabs as a sample type offers a less invasive and more practical option for field sampling, supporting its implementation as a reliable tool for epidemiological surveillance programs in swine populations.

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**Mycoplasma hyopneumoniae circulation in feral pigs: An exploratory spatial analysis**

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Feral pigs are an invasive species with an estimated population of 6 million within the United States. Feral pigs have the potential to transmit various diseases to livestock, including domestic swine. Despite population management efforts, feral pigs continue to spread across the country, becoming a greater potential risk to the commercial swine industry. Recent data has shown detection of Mycoplasma hyopneumoniae in feral pigs in the southeastern U.S. The extent to which feral pigs pose a risk of infection with M. hyopneumoniae and other pathogens to commercial pigs remains unknown. To understand feral pig pathogen detection and transmission, the spatial mapping of the infected individual's location is essential. Therefore, a study was conducted to describe the demographics of feral pigs tested for M. hyopneumoniae and explored the dynamics of pathogen transmission risk among location clusters. Feral pigs (n = 137) were trapped and humanely euthanized at various locations within the southeastern United States. Bronchial swabs were collected from each pig and tested for M. hyopneumoniae by PCR. Spatial analysis was conducted using a comprehensive geographic information system (ArcGIS) to compare data characteristics including PCR results, trapping location, and sex. A subset of M. hyopneumoniae positive samples were submitted for P146 genetic sequencing to establish if strains differed between cluster locations. Of the 47% of pigs that were positive for M. hyopneumoniae, the highest positivity rate was observed in one location cluster, reaching 56%. Genetic sequencing identified two positive samples from the same cluster were identical, while two positive samples from different cluster locations showed varying sequences, possibly indicating strain diversity based on sounder location. Data characteristics of the sampled population were analyzed for demographic patterns. While females were more likely to be positive when compared to males (55% vs. 37%), it can be speculated that the seasonal movement of solitary males may drive pathogen transmission between sounders. This sex-specific activity pattern could be a key component to feral pig transmission for M. hyopneumoniae and other infectious agents. Previous research has shown feral pigs have been infected with agents such as PRRS virus and pseudorabies virus, suggesting the possibility of reservoir status. High rates of pathogen detection, like those observed within this spatial mapping study, could pose risks for commercial production systems. With feral pigs commonly traveling long distances for resources and breeding opportunities, swine barns in low disease areas could be most vulnerable to high feral pig infection rates. Based on this study's results, the key to mitigating preventable commercial system outbreaks and maintaining disease elimination status could be to further understand the infection status, transmission routes, and behavioral patterns of feral pigs.

**Evaluating the Association between Farm Density and Farm Type and PRRSV outbreaks in Breeding Herds**

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Introduction

Studies have shown that farm density is associated with an increased risk of PRRSV infection1,2. However, there is still a gap in understanding how this association varies across different distance ranges and farm types, and to what extent proximity and farm characteristics influence risk. The objective of this study was to investigate the association between farm density and PRRSV classification in breeding herds (BH).

Material and Methods

To conduct this study, we used site location, PRRSV classification and variables such as farm type and production system from the sites participating in the Porcine Regional Information Management Ecosystem (PRIME) project from January 2019 to June 2025. PRIME Automated Classification System currently has 1,864 sites classified weekly as PRRSV-negative or positive, based on diagnostic results and movement information. PRRSV-positive classifications also included vaccine-like strain results. A matched case-control study was conducted based on site classifications for PRRSV from January 2020 through June 2025. Cases were defined as BH classified as positive, considering the entire period during which the farm remained positive until it became negative again. Controls were selected based on three criteria: (1) BH that remained negative during which the entire period the matched case was positive; (2) located 20–50 miles from the case; and (3) with at least one negative PCR result during the study. A conditional logistic regression model was used to identify risk factors for PRRSV classification. Predictors included farm density within 5-, 10-, 15-, and 20-mile radii, with counts calculated for all sites and stratified by farm type. Additional variables captured the number of PRRSV-positive sites within each category. Production system was included as a random effect to account for clustering and unobserved heterogeneity.

Results

Descriptive results showed that, for both the total number of surrounding farms and the subset representing growing herds, higher farm density was significantly associated with increased odds of PRRSV classification in BH, with the strongest associations observed within 5 miles (OR total = 1.84 and OR GH = 2.24). OR progressively decreased as the distance increased, suggesting that proximity plays an important role in risk. Similarly, for BH and for sites used for gilt development and isolation, higher farm density within various distance ranges was associated with increased odds of PRRSV classification in BH. Among BH, the odds were highest within 10 to 15 miles (OR = 4.88), while for GDU and Isolation, the strongest association was observed between 15 and 20 miles (OR = 5.41). Similar results were found when accounting for only positive sites, where higher farm density within 5 miles remained significantly associated with increased odds of BH classification across all farm types. However, at greater distances, the associations weakened and often lost statistical significance, particularly for growing herds, GDU and Isolation sites.

Conclusion

Findings suggest that farm density within up to 20 miles increases the odds of a BH being classified as positive for PRRSV, with the strongest effect observed within 5 miles. Results support targeted biosecurity and surveillance based on local density and farm type.

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## Late Gestation Phase Feeding in Prolific Sows Influences Early Postnatal Bone Development in Progeny

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Nutrient demands rise sharply in late gestation, yet sows are often fed static diets that may not meet maternal or fetal needs. This study evaluated the effects of late gestation phase feeding on sow and piglet nutritional status, mineral metabolism, and early bone development. Thirty females (parity 0–2) at 68-d ± 2-d of gestation were assigned to one of two treatments. Treatments were either (1) a control diet (CON; n = 35) with 11% CP, 0.52% SID lysine, 1.48× NRC trace minerals (organic), and vitamins ≥ NRC; or (2) a late gestation phase diet (LGPHASE; n = 35) with 16% CP, 0.87% SID lysine, 2.48× NRC trace minerals (organic), and >2× NRC vitamins + 500 mg/kg vitamin C. A common diet was fed to all females during lactation. Fifteen piglets per treatment (n = 30) were selected for necropsy at 2 +/1 days of age. Prior to euthanasia, blood was collected from each pig for analysis of serum ferritin, trace minerals, and vitamin D (25(OH)$D_3$). Liver tissue was analyzed for concentrations of 25(OH)$D_3$, vitamin A, vitamin E, and trace minerals. Rib sections were taken near the midshaft to evaluate histological features. A separate subset of ribs was pooled and analyzed for bone ash determination, reported as percentage ash on a fat-free dry weight basis. Histopathological evaluation of the rib growth plates assessed structural and cellular characteristics including the definition of the growth plate-metaphysis interface, cartilage persistence into the diaphysis, periosteal bone development, alignment of chondrocyte columns, expansion of the hypertrophic cartilage zone, presence of osteoblasts and osteoclasts at the growth plate–metaphysis interface, bone spicule development, marrow fibrosis, and lateral bridging. Lesions were scored as absent/normal, mild, moderate, or severe. Birth weights of necropsied piglets were similar between groups (CON: 1.62 kg; LGPHASE: 1.65 kg). Bone ash percentages did not differ between groups (CON: 58.4%; LGPHASE: 59.0%). Among the 43 ribs examined from CON piglets, 2 were classified as mild, 2 as mild to moderate, 17 as moderate, 19 as moderate to marked, and 3 as marked. Among 44 ribs from LGPHASE piglets, 7 were mild, 6 mild to moderate, 16 moderate, 15 moderate to marked, and none were marked. Moderate to marked bone lesions were numerically more frequent in CON piglets (90.0%) than in LGPHASE piglets (71.1%) (P = 0.116). Conversely, the prevalence of mild bone lesions were numerically more frequent in the LGPHASE group (28.9%) compared to CON (10.0%) (P = 0.116). The odds of moderate or worse rib lesions were lower in LGPHASE piglets than CON, with an odds ratio of 0.24. Specifically, 90.7% (39/43) of ribs from CON piglets exhibited moderate or worse lesions, compared to 70.5% (31/44) in the LGPHASE group. In conclusion, phase feeding in late gestation improved rib health and reduced lesion severity, demonstrating clear benefits to skeletal development. However, abnormal rib morphology was not fully prevented, indicating that longer supplementation or repeated application across reproductive cycles may be necessary for more complete skeletal outcomes.

## Late Gestation Phase Feeding in Prolific Sows: Impacts on Reproductive Outcomes and Nutritional Biomarkers in Sows and Their Progeny

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Nutrient demands rise during late gestation; therefore, static gestation diets may not adequately meet the sow's increasing nutrient needs. This study evaluated effects of a nutrient-enriched late gestation diet on reproductive performance and blood-based biomarkers in sows and progeny. Seventy females (parity 0–5) at 68-d ± 2-d of gestation were assigned to one of two treatments. Treatments were either (1) a control diet (CON; n = 35) with 11% CP, 0.52% SID lysine, 1.48× NRC trace minerals (organic), and vitamins ≥ NRC; or (2) a late gestation phase diet (LGPHASE; n = 35) with 16% CP, 0.87% SID lysine, 2.48× NRC trace minerals (organic), and >2× NRC vitamins + 500 mg/kg vitamin C. A common diet was fed to all females during lactation. Blood was collected from the females on days 68 ± 2 and 110 ± 2 of gestation and weaning (lactation day 19 ± 3) for blood counts and serum analysis. Piglet Hb was measured at birth and weaning (birth: n = 974; wean: n = 826). Serum samples were collected from a subset of piglets (2 per litter; n = 136) at 40–48 hours post-birth (d-2) and at weaning. Female and piglet serum was analyzed for copper, iron, zinc, ferritin, and 25(OH)$D_3$. Farrowing duration was shorter in LGPHASE females than CON females (290.4 vs. 359.9 min; P = 0.028). Number of total born (CON: 16.5; LGPHASE: 16.5) and live born (CON: 14.5; LGPHASE: 15.2) piglets did not differ between treatments, but stillbirth rate tended to be lower in LGPHASE females than CON females (3.4% vs. 6.8%; P = 0.099). Piglet and total litter birth weights were similar between groups. The LGPHASE group tended to have lower piglet weaning weight than the CON group (5.7 vs. 6.2 kg; P = 0.087). However, the number of piglets weaned was greater in LGPHASE females than CON females (13.4 vs. 12.3; P = 0.062). Piglet survivability was greater in the LGPHASE group compared to the CON group (90.5% vs. 84.8%; P = 0.019), with lower pre-weaning mortality in LGPHASE litters than CON litters (10.0% vs. 14.9%; P = 0.045). Hemoglobin in LGPHASE females tended to be higher at d-110 gestation (11.2 vs. 10.7 g/dL; P = 0.091) and was higher at weaning (10.7 vs. 9.9 g/dL; P = 0.004) than CON females. Serum 25(OH)D d-110 was higher in LGPHASE females than CON females (54.8 vs. 35.5 ng/mL; P = 0.002). The LGPHASE females also tended have greater serum ferritin at weaning than CON females (38.5 vs. 28.3 ng/mL; P = 0.074). Piglet serum ferritin on d-2 tended to be greater in the LGPHASE group than the CON group (25.1 vs. 19.1 ng/mL; P = 0.079), while 25(OH)D also tended to be greater in LGPHASE piglets than CON piglets (7.5 vs. 6.9 ng/mL; P = 0.080). These results suggest that late gestation needs for amino acids, trace minerals, and vitamins exceed typical commercial levels. Increasing nutrient supply improved farrowing outcomes, piglet survival, and micronutrient status in sows and piglets.

**Low Blood Hemoglobin Levels Predicts Early Sow Removal in Commercial Herds**

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As reproductive intensity increases in modern, highly prolific sows, systemic challenges such as anemia may compromise health, performance, and longevity. Hemoglobin (Hb) is a critical biomarker of iron status and oxygen-carrying capacity; however, its evaluation remains underutilized in commercial settings. This study examined the impact of sow Hb status on reproductive performance and assessed the relationship between Hb levels and the risk of subsequent sow removal. A total of 1,945 females (parities 0–8) across four commercial farms were enrolled. Whole blood was collected via ear vein puncture on gestation day 100 ± 12 and analyzed on-site using the HemoCue Hb 201+ system. Females were categorized as non-anemic (Hb ≥ 10.0 g/dL; n = 792) or anemic (Hb < 10.0 g/dL; n = 1,153). Females were scored 1 (low), 2 (moderate), or 3 (high) for pelvic organ prolapse risk based on established classification methods, and body condition score (BCS) was assessed using the Knauer Sow Caliper (KSC). Sow removals—defined as death, euthanasia, or culling for non-age-related reasons—were tracked over a 70-day period post enrollment. Anemia prevalence averaged 59.3%, varying by farm (46–61%). Anemia rates increased with parity ($P < 0.001$), rising from 40.6% in parity 0 to 82.7% by parity 3. Anemic females exhibited lower BCS compared to non-anemic females (12.5 vs. 13.1 KSC units; $P < 0.001$), with a modest positive correlation between Hb and BCS ($r = 0.21$; $P < 0.001$). Although anemic females had a higher total born count than non-anemic females (16.4 vs. 15.7; $P < 0.001$), they also had increased stillbirth rates (5.3% vs. 4.2%; $P = 0.011$), with no difference in piglets weaned between groups. Removal risk was higher in anemic females than non-anemic females (8.4% vs. 3.5%; $P < 0.001$), with each 1 g/dL increase in Hb being associated with a 43% reduction in the risk of removal during the 70-day tracking period (HR= 0.57; $P < 0.001$). Removal rates were consistently higher in anemic females than non-anemic females across most parities: parity 0 (15.4% vs. 6.9%), parity 1 (8.3% vs. 2.8%), parity 2 (13.5% vs. 6.7%), and parity 3 (11.3% vs. 4.2%) ($P < 0.05$). However, no difference in removal risk was observed in parity 4 and higher sows. These findings support the use of Hb as a practical, on-farm biomarker to identify females at elevated risk of removal due to suboptimal health. Monitoring Hb during gestation offers a valuable diagnostic tool for managing herd retention and optimizing sow longevity. The high prevalence of anemia, especially in early-parity females, highlights the critical need for targeted nutritional and health interventions to mitigate iron deficiency and associated reproductive losses.

**Parenteral Iron Supplementation in Prolific Sows Post-Weaning: A Dose-Response Study**

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Emerging evidence suggests that anemia is common in prolific sows, yet practical strategies to restore iron status in adult females remain underexplored. This study evaluated the hematological and biochemical response of sows to intramuscular iron dextran administered post-weaning. Twenty weaned sows (PIC Camborough) were stratified by parity, body weight, and initial hemoglobin (Hb) concentration, and assigned to one of three intramuscular iron dextran treatments: Control (0 mg, n = 6), Moderate (2,500 mg, n = 7), or High (5,000 mg, n = 7). A corn-soybean meal-based gestation diet, meeting or exceeding requirements for pregnant gilts was fed once daily (2.2 kg/sow) throughout the experiment. Iron dextran injections were administered on day 1 post-weaning. Hemoglobin concentration was measured every other day from day 0 through day 30 using the HemoCue Hb 201+ analyzer. Blood samples for serum iron parameters were collected via jugular venipuncture on days 0 (prior to iron injection) and 30 of gestation. Additionally, sow body weight was recorded on days 0 and 30 of gestation. Throughout the experimental period, no adverse effects from iron treatment were observed. Mean Hb concentration across the 30-day period was higher in both iron-treated groups compared to the 0 mg group (0 mg: 10.3 g/dL; 2,500 mg: 11.4 g/dL; 5,000 mg: 11.2 g/dL; P = 0.005). No difference was observed between the 2,500 mg and 5,000 mg groups (P = 0.768). Serum ferritin concentrations (day 0 vs. day 30) increased in the 2,500 mg group (10.6 → 36.8 ng/mL; P = 0.019) and tended to increase in the 5,000 mg group (10.5 → 38.3 ng/mL; P = 0.057). No change in serum ferritin occurred in the 0 mg group (10.1 → 31.1 ng/mL; P = 0.130). Between-group comparisons for serum ferritin at day 30 were not different. Total iron-binding capacity (TIBC) declined over the 30-day period in all groups (0 mg: 477.1 → 360.7 µg/dL; 2,500 mg: 463.5 → 330.6 µg/dL; 5,000 mg: 458.7 → 330.6 µg/dL; P < 0.001). Serum iron concentrations remained unchanged across time and treatment (range: 82–92 µg/dL; P > 0.10). In conclusion, intramuscular iron dextran administered post-weaning improved Hb concentrations in sows in early gestation and increased serum ferritin, suggesting enhanced erythropoiesis and replenishment of iron stores. A 2,500 mg dose was sufficient to elicit these responses, with no additional benefit observed at 5,000 mg under the conditions of this study. These findings support the post-weaning period as a strategic window for iron intervention in sows recovering from iron losses from farrowing and lactation. Further research is warranted to evaluate long-term benefits on sow blood health and reproductive performance.

## FIELD EVALUATION OF IMMUNE RESPONSE AGAINST A 0,5 ML FOOT AND MOUTH DISEASE VACCINE THROUGH A NEEDLE-FREE INJECTION DEVICE OR CONVENTIONAL NEEDLE

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Introduction

Foot-and-mouth disease is one of the world's most contagious animal viruses affecting swine and other livestock, with major economic consequences. Effective vaccination strategies are essential. Recent studies show that reduced volume (0.5 mL) ultraconcentrated vaccines maintain protective responses in pigs (Mamani et al., 2022). Needle-free (NF) devices also provide operational advantages, improving safety, animal welfare, and ease of use during large-scale vaccination (Ruben et al., 2020).

This paper reports studies evaluating the immunogenicity of this reduced volume vaccine applied by subcutaneous injection or needle-free Free.

Materials and Methods

Sixteen FMD-seronegative piglets (8 weeks old) were divided into two groups (n=8). Both groups received the same vaccination protocol of two doses 30 days apart.

A dose of newly developed Bioaftogen 0,5 ml containing O1 Campos, A24 Cruzeiro, and A2001 Argentina strains (Biogenesis Bago, Argentina) was used in this trial in the 2 groups: Group 1 received vaccination with a commercial needle-free (compressed gas powered) and Group 2 through conventional needle. All animals were blooded at day 0, 30 dpv and 26 days after revaccination. A commercial Liquid Phase Blocking ELISA was used. Titers were analyzed by Student's t-test.

Results and Discussion

All pigs were seronegative for FMD before vaccination. On the other hand, all animals developed protective titters by 30 dpv. Booster vaccination significantly increased responses for all serotypes. For O1 Campos, both groups exceeded the protective threshold after the first dose, and SC titers were slightly higher ($p > 0.05$) after boost. Similarly, A24 Cruzeiro SC titers were higher after boost ($p<0.05$). A2001 Argentina showed similar antibody titers at both evaluated time points and routes. In general, both administration routes showed effective immune responses. These findings confirm the immunogenicity of the newly developed Bioaftogen 0.5 mL FMD vaccine, regardless of delivery method, and the practical advantage of using NF.

Conclusion

The Bioaftogen 0.5 mL FMD vaccine induced protective immune responses via both SC and NF delivery. The comparable efficacy, combined with the logistical and welfare advantages of NF systems, supports its use in modern swine vaccination programs.

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**Evaluation of manure pit agitation and pumping as a factor for porcine reproductive and respiratory syndrome (PRRS) virus detection changes through oral fluids**

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Introduction

Yearly, the onset of the porcine reproductive and respiratory syndrome (PRRS) epidemic occurs between October and November, reaching its peak during the winter months. At the same time the epidemic starts yearly fertilization through pig manure incorporation into the field (manure pumping). When manure is stored in deep pits a layer of foam is built on the top layer capturing gases such as hydrogen sulfide (H2S), and ammonia (NH3). However, when manure is agitated, disturbance occurs and the foam layer collapses and releases significant quantities of these gases. Data supports the fact that manure pit-generated gases can be harmful to the respiratory system as they are a stressor that can lead to complications. There is still a knowledge gap regarding the relationship between manure agitation and pumping and PRRSV outbreak occurrence as the mechanism is poorly understood. Given that there is a temporal relationship between PRRSV occurrence and manure pumping activities, we hypothesize that NH3 and H2S released during the process of manure pit agitation and pumping irritates the respiratory tract leading to inflammation and thus the direct migration of cells from the bloodstream to the lung. This increase in pulmonary macrophages could contribute to viral replication and thus increase the presence of the virus in the bloodstream and thus increase in shedding.

Methods

Seven conveniently wean-to-market or grow-finish farms with pigs originated from a PRRS-positive breeding herds without recent history of PRRS vaccination and located in Minnesota were selected. Farms were divided into two groups, one during the fall and winter of 2023, and the second during the same seasons of 2024. Each farm was visited two times before and two after pit agitation for the collection of oral fluids to assess shedding. A total of 20 pens with approximately 30 pigs each were selected to represent 10 sample collection areas from each farm. One week before the first visit detectors for NH3, H2S, temperature and relative humidity were placed in the middle section of the barn to collect data continuously.

Results

PRRSV detection by RT-PCR varied between farms and within farms' sampling dates for oral fluids. Overall Ct values were high, ranging between 24.6 and 35.9 accounting only positive results. A GLMM was used to assess the association between time of sample collection, pigs' age, and day difference between sampling and event on the probability of having a positive detection for PRRSV using RT-PCR from oral fluid. The odds of having a positive detection were 1.54 times higher during the pre-pumping sampling dates compared to post-pumping, but this result was not statistically significant (OR = 1.54; 95% CI 0.45, 5.26; p-value = 0.49).

Conclusion

This field-based study evidences that PRRSV detection using oral fluids is not affected by manure agitation and pumping in pigs during the growing phase. The consistent detection of the virus suggests that there might a process in the pigs that is triggered by the exposure to these gas concentration changes that maintain the viral shedding.

**Cardiac Puncture Blood Collection as a Practical and Biosecure Method for Postmortem Pathogen Detection in Pigs**

Claudio Marcello Melini[1], Mariana Kikuti[1], Xiaomei Yue[1], Cesar A. Corzo[1]

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Introduction

Non-invasive sample collection methods using swabs, wipes, semen, tonsil oral scraping (TOSc), and oral fluids require a short interaction with the pig and for most, lack of physical restraining. Blood sampling is considered as invasive, and in pigs there is the need for physical restrain for the safety of the animal and sample collector. Post-mortem sampling is an alternative for specimen collection during both endemic and foreign animal disease (FAD) infectious disease outbreak diagnostic investigations. When a pig cadaver is explored by making incisions to reach target organs, this process poses a risk of environmental contamination as blood and other secretions and excretions will be spilled. In the case of a disease such as porcine reproductive and respiratory syndrome virus (PRRSV) which is endemic in most pig producing countries, blood contaminated surfaces are a concern as these can act as fomites. However, in the case of an FAD such as African Swine Fever virus (ASFV), it has been reported that the virus can remain viable in putrefied blood for 15 weeks at room temperature, meaning environmental contamination with blood during these investigations represents an important dissemination risk. Even though blood from live animals has diagnostic value, alternatives to this specimen collection are needed during clinical investigations that require no blood spillage (e.g., ASF, classical swine fever [CSF]).

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. At each farm, recently dead or humanely euthanized pigs were included in the sampling. Pigs were on right lateral recumbency on a flat surface and, by using the proximal end of the ulna, the area within the thoracic cavity where the heart lies would be identified. Once the punction area was identified, a sterile needle was introduced perpendicularly in-between the ribs and through the intercostal muscles to reach the heart. Once the blood sample was obtained, it was transferred to a blood collection tube without anticoagulant. Samples were submitted to the University of Minnesota diagnostic veterinary laboratory for RT-PCR testing for PRRSV as a surrogate for other bloodborne viruses.

Results

A total of 286 CP blood samples were collected from196 suckling and 90 growing pigs. In nine cases, the sample 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 95% of the samples with a median (IQR) cycle threshold value of 21.5 (17.1, 28.5), a minimum of 10.8 and maximum of 35.5.

Conclusion

Blood collection from dead pigs is a viable welfare-friendly alternative for pathogen detection. Furthermore, this method can be safely used when diseases of high impact such as ASFV and CSFV are suspected as it minimizes blood spillage and supports biocontainment. It is an alternative to obtaining

serum for surveillance and diagnosis of pathogens of interest (i.e., PRRSV, ASF, CSF) when a necropsy on site is not feasible and minimizing blood spillage is critical.

**Assessing Environmental Contamination in and around Dead Animal Disposal Structures in Wean-to-Market Farms**

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Introduction

Swine mortality, particularly from infectious disease, poses biosecurity risks and makes it essential to dispose of cadavers in a biosecure manner to prevent disease spread. While transmission routes of swine viral pathogens are well studied, limited attention has been given to the role of dead animal disposal methods as sources of environmental contamination. External areas of farms are often shared by farm personnel, vehicles, maintenance crew, veterinarians, visitors, and crucially, equipment and machinery involved in dead animal removal. It is possible that viral contaminants around dead animal structures represent a breach to both successful biocontainment and bioexclusion practices. Therefore, our objective was to assess the environmental contamination around dead animal disposal structures and determine if the contamination differs according to how dead animals are managed.

Methods

We conducted a cross-sectional study to assess the environmental contamination in dead animal management structures on 33 Midwestern US wean-to-market farms. Those farms were Porcine Reproductive and Respiratory Syndrome Virus 2 (PRRSV-2) or Porcine Endemic Diarrhea Virus (PEDV) positive, according to their attending veterinarian. Ten environmental samples (two each from road, ground, wall, carcass, and leachate) from the vicinity of the dead handling structure were collected using Swiffer pads attached to a mop. Samples were submitted to the University of Minnesota Veterinary Diagnostic Laboratory for PCR testing targeting PRRSV-2, PEDV, PDCoV and TGEV. For PCR-positive farms, samples from the three lowest Ct values were sent for viral isolation.

Results

Out of 33 farms (330 samples) tested, 18 (54.55%) tested positive for at least one of the tested viruses. When stratified by the dead animal handling method, 79.0% (15/19) of the rendering sites and 21.4% (3/14) of the composting sites tested positive for at least one virus (chi-square p-value=0.001). PRRSV-2 was the only pathogen identified at both rendering and composting sites. The average cycle threshold (Ct) value for PRRSV-2 positive tests was lower at rendering sites (30.4) compared to composting sites (33.6, T-test p-value= 0.012). PEDV and PDCoV were exclusively identified on 12.1% and 21.2% of the rendering farms, respectively. The Ct value for all pathogens tested was lower (suggestive of higher viral load) in samples collected from leachate and carcass, respectively. No successful viral isolates were obtained.

Conclusion

Our results indicate that dead animal handling structures in wean-to-market farms are frequently contaminated, and that environmental contamination was more prevalent on rendering sites. Virus isolation was not successful from any of our environmental samples, suggesting that the detected viral material was either not infectious, not viable, present at levels below the analytical sensitivity of the isolation method, or contained inhibitors that hindered the isolation. Despite this, the presence of viral

genetic material in and around these structures supports the possibility of accidental transmission through contact with contaminated surfaces. As expected, lower Ct values (indicative of higher viral load) were found in samples collected from leachate and carcasses suggesting that practices that minimize contact of carcasses or fluids originating from them and commonly used farm areas, such as roads, may improve biocontainment near these sites.

**Longitudinal assessment of PEDV infection dynamics in wean-to-finish herds in the U.S. Midwest**

Juan Mena Vasquez[1], Montserrat Torremorell[1]

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Introduction

Porcine epidemic diarrhea virus (PEDV) is a highly contagious pathogen that causes severe gastrointestinal disease in pigs, resulting in high mortality in suckling piglets1. In older pigs, losses are mostly due to reduced growth and worsening feed efficiency2. However, there is limited information available on the epidemiology of PEDV in growing pigs, particularly regarding its prevalence and infection dynamics. Understanding PEDV status in these populations is essential to guide control and eradication strategies. This study aimed to assess PEDV status and infection patterns in wean-to-finish (WTF) herds across the U.S. Midwest.

Methods

Sixty-three WTF herds from 10 swine production companies in the U.S. Midwest participated in a prospective cohort study from September 2017 to December 2018. Herds were selected based on convenience, logistical feasibility, and veterinarians' willingness to participate in the study. At each site, eight oral fluid samples were collected approximately every four weeks using cotton ropes placed in pens throughout the barns (sampling at ~ 3, 8, 12, 16, 20, and 25 weeks post-placement). After collection, samples were refrigerated, shipped to the University of Minnesota for processing, aliquoted, and stored at –80 °C. RT-qPCR was used to detect PEDV RNA3. Samples with a cycle threshold (Ct) ≤ 36 were considered positive.

Results

A total of 2,585 oral fluid samples were tested for PEDV, yielding 139 positives (5.4%). Positive samples were found in eight WTF herds (13%) across three production companies (Company A: four herds, Company B: three herds, Company C: one herd). Among positive samples, 33.8% (47/139) were detected at 3 weeks (average Ct = 28.8), 30.2% (42/139) at 8 weeks (Ct = 30.5), 25.9% (36/139) at 12 weeks (Ct = 30.5), 5.0% (7/139) at 16 weeks (Ct = 31.4), 1.4% (2/139) at 20 weeks (Ct = 35.5), and 3.6% (5/139) at 25 weeks (Ct = 33.1). The majority of positive herds tested positive from 3 to 20 weeks post-placement, with one herd testing positive at 25 weeks.

Six of the positives WTF herds received piglets from a single sow farm each, while two received piglets from two different sow farms. According to information provided by the Morrison Swine Health Monitoring Project (MSHMP), six of these sow farms were classified as PEDV Status 4 (negative), one as Status 2fvi (positive stable, field virus exposure), and one was unknown.

Conclusion

This study provides valuable insights into the infection dynamics of PEDV in WTF herds in the U.S. Midwest. Most detections occurred early in the production system, suggesting that piglets may be weaned PEDV-positive, acquire infection during transport, or become infected shortly after entering the WTF site. Detection of PEDV towards the end of the growing period may indicate a new infection. These

findings highlight the need for early monitoring and strategies to ensure the weaning of PEDV-negative piglets to reduce transmission and support long-term control and eradication efforts in growing pigs.

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**Longitudinal assessment of influenza A virus infection dynamics in wean-to-finish herds in the U.S. Midwest**

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Introduction

Influenza A virus (IAV) is endemic in swine herds worldwide, contributing to economic losses in pig production and posing a continuous threat to public health1. Epidemiological data on prevalence, incidence, and infection dynamics in growing pigs, particularly in wean-to-finish (WTF) systems, are limited. Thus, a more comprehensive understanding of IAV circulation in WTF herds is critical to inform targeted surveillance, enhance biosecurity and vaccination programs, and reduce transmission risks. This study aimed to evaluate IAV status and describe infection patterns of IAV in WTF herds across the U.S. Midwest.

Methods

Sixty-three WTF herds from 10 swine production companies in the U.S. Midwest participated in a prospective cohort study from September 2017 to December 2018. Herds were selected based on convenience, logistical feasibility, and veterinarians' willingness to participate in the study. At each site, eight oral fluid samples were collected approximately every four weeks using cotton ropes placed in pens throughout the barns (sampling at 3, 8, 12, 16, 20, and 25 weeks post-placement). Samples were tested for IAV by RT-qPCR 2 and samples with a cycle threshold (Ct) ≤ 37 were considered positive.

Results

A total of 2,585 oral fluid samples were tested for IAV, yielding 623 positive results (24.1%). Positive samples were identified in 60 out of 63 WTF herds (95.2%) across all companies. IAV was detected at all six scheduled sampling events throughout the WTF period. IAV was detected in most herds at least once, with positivity and viral load varying across time points. The highest sample level positivity was at 8 weeks post placement (31.0%, mean Ct 29.7), followed by 3 weeks (22.6%, Ct 30.4). Thereafter, positivity declined over time: 15.4% at 12 weeks (mean Ct 29.3), 12.0% at 16 weeks (Ct 30.0), 15.2% at 20 weeks (Ct 30.6), and 3.7% at 25 weeks (Ct 30.7).

Conclusion

IAV circulates widely in WTF herds in the U.S. Midwest throughout the growing period, with peak positivity during the first 8 weeks post-weaning. There were different dynamics of infection, indicating ongoing, recurrent, or new viral introductions. Detection within the first few weeks post-weaning suggests that piglets may be weaned IAV-positive, acquire infection during transport, or become infected shortly after weaning, potentially when commingled with pigs from different sources. The variability in timing and duration of detection highlights the complex infection dynamics of IAV in WTF and the challenges in controlling IAV in these settings. These findings emphasize the need to tailor surveillance and control strategies to growing pigs. Extended monitoring and vaccination are essential to reduce IAV burden and viral persistence, and mitigate risks to swine and people. Molecular characterization, combined with risk

analysis, will improve understanding of transmission and inform more effective prevention and control measures of IAV in growing pigs

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**Experimental comparison of airborne shedding of distinct porcine reproductive and respiratory syndrome virus variants**

Juan Mena Vasquez[1], Wang Lan[1], My Yang[1], Marcelo Melini[1], Montserrat Torremorell[1]

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Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) is considered the most economically devastating swine disease in the U.S., with estimated annual losses exceeding $1 billion 1. Given its ability to spread via aerosols2, controlling PRRSV transmission within and between farms is a persistent challenge. The rapid dissemination of variants such as PRRSV L1C1-4-4 has raised questions about whether newly emergent variants exhibit enhanced aerosol transmission compared to older ones. This study aimed to assess the levels and temporal dynamics of virus-laden aerosols from pigs experimentally infected with distinct clinically relevant PRRSV variants.

Methods

Three PRRSV-2 variants were evaluated: L1C.5 1-4-4 and L1A 1-7-4, associated with recent severe outbreaks, and L9A (D99-30100), a historically documented airborne strain and perceived lower virulence.

Fifty PRRSV-naïve, 3-week-old pigs were randomly assigned to four groups (n=14 per variant; n=8 negative control) and inoculated intranasally with 2 mL of virus ($1 \times 10^{5.5}$ $TCID_{50}$/mL) or mock inoculated. Clinical signs, weight, serum, nasal swabs, air, and surface samples were collected over the 20 days. Air samples were obtained using a non-viable Andersen cascade impactor sampler and the AirPrep sampler, while surfaces, specifically aluminum foil sheets placed to capture settling airborne particles, were swabbed using moistened gauze. All samples were collected over 30 minutes and quantified by RT-qPCR targeting ORF62. Viral load was calculated from Ct values using standard curves and expressed as $log_{10}$ RNA copies/$m^3$ for air samples and $log_{10}$ RNA copies/$cm^2$ for surface samples.

Results

All pigs inoculated with PRRSV exhibited clinical signs, with L1C.5 and L1A showing more severe symptoms and reduced growth rates. The variant L1A produced the highest and most sustained viremia, followed by L1C.5, which had a high viremia during the first 7 days post-infection (DPI)., For both variants, the viremia decreased after 15 DPI. Interestingly, variant L9A had the lowest viremia during the first 7 DPI, but remained relatively elevated throughout the study. Similar trends were observed for nasal shedding, with the difference that shedding of L1C.5 was lower after 11 DPI compared to the other two variants.

All three variants were detected consistently in air and surfaces, although with differing patterns. Detection was similar during the first 10 DPI, with L1A showing the highest and most sustained airborne levels. Interestingly, the L1C.5 became undetectable after 13 DPI, coinciding with reduced nasal shedding. Lastly, all strains could be detected in larger particles (>9.0 µm), with less frequent detection in the 9.0 and 4.7 µm range.

Conclusion

This study advanced the understanding of PRRSV transmission through the air and supports the notion that there are differences among PRRSV variants in their ability to become airborne. These results also point to the need to adjust and possibly enhance biosecurity protocols that may be dose-dependent, including protocols for incoming air biosecurity. Ultimately, results from this study should help guide the development of more effective strategies to prevent the introduction of new variants into farms, including variants with a higher propensity to transmit through the air.

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**Development and Evaluation of Live Attenuated Vaccines for Protection Against Influenza A Virus in Swine**

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Influenza A viruses (FLUAV) pose a threat to the global swine industry, causing significant economic losses. Inactivated vaccines are the main method of controlling FLUAV in swine but often fail to provide protection against antigenically distinct strains. Although effective at inducing systemic IgG antibodies, these vaccines have limited capacity to stimulate cellular and IgA responses, essential for respiratory mucosal immunity and cross-protection. Live attenuated influenza vaccines (LAIV) induce broader immune responses and cross-protection, but recent concerns regarding their safety highlight the need for improvements, minimizing reassortment risk. We have previously developed safe LAIV vaccines capable of inducing robust mucosal immune responses, however their potential for reassortment was unknown. Thus, our objective was to modify these LAIV to improve their immune stimulation further while reducing transmission and reassortment potential in swine.

To achieve this, we designed two vaccines with a rearranged genome (RAM) backbone, a genetic attenuation strategy that relocates the M2 gene from segment 7 to the PB1 segment. In the first vaccine strain, we inserted the IgA-inducing protein (IGIP) gene into the HA segment, and in the second, the interleukin-18 (IL-18) gene was introduced into the NA segment, both aiming to enhance mucosal IgA production and/or promote T cell activation. A third vaccine was produced using a different attenuation strategy carrying a temperature-sensitive mutation in the PB2 ORF (Flu-att) and includes both IGIP-HA and IL-18-NA. In vivo evaluation was conducted in piglets, assigned to groups receiving RAM-IGIP, RAM-IL-18 and Flu-att-IGIP+IL-18. These were compared to three controls: Flu-att (without IGIP/IL-18), an inactivated whole-virus vaccine, and a PBS group. All vaccines contained the HA and NA genes from the same H3N2 strain. Humoral, mucosal, and cellular responses were assessed via HI assay, IgA ELISA, and flow cytometry, and viral replication and transmission were evaluated in vaccinated animals and sentinels.

Our results demonstrate that IGIP and IL-18 enhanced mucosal and cellular immune responses compared to controls. Flow cytometry showed that IGIP+IL-18 increased frequencies of $IgA^+Blimp1^+IRF4^+$ B cells in lymph nodes, suggesting enhanced B cell activation. IL-18-containing vaccines also promoted higher $CD8^+$ T cells in the spleen and elevated $TCR\gamma\delta^+$ T cells in the lungs. ELISA results showed that all attenuated vaccines induced high levels of mucosal IgA in bronchoalveolar lavage and nasal washes compared to the inactivated vaccine, with IL-18 containing vaccines resulting in a trend for higher levels at some timepoints. The attenuated vaccines expressing IGIP, IL-18, or both induced HI titers comparable to the inactivated vaccine, with all groups showing a significant increase after booster immunization, indicating strong systemic antibody responses. Additionally, RAM backbone vaccines reduced viral replication in vaccinated animals and transmission to sentinels compared to the Flu-att control vaccine.

Our findings support the use of IGIP and IL-18 as immunomodulators to enhance the immune response induced by LAIV vaccines in swine. The RAM-based attenuation strategy proved to be genetically stable and safe, contributing to reduced transmission and viral replication. These results highlight a promising strategy to improve influenza control in pigs while minimizing safety concerns.

**Genomic characterization and diversity of porcine astrovirus 4 in oral fluid samples from wean-to-finish herds in the U.S. Midwest**

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Astroviruses (AstVs) infect a wide range of mammals and birds and have been associated with gastrointestinal, neurological, and respiratory clinical presentations, as well as asymptomatic infections. A major limitation in advancing our understanding of AstVs is the lack of widely available diagnostic tools (1). In pigs, five genotypes (PAstV1 through PAstV5) have been identified in both healthy and diarrheic pigs worldwide. In the United States (U.S.), PAstV4 has been detected in nasal swabs, intestinal contents, and fecal samples of pigs. Recently, the ability of PAstV4 to cause clinical respiratory signs as a primary pathogen was confirmed. However, detection has primarily relied on RT-PCR–based methods (2,3) and has been largely limited to individual samples with few reports addressing herd-level characterization2. Oral fluids (OF) are a composite sample type that have been frequently used in swine medicine as a practical tool for herd-level monitoring. The phylogenetic characterization of PAstVs in swine herds from the U.S. particularly using sequencing data from OF samples, has not yet been documented. In this study, we employed probe-enriched long-read sequencing data to recover whole or partial genomes of PAstV4 from OF samples collected between 2017 and 2018 from wean-to-finish herds in the Midwestern United States. Using this novel data, we conducted a phylogenetic analysis of PAstV4 genomes and evaluated their diversity across 10 different production companies comprising 59 sites. A phylogenetic tree was constructed from the aligned sequences using the Randomized Axelerated Maximum Likelihood Next Generation program (RAxML-NG) with the GTR+G model and 1,000 bootstrap replicates. The best tree was selected for visualization using R version 4.4.2. Pairwise genomic distances of the samples were calculated using RAxML-HPC with the GTRGAMMA model5, excluding PAstV4 reference sequences from this analysis. To assess statistical differences in pairwise distances within sites and across systems, the Wilcoxon rank sum test was applied. PAstV4 was the most abundant virus recovered across most samples. Most samples yielded a high genome fraction (ranging from 10.33% to 99.58%), and substantial coverage depth (ranging from 0.11 to 1848.51) was obtained for PAstV4. Genetic distance analysis revealed that PAstV4 sequences were more similar within sites than across different sites and production companies. The observed similarity of within-site and across-company genetic diversity suggests that PAstV4 is evolving locally within production companies or sites. This study is the first to utilize OF samples with target-enrichment and long-read sequencing technology for the recovery of partial and whole PAstV4 genomes and to investigate their genetic diversity in U.S. commercial swine herds.

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**Application of Mitigant to Reduce Viral Trailer Contamination at Harvest Facilities**

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Introduction

Transportation plays an important role in disease dissemination through numerous pathways including farm to farm, farm to market, vehicles for workers, and feed deliveries (Galvis et al., 2022). Transport vehicles at harvest facilities can serve as a major contact point between different farms, and a contamination source when trailers return to pig farms. Trailers are often shared between different farms and producers, and may not always be washed between loads. Research by Lowe et al. has demonstrated that trailers can become contaminated with PEDV during unloading at harvest facilities (2014). During delivery to the harvest facility, drivers enter the trailer through the receiving dock. If assistance is required during unloading, plant personnel will also enter the trailer. Boots may become contaminated while passing through the receiving dock, bringing virus into the trailer. Trailers that become positive during unloading at harvest facilities then return to farms for reloading. One way to reduce the likelihood of viral transmission from negative to positive herds via trailer contamination is to prevent cross-contamination from positive to negative trailers during unloading at the harvest facility. The goal of this study is to provide proof-of-concept that a chemical intervention can reduce the incidence of cross-contamination from positive to negative trailers for both PRRS and PEDV.

Methods

A total of 120 trailers will be enrolled into the study, with 10 trucks enrolled and sampled per month over 12 consecutive months (5 treatment, 5 control). At the start of each sampling window on each sampling day, project personnel will spread 1 pound of Chlorosoab as each treatment trailer backs into its respective dock. The treatment will be re-applied for each truck that enters the “treatment” loading docks during the sampling window. Pigs from all trailers will be unloaded as per standard operating procedure, and all other movements in the loading dock and lairage areas will be as per normal. For both treated and control trailers, swabs will be collected prior to and after unloading of pigs using a standard protocol. Samples will be submitted to the University of Minnesota Veterinary Diagnostic Laboratory for PRRSV and PEDV testing.

Results

During the 5-month sampling period, crude prevalence across all samples was 57%, 25% and 62% for PEDV, PRRSV, and porcine deltacoronavirus respectively. Prevalence before unloading prevalence was 48%, 20%, and 50% for PEDV, PRRSV, and porcine deltacoronavirus, respectively; and prevalence after unloading was 66%, 30%, and 74%, respectively.

Before and after prevalence was then broken down by control and treatment trailers. PEDV prevalence for control trailers was 40% before and 68% after unloading; PRRSV prevalence before unloading was 12% and after unloading was 28%; and porcine deltacoronavirus prevalence was 48% before unloading and 68% after unloading. For treatment trailers, prevalence before unloading was 56% for PEDV, 28% for

PRRSV, and 52% for porcine delta coronavirus; while prevalence after unloading was 64%, 32% and 80% for PEDV, PRRSV, and porcine deltacoronavirus, respectively.

Conclusions

Sampling will continue through January 2026. Results and conclusions will be presented following the completion of testing.

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**Metagenomic Analysis and the Diversity of Preparation Practices of Live Virus Inoculum**

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Introduction

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is an economically devastating disease with an estimated annual cost of $1.2 billion on the U.S. swine industry(1). Outbreaks involving multiple PRRSV strains or recombinant viruses have been associated with more severe production losses (2). Live virus inoculation (LVI) is one strategy employed to manage PRRSV outbreaks (3). However, the uncharacterized nature of LVI material introduces unknown risks to the herd. This study aims to evaluate the genetic diversity of PRRSV and identify the presence of additional swine pathogens within LVI preparations.

Methods

Samples intended for LVI use were collected along with a standardized survey detailing the preparation process. A total of 50 LVI samples from 14 production systems were analyzed. Quantitative RT-PCR (RT-qPCR) and next-generation sequencing (NGS) were performed to estimate PRRSV load and to conduct comprehensive pathogen profiling. Participating veterinarians completed surveys describing their LVI preparation and administration practices, including the type of sample used, dilution media, and route of exposure.

Results

NGS analysis confirmed the presence of PRRSV in all LVI samples. A single PRRSV strain was identified in 86% (n = 43) of cases, while 14% (n = 7) contained multiple strains. One LVI sample contained a recombinant PRRSV strain, while two others harbored MLV-like viruses, with one of them also containing a wild-type strain. In addition to PRRSV, genomic material from several other pathogens was detected, including Salmonella spp. (n = 7), Pseudomonas spp. (n = 2), Porcine Parvovirus (n = 7), Porcine Circovirus Type 2 (PCV2) (n = 1), Orthoreovirus (n = 3), Porcine Astrovirus (n = 2), and Influenza A virus (n = 2). All LVI materials were derived from serum, with 74% (n = 37) pooled from multiple piglet donors with a maxim 150 and mean 14 donors. The majority of preparations (78%, n = 39) did not use antibiotics, with Ceftioufur sodium been the most common in 18% (n = 9) of cases followed by enrofloxacin used in 4% (n = 2). Phosphate-buffered saline (PBS) and saline were the most frequently used diluents, each appearing in 46% (n = 23) of preparations, while sterile water was used in 8% (n = 4). Intramuscular injection was the predominant route of administration (96%, n = 48), while nasal exposure was used in just 4% (n = 2). The viral concentration in LVI samples varied widely, ranging from 49 to 253,491,526 PRRSV particles/ml, with a median of 31,429 particles/ml. For comparison, commercially available MLV products in the U.S. contain between 59,939,654 and 9,440,330,690 genomic copies/ml.

Conclusion

This study underscores the considerable variation in how live virus inoculum (LVI) is prepared and applied across different production systems. In several instances, multiple PRRSV strains were detected within a

single sample, raising concerns about the potential for viral recombination. Additionally, the identification of non-target pathogens points to possible contamination during the preparation process. These findings collectively emphasize the need for rigorous quality control and standardized protocols to ensure the safe and effective use of LVI in herd stabilization efforts.

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**Astrovirus and Anti-Inflammation: A Meloxicam Mechanism in the Swine Trachea**

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BACKGROUND

Porcine astrovirus 4 (PoAstV4) is an emerging pathogen associated with tracheitis and bronchitis in young pigs. 1 Recent research demonstrated that PoAstV4 could independently induce respiratory lesions in cesarean-delivered colostrum-deprived piglets, acting as a primary cause of respiratory disease. 2 PoAstV4 has been detected throughout the U.S., suggesting it is endemic in the national swine herd.

Veterinarians are currently tasked with managing the clinical consequences of PoAstV4. This virus can cause significant tracheal inflammation, which may predispose pigs to secondary bacterial pneumonia. These co-infections can elevate mortality, treatment rates, and economic losses. This pilot study aimed to evaluate whether NSAIDs reduce airway inflammation in PoAstV4-infected nursery pigs, based on histopathologic lesions. The results of this study support a larger trial evaluating Meloxicam's effect on mortality, treatment rates, and average daily gain in PoAstV4 infected systems, given that the proposed mode of action could explain any improvements observed.

METHODS

A conventional nursery flow with confirmed PoAstV4 infection and negative Influenza A (IAV) and PRRSV status was utilized. Twelve coughing pigs were randomly selected from a 1,200 head nursery room and enrolled at two days post-placement. Once enrolled, they were randomly assigned to either a treatment (Meloxicam) or control (placebo) group. Pigs were housed together in one pen for the duration of the trial. Compounded Meloxicam 0.6% soluble was administered orally at 0.4 mg/kg once daily for four days. The control pigs received a sterile water placebo. On day five after initial enrollment, eight pigs (four per group) were euthanized and necropsied. Lung and tracheal tissues were submitted to the Iowa State Veterinary Diagnostic Laboratory (VDL). Prepared slides were sent to Dr. Michael Rahe (NC State) for blinded histological analysis with a scoring system adapted from IAV studies.3

Blood samples were collected, and PCR confirmed a negative PRRSV status. The source farm for these pigs historically tested PCR negative for IAV on udder wipes. Pre-weaning diagnostics confirmed that the sow cohort for these pigs tested PCR IAV negative and PoAstV4 positive on udder wipes. PoAstV4 PCR was performed on the trachea samples collected and yielded a cycle threshold range of 16.8 – 28.1.

FINDINGS

No clinical differences were observed between groups during the study. On day five post enrollment, the nursery room had a moderate cough, emphasizing PoAstV4's herd-level impact. Although not statistically significant, pigs treated with Meloxicam had lower average histological scores in the trachea, bronchi, and bronchioles compared to controls, indicating reduced inflammation and epithelial changes. Two control pigs developed secondary bacterial pneumonia, supporting the association between PoAstV4 and secondary infections and suggesting that Meloxicam may reduce this progression.

DISCUSSION AND LEARNING

Large variation in tracheal scores among treated pigs could reflect differences in immune response or disease progression at time of treatment. Further study is needed to determine if there is a point in the progression of disease where NSAIDs, such as Meloxicam, work most effectively. Though limited in scale, this pilot study established an important foundation for further investigation into NSAIDs as a management tool for PoAstV4.

**Efficacy of Improx in Modulating Immune Response in Nursery Pigs Infected with PRRSV, PCV2d, or Influenza A Virus**

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Introduction

Porcine respiratory diseases such as Porcine Respiratory and Reproductive Syndrome (PRRS), Porcine Circovirus type 2d (PCV2d), and Influenza A virus (SIV) significantly impair swine productivity worldwide, with PRRSV alone contributing to over $1.2 billion in annual losses in the U.S.1. Improx, a mineral-based feed additive supplemented with fructooligosaccharides (FOS), has shown promise as a non-specific immunostimulant 2,3. This study evaluated the efficacy of Improx in enhancing immune responses, reducing lung pathology, and supporting performance in nursery pigs under controlled viral challenges.

Methods

Fifty weaned pigs (21 days old) were randomly assigned into five groups (n = 10 each) and housed under biosafety level 2 conditions. Groups included PRRSV + PCV2d control and Improx-treated, SIV control and Improx-treated, and a negative control. All pigs were unvaccinated against the viruses involved. Improx was included in the feed at 250 g/ton. Viral inoculations occurred on day 0, and pigs were monitored for 28 days. Clinical signs, zootechnical performance (ADG, FCR, ADFI), and mortality were recorded. Flow cytometry assessed immune cell subsets, and lung lesions were scored at necropsy.

Results

Improx-treated SIV-infected pigs exhibited a 70% reduction in lung lesion severity compared to controls (3.1% vs. 10.4%, p = 0.0913). Flow cytometry showed enhanced immune activation in this group, with increased $CD4^+$ helper T cells, γδ T cells, and conventional αβ T cells. Neutrophil-to-lymphocyte ratios were consistently lower, indicating better inflammatory regulation. In contrast, under PRRSV + PCV2d co-infection, Improx showed limited benefits. Lung lesions and mortality (50%) were similar between treated and untreated groups. Although cytotoxic T cells increased across all infected groups, innate γδ T cells were significantly suppressed in the PRRSV + PCV2d groups. Performance metrics did not significantly differ between groups.

Conclusions

Improx showed immunomodulatory benefits in SIV-infected pigs, supporting T cell activation and inflammatory regulation. However, its efficacy was limited in PRRSV + PCV2d co-infection. This may be due to the combined immunosuppressive effects of both viruses. PCV2d infects and replicates in $CD4^+$ and $CD8^+$ T cells and interferes with cytokine signaling (TNFα, IFNα) and Toll-like receptor (TLR) expression, disrupting communication between innate and adaptive immunity. PRRSV infects macrophages, inhibits type I interferon responses, alters cytokine balance, and induces early non-neutralizing antibodies via immune distraction 4. These mechanisms may blunt the host's ability to respond to immunostimulants

like Improx under dual infection. Further research using varied infection models and larger cohorts is needed to explore the scope and limitations of Improx under field-relevant conditions.

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**An evaluation of the effectiveness of a proper cleaning and disinfection protocol in farrowing units and piglet nurseries and its impact on biosecurity, health status and antibiotic use.**

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Introduction

Cleaning and disinfection (C&D) are key for eradicating endemic diseases, and to reduce the risk of introducing new pathogens. The selection of efficient detergents and disinfectants is essential to achieve an effective C&D of farrowing units and piglets nurseries. The objective of this study was to evaluate the effectiveness of a proper cleaning and disinfection protocol in four commercial swine farms.

Methods

The current C&D program, control group (CN group) in all four farms was compared with the advanced program, treatment group (KV group). Including an alkaline foaming detergent, and a concentrated broad-spectrum disinfectant (quaternary ammonium compounds and glutaraldehyde) for barn hygiene and an acidic cleaner and disinfectant to clean and disinfect drinking water systems (peracetic acid, hydrogen peroxide). It was a before-after study, two batches in the CN group were followed and 6 batches in the KV group. All clinical incidences (mortality and antibiotic use) were recorded daily. 542 and 1621 litters in the CN and KV groups were followed up in maternity and 24,814 weaned piglets (28 days) from 32 batches in the nursery. The weaned piglets were followed until the end of the transition phase (5weeks).

Results

Pre-weaning mortality was reduced (13.2% vs 15.8%; $P<0.01$), mainly linked to less digestive problems (especially in one farm, which had high incidence of diarrhoea) and lameness and the number of weaned piglets per litter was increased (12.0 vs 11.8; $P<0.05$) in the KV group. The percentage of piglets treated with antibiotics in maternity was reduced 4.7 times in the KV litters in all farms, especially to treat diarrhoea (18.0% vs 3.8%; $P<0.0001$). Antibiotics used for the weaned piglets in the nursery was reduced from 6.40% to 4.07% ($P<0.05$). this was mainly due to a reduction of respiratory problems (1.67% vs 0.66%; $P<0.05$), lameness (2.47% vs 1.01%; $P<0.05$) and meningitis (1.19% vs 0.72%; $P<0.05$) after applying the KV program. The incidence of digestive problems increased in the KV group ($P<0.05$), this was most likely due to a one-time outbreak in the before-after study. Mortality in the nursery was reduced from 6.45% to 5.39% ($P<0.05$) after application of the KV program, the main causes were lameness and meningitis, which were heavily decreased (0.72% vs 0.38% and 1.48% to 0.86%; $P<0.05$).

Conclusion

The application of proper and effective cleaning and disinfection is not only resulting in a reduced use of antibiotics administered to the piglets in maternities and nurseries, it also helps to reduce piglet mortality and to improve the health status of the piglets by lowering disease incidence on commercial farms.

**Novel rPICV-Vectored Vaccine for PRRSV: Development, Safety, and Efficacy in Porcine Model**

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Porcine reproductive and respiratory syndrome virus (PRRSV) causes significant economic losses in the swine industry due to its immune evasion and high genetic variability. We aim to develop an effective PRRS vaccine using a recombinant tri-segmented Pichinde virus (rPICV) vector. rPICV targets antigen-presenting cells (APCs) to elicit robust antibody and T-cell responses. It has a good safety profile, causing a limited replication in local lymph nodes with no viremia or viral shedding. This study evaluates the safety, immunogenicity, and protective efficacy of a rPICV vector expressing PRRSV envelope glycoproteins. Four-week-old pigs were divided into three groups: Group 1 (vaccinated, unchallenged), Group 2 (vaccinated, PRRSV-challenged), and Group 3 (vector-only, PRRSV-challenged). Vaccinations were administered intramuscularly at 4 and 7 weeks of age, followed by a homologous PRRSV challenge at 9 weeks of age. A 9-plex fluorescent microsphere immunoassay (FMIA) was used to assess serum cytokine responses. The vaccinated groups exhibited a lower level of proinflammatory cytokines, including IFN-α, IFN-γ, IL-1β, IL-6, and TNF-α, which were observed in the first week post-challenge, as opposed to the non-vaccinated group. Similarly, TH2 cytokines IL-4 and IL-10, as well as innate IL-8 cytokine levels, were significantly lower in the vaccine group, suggesting a shift toward a Th1 response and a suppression of neutrophil activity during the challenge phase of the study. qPCR analysis revealed significantly lower viral loads in vaccinated pigs at 42, 49, and 63 days of age (7, 14, and 28 days post-challenge), with serum viral RNA levels reduced by 24.7-fold at day 7 ($p=0.0104$), significant reductions in both serum and nasal swabs at day 14 ($p=0.0286$), and complete viral clearance in vaccinated pigs by day 28 ($p=0.0319$). Neutralizing antibodies emerged post-challenge in vaccinated pigs, with none detected before exposure. The rPICV-based PRRS vaccine triggered a balanced immune response, improved viral clearance, and reduced tissue inflammation, underscoring its potential as an effective vaccine for controlling PRRSV. These results support further research and development of rPICV as a vector platform in swine vaccinology.

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**Intradermal Application of Liquids (IDAL®) device for easy vaccine delivery in swine**

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Introduction

Merck Animal Health recently licensed a new prescription platform for intradermal vaccination of pigs. Skin-based vaccination has long been a focus of human and animal vaccine development, due to the ease of administration, reduction of pain, and the diversity of skin immunology.1 Likewise, vaccine delivery device attributes like safety, components, ease of use, etc. play an integral role in effective vaccination programs. Here we will review the principles of skin immunology as well as features of the IDAL device recently registered in the U.S. for intradermal vaccinations of swine.

Skin Immunology

The layers of the skin are rich with both innate and adaptive immune cells, capable of stimulating a variety of immunological responses. Multiple antigen presenting cell phenotypes are present in the epidermis and dermis, such as Langerhans cells (LC), dermal dendritic cells (DDC) and dermal macrophages, specially equipped to drive humoral and cell-mediated immune responses through antigen presentation.2 The resident lymphocyte population is also diverse, and includes CD4+, CD8+ and γδ T cells, as well as memory and plasma B cells.3,4 In both humans and pigs, intradermal vaccination has been explored to combat multiple diseases, including respiratory disease caused by influenza.1,5

IDAL device

The IDAL device is a hand-held precise delivery system that delivers 0.2 mL into the dermis via a jet injector. Vaccine is delivered using a dual- pressure injection for vaccine delivery at the desired skin plane. Product is delivered within milliseconds. The device delivers vaccines without the use of needles. It has been ergonomically designed for vaccinator comfort especially for vaccinating large swine populations. Device settings are available in multiple languages to make it easy for the operator to use. There is also a supporting device app (IDAL way) that helps manage vaccination events as well as the device. The IDAL device has a two-step injection delivery activation step as a safety feature to prevent accidental injections.

Device Attributes

This needle-free device reduces the risk of iatrogenic spread of pathogens (demonstrated for PRRSV and ASFV) during the vaccination event.6,7 The use of the IDAL device eliminates the risk of needle sticks and broken needles. Delivery of vaccines into the skin provides enhanced meat safety as it minimizes potential damage of carcasses. The device is easy to use which helps with vaccination compliance amongst a variety of experience leveled vaccinators. Intradermal vaccination using the IDAL device has been shown to reduce stress and improve animal welfare during the vaccination process compared to intramuscular injections. 8,9 Intradermal vaccination allows for increased flexibility in selecting vaccination sites for sows, allowing for an easier and safer process for vaccinators.

Conclusion

In the U.S., the Sequivity prescription vaccine platform has been formulated and licensed for intradermal delivery of vaccines using an intradermal device (IDAL).

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**SEQUIVITY® ID: a novel intradermal prescription vaccine**

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Introduction

Intradermal vaccination provides easy administration, reduced pain, and robust immune response.1 Sequivity ID is the first intradermal vaccine licensed for U.S. swine. This paper summarizes the studies performed by Merck Animal Health to evaluate the safety and efficacy of Sequivity ID adjuvanted with Microsol Diluvac Forte® and based on the hemagglutinin of H1N1 IAV-S.

Methods

All vaccinations were 0.2 mL given with the IntraDermal Application of Liquids (IDAL®) device. In Study 1, 64 IAV-S negative pigs were enrolled at 21 DOA; 32 pigs were administered test vaccine and 32 were administered placebo vaccine and all were boostered three weeks later. Blood was collected on the days of vaccination and weekly thereafter and analyzed for hemagglutinin inhibition (HI) titer. At 31 days post-booster, pigs were intratracheally challenged with 6.1 logs of homologous virus. Twenty pigs were necropsied 5 days post challenge (DPC) to evaluate macroscopic lung lesions and viral load and 12 pigs had nasal swabs collected and tested for live virus on DPC 0-10. In study 2, 733 three-week-old pigs from three farms were vaccinated twice, three weeks apart and were monitored daily for adverse events for three weeks following vaccinations. In study 3, 479 sows were vaccinated twice, three weeks apart. Sows were either in early (30-40 days), mid (50-60 days), or late (70-80 days) gestation at the time of enrollment. 237 non-vaccinated sows in each phase of gestation served as controls. Sows were observed for three weeks post vaccinations and again at farrowing and seven days thereafter.

Results

In study 1, pigs receiving test vaccine were seropositive at time of challenge, with geomean titers peaking at 1733.5 on day 7 post-booster. Following challenge, no vaccinated pigs shed live virus versus 92% of placebo pigs. Peak shedding occurred on 3 DPC and resolved by 7 DPC. At necropsy, percent lung lesions was reduced in vaccinated pigs by 95% versus controls. There was no detectable live virus in the lungs of vaccinated pigs versus 45% of placebos.

In study 2, no systemic adverse events post vaccination were observed. Local injection site reactions occurred in 5% and 30% of pigs following the first and second vaccinations, respectively. Most reactions measured less than 1.5 cm and resolved by 1.4 and 3.9 days following first and second vaccinations, respectively.

In study 3, the incidence of adverse events in vaccinated sows was not different versus controls or between gestation phases. Injection site reactions were observed in 35% sows, of which 71% were less than 1.5 cm in diameter. Most reactions appeared within one day and resolved by an average of 8 and 10 days after the first and second vaccinations, respectively. The incidence of miscarriage was 1.3%, with no difference between groups for any reproductive performance indices.

Discussion

These studies demonstrated the safety and efficacy of SEQUIVITY ID administered in a two-dose regimen. The pairing of SEQUIVITY ID and IDAL technologies presents veterinarians and swine producers a new set of innovative solutions to combat swine diseases.

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**Portable Magnetic Particle Spectroscopy (MPS) platform for multiplex detection of swine pathogens**

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Introduction

Rapid detection of pathogen(s) at the farm is essential for control and containment strategies to curtail disease outbreaks in swine production systems. Simultaneous detection of multiple pathogens in a single test would further reduce time of intervention, effort, and cost for producers. MPS bioassays rely on the nonlinear magnetic responses of magnetic nanoparticles (MNPs). Upon application of AC drive field, the response of each MNP contains higher harmonics in addition to the drive field frequency. The aggregate response can be separated by means of appropriate filtering. Fine-tuning MNPs' material, size, shape, structure, etc., results in each kind of MNP to have its own unique 'fingerprint' allowing multiplexed bioassays.

Materials and Methods

Concurrent quantification of commercially available MNPs was carried out to mimic the surface-based bioassay. Multi-core MNPs such as SPG0050 (50 nm, 1mg/mL), SC0102 (100 nm, 10 mg/mL), and MV1001 (1µm, 5 mg/mL) from Ocean Nanotech LLC (San Diego, CA, USA) and nanomag-D-SPIO (50 nm, 5 mg/mL) from micromod Partikeltechnologie GmbH (Rostock, Germany) were used. A single-frequency MPS implementation was used. Magnetic response curves for these MNPs were recorded using a portable MPS device consisting of a balanced set of pickup coils.

Results and conclusions

As the MNPs undergo magnetic relaxation, one observes a phase lag between their magnetization response and the drive field. Under such excitation, the magnetization response yielded MPS spectra consisting of harmonic amplitude and phase information for each MNP. MNPs exhibiting the greatest dissimilarity in their response generate optimal multiplexing performance. This study demonstrated the feasibility of multiplexed MPS bioassays. When different types of MNPs are functionalized with capture probes specific to target analytes, the binding events immobilize these MNPs on a reaction surface. Assuming that the collective response of MNPs in a mixture is the weighted linear sum of individual MNP's harmonics, one can deconvolve the quantities of MNPs in binary, ternary, or even quaternary mixtures. These findings provide a high accuracy solution for multiplexed MPS bioassays and offer valuable insights for further development in this field.

**Meloxicam benefits for sows: an international review with new data**

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Introduction

Meloxicam is a selective COX-2 inhibiting, non-steroidal anti-inflammatory drug that exerts analgesic, antipyretic and anti-endotoxic effects. Its administration around parturition targets pain and inflammation that can impair sow behavior, lactation, and piglet outcomes. Meloxicam impact on lameness has also been studied. New findings, here, align with findings from global controlled field studies, pharmacokinetic evaluations, and clinical trials are summarized, demonstrating meloxicam's overall impact on sow health, litter performance, lactational efficiency, lameness, and breed-back metrics.

Methods

The reviewed body of evidence encompasses more than two decades of global studies on meloxicam use in adult swine and their offspring. These include randomized controlled trials in healthy sows, those with postpartum dysgalactia syndrome/mastitis-metritis-agalactia (PPDS/MMA), translactational studies assessing piglet immunology and pharmacodynamic assessments of optimal dosing. Outcomes include maternal behavior, rectal temperature, inflammatory biomarkers, locomotion, sow feed intake, piglet average daily gain (ADG), pre-weaning mortality, colostrum immunoglobulin content, colostrum intake, cytokine profiles, and sow reproductive parameters.

Results

Lactation and piglet performance: Multiple studies show improved piglet ADG and survival, particularly among low birthweight piglets, with gains of +30 g/day and mortality reductions up to 66%. Litters from meloxicam-treated sows consistently showed higher weaning weights, even when birthweights were lower. A reduction in antibiotic treatments in piglets from meloxicam dams have been observed in several studies.

Immunity transfer: Studies demonstrated significantly elevated antibodies (IgG, IgA) in sow colostrum and piglet serum following sow meloxicam administration. Cytokine profiles (IL-2, IL-4) were also improved, promoting more robust piglet immune development. Piglet colostrum uptake (immunocrit and piglet weight gain from pre- and post-suckling) has been demonstrated.

Behavior and lameness: Meloxicam-treated sows exhibited improved laying posture in farrowing. In a sow lameness study, there was reduced lying and increased standing with meloxicam, outperforming flunixin in pain behavior scores. One study noted significantly better pain control behaviorally and physiologically in meloxicam-treated sows vs. placebo and flunixin. Two boar treatment-control studies showed lameness reduction and improvement in longevity in the herd.

Reproductive health, treatments and retention: Meloxicam treatment reduced post-farrowing fever for 12-48-hours and supported earlier return to estrus, especially in parity 2–3 sows. Sow retention through the subsequent parity improved by 9.2% in one trial. Fewer therapeutic antibiotic and injectable anti-inflammatory treatments during lactation for younger parities have been demonstrated.

Pharmacology: Meloxicam demonstrated a favorable safety profile and high oral bioavailability (87%). Dose-response in younger pigs confirmed 0.4 mg/kg IM as an optimal dose during endotoxin studies. A residue study utilizing FDA-withdrawal stats package showed withdrawal period of 12-days for 2 x 90mg doses, SID for the US-available compounded meloxicam suspension.

Conclusion

Administering meloxicam to sows during early postpartum significantly benefits health, welfare, and productivity. Benefits include enhanced piglet growth and immunity, improved sow comfort and behavior, reduced medical interventions, and potentially better reproductive outcomes. Effective lameness treatments may also reduce culling rates. Meloxicam's proven safety and reliability make it essential for modern sow management.

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**Proactive tail bite management: a field study comparing two products on the healing and prevention of tail bites**

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Introduction

Tail biting is a welfare and productivity issue. Previous treatment protocols have included spraying tails with unproven products to "treat" the wounds. Healicin-ABF™, a unique colored formulation of ingredients designed to be applied to skin, has shown healing dominance in previous sow shoulder sore studies across multiple farms. This pilot study compared Healicin-ABF to Stop Bite™ in promoting healing of existing tail bite wounds and preventing new incidents over an eight-day period.

Methods

The study involved finishing pigs (n=1,380, 130 days of age) in finishing pens (n=15; 92/pen). Treatments were assigned at the pen level using a systematic alternation approach, beginning with a randomly selected pen and continuing with every other pen thereafter. Tail-bitten pigs were objectively scored on an open wound scale (1-4) and treated with either Healicin-ABF or Stop Bite (n=9 and 6 pens) from days 1-5, based on their assigned pen-level treatment. Healing success was assessed by the proportion of tail wounds that were "dry/scabbed" on day 5 and three-days post-cessation of treatment (day 8). Average healing days per pen were calculated. The incidence and total number of tail bites were measured from days 1-5. Pen served as the experimental unit. Statistical analysis included generalized linear models (binomial and Poisson), ANOVA, and correlation analysis between initial wounds and subsequent new cases.

Results

Healicin had a statistically higher healing success rate (56.9%) compared to Stop Bite (32.2%) at day 5 ($p=0.01$), with a trend toward statistical significance three days after treatments were stopped (60.8% and 44.1%, respectively, $p=0.08$). Mean healing time was similar between treatments (Healicin: 6.56 days; Stop Bite: 6.51 days; $p=0.82$). The incidence of new bites between days 2–5 was lower in the Healicin group (1.74 vs 3.26; $p=0.075$), adjusted for initial day 1 bites. Mean tail bites per pen from days 1–5 were significantly lower for Healicin (5.78) than for Stop Bite (10.67; $p=0.001$), as were day 1 bites alone (4.11 vs 6.67; $p=0.034$). A moderate, statistically significant correlation ($r=0.53$, $p=0.04$) was observed between the number of day 1 bites and new bite incidence, with a 0.32 increase in new bites per additional initial bite.

Conclusions

This study highlights enhanced healing success and reduced incidence of tail bite wounds using Healicin-ABF over Stop Bite. Healicin significantly lowered the total tail bites during the treatment period, factoring in the initial prevalence of the bites in each pen. These findings provide additional evidence to previous studies that Healicin promotes better wound healing than alternative treatments. Healicin's formulation includes an ingredient that deters pigs from biting treated wounds due to its bitter taste, reducing further

biting incidents. Additionally, the strong correlation between initial and subsequent tail bite wounds underscores the importance of early intervention. A replicated study in a larger population should be conducted to further validate these findings.

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**Large scale evaluation of the effects of oral compounded meloxicam on mortality in grow-to-finish pigs laterally challenged with PRRSV and IAV**

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Introduction

Respiratory viral infections, specifically Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) and Influenza A Virus (IAV), remain major threats to swine production, causing increased mortality and treatment costs. Meloxicam has demonstrated positive effects on clinical and production outcomes in respiratory diseases. The timing of administration of any drug impacts the level of effectiveness. This large-scale, paired-barn field study evaluated the reduction of mortality in pigs naturally exposed to these pathogens when treated with compounded meloxicam, regardless of proper timing of administration. Economic return across blocks and whole-system were evaluated.

Methods

All sites were commercial finishing herds (mean=1,536 head/barn) in the Midwest. Blocks were created from paired barns (50 CON; 50 MEL) on the same sites, with the same sourced/aged weaned pigs, and managed by the same caregivers. Sites were enrolled (9.7 weeks old) when clinical respiratory signs were identified (day 0). Oral fluids were collected to confirm pathogen presence. A trained third party evaluated whether enrollment was on-time or late based on treatment/mortality records, clinical observation and caregiver communication. Treatment was assigned at the barn level using a systematic alternation approach, beginning with a randomly selected barn and continuing with every other barn on the same site thereafter. MEL groups received compounded meloxicam 0.6% soluble through drinking water (1pint/4gallons of stock solution, 5 days). All additional medicines were administered to both CON and MEL per normal protocol. Mortality rates were assessed in time segments for 10 weeks after day 0. Additional oral and injectable medication costs per barn were assessed. Statistical analysis involved generalized linear mixed models (GLMMs) for binomial outcomes and linear mixed models for cost outcomes, incorporating fixed effects for treatment and disease, and random effects for experimental blocks.

Results

Treatment occurred on time in 72% of barns and was late in 28% of barns. MEL pigs demonstrated statistically lower cumulative mortality rates compared to CON at: 4 weeks (2.79% MEL vs. 3.17% CON); $p<0.0001$), 8 weeks (4.22% MEL vs. 4.65% CON; $p<0.0001$), and 10 weeks (4.73% MEL vs. 5.14% CON; $p<0.0001$). Cost analyses showed no statistical differences in oral or injectable medication cost per pig. Costs of the compounded meloxicam in MEL was $0.05/pig/day.

Discussion

Oral meloxicam statistically reduced cumulative mortality over 4, 8, and 10 weeks across the system regardless. The previous report, including only timely treatments, had even more improved cumulative

mortality rates at 4- and 10-weeks post meloxicam, 1.1% and 0.9% for the MEL groups. MEL averaged 13.8 more pigs to market in the on-time barns and 6.6 more across all barns. These findings support health protocols including adjunctive oral meloxicam in systems with growing pig respiratory disease. However, ongoing caregiver training for clinical signs identification and early disease treatment can improve the ROI. Training, feedback, and communication should be emphasized. More research into further cost savings by reducing the use of antibiotics for secondary infections during viral disease, which was not evaluated here, may be warranted.

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**Genotypic diversity of Porcine circovirus 2 (PCV2) on a global scale and within the United States**

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Background

Porcine circovirus 2 (PCV2) evolution has led to the emergence of multiple genotypes. The capsid protein (Cap), encoded by the open reading frame 2 (ORF2), serves as the primary immunogenic component and is fundamental for viral classification and phylogenetic studies. This study aimed to compare the global and United States (US) PCV2 genetic diversity over time based on ORF 2 sequences.

Materials and Methods

A total of 10,151 PCV2 ORF2 sequences available in GenBank from 2010 to January 2023 were analyzed. Sequences derived from patents, cell culture-adapted strains, partial sequences, and those lacking reliable collection dates were excluded, resulting in 7,652 sequences available for analysis. The same criteria were applied to 1,743 sequences obtained from samples processed at the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL) between 2010 and 2022. Sequence alignments were performed using MAFFT, and genotyping was conducted based on genetic distance analyses and phylogenetic inference using RAxML. Further phylogenetic analyses were performed with BEAST v1.10.4, while selection pressure assessments utilized MEME, FEL, SLAC, and FUBAR methodologies via the Datamonkey server.

Results

The findings revealed the presence of eight genotypes globally (PCV2a–PCV2h), whereas four genotypes (PCV2a, PCV2b, PCV2d, and PCV2e) were identified within the ISU-VDL dataset. In the US, PCV2d was predominant, accounting for 73.38% of sequences, followed by PCV2a (15.09%), PCV2b (8.03%), and PCV2e (3.5%). Globally, PCV2d also exhibited the highest frequency of detection at 45.2%, succeeded by PCV2b (36.7%), PCV2a (15.05%), and PCV2e (0.44%). The PCV2d genotype became predominant globally starting in 2014–2015 and the ISU VDL data demonstrates this dominance began between 2012 and 2014. Between 2010 and 2013, PCV2a and PCV2b were the most prevalent genotypes, with the exception of 2012 in the ISU group. However, both genotypes experienced a significant decline in frequency after 2014, both globally and within the ISU group. The measured genetic distances within clades indicated that PCV2a harbors greater intra-clade variability compared to other genotypes, both globally and within the ISU sequences. Selection pressure analyses identified multiple sites under positive selection within immunoreactive regions of the capsid protein, notably at positions 63 (global A), 64 (ISU B), 134 (global D and ISU A, B, D), and 169 (ISU D).

Discussion and Conclusions

Numerous amino acids have been positively selected over time, particularly at position 134 of the capsid protein, which has been associated with immune evasion and failures in virus neutralization. Moreover, structural analyses suggest that these sites are located in exposed regions of the capsid, potentially influencing host immune responses. In conclusion, this study not only underscores the extensive genetic

diversity of PCV2 at both global and national scales, with a clear shift to PCV2d genotype prevalence, but also demonstrates that PCV2 undergoes continuous positive selection in critical regions of the capsid. These findings highlight the necessity for ongoing surveillance and molecular characterization of PCV2 to effectively implement targeted vaccination strategies.

**Weaning Acclimation Impacts Feeding Behavior , Thermoregulation, and Growth Performance of Piglets**

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Weaning represents an abrupt exposure of the pig to new social, nutritional, health and environmental challenges. This convergence of stressors often suppresses appetite, feeding behavior and compromises feed intake for days in a high-risk segment of weaned pig groups. Later weaning increases the robustness of the pig but a loss of reproductive efficiency. Strategies that reduce environmental and social disruption during this period may improve post-weaning health in these pigs. This study evaluated the effects of housing environment stability during weaning on growth performance, thermoregulation, and feeding behavior. A total of 293 piglets from 21 litters (weaning age: 18 ± 3 days; BW: 5.65 ± 0.55 kg) were enrolled. Eleven litters remained in their farrowing stalls post-weaning (STALLS), while ten litters were moved to conventional nursery pens (PENS). All pigs were fed a common, complex nursery diet formulated to meet or exceed NRC requirements. Individual body weights (BW) were recorded on days 0, 3, and 7 post-weaning. Feed disappearance was measured by PEN or STALL to estimate average daily feed intake (ADFI) from days 0 to 7. Body temperatures (BT) were recorded every 24 hours for the first 72 hours post-weaning from a representative small, medium, and large pig in each PEN and STALL (STALL; n =33; PEN; n = 30). Feeding behavior was monitored for 6 PENS and 6 STALLS via video analysis to determine average eating time during the first 72 hours post-weaning. Individual BW did not differ between groups at any time point. However, pigs housed in STALLS tended to have reduced BW loss from day 0 to 3 (−6.7 vs. −22.1 g/d; P = 0.103) and greater average daily gain (ADG) from day 3 to 7 (191.5 vs. 163.4 g/d; P = 0.081) compared to the PEN group. Overall ADG from day 0 to 7 was greater in the STALL group than the PEN group (106 vs. 83 g/d; P = 0.034). Additionally, pigs in STALLS tended to spend more time eating during the first 24 hours post-weaning (17.9 vs. 1.9 minutes; P = 0.071) and maintained higher BT in the first 24 hours than the PEN group (102.6 vs. 101.9°F; P < 0.001). These findings suggest that housing and social stability at weaning promotes early post-weaning feeding behavior and intake. Improving feed intake supports thermo-regulation and early post-weaning growth which are key indicators of health and survival.

**Coexist or Eliminate: The Challenge of Endemic PRRSV from the Breeding Herd to Finishing Phases in Mexico**

Ana Paula Poeta Silva[1], Gustavo Lima[1], Edison Magalhaes[1], Daniel Linhares[1], Lucina Galina[2]

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The costs resulting from PRRSV infections in affected breeding herds task producers to choose to tolerate or manage the infection rather than eliminate it. It is important to highlight that low-prevalence breeding herds are likely subclinical; however, herd immunity wanes, virus transmission increases, and clinical consequences become evident in the grow-finish phase. This work describes the production impact of PRRSV on naïve breeding herds alongside two scenarios of low-prevalence breeding herds and their downstream wean-to-finish (WTF) phases in Mexican farms.

Production data were collected from two 10,000-sow breeding herds (System A) which experienced outbreaks of PRRSV lineage L1B. Additionally, two System B's breeding herds were included: a 1,750-sow herd (Herd B1), initially PRRSV-negative but exposed to PRRSV in the past (L1C.29), became infected with L1C.9 and used test-removal of PRRSV-positive sows; a 6,300-sow herd (Herd B2), previously low-prevalence and experienced a new introduction of L1C.28. System B's production data were compared across three predefined phases: negative (21 weeks before outbreak), epidemic (first 16 weeks after outbreak), and endemic (17 to 37 weeks post-epidemic). WTF closeouts (n=224 between 2022-2024) were integrated alongside their PRRSV statuses based on the results of weekly PCR testing in pooled processing fluids (PF). Closeouts were defined as negative when 100% PCR-negative of PF pools, positive 100% PCR-positive, and endemic if they were derived from the endemic breeding herd (B2). Regression models were used to estimate adjusted means for analyses separately into System A (2 herds), Herd B1, B2, System B's closeouts.

During the System A's epidemic phase, the number of live-born piglets per litter significantly (p-value<0.01) decreased by 46% (from 15.3 to 8.2) compared to negative, as well as pre-weaning mortality increased by 87% (from 13.5% to 25.3%), and total piglet weaned per 1,000 sows (TPW) reduced by 50% (from 602 to 242).

Herds B1 and B2 had a milder impact due to PRRSV outbreaks, with only TPW reduced significantly by 11% (from 647 to 559) and by 4% (from 620 to 602), respectively, during epidemic phases compared to the negative. Regarding System B's closeouts, the WTF mortality was 58% significantly higher (p-value<0.01) in closeouts weaned during the breeding herd's PRRS-epidemic (4.7%) and -endemic (4.6%) than negative (3.0%) weeks. Likewise, the ADG decreased by 0.06 kg/day (−6.7%) in PRRS-epidemic weeks and 0.03 kg/day (−3.4%) in -endemic in relation to negative (0.90 kg/day) (p-value<0.01). On-feed days were significantly longer in herds with PRRS (p-value < 0.01). Compared to PRRS-negative herds (143.4 days), the epidemic and endemic weeks added 5.9 and 3.2 days, respectively.

Aligned with findings from the USA, currently circulating PRRSV strains caused a substantial impact on the productivity of previously naïve breeding herds in Mexico, while herds with previous exposure experienced milder effects. However, analyses from the WTF phase revealed that PRRSV continues to exert a significant downstream impact. Despite the relatively modest effects observed in breeding herds,

all WTF production indicators were notably affected. These findings underscore the importance of PRRSV elimination efforts to ensure the long-term sustainability of the swine industry in Mexico.

**Evaluating Flank-to-Flank Tape as a Screening Tool for Gilt Breeding Decisions**

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Introduction

Breeding gilts at the recommended body weight for first service is essential for reproductive performance, along with age, and ensuring that breeding occurs at least on the second recorded estrus. In commercial settings where scales are not always available, flank-to-flank measuring tapes have been promoted as a practical alternative to estimate body weight. However, there is typically substantial variability in gilt weight across different levels of flank-to-flank length, which raises concerns about the tool's validity for predicting precise weight. Additionally, the relationship between body dimensions and weight is expected to vary across genetic lines, highlighting the need for line-specific validation. This study evaluated the correlation between flank-to-flank tape measurements and actual gilt weight, and explored whether the tool could be better applied as a classification method to determine whether a gilt has likely reached the target minimum weight for breeding.

Methods

Flank-to-flank tape measurements (cm) and body weight at insemination (kg) were recorded from 409 Large White gilts (Topigs Norsvin Z-line). The correlation between tape length and weight was assessed using Pearson's correlation coefficient. A binary outcome variable ("Breed" vs. "Don't Breed") was created based on whether the gilt met the recommended minimum weight of 150 kg. A receiver operating characteristic (ROC) curve was generated to evaluate the ability of tape measurements to classify gilts based on this weight threshold and to guide the selection of a tape length cutoff. The performance of different cutoffs was evaluated using confusion matrices, with sensitivity (Se), specificity (Sp), positive predictive value (PPV), and negative predictive value (NPV) calculated.

Results

The correlation between tape length and body weight was low (r = 0.36), indicating substantial variability in weight across measurement levels. The ROC curve yielded an area under the curve (AUC) of 0.71, suggesting fair discriminative ability. While the cutoff that maximized sensitivity and specificity was 93.5 cm, a more permissive threshold of 91.5 cm was selected.

At the 91.5 cm cutoff, sensitivity was 83.8% and specificity was 49.5%. PPV was 82.4%, and NPV was 52.0%. These results indicate that most animals recommended for breeding (i.e., at or above 91.5 cm) meet the 150 kg weight threshold. The lower specificity reflects a management decision to avoid delaying gilts that may already have or be close to the target weight. This trade-off supports the use of the tape as a screening tool rather than a precise predictor of weight.

Conclusions

Flank-to-flank tape measurements can serve as a practical screening tool to assess whether a gilt has likely met the minimum target weight. Using a cutoff of 91.5 cm resulted in acceptable Se and PPV values, allowing most eligible gilts to be correctly identified. A more restrictive cutoff would delay more gilts,

increasing the risk of excessive weight gain before the next estrus and negatively impacting performance and longevity. When used alongside age and confirmation of a second recorded heat, the tape can support field decisions in systems where scales are not available. This is an ongoing project. Therefore, results may change slightly as the study is finalized.

**A spatial network analysis of PEDv from 2017 to 2024 in a swine production group.**

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Introduction

Porcine Epidemic Diarrhea virus is a major endemic cause of production loss in the swine industry. Understanding the epidemiology of the disease is important for disease prevention, disease treatment, and the development of biosecurity protocols.

Methods

Data were collected between 2017 and mid-2024 by a single swine production company owning the individual premises. Variables included the year of the outbreak, the premiseID and location of the property, the barn type (broken between sow barns, nursery barns, and finishing barns), whether the outbreak was a new break or a repeated one, and the number of outbreaks that the premise has had. All data were anonymized, with the spatial plane and relationship kept constant to allow for a spatial analysis.

A point pattern object was created using 'sf' and 'spatstat' in R, and fixed characteristics of the premises were designated as marks on the points. The point pattern intensity was estimated and tested for complete spatial randomness using the chi-squared test. Intensity was broken down by year and examined based on the marks 'type of outbreak' (new or recurring) and 'barn type'. Lastly, complete spatial randomness was tested with Ripley's K function, used to assess spatial dependence in point pattern data.

Results

Outbreak intensity varied by year, break type, and barn type. Outbreaks exhibited a clustered point process, indicating a localized spread.

Conclusions

Point pattern intensity changed over time and between barn types. In later years, outbreaks were re-breaks instead of new infections; therefore, most outbreaks on the farms were likely from internal sources rather than external sources of infection. Spatial clustering explains these patterns, showing that the infection did not spread across the entire production group but was focused on a select number of farms. Thus, biosecurity and control focused on high-risk farms may be a successful strategy.

**Comparison of supplemental heat lamps and heat mats on sow and piglet performance during lactation**

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Supplemental heat lamps have long been an industry standard in lactation stalls. However, supplemental heat mats have been suggested to be more energy efficient and provide a more uniform heat dispersion for the litter, while lowering ambient heat effect on the lactating sow. There has been little controlled research evaluating effects of supplemental heat sources on sow and piglet performance in lactation. A total of 214 sows/litters (PIC 1050 or DNA 241) were used in a randomized complete block design evaluating two treatments: 1) Supplemental heat lamp and 2) Supplemental heat mat. Heat lamps with 175 W heat bulbs were initially suspended 18 inches over black rubber mats in the farrowing stalls. Lamps were raised to 23 inches after the piglets were 10 days of age. Heat mats measuring 2 ft × 4 ft were placed under a stall divider providing 4 sq. ft. in each stall. Two heat lamps or mats were placed in each stall. Two farrowing rooms, each consisting of 108 stalls measuring 6 ft × 8 ft (sow area = 2 ft × 8 ft), were equipped with an electronic feed system capable of recording feed deliveries to each individual sow. Sows were allocated to a treatment at entry into the farrowing room based on individual animal parity, genetic line, and sow entry weight. Pigs were individually weighed at birth (± 24 h) and weaning. Daily sow feed intake was recorded. Supplemental heat sources were turned on at farrowing and remained on through weaning. Using an infrared thermometer, temperature recordings were collected in each stall approximately every 6 inches across the heat mats and the black rubber mats under the heat lamps. There was no effect (P > 0.05) on litter or piglet wean BW or ADG, nor on sow intake performance. While not significant (P > 0.05), pre-wean mortality was numerically lower for heat lamps vs. heat mats (0.8% unit). Average temperature recordings on the rubber mat under the heat lamp ranged from 68.9$^{o}$F on the mat edges to 95.0$^{o}$F in the center with an average of 81.3$^{o}$F, whereas the supplemental heat mat temperatures ranged from 88.4$^{o}$F on the mat edges to 102.7 $^{o}$F in the center with an average of 98.3$^{o}$F. Records indicate the farm crew has replaced approximately 120 heat bulbs and 10 heat lamp fixtures each year the farm has been in operation. However, heat mats installed in part of the farrowing facility in 2018, have not required replacement to date. Collectively, energy and replacement costs were estimated to be reduced by $150/stall/year for supplemental heat mats vs. lamps, suggesting approximately an 18 month break even cost. This study suggests similar performance and economic energy savings with the use of supplemental heat mats vs. traditional supplemental heat lamps.

**Impact of Lawonia Intracellularis vaccination on biodigester performance**

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Introduction

In the coming years, the demand for agricultural and livestock products is estimated to increase significantly due to population growth, leading to a need to intensify production and greater pressure on natural resources. It is necessary to establish responsible and sustainable use of antibiotics, being aware that they are essential for the treatment of certain bacterial infections. The "One Health" concept, among other approaches, involves the recycling of waste and sanitary effluents, which, once misused, become a source of contamination and antibiotic-resistant bacteria (ARB).

Composting and biodigesters allow for the recycling of nutrients, achieving environmental, quality of life, and economic improvements by reducing dependence on mineral fertilizers. In the case of biodigesters, they also provide a renewable energy source, improving energy sovereignty (CARVALHO, 2022). Studies show that the presence of antibiotics in waste can have effects on biogas production and cause the selection of resistant bacteria, which can share their antibiotic resistance genes (ARG) in these environments, raising awareness about this public health problem, in addition to the presence and resilience of antibiotic resistance genes in the treated liquid fraction.

Materials and Methods.

A farm (6300 sows) with a history of Ileitis and operating a biodigester for manure processing was followed up from August 2020 to March 2023. Intramuscular LI vaccination (Porcilis Ileitis) was implemented in November 2021 to control clinical disease. An historical comparison was done comparing a period before (Aug20-Nov21) and after (Dec21-Mar23) implementation of vaccination. Antibiotic consumption and energy production of the biodigesters were measured in mg/kg and Megawatts produced (MW) per biodigester, respectively. The relationship between both variables was investigated by a linear model (Statgraphics Centurion XVI).

Results

Antimicrobial consumption was reduced after vaccine implementation (before: 146,61mg/kg; after: 64,57mg/kg). Similar findings were described for antimicrobials used against enteric disorders (before: 80,8mg/kg; after: 36,6mg/kg)

Energy production was increased after vaccination (before: 322 MW; after: 8793 MW).

The equation of the Linear model, fitted to describe the relationship between antimicrobial consumption and energy production was:

Energy production (MW) = 14493 - 117.575*antimicrobial consumption (mg/kg). A significant strong correlation ($R2=-0.964186$; $P<0.05$) was determined.

Conclusion

Under the conditions of this case report, LI vaccination reduced antimicrobial consumption, having a potential impact on the performance of the biodigester. It is hypothesized that this antimicrobial reduction led to an optimal bacterial growth needed for manure bio-digestion, and therefore, improving the efficiency in the generation of biogas and energy through the effluents.

Vaccination does not only support animal health but also may improve sustainability in pig production under the One Health umbrella, promoting circular economy, less antimicrobial usage and optimizing this renewable energy source.

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**Spray-dried plasma top-dressed in feed reduces mortality and medications for grow-finish pigs.**

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Introduction

Spray-dried plasma (SDP) is a highly digestible functional protein commonly used in weaned pig diets. This study aimed to assess the impact of top-dressed SDP on mortality and injectable medication use in grow-finish (GF) pigs under commercial conditions in Brazil.

Material and Methods

A total of 1,536 grower pigs (65 days old) were randomly assigned to a control or SDP treatment group, with 24 pens of castrated males and 24 pens of females (32 pigs/pen; 24 replicates/treatment). Both groups shared the same health status, feed, and vaccination program. The SDP group received 2 g of SDP top-dressed daily during the 98-day GF phase. Each day 64 g of SDP was added on the feed in the trough using a scoop and hand-mixed into the feed for each pen of 32 pigs to provide 2 g of SDP per pig. Mortality and injectable medications were recorded per pen throughout the study. Pen was used as the experimental unit, and data were analyzed using a mixed model for the main effects of treatment and sex with replication as a random effect. Chi-square probabilities were reported for results expressed as a percentage.

Results and Discussion

There were no significant effects of sex or interactions of sex and treatment. The SDP group had a lower (P=0.0007) average number of deaths per pen (control, 1.08; SDP, 0.25) and a lower (P=0.0003) percentage of mortality (control, 3.39%; SDP, 0.78%). The SDP group required less (P=0.0016) injections per pen of the antibiotic Tulathromycin (control, 0.75; SDP, 0.13) with a trend (P=0.0877) toward less use of total injectable medications (control, 1.70; SDP, 1.11). Other medications used included Dexamethasone (control, 0.38; SDP, 0.46) injections per pen and Metamizole sodium (control, 0.55; SDP, 0.51) injections per pen, but their use did not differ between treatment groups. The main reason for the use of injectable antibiotics was for symptoms of pneumonia. These findings align with previous research demonstrating the benefits of SDP on performance, gut health, immune function, and general systemic health (1,2), as well as reduced antibiotic use in grow-finish pigs (3).

Conclusions

Providing 2 g of SDP per pig per day top-dressed on feed during the GF phase offers a novel approach to support health of grow-finish pigs and aligns with current regulations to reduce reliance on antibiotics.

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**Effect of antioxidant supplementation with ImmuFend pre-farrow and during lactation on sow performance on subsequent reproductive events**

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Introduction

Optimizing sow health and productivity around farrowing is critical for swine operations. This study evaluated the effect of antioxidant supplementation with ImmuFend administered pre-farrow and during lactation on sow key performance indicators, measured across the subsequent parity, in a system under a natural porcine reproductive and respiratory syndrome (PRRS) challenge.

Materials and Methods

• Study design: A randomized block design was used to enroll a total of 804 gestating sows which were followed for their next two litters.

• Treatments: Group A was supplemented with ImmuFend top-dressed from farrowing load-in until weaning. Group B received ImmuFend from farrowing load-in to day 5 post-farrow. Group C, the control group, was not supplemented with ImmuFend during this trial.

• Parameters measured across the subsequent parity included wean to first service interval, wean to farrow interval, farrowing rate, culling rate, and sow mortality.

• Methods: 2.5 grams of ImmuFend was supplemented to each sow individually as a top dress daily. All key farrowing performance metrics were extracted from the farm's record-keeping software. Statistical analysis was performed using Generalized Linear Mixed Model and MANOVA Repeated Measures functions of JMP PRO 18. Results were considered significant if $P < 0.05$. A trend toward significance was established at $0.05 < P < 0.10$.

Results

• Wean to service interval (days): Groups A (12.77a) and B (12.74a) were significantly higher compared to group C (14.60b). ($P < 0.074$). ab: Means with different superscripts differ ($P < 0.05$).

• Wean to farrow intervals (days): Group A: 127.9a, Group B: 129.65b, and Group C: 131.06b. ($P < 0.083$). ab: Means with different superscripts differ ($0.05 < P \leq 0.10$).

• Sow culling rates: Group A: 0.82a, Group B: 2.02b, and Group C: 2.24b. ($P < 0.001$)

• Farrowing Rate: Groups A (87.3%a) and B (87.5%a) had significantly higher farrowing percentages than C (78.85%b). ($P < 0.05$)

• Sow mortality: Group A (3.68%) had the lowest percentage compared to group B (4.03%) and group C (6.41%), numerically.

Conclusions

Supplementing sows with antioxidants via ImmuFend during the periparturient period until weaning yielded notable benefits in both immediate and subsequent sow reproductive performance. The most pronounced improvements were observed in:

- Significant increase in number of piglets weaned (Bohr et al, 2025)
- Improvement in piglet ADG during lactation (Bohr et al, 2025)
- Shortened wean-to-service and wean-to-farrow intervals
- Higher farrowing rate
- Significantly lower sow culling rates
- Potential reduction in sow mortality

The reduction in wean to service and wean to farrow intervals have direct implications on non-productive days (NPD). Even modest reductions in NPD translate into measurable economic gains by increasing the number of litters per sow per year, enhancing throughput and reducing costs per piglet produced without increasing sow inventory. Similarly, lower culling rates and increased farrowing rates yield important economic advantages for weaned pig producers.

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**Early detection after oro-nasal inoculation of African Swine Fever virus in boars**

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Introduction

African swine fever virus (ASFV) can cause devastating losses in swine and has far reaching economical and trade implications. ASFV has previously been shown to be shed in semen from 4 boars inoculated intramuscularly with the moderately virulent ASFV Estonia 2014 strain. The virus was detected as early day 1 day post infection (dpi) in blood, and 2 dpi in semen. Seven of 14 gilts inseminated with the infected semen tested positive for ASF within one-week post-insemination. The purpose of this study was to determine the shedding patterns of ASFV in semen and various sample types along with establishing the timeline for the onset of clinical signs, following natural (oronasal) exposure to highly virulent ASFV Georgia 2007/1.

Materials and Methods

Nine boars (8 intact and 1 vasectomized), 9-10 months of age, were acclimated prior to inoculation with ASFV Georgia 2007/1. Boars were collected using the 3-glove method, once before and daily after the inoculation. In addition to semen, oral fluids (daily), oral swabs, whole blood, serum and blood swabs were collected on the collection days. Boars were monitored daily for fever and for other clinical signs. Upon reaching the humane end point, boars were euthanized, complete postmortem examination was performed, and tissue samples were collected for PCR, virus isolation and histopathology.

Results and Discussion

In one of the boars, ASFV genome was detected in blood (viremia) by 2 dpi, and in semen by 3 dpi. On 3 dpi, viremia was detected in three more boars, and by 4 dpi, all nine boars developed viremia. On 4 dpi, semen from three boars had detectable levels of ASFV genomic material. Out of those three, two started viremia on 3 dpi and the other on 4 dpi, coinciding with semen detection. Onset of fever was observed in 3 boars on 3 dpi and by 4 dpi, all boars had developed fever. Two boars were mildly depressed on 3 dpi while others appeared clinically normal. One boar was humanely euthanized due to a non-ASF related condition on 4 dpi. As clinical disease progressed 4 dpi on, two boars reached the humane end point on 5 dpi. On 5 dpi, five out of six boars showed ASFV genome in semen, including two strong positive detections. Three of those boars were showing consistent detection in semen on 4 and 5 dpi. On 6 dpi, semen was collected from only one boar, and it was positive for ASFV genomic material for the first time, two days after it developed viremia. All boars displayed clinical signs of acute ASF and reached humane end point by 7 dpi. Conclusions and additional results will be discussed at the Leman Conference.

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**Use of Mycoplasma hyosynoviae and Mycoplasma hyorhinis serology to differentiate herd status**

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Mycoplasma hyorhinis (Mhyor) and M. hyosynoviae (Mhyos) are insidious pathogens associated with clinical disease in post-weaning pigs. Mhyor is increasingly detected in cases of serositis and arthritis submitted to a U.S. VDL with a primary focus on swine diagnostics (1). While Mhyos the rate of detection declined to 6.4% from 2017-2022, it remains a significant etiology of lameness in finishing pigs (1).

To evaluate the serologic differentiation of herd status, two 2000-sow farrow-to-finish sites were selected: one with known Mhyos and Mhyor infections confirmed by PCR (CONV) and one considered free of both agents (NEG), as previously described (2). Serum antibodies were evaluated using two ELISAs: one targeting a recombinant chimeric polypeptide representing the seven known variable lipoproteins (A-G) of Mhyor and the other using a detergent-extracted cocktail of Mhyos surface proteins. The suitability and use of these antigens as serologic biomarkers of Mhyor and Mhyos exposure was previously described (3).

Twenty pigs per farm from the same birth cohort (birth lot) were sampled at 4, 7, 10, 15, 20, and 23 weeks of age. In the NEG cohort, no pigs were positive for Mhyos at any time point. For Mhyor, the percentage of NEG pigs testing positive varied over time: 25%, 5%, 10%, 37%, 55%, and 35% ($p=0.005$). In the CONV cohort, the percentage positive for Mhyos was 45%, 17%, 6%, 5%, 56%, and 81%, and for Mhyor: 90%, 67%, 90%, 100%, 100%, and 100%.

ELISA S:P values for both Mhyos and Mhyor were statistically different between the NEG and CONV cohorts at all time points (Mann-Whitney U-Test, exact $p < 0.001$), with the NEG cohort consistently showing lower mean ranks.

These results demonstrated that Mhyos and Mhyor ELISAs tests can differentiate herd health status. None of the NEG pigs showed evidence of Mhyos exposure. Although the Mhyor ELISA showed variable reactivity among NEG pigs (S:P values from 0.4 to 3.7), oral fluid PCR results collected from the same cohort (data not shown) suggested these are non-specific reactions. Further, positive S:P values in CONV pigs ranged from 0.442 to 6.374. In the future, adjusting the Mhyor ELISA cut-off value may reduce false positives in naïve herds. Alternatively, applying statistical process control to cohort-level mean S:P values may improve monitoring and interpretation in Mhyor-free populations.

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# PHYTOBIOTIC–PREBIOTIC ADDITIVE AS A SUBSTITUTE FOR ENRAMYCIN AS A GROWTH PROMOTER IN SWINE PRODUCTION

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## Introduction

The use of antimicrobial growth promoters in swine production has traditionally aimed to improve feed efficiency and animal performance. However, increasing regulatory restrictions in Brazil, prompted by public health concerns and international trade requirements, have stimulated the search for natural alternatives. Phytobiotics and prebiotics, with antimicrobial, anti-inflammatory, and antioxidant properties, have emerged as promising solutions. This study aimed to evaluate the efficacy of a phytobiotic–prebiotic additive (Improver), composed of thyme, sage oil, carob seed, Jerusalem artichoke, and chicory, in comparison with enramycin in finishing pigs.

## Methods

A total of 120 pigs (PIC 337 × Camborough), 70 days old with an initial body weight of 31.296 ± 2.738 kg, were randomly assigned to two treatment groups with 12 replicates of five pigs per pen. The treatments were: (1) Positive Control – diet with enramycin (5–10 ppm); and (2) Improver – diet supplemented with 500 g/ton of the phytobiotic–prebiotic additive. Animals were fed ad libitum from day 70 to 168 under a four-phase feeding program.

Performance indicators – average daily gain (ADG), daily feed intake (DFI), and feed conversion ratio (FCR) – were evaluated weekly. At the end of the trial, carcass traits were measured using the Hennessy Grade Probe, including backfat thickness, loin depth, lean meat percentage, and meat color (PSE classification). Data were analyzed using ANOVA and Chi-square test with a significance level of $p \leq 0.05$.

## Results

No significant differences ($p > 0.05$) were observed for any performance parameters. The average daily gain was 1.015 kg/day and 1.019 kg/day for the Improver and enramycin groups, respectively. Daily feed intake and feed conversion ratio were also comparable: 2.410 vs. 2.421 kg/day, and 2.370 vs. 2.373, respectively. Final body weights at 168 days were 130.836 kg in the group receiving the phytobiotic–prebiotic additive and 131.231 kg in the control group, confirming equivalent performance ($p > 0.05$).

Carcass characteristics followed the same trend of similarity. The average carcass weight was 94.500 kg in pigs supplemented with Improver and 94.092 kg in those receiving enramycin. Backfat thickness (16.074 mm vs. 16.071 mm) and loin depth (61.233 mm vs. 60.503 mm) were also comparable. Lean meat percentage, calculated using the Hennessy method, showed minimal variation between treatments, with values of 55.237% vs. 55.166%. The meat color index, used to assess the presence of pale, soft, exudative (PSE) meat, remained within the normal range (≤90) in both groups, 69.259 (Improver) and 67.982 (enramycin), indicating no adverse effects on meat quality.

Conclusions

The phytobiotic–prebiotic additive Improver at 500 g/ton effectively replaced enramycin as a growth promoter in finishing pigs. It maintained animal productive performance and carcass quality with no statistically significant differences. These findings support its application as a viable, antibiotic-free alternative in swine production systems.

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**One Health perspective of swine diseases: The impacts of African swine fever emergencies on veterinarian responders**

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For animal health emergencies, veterinarians are critical first responders and may participate in distressing tasks like depopulation of infected animals and protective culling of healthy animals. African swine fever (ASF) is a global pandemic, affecting nearly 2 million pigs since 2022 alone and causing significant disruption to food security and trade[1]. The Philippines and Dominican Republic (DR) have been affected by ASF since 2019 and 2021, respectively. In both countries, public and private veterinarians have been crucial for implementing control measures such as depopulation, surveillance, and quarantines to prevent further disease spread and minimize the epidemics' impacts to swine health and production. Despite these burdens, the effects of prolonged emergency response on the well-being of veterinarians has not been well-characterized. The objective of this work was to assess the impacts of the ASF epidemics in the Philippines and DR on the mental and social health of swine veterinarians. We developed a questionnaire based on the World Health Organization's Quality of Life assessment[2] and distributed it to 42 swine veterinarians at two in-person workshops, in the Philippines in December 2023 and in the DR in January 2025. In the DR, semi-structured focus group interviews were used at a second workshop in March 2025 to explore the root causes of symptoms reported from the questionnaire. Questionnaire responses were analyzed using social network analysis to visualize and explore the connectivity between reported negative symptoms. In the network, nodes represented negative symptoms, and edges represented high positive agreement between two symptoms (the proportion of individuals who responded with both symptoms present). Graph and node-level centrality measures were estimated. Qualitative data from the focus groups was coded and thematically analyzed. Overall, veterinarians that responded to the ASF outbreaks experienced high levels of anger (72%), reduced energy (68%), hopelessness (60%), reduced sleep (60%), and reduced enjoyment of life (56%). A small number of veterinarians reported more significant symptoms or behaviors, including suicidal thoughts (n=2) and starting mental health visits (n=4). Anger and hopelessness were highly centrally located in the network with the highest betweenness, closeness, and Eigenvector scores, and were directly connected to other highly prevalent symptoms such as reduced sleep and reduced enjoyment of life. Veterinarians from the DR reported that anger and hopelessness were worsened by a heavy work burden, perceived insufficient response to the disease, and a lack of communication, trust, and transparency between government authorities, veterinarians, and farmers. The veterinarians also reported that they felt they had conflicting

responsibilities between supporting producers' livelihoods and professional obligations to control ASF. Many sources of positivity and hope were also identified, such as improved technical capacity to respond to ASF, a sense of responsibility, and family and social support. As animal, human, and zoonotic diseases, such as ASF and avian influenza, continue to emerge and expand, these results bring attention to the need for considering actions to prevent and mitigate their impact on the mental health of veterinary first responders and, ultimately, improve the effectiveness of the disease response.

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**Evaluation of sick pig laboratory surveillance at University of Minnesota and Iowa State University Veterinary Diagnostic Laboratories**

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The US is currently free of African swine fever and classical swine fever (ASF, CSF), two foreign animal diseases that would have severe impact if detected. To help protect the US swine industry and detect a potential disease introduction as early as possible, the US Department of Agriculture operates an ASF/CSF surveillance plan with multiple components1. The Sick Pig Veterinary Diagnostic Laboratory (VDL) component uses a risk-based approach for active surveillance by targeting sick pig cases submitted to VDLs and is conducted at 12 VDLs in the US2. Cases with an approved specimen type (spleen/spleen swabs, tonsil, lymph nodes, whole blood/blood swabs) and clinical signs, pathology, or history consistent with ASF/CSF can be tested at no charge to producers or veterinarians. This component is highly valuable due to its risk-based approach, but its coverage and representativeness compared to the general swine population have not yet been fully evaluated. Here, we aimed to evaluate the Sick Pig VDL surveillance component at two major VDLs for swine, the University of Minnesota (UMN-VDL) and Iowa State University VDLs (ISU-VDL). De-identified data from all swine cases were received from UMN-VDL, and from tissue cases (histopathology, necropsy) from ISU-VDL, from approximately 2022-2024. The date received, state of origin, age/production class, farm type, diagnostic procedures, tested specimens, and test results were available for analysis. Data were descriptively analyzed, and choropleth maps were produced. Odds ratios (OR) and unpaired t-tests were used for comparisons between ASF/CSF-tested and non-tested cases. In total, UMN-VDL had 29,012 swine cases from 35 states. Of these, 1,490 cases (5% of all cases/54% of tissue cases) from 18 states were tested for ASF/CSF. ISU-VDL had 20,601 tissue cases from 46 states. Of these, 6,864 cases (33%) were tested for ASF/CSF. All ASF/CSF tests from both labs were negative with no false positives. Testing was concentrated in swine-dense states (IA, MN, NC) and was consistent over time. The majority of cases with an ASF/CSF-approved specimen were tested for ASF/CSF (UMN=81%, ISU=63%). ASF/CSF-tested specimens were mainly spleen or spleen swabs (>80%). At both labs, tissue cases with pigs <180 days were significantly more likely to be tested than those >180 days (UMN-VDL: OR=1.70, 95% CI: 1.21-2.39; ISU-VDL: OR=1.74, 95% CI: 1.42-2.12). The odds of being an ASF/CSF-tested case were higher in nursery and finishing farms compared to sows and breeding/replacement. The eligibility of cases for the sick pig VDL component could not be fully evaluated here because data on presenting clinical signs/history and a full list of specimens submitted with each case were not available. Despite these limitations, these results strongly support that the sick pig VDL component is being implemented at a high level in both UMN-VDL and ISU-VDL, and that it efficiently rules out ASF/CSF in sick commercial pigs in the US. Producers and veterinarians are encouraged to submit spleen or other approved specimen types with sick pig cases to help rule out ASF/CSF, which will ultimately protect the US swine industry.

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**Phylogenetic Lineages of PRRSV-2 from Canada Reveal Patterns of Transboundary Spread and Two Novel Sub-Lineages in North America**

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Introduction

PRRSV-2 represents a threat to the global swine industry. PRRSV-2 is classified into lineages, sub-lineages, and variants based on phylogenetic relationships and genetic distances of the ORF5 gene. Currently 21 sub-lineages are described globally and 205 variants in the USA. Canada ranks among the world's leading pork producers and exports approximately 6 million live pigs annually to the USA. Historically, certain sub-lineages of PRRSV-2 were introduced into the USA from Canada, but the number of Canadian sequences analyzed in these studies is limited to a few hundred. Therefore, the evolutionary dynamics and dispersal patterns of PRRSV-2 in Canada remain uncertain, and the extent to which PRRSV-2 evolution in Canada and the USA is characterized by extensive gene flow or on independent evolutionary trajectories is not clear.

Methods

To understanding of PRRSV-2 diversity in Canada and its patterns of spread between different regions of Canada and the USA, we analyzed a dataset of over 3,000 ORF5 sequences collected over 24 years from five Canadian provinces (Aberta n=11, Manitoba n=316, Ontario n=563, Quebec n=2678, Saskatchewan n=5) and 76,000 sequence from USA. Sequences were classified into sub-lineages; maximum likelihood phylogenies inferred with IQ-TREE and pairwise genetic distances were computed using SDTv1.2. Time-scaled phylogenies and discrete trait phylogeographic reconstructions were conducted in BEAST v1.10 to infer sub-lineage origins and cross-border dispersal events. For the phylogeographic analyses, we combined the Canadian data with a comprehensive data set from the USA composed of sequences originating from the University of Minnesota's Morrison Swine Health Monitoring Project (MSHMP) and GenBank.

Results and Conclusions

Thirteen distinct sub-lineages (1A–1C, 1E–1I, 5A, 7, 8A, 8C and 9A) were identified circulating within Canada. Nearly one-third of Canadian sequences were assigned to an undetermined sub-lineage. Phylogenetic analyses incorporating representative sequences from all known sub-lineages revealed that the majority of the unclassified sequences clustered into four distinct monophyletic clades, most closely related to sub-lineage 1F. These clades exhibited average genetic distances exceeding 9.5% from other sub-lineages, suggesting they may represent novel sub-lineages. For two of these groups, we propose the designation of two new sub-lineages: 1K and 1L. The other two clades represent less than 2% of Canadian sequences and were not detected after 2021. Our results suggest that sub-lineages 1C, 1F, 1H, 1I, 1K, and 1L originated in Canada, while 1A, 1B, and 1E 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

indicative of founder effects and local diversification. In contrast, 1B showed unidirectional movement from the USA into Canada, and 1E and 1I exhibited bidirectional transmission. Sub-lineage 1L and the two undetermined clades appeared restricted to Canada. Our findings help clarify PRRSV-2 diversity in the USA by situating Canadian sub-lineages in the global phylogenetic framework and mapping cross-border spread. These results highlight the need for coordinated surveillance and a unified nomenclature across Canada and the USA, which would aid in rapid detection cross-border transmission and mitagate the introduction of new sub-lineages.

**Timing the Regional Dispersal of PRRSV-2 Variants Across the U.S. to Improve Preparedness**

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Introduction

Porcine Reproductive and Respiratory Syndrome Virus 2 (PRRSV-2) is a positive-sense single-stranded RNA virus (+ssRNA) in the Arteriviridae family and represents a major threat to the global swine industry. It is classified into 11 lineages based on genetic distances in the ORF5 gene, which are further subdivided into sub-lineages and variants. Over the past decade, at least 19 variants (i.e., phylogenetic clades with a mean nucleotide distance of ~2.5%) are estimated to have emerged annually in the U.S. Long-distance PRRSV-2 spread is primarily driven by animal movement across geographic regions. Measuring the timing in which a new variant emerges in one region and spreads to other regions could inform preparedness.

Methods

To address this, we analyzed 19,034 sequences sampled between 2015 and 2024, retrieved from the Morrison Swine Health Monitoring Project (MSHMP). Variants associated with vaccine strains and unclassified variants were excluded, yielding a final dataset of 9,257 sequences representing 102 variants across the five major swine-producing regions in the USA: the Upper Midwest (UM), Lower Midwest (LM), Atlantic Seaboard (AS), Northeast (NE), and Great Plains (GP). The time between emergence and dispersion of variants were assessed using survival analysis and structured coalescent models to estimate regional persistence times and the time between emergence and spread to new regions. Genetic diversity was measured using Hill numbers.

Results and Conclusions

The UM had the highest variant richness (n=65), which reflects the number of unique variants present in a population irrespective of their relative abundance, followed by the LM (n=27), AS (n=26), NE (n=20), and GP (n=17). Of the 47 variants that initially emerged in the UM, 11 later spread to other regions. The UM also received the highest number of variant introductions (n=22), followed by LM (n=16), NE (n=12), AS (n=5), and GP (n=2), highlighting regional differences in connectivity and risk. Other regional patterns were also noted. For example, variants originating in AS never dispersed to GP, and vice versa. On average, variants remained in a region longer before spreading onwards in the UM, GP, and AS (2–3 years) compared to LM and NE (0.5–1.8 years). Dispersal times varied among variants and also among regions, likely reflecting differences in animal movement and production practices between regions. These findings may help anticipate the risk of PRRSV-2 variant introduction and provide more accurate dispersal time estimates, which are useful for improving epidemiological models.

**Multivariate analysis reveals superior gut integrity in suckling piglets treated with dual early application of postbiotic**

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Introduction

Postbiotics are byproducts of microbial fermentation (metabolites, cell wall components, organic acids, etc.) that can exert beneficial effects on the host's health. Its use is increasingly recognized as an effective tool to improve gut health and reduce diarrhea in swine, particularly when applied during critical developmental windows [1-3]. This study evaluated the impact of different timing strategies of a postbiotic on intestinal morphometry, mucosal permeability, immunoglobulin profiles, and fecal consistency in suckling piglets. The central hypothesis was that earlier or reinforced administration protocols would enhance gut structural and functional integrity.

Methods

Sixty sows and their litters were equally distributed into five groups: NC, no postbiotic treatment; PB1 (postbiotic on D1 via pig doser); PB1/3 (postbiotic on D1 and D3 via pig doser); PB1/14 (postbiotic on D1 and D14 via pig doser); and PB1/13-14 (postbiotic on D1 via pig doser; D13 and D14 via feed). Litters had their fecal score monitored throughout the study [4]. On day 21, five piglets per group were selected for laboratory analysis. The same animals were used for all biological sample collections to ensure consistency across datasets. Blood samples were collected 6 hours after oral administration of FITC-dextran to assess intestinal permeability, and tissue samples (duodenum, jejunum, and ileum) were collected postmortem for histomorphometry and tight junction protein quantification (Claudin-1 and Occludin). Data were analyzed using ANOVA followed by Tukey's post-hoc test ($\alpha$=0.05), and a Principal Component Analysis (PCA) was conducted to integrate the morphometric, permeability, immune, and clinical (diarrhea) variables. PCA was used as an unsupervised multivariate tool to reduce data dimensionality and identify latent structures in the dataset. The first two components (PC1 and PC2) explained the majority of the variance, with PC1 capturing morphometric and clinical health variables (villus height, villus/crypt ratio, fecal score), and PC2 capturing immune and epithelial barrier markers (IgG, IgM, Claudin-1, Occludin).

Results

ANOVA showed no significant differences (p>0.05) among groups for villus height, crypt depth, or FITC-dextran levels, although trends toward improved morphology were observed in PB1/3 and PB1/14. PCA, however, revealed robust treatment-driven clustering. Piglets in PB1/3 clustered positively along PC1 and PC2, indicating a profile of enhanced intestinal architecture, reduced fecal scores, and higher Claudin-1 levels, suggesting epithelial fortification. PB1/14 animals also showed improved distribution in the PCA space, particularly associated with higher Occludin expression and better fecal score. PB1/13-14 presented variable positioning, likely due to inconsistent intake of the postbiotic when administered via feed. In contrast, NC animals consistently occupied the lower PC1 quadrant, indicative of poorer mucosal

development and higher diarrhea burden. Immune markers did not differ statistically among groups, though IgA and IgG means were numerically higher in PB1/13-14, suggesting a non-significant trend toward immunomodulation.

Conclusions

PCA analysis demonstrated clear patterns associating dual early applications (especially PB1/3) with superior intestinal health. These findings emphasize the value of multivariate approaches for gut integrity assessment, support the early and reinforced administration of postbiotics in piglet management, and are consistent with recent evidence that postbiotics modulate intestinal structure and improve gut health in piglets.

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**Impact of Pre-Farrow Ceftiofur Sodium Administration to Dams on Progeny Prewean Production Parameters**

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Introduction

Streptococcus suis (S. suis), a swine pathogen capable of inducing high morbidity and mortality early in life, continues to challenge producers and veterinarians worldwide. A known route of S. suis infection in piglets is during transit through the vaginal canal. As a result, routine medication of piglets is common practice. Maternal interventions, such as a single pre-farrow dose of ceftiofur sodium (Naxcel®) in dams, have shown potential to reduce S. suis colonization in piglets. The production impacts associated with this decreased early colonization remain unclear. The objective of this study was to assess the impact of periparturient Naxcel® administration to dams on the prewean production parameters of their progeny.

Materials and Methods

A single 2,500-head, PRRSv, Mhp, and PEDv/TGEv/PDCoV negative commercial sow farm was utilized for this study. Twenty-four farrowing rooms were assigned to either a “Treated” or “Control” group (n=12/group). Dams in Treated rooms received Naxcel® (5 mg/kg) IM at induction. Piglet cross-fostering between rooms was prohibited. During the study, no mass treatment to progeny was used; piglets were spot-treated based on observed health concerns. Key production parameters were recorded at the room level, including pre-wean mortality (PWM%), farrowing performance, and piglet treatment timing and frequency. Data analysis was conducted in R. Farrowing metrics (average total born (TB), live born (LB), stillborn (SB)%, mummies%, and PWM%) were compared between groups using Mann-Whitney tests. Treatment incidence rates per pig-day within each room were analyzed by Poisson regression model with pig-days as an offset. Peak of treatment frequency based on piglet age within the room was described.

Results

Preliminary results from 16 rooms (n=8/group) are presented, as the remainder of rooms will wean early September. Farrowing performance was similar across groups (p>0.10), with averages of 18.8 TB, 16.6 LB, 6.6% SB, 4.9% mummies, and 11.9% PWM. A total of 398 piglet treatments occurred in Control rooms vs. 254 in Treated rooms. Treatment incidence rates were 0.0124 and 0.00934 per pig-day for Control and Treated groups, respectively. Poisson regression showed a significant 24.7% reduction in treatment incidence in Treated rooms (rate ratio: 0.753; 95% CI: 0.64–0.88; p<0.001). Treatment timing analysis revealed that 59% and 33% of treatments were administered between days 1–6 and 7–12 of piglet age, respectively.

Discussion and Conclusion

Results of this investigation suggest that periparturient Naxcel® administration to dams can reduce the amount of piglet treatments prior to weaning. Farrowing performance and timing of piglet treatments were not impacted, with the majority of individual piglet treatments occurring within the first 6 days of age, regardless of dam treatment.

**Use of an environmental sample collection device to determine Salmonella status of swine transport trailers**

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Introduction

Salmonella infections are often subclinical with intermittent shedding in finishing pigs making detection difficult. However, the stress of transportation has been shown to induce more Salmonella shedding, potentially facilitating detection. The objective of this study was to evaluate if an environmental sample collection device worn over shoes could be used to determine the Salmonella status of swine transport trailers.

Methods

Within three hours prior to load-out, six environmental samples were collected from five finishing barns using a fabric environmental sample collection device worn over shoes (EnviroBootieTM, Hardy Diagnostics). Pens selected for sampling were spatially distributed throughout the barn and walked in the same pattern every time. Two samples using the same collection system were taken from one trailer at each of the finishing farms immediately before loading pigs, one from the lower and one from the upper deck. Two additional samples were collected from the same trailer after pigs were off-loaded, one from each the upper and lower deck. Trailers were walked in the same pattern every time. Samples were evaluated by Salmonella enrichment culture.

Results

Salmonella was cultured from 13% (4/30) of farm samples, all positives were from the same farm. Salmonella cultures were 70% (7/10) positive on trailers prior to loading and 90% (9/10) positive after the pigs were unloaded at the packing plant.

Conclusions

The use of this environmental sample collection device was a successful method to sample and culture Salmonella from swine transport trailers. This method could easily be used to investigate trailer sanitation and points of contamination. Furthermore, if swine transport trailers were only positive for Salmonella after the pigs were unloaded, as in one farm in this study, trailers may be useful in measuring the Salmonella status of a farm, indicating that this sampling method merits further exploration.

**Inactivation of PRRS virus on surfaces and in air by far-UVC light (222 nm)**

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Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) causes huge economic losses to the swine industry and has not been controlled even with extensive vaccination programs. The virus is believed to be spread by fomites and by air. It is particularly difficult to control because of rapid mutations that generate variant strains. The industry is always looking for better and cost-effective methods to inactivate PRRSV on swine farms. The far-UVC light (207 to 222 nm) represents a new era in UV application for virus control because it can kill human and animal pathogens in occupied spaces without negatively affecting skin or eyes; thus, it is a safer option for disinfection compared to the traditional UVC light (254 nm).

Methods

In this study, the effect of far-UVC light (222 nm) was investigated against aerosolized PRRS virus and on PRRS virus-contaminated surfaces. A special environmental chamber was designed to aerosolize PRRS virus and measure the inactivation effects of different doses of far-UVC. Experiments were conducted using one, two, and three pairs of UVC lamps. For testing the effect of far-UVC on PRRS virus-contaminated surfaces, the virus was loaded onto discs of stainless steel (SS), polypropylene plastic (PP), polyvinyl chloride (PVC) plastic, and aluminum (AL). The PRRSV was loaded onto coupons (~1 $cm^2$) of these fomites (at 30 µL of virus per coupon), air-dried for one hour, and then exposed to far-UVC at distances of 8 and 12 inches for 1, 2, 4, 6, 8, and 10 minutes.

Results

The rates of inactivation of aerosolized PRRSV were 50% and 90% with two and three pairs of lamps, respectively, while a single pair did not cause any inactivation. The rates of viral inactivation after a 10-minute exposure at 8 and 12 inch distance on SS, PP, PVC, and AL were (99.72% and 99.40%), (99.22% and 98.34%), (97.25% and 97.25%), and (99.22% and 99.24%), respectively.

Conclusion

Far-UVC light has the potential to be used on swine farms for PRRSV (and perhaps other viral) inactivation.

**Individual Sow Care outcomes and challenges: A case study**

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Introduction

Individual Sow Care (ISC) is a training program that teaches caregivers the value of conducting health, welfare, and performance assessments on every sow every day to improve early detection and treatment of sows needing care.

Methods

ISC trainings were held quarterly on a 5000-sow open pen gestation farm specifically targeted for sow mortality reduction. Health of the farm was considered porcine reproductive and respiratory syndrome virus (PRRSV)-stable and Mycoplasma hyopneumoniae (Mhp)-negative from April 2024 through May 2025. This farm had recently completed a PRRS and Mhp elimination program at the onset of the initial training period, during which sows received whole herd tulathromycin injections which may have additionally contributed to improved health outcomes. ISC training consisted of both classroom and in-barn portions, with walking pens daily as a team being the primary point of emphasis. Training involved all phases of production on the farm: breeding, gestation, and farrowing. During this time, lame, off feed, or injured sows were identified, and farm staff would return to treat, or remove, sows according to farm protocol. Weekly sow deaths were the primary outcome measured.

Results and Conclusion

Sow mortality data were analyzed for a 3-week period prior to, and after, each of four quarterly training sessions. Prior to the initial training, the average three-week mortality rate was 13.1% which declined to an average 3-week post-training mortality of 12.2%. Thereafter, the second, third, and fourth pre- and post-training 3-week averages were 10.5% and 12%, 8.5% and 7.6%, 5.0% and 5.2%, respectively. Overall, this farm exhibited a consistent downward trend in sow mortality throughout the study period, with a cumulative reduction exceeding 7%. Sow health and key performance indicators are multifactorial. A notable challenge in maintaining continuity of a training program was employee turnover. Each training session included a significant number of new employees, while also serving as a refresher for experienced personnel and the designated training team. These findings suggest a regular, structured training focused on early identification of at-risk sows can positively influence mortality rates. However, achieving a consistent and sustained reduction remains complex, even with ongoing education. The overall success of a plan to reduce sow mortality will require more than periodic outside training programs like ISC. All personnel including production and farm managers, caregivers, training team, nutrition and veterinary teams are needed to successfully initiate process changes aimed at reducing sow mortality.

**Evidence of coinfection by Swine Teschovirus and Streptococcus suis in piglets with neurological disease**

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Encephalitis poses a significant health challenge in modern swine production, particularly affecting piglets during the nursery phase, where it is associated with high morbidity and mortality rates. Several infectious agents are involved in its etiology, including bacteria such as Streptococcus suis, a common cause of meningoencephalitis, and viruses such as swine Teschovirus, known to cause lymphoplasmacytic polioencephalomyelitis. It is well-established that prior viral respiratory infections can predispose animals to secondary bacterial infections; however, until now, there have been no documented cases of coinfection involving Teschovirus and S. suis in piglets presenting neurological signs.

This study aimed to investigate the simultaneous presence of these two pathogens in piglets with neurological symptoms and to correlate pathological findings with bacteriological and molecular analyses. The research was conducted in 2024 on a nursery farm in the midwestern region of Santa Catarina, Brazil, with piglets approximately 40 days old. Three outbreaks involving neurological signs such as paresis, paralysis, and opisthotonus were monitored. Sixteen piglets were euthanized for necropsy and tissue collection.

Samples from the brain, joints, spleen, heart, liver, lungs, and spinal cord were collected for bacteriological culture and histopathological examination. Bacterial isolation was performed using blood agar incubation, followed by PCR for species and capsular type identification. Frozen fragments of the central nervous system (CNS), including spinal cord and brain, from eight animals were subjected to RT-qPCR for the detection of swine Teschovirus.

Streptococcus suis was the only bacterium isolated in 13 of the 16 piglets (81.25%), with serotypes SV1, SV2, SV7, and one untypable strain identified. Histopathological findings revealed lymphoplasmacytic encephalomyelitis as the most frequent lesion, followed by histiocytic and neutrophilic meningoencephalitis, and fibrinosuppurative meningoencephalitis. Among the piglets with CNS lesions, three tested positive for swine Teschovirus, and two of these also had positive S. suis isolations, indicating coinfection. These findings suggest a possible synergistic interaction between viral and bacterial pathogens, complicating the clinical diagnosis and potentially worsening neurological outcomes. The study underscores the importance of a comprehensive diagnostic approach—including necropsy, histopathology, bacterial culture, and molecular techniques—for accurately identifying the etiological agents involved in porcine encephalitis.

In conclusion, viral infections may predispose animals to secondary bacterial invasions, thereby intensifying clinical signs and adding complexity to disease management. This study presents the first evidence of coinfection between swine Teschovirus and Streptococcus suis in piglets with neurological

symptoms. Further research is needed to determine the field prevalence of this association and to better understand its role in the pathogenesis of encephalitic conditions in pigs.

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**Monitoring of Influenza A Virus in Pigs from Different Production Systems in Brazil**

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Influenza is endemic in pigs worldwide, primarily circulating as H1N1, H1N2, and H3N2 subtypes. Due to significant genetic and antigenic diversity across different geographic regions, a phylogeny-based global nomenclature system was established for H1 and H3 viruses. Swine influenza H1 viruses (swIAVs) are classified into three main lineages—1A (or classical, including the H1pdm09 clade), 1B (human seasonal), and 1C (Eurasian avian). In Brazil, four main genetic clades of H1 viruses (1A.3.3.2 [H1pdm09], 1B.2.3, 1B.2.4, and 1B.2.6) and three clades of H3 viruses (1990.5.1, 1990.5.2, and 1990.5.3) have already been identified. The objective of this study was to monitor influenza in pigs to identify the main genetic clades of circulating H1 and H3 viruses in farms of two intensive swine production systems: single-site and multiple-sites. From February to December 2024, monthly nasal swabs were collected from pigs in multi-site (four companies: A-D) and single-site (four companies: E-H) production systems, located in the South, Southeast, and Central-West regions of Brazil. Pigs of the following ages and categories were sampled: UPL (Piglet Production Unit; including gilts and sows at 90 days of gestation), piglets at 45 days (45d), 70 days (70d), and 130 days (130d). Samples were analyzed by RT-PCR and sequencing. Of 1,980 samples tested by RT-PCR, 255 were IAV positive. Phylogenetic analysis of H1 viruses revealed the circulation of the H1pdm-C04 genetic clade, previously described and widely disseminated in the country's herds, as well as four new genetic clades (NC-#1 to NC#-4) within the H1pdm09 lineage. Regarding H1N2 and H3N2, representatives of the H1 -1B.2.4 and H3 -1990.5.1 clades were detected. The four multi-site production companies (A-D), located in the South region, have 1 to 6 UPLs and 4 to 9 finishing farms sampled. Viruses of the 1A.3.3.2 (H1pdm09) lineage were detected in all sampled companies, supporting previous studies showing that this lineage is widely spread in swine in Brazil. Additionally, the identification of potential new genetic clades reinforces the role of human-to-swine transmission in expanding the genetic diversity of swIAVs. A high diversity of IAVs was detected in pigs from companies A-D, especially in nursery and finishing phases, possibly due to the mixing of animals from different origins. In companies E-H, different genetic clades of H1N1pdm (NC#-1 - 4) and H3N2 were detected in nursery (45d) and early finishing (70d) phases. In two UPLs (A and B), an H1N2 was detected in a 26-day-old piglet and an H1N1pdm (H1pdm-C04) in a gilt. It is important to note that in multi-site production companies, sample collections were not always conducted on the same farm, which may have contributed to the detection of greater viral diversity. This study revealed extensive circulation of H1N1pdm (1A.3.3.2) in pigs in all sampled farms, and new genetic viral clades were identified. In addition to H1N1pdm, the H1 -1B.2.4 and H3 -1990.5.1 lineages were detected. A higher genetic diversity of IAVs was found in pigs from multi-site production companies, with nursery piglets and finishing pigs being the most affected phases.

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**Digital PCR, a new technique for improved detection of Mycoplasma hyopneumoniae**

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Mycoplasma hyopneumoniae is the primary cause of enzootic pneumonia in pigs. This bacterium increases the susceptibility of pigs to secondary infections, affects animal health, and leads to a reduced average daily gain and poor feed conversion. The main form of transmission occurs when sows that are positive for M. hyopneumoniae shed the bacterium and infect their piglets. However, clinical signs such as coughing and growth setbacks may not be observed until the grow/finish stage due to the slow replication rate of the bacterium. An early diagnosis is crucial to control the spread of infection and shedding of the bacterium. The current diagnostic method with the highest sensitivity in live animals includes the collection of tracheal secretions to perform real-time PCR (rtPCR), which can detect the presence of M. hyopneumoniae DNA. Digital PCR (dPCR) is an emerging technique that uses partitioning to provide a higher sensitivity than other PCR methods. Therefore, this study aimed to evaluate whether dPCR enables higher sensitivity of M. hyopneumoniae detection compared to rtPCR. Both rtPCR and dPCR were used to test for the presence of M. hyopneumoniae DNA in single samples. Here, we examined the sensitivity of rtPCR in comparison to dPCR. Six ten-fold dilutions up to 1:10^6 were created from M. hyopneumoniae 232 extracted DNA from a pure culture (reference strain) and stored at -20ºC. Both the original sample and the dilutions were run through rtPCR to obtain Ct values and then through dPCR in triplicates. Four known-negative samples were also run through dPCR and rtPCR. The original sample and dilutions up to 1:10^5 all showed a positive result for M. hyopneumoniae DNA in all three dPCR replicates. The 1:10^6 dilution showed a positive result in two of the three replicates. The rtPCR showed a positive result for M. hyopneumoniae DNA for the original sample and dilutions up to 1:10^4. The 1:10^5 dilution produced a Ct value of 38.2, which is considered to be inconclusive or suspect by most veterinary diagnostic laboratories, and the 1:10^6 dilution showed a negative result. Ct refers to the cycle threshold, or the number of cycles needed to replicate enough DNA during rtPCR to be detected. The known-negative samples showed a negative result and positive controls showed a positive result in both the dPCR and rtPCR. The results indicate that dPCR was able to detect a lower concentration of M. hyopneumoniae DNA in comparison to rtPCR. Specifically, dPCR showed at least one 10-fold higher sensitivity than rtPCR. The ability of dPCR to detect very low concentrations of pathogen DNA could be used to identify an infection earlier than using rtPCR.

**Development of a Sensitive and Rapid Homogeneous Bioluminescent Assay Platform for Detection of Animal Infectious Diseases**

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[1]Promega

Rapid and accurate diagnosis of animal infectious diseases is essential for effective management and control. Current methods, limited by slow turnaround times, low sensitivity, and complex equipment requirements, often fall short in diverse settings. This study introduces a novel bioluminescent analyte detection assay platform using ternary split NanoLuc® luciferase complementation as the reporter system in a homogeneous immunoassay (Lumit Flex®). This system features three non-functional, engineered fragments of NanoLuc® luciferase that reassemble into an active enzyme only in the presence of a target molecule, producing a bioluminescent signal. Enhanced through directed evolution for better chemical and thermal stability and reduced background noise, this technology enables dual epitope analyte detection resulting in highly sensitive and specific target detection suitable for real-time monitoring in various complex biological samples.

To showcase the utility of this low affinity, split complementation reporter chemistry platform, we developed bioluminescent, homogeneous immunoassays for the rapid detection of African Swine Fever and Leptospirosis antigens that outperform conventional ELISAs in LOD, ULOQ, and ease of workflow. We also demonstrated the feasibility of lyophilizing the assay components to create a shelf-stable, aqueous buffer soluble, point-of-care test using a handheld luminometer. This study highlights the system's adaptability, operational simplicity, and rapid result delivery.

The development of the ternary, low-affinity complementation bioluminescent system, tailored for increased stability and usability, offers a robust tool for analyte detection in diverse challenging environments. This advanced system provides transformative solutions for potential accurate diagnoses in animal infectious disease as well as relevant health status needing rapid testing, enhancing disease surveillance and management, and simplifying the diagnostic process across various settings.

**Effects of a second iron injection and sire line on growth performance, hemoglobin levels, antioxidative status and whole-body iron retention in piglets**

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Introduction

A single iron injection at birth is common practice in pig production to prevent iron deficiency anemia. While a second iron injection improves hematological status and postweaning growth (Johnson et al., 2024), limited information is available on its effect on whole-body iron retention and antioxidant status in piglets. Additionally, genetic factors may influence piglets' responses to iron administration. Therefore, this study aimed to evaluate the effects of a second iron injection on growth performance, hemoglobin and antioxidant status, and whole-body iron retention in piglets from two sire lines.

Methods

143 newborn piglets from 15 litters (7 from PIC337 and 8 from PIC800 sire lines, all bred to Camborough sows) were allotted to 6 treatments in a 2x3 factorial arrangement. The main factors were: 1) sire line (PIC337 vs PIC800), and 2) iron injection frequency (0, 1, or 2 intramuscular injections of 200 mg iron; UNIFERON®200, Pharmacosmos, Inc.) administered on d 3 (1 injection), or d 3 and 8 (2 injections) of age. Colostrum and milk (d 15 of lactation) were collected. Six piglets per sire line at birth and six per treatment at weaning (d 18.9 ± 1.6 of age) were euthanized for collection of liver, spleen, kidney, heart, whole blood and remaining body tissue for iron analysis. The remaining pigs were transferred to a nursery facility and fed a common diet for 28 d. Hemoglobin levels were measured at d 3, 8, 15 of age, at weaning, and weekly in the nursery period. Plasma malondialdehyde, catalase, and superoxide dismutase levels were measured at weaning and d 14 and 28 postweaning.

Results

PIC337 pigs had greater overall nursery feed intake (P=0.10, tendency) and were 1.5 kg heavier at d 28 postweaning (P=0.06) than PIC800 pigs. PIC337 pigs had lower hemoglobin levels than PIC800 pigs from d 15 of age to d 7 postweaning (P≤0.05; 101.7 and 108.5 g/L respectively). Increasing iron injection frequency from 0 to 2 linearly increased weaning weight (P≤0.05; 4.99, 5.30, and 5.50 kg, respectively), body weight and average daily gain through d 28 postweaning (P≤0.05; 0.295, 0.353, and 0.362 kg/d, respectively). Hemoglobin levels also increased linearly and quadratically from d 15 of age to d 14 postweaning (P≤0.05; 72.5, 108.9, and 114.2 g/L at d 14 postweaning, respectively). Plasma malondialdehyde levels increased quadratically at weaning (P=0.06) and d 14 postweaning (P≤0.05; 13.8, 16.2, 15.6 µM, respectively), with a peak in the 1-injection group. Plasma catalase level increased linearly at d 14 postweaning (P≤0.05). Total iron retention in individual organs and whole-body (P≤0.05; 121.3, 291.5, and 509.1 mg, respectively) increased linearly with iron injection frequency. No differences were observed between sire lines in whole-body iron retention at birth (P>0.19; 47.0 and 55.1 mg for PIC337 and PIC800, respectively), at weaning, or in iron content of colostrum and milk (P>0.56).

Conclusion

A second iron injection on d 8 increased hemoglobin levels through d 14 postweaning, nursery weight gain, antioxidant status, and whole-body iron retention, confirming that most of the injected iron was retained in the body.

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**EC-110 reduces mortality of nursery pigs during a known F18 E. coli challenge**

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Three studies were conducted at two commercial nursery barns in Iowa to evaluate the impact of a unique Essential Oil blend (EC-110) on piglet mortality during a natural F18 Escherichia coli challenge. In study one, 4,117 pigs were used across 8 rooms. Rooms were assigned to one of two treatments: 1) Control or 2) EC-110. EC-110 was administered at a rate of 64 oz/5 gallons of stock solution for 7 days. In study two, 5,017 pigs were used across 8 rooms. Rooms were assigned to one of four treatments: 1) Control, 2) EC-110 at a rate of 64 oz/5 gallons stock solution for 7 days, 3) EC-110 at a rate of 64 oz/5 gallons stock solution for 14 days, or 4) EC-110 at a rate of 64 oz/5 gallons stock solution for 7 days followed by EC-110 at a rate of 32oz/5 gallons stock solution for 7 days. For the first two studies, the EC-110 treatments began at 24 hours post-placement, and all pigs received an E. coli vaccine 3 days prior to weaning. These studies were 8 weeks long. In study three, 3,350 pigs were used across 3 rooms in a 7 week study. Rooms were assigned to one of two treatments: 1) E. coli vaccine administered via water upon arrival in the nursery, 2) EC-110 at a rate of 64 oz/5 gallons stock solution for 14 days with no E. coli vaccine administered. All EC-110 administration began on the day of placement. For all studies, the stock solutions were metered at 1:128 in the drinking water. Weekly mortalities were reported by room. Mortality numbers were analyzed using the Chi Squared test in the FREQ procedure in SAS. In study one, mortality was decreased ($P < 0.05$) with the use of EC-110 in weeks 2 (3.3% v 0.9%), 3 (3.4% v 2.1%), and 7 (0.5% v 0.1%). Furthermore, cumulative mortality was decreased ($P < 0.05$) throughout the study with the use of EC-110 (12.8% v 8.6%). In study two, mortality was decreased ($P < 0.05$) with the use of EC-110 in week 2 and in turn, cumulatively throughout the study. The lowest mortality was observed for the 14-d EC-110 administration (4.0%), followed by the step-down EC-110 administration and 7-d EO administration (6.3% and 6.9%, respectively), and the control group had the highest cumulative mortality (8.9%). In study three, mortality was decreased ($P < 0.05$) with the use of EC-110 during weeks 2 (1.0 %, v 0.3%) and 4 (1.7% v .7%). Additionally, cumulative mortality was decreased ($P < 0.05$) throughout the study (6.6% v 3.4%) compared to the E. coli vaccinated pigs These studies indicate that EC-110 delivered through the water during the early nursery period successfully reduced mortality both when given in addition to a vaccine as well as when given independent of and, in comparison to an E. coli vaccine. A minimum of 14 days of EC-110 use is needed to obtain the best results.

**Validation of E. coli challenge model and impact of Siderophore Receptors and Porins (SRP®) vaccine in nursery pigs**

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Introduction

Escherichia coli is a gram negative, facultative anaerobic, rod-shaped coliform found in the gut of warm-blooded animals, including swine1. While considered part of the normal gut flora, certain variants possess pathogenic potential, particularly in young pigs1. Over the past decade, there have been increased reports, and increased severity of outbreaks associated with pathogenic E. coli among recently weaned pigs2. Veterinarians and pig care givers experience frustration with outcomes of common preventative and therapeutic treatments, as well as production management practices to reduce these outbreaks.

A common feature among pathogenic gram-negative organisms is metabolic requirement for iron. They have evolved mechanisms for obtaining iron from the host utilizing a conserved set of transmembrane proteins known as siderophore receptors3. These proteins have been purified into vaccines against gram negative cattle and poultry pathogens with successful outcomes for decades4,5. The studies presented here were designed to validate an E. coli challenge model, explore the importance of intestinal receptor genotype on the susceptibility to E. coli, and study the impact of a proprietary autogenous SRP® vaccine in a challenge study.

Methods

In the first study, 3 different E. coli isolates were evaluated for ability to cause mortality in weaned pigs, and 3-week-old pigs were orally challenged following previously described methods6. The isolate that produced the highest mortality was selected for the intestinal receptor genotype and vaccine challenge studies. In the second study, 3-week-old pigs with different genotypes (A/A – resistant, A/G – susceptible, and G/G – susceptible) for E. coli receptors were orally challenged as described above and mortality was measured over a 28 day period. In the third study, SRP® vaccinated, and non-vaccinated, 3-week-old, G/G genotype pigs, from 2 different sow sources were orally challenged as described above and mortality was measured over a 28 day period.

Results

In the first study, one isolate produced the highest mortality (38.9%). The isolate was F18, Lt, Sta, Stb, Stx2, Stx2e, PAA positive and classified as ETEC/STEC hybrid. In the second study, there was an effect of genotype on mortality after challenge where A/A = 1.7%a, A/G = 20.0%b, and G/G = 26.2%b (p=0.0166). In the third study, there was an effect of vaccine on mortality after challenge with 20.0% for vaccinates and 46.0% for non-vaccinates (p=0.0100) in piglets from sow source A (enteric disease not present in piglets). In sow source B (enteric disease present in piglets), mortality among the vaccinates was 16.2% and non-vaccinates 3.7% (p=0.2200).

Conclusions

The results of the first two studies validated a previously described challenge model, and demonstrated the impact of E. coli susceptibility genotype. In the third study, the effect of the SRP vaccine was evident in one sow source, as a reduction in mortality after a strong E. coli challenge was observed. Additional studies are planned to better understand the use of SRP vaccine in other sow sources where intestinal disease is present in suckling pigs. Autogenous SRP® vaccines should be considered in prevention programs against post-weaning E. coli in swine.

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**Medial Canthus Blood Collection in Neonatal Piglets as a Welfare-Focused and Efficient Alternative to Jugular Venipuncture**

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Blood sampling in neonatal piglets is routine in research settings to evaluate parameters such as colostrum intake via IgG levels. Traditionally, jugular venipuncture requires a "blind stick" technique due to thick skin and poor vein visualization, demanding significant skill to minimize stress and time. The medial canthus approach has been suggested as an alternative, but few published resources describe its technique, anatomical basis, or potential welfare advantages in piglets (Dove and Alworth).

This pilot study aimed to (1) characterize the anatomical features relevant to medial canthus blood collection in neonatal piglets and (2) compare its sampling efficiency to traditional jugular venipuncture. At the Michigan State University Swine Teaching and Research Center, blood samples were collected from neonatal piglets across 24 litters to assess IgG levels, confirming colostrum intake. Two stillborn piglets were dissected to study the orbital sinus anatomy, the medial canthus region, and to determine the optimal plane of entry for the hematocrit microtubes.

For live sampling, topical proparacaine was applied to the selected eye prior to collection. Piglets were placed in dorsal recumbency with one handler restraining the body and limbs while the phlebotomist stabilized the head. Anatomical landmarks, including the lower eyelid margin and the vertical orientation of the snout, were identified to guide placement. Heparinized hematocrit microtubes were inserted at approximately a 45-degree horizontal plane from the medial canthus toward the contralateral mandible. A subtle "crunch" indicated penetration of the orbital sinus. The tube was then withdrawn slightly until blood flow was observed. The duration of blood collection and number of litters completed within a 3-hour window were recorded for both the medial canthus approach and jugular venipuncture sessions.

In timed pilot sessions, the medial canthus technique allowed sampling of about 16–17 piglets from 6 litters within 3 hours (around 30 minutes per litter), while jugular venipuncture only completed 3 litters in the same period. Handlers reported that the piglets showed minimal stress during medial canthus sampling, which they attributed to shorter restraint times, the use of local anesthesia, and more consistent anatomical landmarks. In the next cohort (August 2025), we plan to evaluate potential adverse effects such as hematomas, ocular trauma, or visual impairment after sampling.

The medial canthus approach shows real promise as a safe, efficient, and welfare-friendly alternative to traditional jugular venipuncture in neonatal piglets. It's essential that anyone performing this technique is well-trained and comfortable with the anatomy beforehand, as the piglets are awake and the goal is to minimize stress through quick and accurate sampling. We have developed an instructional video, which has been shared with the MSU Attending Veterinarian, Farm Veterinarian and IACUC reviewers.

The outcomes of the next cohort will include long-term piglet safety, time to sampling, and the provision of clear, practical guidelines for use in clinical and on-farm research, incorporating anatomical landmarks and safety protocols. These results will be available for presentation at the 2025 Allen D. Leman Swine Conference.

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**Spatial-Temporal Dynamics and Seasonal Patterns of African Swine Fever in Vietnam, 2019 – 2024**

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Introduction

African swine fever (ASF) is a highly contagious viral disease that affects both domestic and wild pigs, with significant economic and food security implications. Since its introduction in Vietnam in February 2019, ASF has spread nationwide, causing severe disruptions to pig production. Biosecurity, early detection, and timely intervention are the primary tools for containment. Understanding the spatial and temporal dynamics of ASF is essential for developing targeted control strategies. This study aimed to identify spatial-temporal clusters of ASF outbreaks in Vietnam from 2019 to 2024 and to examine seasonal patterns across northern, central, and southern regions of the country.

Methods

ASF outbreak data (2019–2024) were made available from the Vietnam Department of Animal Health. Outbreaks were reported via passive surveillance. Data were compiled at the commune level and georeferenced using centroid coordinates. Communes were classified as cases if outbreaks occurred in a given month and as controls otherwise. Spatial-temporal clustering was analyzed using SaTScan v10.1 with the Bernoulli model, a 10% spatial window, and a 3-month temporal window. Cluster locations were mapped using ArcGIS Pro and categorized into North, Central, or South based on provincial boundaries. Seasonality was assessed nationally and regionally using a 3-month centered moving average of the seasonal index (Si), which was calculated by dividing monthly outbreaks by the overall monthly average.

Results

Across Vietnam, 17,562 commune-level outbreaks were reported from 2019 to 2024. In total, 72 spatial-temporal ASF clusters were identified. The highest number of clusters occurred in 2021 (17), followed by 2019 (14) and 2020 (13), indicating intense early epidemic activity. Between 2022 and 2024, the number of clusters stabilized at 8–10 per year. Regionally, the North accounted for 35 clusters (48.6%), concentrated in provinces such as Lang Son, Ninh Binh, and Son La. The Central region reported 27 clusters (37.5%), with Nghe An (8 clusters) as the most affected. The South had fewer clusters (10, or 13.9%), mainly in Binh Phuoc and Dong Nai. Overall, 61.1% of clusters occurred from January to August, and 38.9% from September to December.

Nationally, the seasonal index (Si) peaked in May (1.46) and June (1.48), and was lowest in January (0.59) and February (0.58). In the North, ASF activity peaked from April to June, with the highest Si in May (2.06) and the lowest in February (0.26). The Central region exhibited mild seasonality, characterized by a gradual increase from June to October, with a peak in September (1.25). In the South, outbreaks peaked in July (1.97) and August (1.80), corresponding with the rainy season, and were lowest in March (0.30) and April (0.16).

Conclusions

ASF outbreaks in Vietnam showed clear spatial-temporal clustering, with early epidemic waves followed by sustained regional activity. Distinct seasonal patterns were observed across regions, with the North showing sharp spring peaks, the Central region showing milder, prolonged activity, and the South peaking mid-year. These findings support the need for region-specific and seasonally targeted ASF control strategies.

**Probe capture enrichment method for PRRSV whole genome sequencing**

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Porcine reproductive and respiratory syndrome (PRRS) has been damaging the pig industry for about four decades worldwide since its initial recognition in 1987 in the USA. Two genotypes, PRRSV-1 (European type) and PRRSV-2 (North American type), have been identified. PRRSV infects all ages of pigs and causes reproductive impairment in sows and gilts and respiratory and pulmonary syndrome in young pigs, especially in wean-to-finish pigs. Next-generation sequencing (NGS)-based whole-genome sequencing (WGS) of PRRSV is commonly used in the diagnostic field for genotyping, providing a significantly higher discriminatory power than ORF5 sequencing and thus improving viral genomic surveillance. Metagenomics-based WGS for PRRSV has a lower diagnostic sensitivity but works well only for clinical samples with high viral loads. In the present study, we applied a probe capture-based method to increase the sensitivity of PRRSV WGS. We first evaluated the capture approach to lab isolates and then different types of clinical samples, including serum, processing fluid, oral fluid, and tissue samples. For laboratory isolates, the probe capture enrichment method showed effectiveness in enhancing genome coverage ranging from 2.6% to 95% and obtained over 90% genome coverage for RNA with Ct values up to 29.8 for three PRRSV-2 strains (11604, PA8, and VR2332). For the PRRSV-1 strain (Lelystad), the genome coverage was between 2.2%-32.5% acquiring 90% genome for samples with Ct values up to 30.2. For serum samples, the probe capture enrichment enhanced genome coverage by 22% (0-89%) for 15 samples (Ct 21.20-33.78) and consistently obtained 90% genome for samples with a Ct value below 26. For processing fluid, the probe capture enrichment increased genome coverage by 32% (0.25%-72%) for 33 samples (Ct 21.83-33.83) and consistently obtained 90% genome for samples with CT value below 27. For oral fluid, the probe capture enrichment increased genome coverage by 36% (0.51%-78%) for 19 samples (Ct 26.86-33.25), but could not determine the Ct value cutoff due to the unavailability of samples with Ct values. For tissue samples, the enrichment method enhanced genome coverage by 64% (53%-72%) for six samples (Ct 20.91-29.49). Further improvement for WGS for tissue samples through a combination of capture enrichment and host genome depletion, and sequencing additional oral fluid samples with lower Ct are in progress. Overall, our data demonstrate that probe capture-based enrichment significantly increases PRRSV WGS and genome surveillance.

**Effect of organic acids and monoglycerides supplementation in feed and water on growth performance of nursery piglets**

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Introduction

Enteric health of nursery pigs is an ongoing challenge, resulting in poor performance and health in animals. Organic acids have been shown to improve performance in post-weaning pigs, due to acidification of the gastro-intestinal tract and pathogenic microbial inhibition. Additionally, monoglycerides have been shown to have potent effects on pathogen inhibition, while supporting intestinal integrity and modulating immune response.

Methods

A trial was conducted at a commercial swine research nursery to evaluate inclusion of Entero-NovaTM 410C (feed additive consisting of short- and medium-chain monoglycerides, Eastman Animal Nutrition) in feed, with or without inclusion of MonoSolTM (blend of organic acids and short- and medium-chain monoglycerides, Best Veterinary Solutions and Eastman Animal Nutrition) in water, on pig performance. A total of 2,184 weaned pigs (˜21d, 13.2 lb, PIC 1050x337) were assigned to one of 3 treatments (14 replicates/treatment, 52 pigs/pen) using a randomized block design. A five-phase feeding program was used for the 42d study.

Dietary treatments are: 1) control (CON) basal diets; 2) (EN410C) basal diets with Entero-Nova 410C provided at 6 lb/ton (d0-21) and 2 lb/ton (d21-42); and 3) (EN410C+MonoSol) with same diets as EN410C but also MonoSol provided in the water at 0.27 oz/gal, targeting a water pH of 4. Pigs were weighed at the start of the trial (d0), and the end of Phase 1 (d7), Phase 3 (d21) and end of the nursery trial (d42) and feed consumption determined during same time periods.

Results

A total of 58 pigs were removed from test, along with 19 mortalities. Pig removals and mortalities were similar among treatments (P>0.10). EN410C+MonoSol pigs weighed greater than CON pigs for d7 and d21, with EN410C intermediate. At the end of the trial, pigs on EN410C or EN410C+MonoSol were numerically heavier (0.7 lb greater) than CON pigs.

During Phase 1, ADG was greatest for EN410C+MonoSol compared to CON, with EN410C intermediate (P<0.01). ADFI tended to be greater for EN 410C+MonoSol compared to CON (P=0.09). During Phase 2, ADG tended to be greater for EN410C+MonoSol compared to CON, with EN410C intermediate (P=0.06), resulting in greater ADG for the first half of the nursery period (d0-21) for EN410C+MonoSol over CON (P<0.01). Feed conversion was improved numerically 4.7% and 3.1%, respectively, for EN410C+MonoSol or EN410C compared to CON.

For the final two phases (d21-42), treatments did not differ for ADG, ADFI, or F:G. Overall, growth performance did not differ significantly for the entire 42d trial period, although numerically, ADG increased 10.9%.

Conclusions

The combination of Entero-Nova 410C at 6 lb/ton in feed and MonoSol in water increased ADG and ending bodyweight for Phase 1 and Phases 1-3 over the control group. During the final 21 days of trial, when Entero-Nova 410C level was reduced to 2 lb/ton, there was no significant further improvement on growth performance. Under the conditions of this study, a combination of Entero-Nova 410C and MonoSol improved growth performance of nursery pigs during the first 21 days of the nursery period.

**Emergence of a structurally and immunologically distinct strain of Porcine Circovirus 3 in the US Swine Herd, and implications for vaccination.**

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Porcine circovirus strains have been a universal challenge for the swine industry, and also a subject of widespread vaccination. Although vaccines have been largely effective in control, they also have been the subject of speculation regarding shifts in the relative prevalence of unique strains. Despite widespread use of PCV2 vaccines incorporating protection against PCV2a and PCV2b, the past decade has seen emergence of PCV2d and more recently PCV2e, requiring additional studies to determine cross protection and potential need for updated vaccines. In 2017, PCV3 was identified in the United States associated with dermatitis, nephropathy syndrome, and reproductive failure(1). Sequence analysis was used to demonstrate the existence of 3 distinct clades of PCV3, termed PCV3a, PCV3b, and PCV3c(2). These three clades could be differentiated by unique mutations targeted to two amino acids, A24V and R27K, representing less than 1% difference between PCV3a, PCV3b, and PCV3c. The relevance of these mutations to broad cross-protection remains unclear. The purpose of these studies was to monitor for occurrence of the three PCV3 clades in the face of vaccination.

As part of the ISPrime(TM) process, diagnostic sequences are routinely monitored for emergence of variant viruses. In addition, publicly available databases are routinely probed for occurrence of new viral sequences corresponding to the potential need for new vaccine constructs. For PCV3, sequences for the Orf2 CAP region were subjected to Medgene Spice(TM) predictive bioinformatic analysis to monitor for potential sequence changes that could alter the protein structure and contribute to antigenic drift of the protein at key epitopes.

Over the course of the past 3 years, increased isolation of PCV3c sequences has been observed among our sample population. Despite the very limited sequence diversity between PCV3 clades, there was a noticeable increased identification of PCV3c relative to PCV3a and PCV3b. Bioinformatic analysis of target epitopes on the three strains indicated potential cross-protection between PCV3a and PCV3b, whereas PCV3c demonstrated clear structural deviation in a key target epitope region. Interestingly, the structural deviation appeared to affect a structural epitope distant from the actual region of the target amino acid changes. Although minor, these two amino acid changes appear to directly contribute to alteration of the immunological epitopes at a distant key protective site, indicating a need for adjusted vaccine formulations to provide complete protection.

Although not widespread, PCV3c is potentially immunologically unique from PCV3a and PCV3b. This variation may directly impact both naturally occurring immunity associated with prior infection as well as vaccination strategies. While Circoviruses do not appear to be subject to significant antigenic drift, vaccination strategies must incorporate antigenic specificity against field variants to maintain protection. While this study focused on PCV3, the recent emergence of PCV2e strains may also reflect antigenic diversity that must be accounted for in the formulation of protective vaccines.

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**Does increased feed intake in late gestation enhance the success of rearing one surplus piglet in relation to functional teats in hyperprolific sows?**

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Introduction

In recent years, genetic selection and nutritional advances have significantly enhanced swine productivity, resulting in averages of more piglets born per sow, which exceeds the number of functional teats. Thus, cross-fostering with surplus piglets can be a strategy to increase farm productivity (1). Studies indicate that higher milk yield (≥ 10.2 kg/day) during lactation favors the weaning of surplus piglets (2). In this context, bump feeding, which increases feed intake in late gestation, has the potential to improve milk yield. This study evaluated the effects of bump feeding on piglet performance and milk yield in hyperprolific sows.

Methods:

Sows (n=201; parity 2-5) were selected and randomized into the CONT (n=101) and BumpFe (n=100) groups at 70 days of gestation. Between days 70–89, the sows in the CONT group received 1.8 kg/d of feed (5.85 Mcal ME and 10.8 g/d SID Lys) and the BumpFe sows received 2.5 kg/d of feed (8.10 Mcal ME and 15.0 g/d SID Lys). From day 90 until farrowing, the CONT group received 2 kg/d of feed (6.48 Mcal ME and 12.0 g/d SID Lys) and the BumpFe group received 3 kg/d of feed (9.72 Mcal ME and 18.0 g/d SID Lys). All sows were fed individually and manually in the morning. At 112 days of gestation, the sows were moved to the farrowing room. All litters were equalized with one piglet exceeding the number of functional teats and were weighed on D0 and D20. The milk yield was calculated from litter weight and growth rate following equations (3), and weaning ability was analyzed by subtracting the number of weaned piglets from the initial litter size, ranging from +1 to ≤ -3 (sows that lost three or more piglets during lactation). Statistical analysis was performed using the GLIMMIX procedure (SAS 9.4®), and significance was considered when P≤0.05.

Results

No differences were observed between the CONT and BumpFe groups for piglet weight on D0 (1.41 vs. 1.38 kg; P = 0.62) and D20 (5.99 vs. 6.06 kg; P = 0.62). Likewise, the number of piglets on D0 (15.08 vs. 15.07 piglets; P = 0.97) and D20 (13.80 vs. 13.71 piglets) was similar between groups, respectively. Regarding the piglet loss rate (deaths and removals), there was no difference between the CONT and BumpFe treatments (8.41 vs. 9.06%; P = 0.53). Milk yield during lactation was also similar between groups (11.26 kg/day; P = 0.89). Additionally, the distribution of sows according to the number of piglets weaned about initial litter size; sows weaning +1 (29.0 vs. 25.74%), sows losing 1 (29.0 vs. 45.54%), 2 (27.0 vs. 14.85%), or ≥3 piglets (15.00 vs. 13.86%) was similar between the CONT and BumpFe groups (P=0.44).

Conclusion:

Bump feeding did not significantly affect litter performance and milk yield. Furthermore, the ability of sows to wean surplus piglets remained similar between treatments under the conditions of this study.

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**Evaluating high-dose oxytocin as an intervention to increase immunoglobulin transfer to piglets**

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## Introduction

Colostrum intake is critical for piglet survival, especially as litter sizes increase (1,2). Colostrum supplies immunoglobulins (Ig) and leukocytes, with survival most closely linked to Ig transfer. An administration of high-dose oxytocin to the sow shortly after farrowing may prolong the period mammary tight junctions remain open, potentially enhancing Ig transfer (4,5). This study evaluated whether post-farrowing high-dose oxytocin influences quantitative Ig transfer, as measured by serum Brix values in piglets.

## Materials and Methods

The study was conducted at a 2,500-sow commercial farm using batch farrowing. Ninety-six sows were assigned to treatment (n = 48; 4 cc oxytocin IM 12–20 h post-farrowing) or control (n = 48; no intervention) in a systematic controlled trial. Sows were excluded if piglets weighed < 0.91 kg at birth, required cross-fostering, or had excessive body condition scores. Room temperature and mammary assessments were recorded. Colostrum samples were collected at ~1 h and ~4 h post-treatment and analyzed by Brix refractometer. Blood was collected from two piglets per litter at 4 h post-treatment; serum was analyzed by Brix refractometer. Passive transfer adequacy was defined as serum Brix ≥ 7.9% (3), based on Schoos et al. (2021). Five piglets per litter were weighed at birth and 24 h; colostrum intake was estimated from weight change using the Devillers et al. (2004) equation (6).

## Results

A total of 477 piglets were included in the weight/intake analysis and 181 in the colostrum/serum analysis. Mean serum Brix was higher in treatment piglets (8.15%) than controls (7.63%; $p = 0.007$). Using the 7.9% cutoff, 59.1% of treatment piglets and 40.9% of controls were adequate (OR = 2.09; $p = 0.017$). Colostrum Brix at ~1 h tended to be higher in treated sows (6.84% vs. 4.76%; $p = 0.075$) but did not differ at ~4 h (3.94% vs. 3.82%; $p = 0.906$). Control piglets were heavier at birth (1.59 kg vs. 1.50 kg; $p < 0.001$) and at 24 h (1.71 kg vs. 1.59 kg; $p < 0.001$). Weight change (119.4 g vs. 96.0 g; $p = 0.168$) and estimated colostrum intake (360.5 g vs. 323.6 g; $p = 0.091$) did not differ significantly.

## Discussion

High-dose oxytocin increased mean serum Brix and the proportion of piglets achieving adequate passive transfer, indicating improved quantitative Ig transfer. Colostrum quality tended to be higher at ~ 1 h in treated sows but was similar between groups by ~4 h, suggesting the benefit may be short-lived. Although differences in estimated colostrum intake and weight gain were not statistically significant, the positive trends observed may be valuable in pork-producing systems. In high-volume operations producing millions of pigs annually, even a modest chance that these trends reflect true differences could have meaningful performance and economic implications. Lower average parity in the treatment group – due to sow availability and time constraints – likely contributed to lower birth weights and may influenced

intake and growth outcomes. Future studies should balance parity, extend sampling period, and assess whether early Ig improvements translate to improved survival or performance.

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**The Changing Challenges for Swine Worker Health and Safety**

Jeff Bender

Upper Midwest Agricultural Safety and Health Center

September 22, 2025

The Upper Midwest Agricultural Safety and Health Center (UMASH) is a multidisciplinary Center of Excellence in Agricultural Disease and Injury Research, Education, and Prevention. UMASH was formed as a collaboration of the University of Minnesota School of Public Health, University of Minnesota College of Veterinary Medicine, University of Minnesota School of Medicine, National Farm Medicine Center of the Marshfield Clinic, Migrant Clinicians Network, and the Minnesota Department of Health. The central theme of UMASH is to promote a One Health approach that emphasizes the inter-connections between human, animal, and plant health and the health of the environment for addressing the changing health and safety conditions for the people who are feeding the nation and the world. The long-term objective of the UMASH center is to improve the health and safety of agricultural owners, producers, and workers in the Upper Midwest. This has broad impact on agricultural families and rural communities.

It is an understatement to say that farming is dangerous work, and agricultural workers are at risk of injury and illnesses. Most worker injuries on livestock operations are related to animal handling. However, machinery, noise and repetitive activities all contribute to injuries, illnesses, disability, and fatalities related to swine production. As such, health and safety on livestock and poultry facilities requires a team approach requiring input and support from a number of individuals.

UMASH identified veterinarians as key partners in creating a health and safety team on agricultural operations. To support our producers, employees and family members, we should include veterinarians to work with producers and herd managers to ensure a holistic One Health approach to animal welfare, create a healthy work environment to minimize injuries and illnesses, and educate agricultural workers.

As part of the health and safety care team, there are a number of ways we can support employee health and safety. First, is the recognition of potential hazards. This can include identifying zoonotic disease risk while working with pigs. It may involve rapid detection of potential zoonotic agents (i.e. Salmonella or Swine Influenza) and ways to improve biosecurity to minimize disease spread. This should include disease prevention education. This could include a preventive approach with a simple checklist to identify hazards and propose solutions to minimize those risks by working with the producer. Yet veterinarians are only part of the team. The development and inclusion of safety managers and others is key in identifying production injury and illness risks, training new workers, and monitoring worker safety issues.

This focus on swine health and safety falls well within the stated goals of the Pork Quality Assurance Plus® Program “to help pig farmers and their employees continually improve production practices.” This includes food safety, animal well-being, environmental stewardship, worker safety, public health and community. Agriculture is dynamic and changes represent new challenges. Therefore, the industry and the profession need to be nimble to support the food production system which includes agricultural workers and their family.

For more information see umash.umn.edu

**Investigating waterless decontamination and application potential in transportation biosecurity**

Alyssa Betlach[1], Erin Kettelkamp[1]

[1]Swine Vet Center

## Introduction

Effective biosecurity protocols for swine transport are critical to controlling endemic pathogens like porcine epidemic diarrhea virus (PEDV) and preparing for foreign animal diseases. Current trailer disinfection methods using power washing, chemical disinfectants, and thermos-assisted drying are labor-intensive, water-dependent, and impractical for rapid or mobile use during outbreaks. Modified vaporous hydrogen peroxide (mVHP) has been successfully utilized in military and Biosafety Level 4 laboratory settings due to its effectiveness in neutralizing biological agents across diverse materials without equipment degradation (IS4S, 2023; USDA, 2024). Hydrogen peroxide-based aerosol disinfectants have been previously shown to inactivate swine pathogens (Kettelkamp et al., 2021). Broader adoption of hydrogen peroxide disinfectants in swine production requires more research and field optimization, including assessing the removal of organic material using a portable industrial vacuum to reduce labor, conserve resources, and improve biocontainment. This approach presents a promising portable, scalable, waterless alternative for enhanced biocontainment in swine production systems; however, its application needs to be proven. Therefore, this study aimed to evaluate the feasibility and efficacy of integrating an mVHP system with an industrial vacuum solution for decontaminating swine transport trailers for PEDV.

## Materials and Methods

An experimental study was conducted to evaluate the effectiveness of an mVHP system in inactivating PEDV under two simulated swine transport conditions: (1) in-vitro conditions using a sealed chamber, and (2) field-simulated conditions using a shrouded trailer model. PEDV inoculum (USA/NC49469/2013; $10^4$ $TCID_{50}$/mL) was mixed with feces and shavings to prepare the contamination material. Aluminum trailer models were contaminated with PEDV fecal inoculum and treated with mVHP for 30, 60, or 120 minutes. Four replicates per treatment duration were performed, with positive controls held at ambient temperature. Post-treatment, environmental samples were collected and analyzed for PEDV RNA using RT-PCR. A subsequent bioassay was conducted in a BSL-2 facility. Thirty piglets were orally inoculated with post-treatment environmental samples. Clinical observations and fecal swabs were collected up to 7 days post-inoculation. Fecal swabs were tested via PEDV RT-PCR. Necropsies were performed for histopathological and immunohistochemical evaluation and intestinal villus atrophy scoring. Data were analyzed in R Studio using linear regression to assess PEDV Ct differences by treatment, holding time, and their interaction. Bioassay results were summarized descriptively.

## Results and Discussion

Modified vaporized hydrogen peroxide treatment reduced detectable PEDV RNA levels on contaminated trailer surfaces under both in-vitro (chamber) and field-simulated (shroud) conditions ($p < 0.005$). No effect of holding time or interaction between treatment and time was observed ($p>0.10$). Despite the reduction in viral RNA, PEDV remained detectable in most samples post-treatment. All samples failed to induce PEDV infection, as fecal swabs were PEDV RT-PCR negative at all time points, and no post-mortem findings indicative of PEDV disease were obtained. These findings support the potential of mVHP

combined with industrial vacuum technology as a scalable, waterless trailer disinfection method for PEDV RNA reduction. Further studies are needed to evaluate effectiveness against live virus under varied conditions. Limitations in viability and sensitivity highlight the need to refine and validate virus inoculum preparation.

**Dry Fog for PRRSV and Salmonella Inactivation**

Lindsey Britton

NC State University

Introduction

Supply entry on swine farms is a critical area for disease introduction. A common biosecurity practice for supply entry is disinfection via time and temp, which often requires extended periods and may not be entirely effective, highlighting the need for alternative procedures. Dry fogging systems (e.g., Micro-Spray) offer an alternative disinfection method and have demonstrated efficacy in reducing pathogen viability, including Salmonella spp. The system converts a liquid disinfectant into a dry fog of vapor particles <10 microns. This small particle size enables rapid, thorough diffusion, making it ideal for disinfecting supplies. Limited research is available evaluating the effectiveness of this system against other swine-specific pathogens under shortened durations. Therefore, the objective of this pilot project was to evaluate the efficacy of a commercially available Micro-Spray system in inactivating Salmonella spp. and PRRSV during supply entry disinfection, under simulated, shortened durations.

Materials and Methods

A supply entry room (11’ x 13’ x 9’) of a depopulated farm was utilized for the project. The room contained metal shelving, in which cardboard boxes were randomly dispersed to replicate a typical supply entry event. The Micro-Spray system was installed within the center of the room on the ceiling and two different disinfectants (hypochlorous acid (Disinfectant A) and hydrogen peroxide with peracetic acid (Disinfectant B) were evaluated. Petri dishes were aseptically plated with either 1 mL of modified-live PRRSV MLV, Salmonella TC vaccine, or PRRSV positive serum. One MLV dish and one Salmonella dish served as positive controls and placed outside of the room. The remaining plates were placed into the fogging chamber at various locations: in open air on the metal rack, between two cardboard boxes, and under a cardboard box flipped upside down. This procedure was repeated for both disinfectants using three different durations: 10-, 30-, and 60-minutes of contact time post-fogging. Salmonella plates were cultured at an accredited veterinary diagnostic lab. The PRRSV MLV and PRRSV serum plates were analyzed with a viability RT- qPCR assay developed in the Schroeder Lab.

Results

Disinfectant A was ineffective against PRRSV-positive serum at all contact times, while Disinfectant B inactivated PRRSV in both the 30- and 60-minute treatments. Similarly, Disinfectant A showed no efficacy against Salmonella at any contact time, whereas Disinfectant B successfully inactivated Salmonella on all fogged plates across all contact times.

Conclusions

When utilized at a higher than recommended rate, Disinfectant B successfully reduced PRRSV viability with a contact time of 30- and 60-minutes and inhibited culture of Salmonella at all contact times. This study should be replicated with other PRRSV strains, supply room designs, and disinfectants to better understand dry fog system capabilities.

**Piglet diarrhea and vaccine efficacy: Observations from the field**

Laura Bruner

Swine Vet Center

Neonatal diarrhea has a major impact on piglet health and performance, with effects that extend well beyond the first 21 days of life. In my experience, it can generally be divided into two categories: early scour (occurring around 3–5 days of age) and late scour (typically beginning around day 10 and continuing until weaning).

Early scour is often caused by viral agents such as Rota A, B, and C. The severity can range from high mortality to mild clinical signs—such as loose stools, reduced weight gain, and increased post-weaning diarrhea. To add to the complication, these viral infections often pave the way for secondary bacterial scours, such as Clostridium perfringens or E. coli.

Historically, our tools for managing these outbreaks have been limited, relying mainly on sanitation and sow-derived immunity.

Late scour is more commonly linked to Sapovirus or Coccidia, though Rota A, B, or C can also appear as primary or secondary pathogens. These cases tend to have a greater effect on post-weaning health and contribute to poor starting pigs, increased nursery mortality, and long-term gut health issues. A compromised gut leaves piglets more vulnerable to post-weaning E. coli and other bacterial challenges.

Recent advances in technology have provided highly effective tools for controlling both clinical and subclinical diarrhea caused by these viruses. Vaccinating sows twice within six weeks pre farrowing has led to dramatic reductions in Rota C cases—sometimes virtually eliminating them overnight as immune sows farrow. While Sapovirus has been more challenging to manage, careful antigen selection has also yielded strong control in many herds.

In my presentation, I will share real-world cases of both early and late scour, highlighting the impact vaccination has had on piglet health, diarrhea reduction, and overall production performance.

**Field performance of a point-of-care PCR test for influenza in growing pigs: A domestic case study**

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Point-of-care (POC) testing involves conducting diagnostic assays near patients to enable rapid decision-making and timely intervention. In order to meet basic criteria and be informative, POC tests must be evaluated and validated in the field, and their diagnostic performance must be compared to results generated by reference diagnostic laboratories. To date, evaluation of POC devices under field conditions in veterinary medicine is largely lacking. Therefore, the objective of this study was to describe the use and performance of a POC system in the field for the detection of swine influenza A virus with varying sample conditions. To do this, we compared PCR test results from a POC platform to results from an accredited veterinary diagnostic laboratory. Seventy oral fluid samples were collected from ten swine farms and aliquoted into five treatment groups: portable PCR performed 1) on swine farms (FARM), 2) on the road (RIDE), after 24 hours incubation 3) at room temperature (RT) and 4) on ice (ICE) in a laboratory (Ohio State University). Samples were also submitted for testing at a reference diagnostic laboratory (LAB; the Ohio Animal Disease Diagnostic Laboratory). Quantitative analysis included linear mixed regression models with Ct of LAB as the outcome and Ct of the other POC PCR treatments as the fixed effects; and qualitative analysis included logistic mixed effect regression models with binary LAB results as the outcome and POC PCR treatment groups as the fix effects. Finally, a Bayesian Latent Class Model was used to estimate the diagnostic sensitivity and specificity (along with 95% credible intervals, CrI) of the POC test scenarios for disease detection, without assuming a perfect reference test. Influenza A virus was detected at least in one oral fluid sample for six out of the ten farms sampled according to the LAB results; within-herd prevalence in positive farms varied from 16.7 to 100.0%. POC system's Ct values were statistically associated with the gold standard results. POC tests showed high specificity, with median estimates ranging from 95.4% to 95.8% with the lower boundary of 95% CrIs consistently above 91%. Sensitivity of POC tests varied more substantially, with the lowest observed in the ICE setting (median 80.5%; 95% CrI: 60.7%–94.5%) and the highest in the RT setting (median 92.6%; 95% CrI: 76.6%–99.5%). Our study showed that the POC PCR system was a promising method for on-site diagnostic testing, providing results consistent with official laboratory results.

**Turning data into decisions: Opportunities and challenges of AI application in swine farming**

Isabella Condotta

University of Illinois at Urbana-Champaign

The swine industry faces growing pressure to meet rising global demand for animal protein while improving animal health, welfare, environmental sustainability, and farm profitability. Precision management, which encompasses continuous, automated, real-time monitoring of individual animals, is a potential solution to address these challenges. Artificial intelligence (AI), particularly computer vision and machine learning, enables the transformation of raw sensor data into information that supports timely decision-making on farms. This presentation will highlight AI-driven approaches developed for swine production, including systems for estimating body weight and body condition score from RGB-D images, predicting feed intake from visual and sensor-based monitoring, detecting postures and behaviors relevant to health, welfare, and reproductive status, and enabling individual animal identification in group housing environments. Case studies will illustrate the integration of sensor data with advanced algorithms to deliver accurate, non-invasive, and scalable solutions. The talk will also address critical challenges such as variability in animal appearance and behavior, environmental and equipment constraints, data volume and integration, and the need for robust validation under commercial conditions. Finally, opportunities for future development will be discussed, including the need for multidisciplinary collaboration, farmer-centered design, and the potential for AI to improve efficiency, reduce labor demands, and enhance decision-making in swine production systems

**Academia and industry partnership results**

Joel DeRouchey[1], David Rosero[2], Stacie Matchan[2]

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The Improving Pig Survivability project began in 2018 encompassing research, education, and extension efforts with the goal of reducing overall mortality in the U.S. commercial swine industry. The project is currently funded through 2027 by the National Pork Board and the Foundation for Food and Agriculture Research (FFAR). Team members represent multiple institutions, including Iowa State University, Kansas State University, and formerly Purdue University. The consortium is guided by an advisory board consisting of representation across a wide spectrum of the US swine industry and multiple research projects are the result of direct collaborations with producers and allied industry partners in a field setting. Research efforts in this project seek to identify factors contributing to swine mortality in commercial production, and to develop strategies and information that can be utilized to reduce mortality and maximize pig livability.

Academic and Commercial Industry partnership

The project has and continues with a focus on conducting on-farm discovery and validation research. To date, commercial industry partners have provided over $1.6 million of in-kind donations in the form of facility and pig use, personnel time, database information, laboratory expenses, and other support to expand the impact of this project. This has allowed information generated to be more likely to be adopted due to the high level of research conducted in commercial facilities for more confident validation. This has reduced the cost burden to other US pork producers as all information generated is publicly available. Also, this information can be utilized so that they may not have to conduct similar research themselves. Further leveraging of new information generated from this project has led to over 1.7 million in additional grants focused on pig livability by the PI's due the ongoing findings for the swine industry.

Project Outcomes

Through the collaborations of the Pig Survivability Project, a vast variety of practical resources have been generated and made available to different audiences including peer-reviewed publications, factsheets (English and Spanish), short informational videos, and the PigX podcasts. Also, the generated resources are available on the Improving Pig Survivability website (www.piglivability.org).

The second International Conference on Pig Survivability will held November 7 and 8th, 2025 in Omaha, Nebraska, at the Hilton Omaha. The conference's objective is to facilitate the discussion and dissemination of the most current information relative to sow, litter, weaned pig, and grow-finish mortality. Full information and registration is available at www.piglivability.org. In 2021, 451 participants from 29 states, 5 countries representing 175 different swine operations and allied industry business attended.

Key Findings of the Improving Pig Survivability Project.

More detailed information will be presented in this conference session highlighting information that has shown to improve pig livability in sow, preweaning and wean to finish production phases. Also, practices that did not improve pig livability will be discussed to determine whether alternative approaches should

be evaluated and more awareness of some current practices may not be improving pig livability as expected.

**Mechanistic insights into key soy-derived bioactives (isoflavones, saponins): Modulating immunity and improving disease resilience in swine**

Ryan Dilger

University of Illinois

Introduction: Swine respiratory disease (SRD) involves complex interactions between host immunity and a range of viral and bacterial pathogens. Nutritional interventions that target immune modulation represent a promising approach to improve resilience and reduce reliance on therapeutic agents. Soybean meal, long used as a protein source in swine diets, also contains bioactive compounds (most notably isoflavones and saponins) that are proven to exert immunomodulatory, anti-inflammatory, and antiviral effects. These compounds offer mechanistic potential for mitigating the pathophysiological impacts of SRD.

Methods: Evidence was synthesized from in vivo and in vitro studies in swine and model systems to evaluate biological pathways influenced by soy-derived isoflavones and saponins. Emphasis was placed on immunological, molecular, and physiological endpoints relevant to respiratory disease pathogenesis, including cytokine signaling, epithelial barrier integrity, oxidative stress, and adaptive immune cell profiles.

Results: Isoflavones, particularly genistein and daidzein, inhibit NF-κB activation and downstream pro-inflammatory cytokines such as TNF-α and IL-6. These effects are associated with reduced immune-mediated tissue damage and improved systemic resilience during pathogen challenge. Saponins, owing to their amphiphilic structure, influence mucosal immunity and barrier function, potentially reducing pathogen entry and secondary bacterial complications. Both compound classes have demonstrated antioxidant activity and the ability to modulate acute-phase responses and hematological parameters. Although bioavailability varies across soy processing methods, strategic inclusion of soy protein sources or concentrated bioactive fractions can support immune homeostasis during respiratory infection.

Conclusions: Soy-derived isoflavones and saponins exert complementary effects on host immune function through suppression of inflammatory signaling, maintenance of epithelial integrity, and modulation of cellular immune responses. These mechanisms are relevant across diverse SRD pathogens and support the broader use of soy-based functional ingredients as part of an integrated strategy for disease resilience in swine production.

**Viability PCR: A New Frontier in Monitoring Infection and Sanitation**

Nathan Feirer

Promega Corporation

Culture-based detection methods remain a cornerstone of microbial and viral testing due to their specificity and regulatory acceptance. However, these methods are often hampered by prolonged time-to-result and an inability to detect viable but non-culturable (VBNC) microorganisms. These limitations pose a significant challenge in accurately assessing microbial threats, particularly in applications involving environmental surveillance, clinical diagnostics, and food and water safety monitoring. To overcome these shortcomings, several non-culture-based techniques have been developed, including microscopy, ATP quantification, RNA analysis, and flow cytometry. While these methods offer faster turnaround times, each has notable limitations such as sensitivity, complexity, and inability to provide accurate live-dead differentiation. PCR-based methods have become increasingly popular due to their high sensitivity and specificity. However, traditional PCR cannot discriminate between viable and non-viable organisms, frequently resulting in an overestimation of viable pathogen load. Viability PCR (vPCR) addresses this critical gap by incorporating the use of membrane- or capsid-impermeable chemical reagents that selectively bind to and modify nucleic acids from dead cells or compromised viral particles. Once modified, these nucleic acids cannot be amplified by PCR, effectively excluding signals from non-viable organisms. In this presentation, I will provide a detailed overview of the Viability PCR methodology, including key chemical reagents currently available on the market, such as intercalating dyes and photoreactive compounds that enable this selective inhibition. Case studies and experimental data will be shared to illustrate the utility of vPCR in real-world applications. Examples include detection of viable vs. non-viable bacteria such as Legionella, RNA viruses like Norovirus and SARS-CoV-2, and fungal pathogens such as Colletotrichum. These examples highlight the versatility of Viability PCR across diverse microbial types and sample matrices. Viability PCR offers a powerful, rapid, and accurate alternative to conventional culture-based detection, enabling more reliable assessments of microbial contamination. By enhancing the precision of viability determinations, this method supports faster decision-making in outbreak response and risk mitigation. Its implementation across public health, food safety, and industrial hygiene sectors holds the potential to significantly improve global biosurveillance and safety standards.

**Assessment of trailer contamination at the harvest facility**

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Introduction

Harvest plants serve as concentration points, receiving dozens to hundreds of trailers from multiple sources with varying infectious statuses, which may contribute to facility contamination. Limited information is available on trailer contamination risk and factors associated with unloading pigs at harvest plants. Therefore, this study aimed to quantify market hog trailer contamination during unloading and identify associated risk factors.

Methods

In this ongoing study, fifteen environmental samples have been collected biweekly since calendar week 47 of 2024 at a Midwestern US harvest plant. Samples are collected from the unloading dock and trailers (both before and after unloading pigs) and RT-PCR tested for PRRSV, PED/PDCoV/TGE and SVA. Associated metadata, including trailer origin, sanitation status, destination, and driver or plant employee behavior during unloading are also recorded.

Results

As of this writing, 61,5% of samples have been collected with PRRSV, PEDV, PDCoV, and SVA being detected in 56.7%, 70.8%, 77.5% and 32.5% of the dock samples, respectively. Most of the SVA positive samples were detected at the end of 2024 and early 2025.

Before unloading pigs, PRRS, PEDV, PDCoV and SVA were detected in 36.2%, 33.3%, 45%, and 15.8% of the trailers, respectively. After unloading, the percentage of contaminated trailers increased for all pathogens as PRRS, PEDV, PDCoV and SVA were detected in 49.6%, 59.6%, 70.8%, and 25% of the trailers, respectively.

Furthermore, a total of 64 (26,7%) out of 240 trailers tested negative on arrival at the plant, and 47 (73,4%) out of the 64 were contaminated with at least one pathogen. When the dock was contaminated, the odds of the trailer becoming contaminated increased significantly for PRRSV, PEDV, and SVA, but not for PDCoV. Specifically, the odds of trailer contamination were 2.19 times higher for PRRSV (95%CI: 1.10, 4.38), 2.50 times higher for PEDV (95%CI: 1.26 to 4.96), and 5.78 times higher for SVA (95%CI: 2.62 to 12.79). For PDCoV, the odds of becoming contaminated were 1.18 times higher, although it was not statistically significant (95% CI: 0.60 to 2.32).

A total of 10.0% of PDCoV-contaminated, 8.8% of PEDV-contaminated, 5.8% of PRRSV-contaminated, and 3.3% of SVA-contaminated trailers went on to load new pigs on a farm without being washed after unloading. The RT-PCR Ct values observed after unloading varied by pathogen. For PRRSV, values ranged from 26.09 to 38.74, with a mean of 34.00 (±2.23). For PEDV, Ct values ranged from 26.63 to 37.99, mean of 33.71 (±2.71). PDCoV ranged from 14.45 to 37.95, mean 32.82 (±3.53), while SVA ranged from 22.06 to 39.94, mean 34.26 (±3.86).

Conclusion

These findings indicate that a significant proportion of trailers arrive at harvest facilities already contaminated, likely due to pathogen shedding by pigs or inadequate sanitation between loads. PEDV and PDCoV contamination was consistently detected throughout the study. These results underscore the urgent need for stringent cleaning and disinfection protocols following unloading and highlight opportunities to enhance biosecurity measures during the unloading process.

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**Piloting a tool to assess the usability of point-of-care testing (POCT): A case study from Thailand**

Richard French

Global Animal Health Partners, LLC

Piloting a tool to assess the usability of point-of-care testing (POCT): A case study from Thailand. Richard A. French, Joint NAHLN/NADPRP Grant, UMN, OSU. Improving national capacity for early detection of foreign animal disease incursions: critical evaluation of field accuracy, standard of procedures, risks, challenges, and opportunities for the implementation of point of care platforms for NAHLN target diseases.

Biosecurity is the leading defense against foreign animal disease (FAD). Second to biosecurity is early detection and rapid response. The advancement of diagnostic technologies to smaller, portable, integrated, and user-friendly devices allows for potential field applications for the timeliest detection. The usability and of a mobile PCR unit (IndiField™, Indical Bioscience) is used as a Point-of-Care Test (POCT) in Thailand where ASF outbreaks have been detected and reported. Units are used on two farms reported to have experienced ASF outbreaks as confirmed by regional laboratories and by use of pen-side lateral flow tests. Onsite personnel are trained in the use of the IndiField™, Trainees included veterinarians, animal health technicians and farm staff and/or owners. All data and usage is accessible via Indical's link with the cloud-based application, 'BIomeme Go' (Biomeme, Philadelphia, PA). All data is accessible in real-time if the units are used in regions with good internet access. All data is accessible globally and includes GPS coordinates and other data as entered regarding the premise. Trainees used the testing platform without significant issue and found the device to be useful for farm operations and disease surveillance. The primary complaint is the cumbersome DNA extraction, which was a series of pipetting stages. The device is compact, durable, and easily disinfected. The primary problems reported are with the reagent storage and shelf life. There are also reported issues with test results possibly related to the vaccination of animals. As there is no registered or approved vaccine foe ASF in Thailand, this could not be confirmed. The IndiMag48 (Indical Bioscience) was provided for automated RNA/DNA processing but is not practical in field and farms applications. Use of IndiField™ was, overall, found to be practical in disease monitoring and surveillance during an outbreak and significantly shortened the time for on farm diagnoses and rule out of other diseases. Note, in Thailand, ASF is a reportable disease but access to authorities and testing is limited and not timely often worsening the situation for the producer and farm management. In the hands of trained professionals and with real-time data access, the system can be used for early detection.

**Early detection of African swine fever and classical swine fever in swine processing fluid following oronasal inoculation**

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African swine fever (ASF) and classical swine fever (CSF) are devastating hemorrhagic swine diseases that could cause significant economic losses to the North American swine industry. Highly virulent ASF and CSF viruses cause acute disease characterised by high fever, hemorrhages and high mortality. In contrast, low to moderately virulent ASFV and CSFV strains induce subacute/chronic infections that could go unnoticed due to mild/nonspecific clinical signs [1]. Swine processing fluid (PF) is an aggregate sample type generated from a routine industry practice [2]. The objective of this study was to evaluate the use of PF for early detection of ASF and CSF collected upon natural oronasal exposure to low/moderately virulent ASFV and CSF strains.

Forty and twenty-four newly weaned 3 -weeks old piglets were sourced from a local supplier for each ASF and CSF experiment respectively. The piglets were acclimatised for one week and infected oronasally with ASFV Estonia 2014, ASFV Malta'78, CSFV Pinillos 2016 or CSFV Brazil 2019. Four ASFV infected piglets were castrated, and tail docked (processed) under general anaesthesia daily until 5 days post-infection (dpi) and on every other day thereafter. Similarly, three CSFV infected piglets were processed every other day. Following piglet processing, they were humanely euthanized, complete postmortem examinations were performed and tissue samples were collected. Individual processing fluids generated from the testicles and tails following approximately 2 hours were collected and frozen at -80C. Nucleic acids were extracted using the MagMax ® Core and/or Pathogen RNA/DNA kits and real time PCR was performed on individual PF samples. Several samples with the highest genomic detections were diluted ten-fold in known ASFV/CSFV negative PF to simulate aggregate PF and tested.

ASFV genome was detected in individual PF as early as 2-3 dpi coinciding with the onset of viremia. The serially diluted PF indicated possible detection as early as 3-4 dpi, in aggregate swine PF originating from a pool of up to 100 tissues. Pigs appeared clinically normal during this early detection point. Anti ASFV antibodies were detected in individual PF on 9-10 dpi. CSFV genomic material was detected earliest in individual PF on 4 dpi. Based on serial ten-fold dilution testing, one CSFV infected pig could be detected in aggregate PF generated from a pool of 100 pigs' tissues as early as 6-8 dpi. At this early point of viral detection, the piglets appeared normal. This study indicates the utility of swine PF as a valuable aggregate sample type, generating from a routine industry practice, that can help to detect ASF and CSF in piglets, as a surveillance tool.

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**An estimation cost calculator to assess the economic impacts of Mycoplasma hyopneumoniae disease**

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Mycoplasma hyopneumoniae (M. hyopneumoniae) is a bacterium that affects swine, resulting in significant production losses to the industry. The pathogen causes respiratory issues, which decrease the growth rate of pigs and negatively impacts animal welfare. Currently, tools for producers to help calculate the cost of disease caused by M. hyopneumoniae are not widely available. This project developed a simple calculator that allows producers to input their specific farm data to receive an estimated value of the cost of M. hyopneumoniae in their operation type. The calculator was created using Google Apps Script, which was linked to a Google Sheets backend for real-time calculations. Artificial intelligence (ChatGPT) was utilized to assist with setting up the Google Sheet and creating code snippets for the application. Data was provided from several production systems and published literature across the United States (Britton, L. 20241; Schwartz, M. 20252). A partial budget, which included data from various farms across the Midwest, was provided by a swine practitioner (Yeske, P., personal communication). The data served as the baseline for comparing M. hyopneumoniae production factors. Values also became the negative standard that producers could compare their data to. More information was obtained evaluating the effect of M. hyopneumoniae on sow farm production indicators. In addition, data were utilized from a large Midwest production system, examining an M. hyopneumoniae with a PRRSv co-infection. Altogether, values were used to obtain ranges for various production factors, including litters farrowed per year, number of non-productive days per year, average daily gain, and mortality rate. The calculator was meant to be simple and make efficient use of time. Producers can input already calculated farm-specific factors, including piglets weaned per year, mortality rate, ADG, and elimination protocol information, if applicable. The calculations will appear on a new tab in a clean and user-friendly format, including tooltips that provide further explanation of the analysis. This calculator allows producers to visualize how much M. hyopneumoniae may be costing their operation. Producers can also learn about the return on investment if they choose to undergo an elimination protocol. Elimination protocols have been proven successful and continue to maintain a negative status even in pig-dense areas. While these values are not exact, this calculator can help inform producers of possible opportunity losses that can be further discussed with their veterinarian. This information will aid in realizing the potential loss that M. hyopneumoniae is contributing to at their farm, and encourage producers to take the next steps in helping Minnesota eradicate M. hyopneumoniae.

**Managing large litters: Practical strategies for split-suckling and teat optimization**

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Recent benchmarking reports for U.S. swine production systems indicate that the top 10% of farms are achieving an average of 15.7 liveborn pigs per litter (1).However, recent research has shown that sows in some commercial swine herds average only 13.9 functional teats (2). This mismatch between liveborn pigs and teat capacity has increased interest in management strategies such as split suckling and teat optimization.

Split suckling is used to ensure all pigs, especially those in large litters, receive adequate colostrum. Colostrum is critical for survival and productivity: immediately after birth it provides energy and supports thermoregulation, while its immunoglobulins improve lifetime immunity, and its bioactive factors contribute to reproductive tract development. The process of split suckling involves temporarily removing a portion of the litter from the sow so the remaining piglets have greater access to the sow's underline. Selection criteria for removal and the duration of split suckling vary by production system, but typically the first-born or heaviest piglets are removed to give lighter or later-born pigs more opportunity for colostrum intake. However, modern research trials have shown no improvement in growth performance when split suckling was practiced and inconsistent effects on mortality (3,4,5,6). Recently, a large trial utilizing 22,800 piglets was conducted at a commercial sow farm which compared two split suckling methods, either split suckling based on birth weight or based on birth order, to a control treatment with no split suckling and observed no differences in pre-weaning or lifetime growth or mortality (7).

Historically, the practice of matching the number of pigs to the number of functional teats during cross-fostering has been widely followed (8). This principle was based on studies demonstrating a high level of teat fidelity observed in nursing pigs. However, when litter size exceeds teat count, producers must decide between artificial rearing, fostering to nurse sows, or allowing the sow to nurse more pigs than teats. Recent interest in allowing sows to raise more pigs than functional teats has prompted more research in this area (9,10,11,12). The optimal litter size relative to functional teat count depends on the performance measure of greatest interest. Sows nursing below teat count have lower pre-weaning mortality and sow BW loss and greater pig weaning weights. However, as litter size relative to functional teat count increases, overall farm throughput improves by increasing pigs weaned per litter, litter weaning weight, and pigs weaned/sow/year.

**Programming for performance: Early-life pig nutrition**

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Historically, "early-life" nutrition conjured images of suckling pigs and pigs in the early postweaning period. Advancing science is encouraging nutritionists, veterinarians, and pig farmers to think about early-life nutrition of pigs as starting in the uterus during pregnancy. Feeding the pregnant sow with special focus on supplying nutrients to the developing fetuses in utero is a new twist on traditional approaches to sow feeding. This updated approach is termed "fetal programming". Fetal programming potentially influences performance and health of the pig throughout its lifetime. Birth weight can be an important indicator of fetal programming especially if pigs suffer from Intra-uterine Growth Retardation (IUGR). Pigs suffering from IUGR are lighter than normal littermates and experience more and greater negative consequences for growth and survival than normal birth weight pigs. Increased occurrence of IUGR pigs is an unintended consequence of increasing litter size. Economic and sustainability metrics favor large litter sizes so pig farmers must find ways to mitigate negative effects of low birth weight resulting from elevated litter size. One such approach is to impose targeted nutritional interventions during specific periods of gestation that program fetuses in utero for improved performance and survival after farrowing. Hydroxy methyl butyrate (HMB) fed to sows during mid and late or late pregnancy can increase piglet birth weight and improve bone strength of offspring. These effects can improve pig performance. Feeding sows about 600 ppm Zn from day 80 of gestation to farrowing improved piglet survival to weaning compared with feeding the standard Zn concentration of 125 ppm. Similarly, increasing dietary Zn concentration from 125 ppm to 353 ppm throughout gestation improved intrapartum survival of pigs. Brazilian researchers reported that feeding 850 ppm Zn throughout gestation increased survival of pigs to weaning and increased pig weight at marketing compared with feeding sows 125 ppm Zn. Strategic supplementation of gestating sow diets requires sophisticated equipment that can feed group-housed sows individually and determine daily whether an individual sow requires supplementation or not. Modern electronic sow feeders (ESF) with their associated sow identification systems and computer software are up to this task. Fetal programming of piglets will become more reliable and predictable as researchers learn more about the physiological connections among specific nutrients, the timing necessary for those nutrients to exert positive impacts, fetal development, and impacts of fetal development on lifetime pig performance and health. Improved ESF design and reliability along with reduced feeder costs will increase penetration of ESF's in the commercial swine industry. Greater availability of ESF's will make feeding pigs in utero to optimize lifetime performance more realistic.

**Tick bites, allergy, and diet: alpha-gal syndrome in the United States**

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First described in 2008, alpha-gal syndrome (AGS) is an allergy to the carbohydrate galactose-alpha-1,3-galactose (aka alpha-gal), a molecule found in all mammals except for humans and Old World monkeys. Humans can therefore develop IgE antibodies to alpha-gal and have allergic reactions after ingestion of alpha-gal containing products. These reactions typically occur 2-6 hours after ingestion and can be quite severe. The most common way that humans develop IgE antibodies against alpha-gal is through the immune response to tick bites, with bites from the lone star tick by far the most common inducer of alpha-gal IgE in the United States.

The prevalence of AGS in the U.S. has been estimated by looking at laboratory testing for alpha-gal IgE. Between 2017 and 2022, over 90,000 persons tested positive for alpha-gal IgE in the U.S. The geographic distribution mostly overlapped with the known distribution of the lone star tick, with high prevalence in the south-central and mid-Atlantic states.

Although AGS is rapidly emerging in certain areas, we have found that healthcare provider knowledge about AGS has been slow to expand. In a 2022 healthcare provider survey, 42% were not aware of AGS, and another 35% were not confident in their ability to diagnose or manage AGS patients. Considering the low healthcare provider knowledge may lead to missed diagnoses of many AGS cases, we have estimated that as many as 450,000 people were impacted by AGS in 2022.

Many patients experience difficulties before and after diagnosis. The symptoms, such as stomach pain, are sometimes difficult to relate to consumption of a meat product hours before. Many report multiple ER visits before diagnosis. After diagnosis, it can be difficult to navigate the changes in diet that are required, and many cannot correctly identify food products that are derived from mammals. Prevention of tick bites through personal protection behaviors is important to avoid AGS and reduce symptoms after diagnosis.

“The findings and conclusions in this report are those of the author and do not necessarily represent the official position of the Centers for Disease Control and Prevention”

**Science-driven approaches to enhancing sow livability**

Mark Knauer

North Carolina State University

Sow livability continues to challenge U.S. swine production systems. While scientific understanding in this area is expanding, concrete solutions remain limited. On-farm sow deaths encompass both euthanasia and sudden death. The primary farm-recorded reasons for sow mortality include lameness, prolapse, and unknown causes. Regarding euthanasia, five necropsy studies have reported arthritis and cartilage disorders in 39% to 88% of euthanized sows. For sudden deaths, six necropsy investigations indicated a range of causes, including ulcers (4% to 80%), torsions (0% to 49%), and urinary disorders (5% to 41%). Engblom et al. (2008) reported 29% of sows that experienced sudden death had exhibited previous symptoms. Knauer (2023) found that abnormalities were recorded significantly more often in sows that later died (15.3%) than in those that survived (4.5%). Knauer (2023) reported the most common abnormality in late gestation was perineal swelling, affecting 1.7% of all sows. Of those sows with perineal swelling, 4% subsequently died from lameness, 14% prolapsed, and 7% died suddenly. Harshman et al. (2023) reported that prolapsed sows had decreased serum concentrations of trace minerals, including Fe (2.77 vs. 3.76ppm), Mo (9.22 vs. 13.02ppb), and Zn (1.07 vs. 1.19ppm), compared to non-prolapsed sows. Multiple feeding practices have been related to sow livability. Abiven et al. (1998) found that herds feeding gestating sows three times per day were more likely to have lower sow mortality than those feeding less frequently. The same study also reported that herds where the maximum daily lactation feed intake was less than 8 kg and was reached early in lactation had better sow survival compared to those with ad libitum feeding. According to Deen (2005), sows with minimal feed intake during the first week after farrowing were at a greater risk of mortality. Ross (2019) observed that herds that "bump fed" in late gestation had superior sow survival, as did those that fed antibiotics. The same author reported that feeding ≥2.3 kg pre-farrow, a low-fat diet during lactation, and generally higher levels of fiber were associated with fewer sow prolapses. Knauer (2023) found that sows supplemented with vitamins C and E tended to have a lower incidence of sudden death and prolapse compared to the controls (3.0% vs. 6.0%). Nickell et al. (2023) reported that a lactation supplement containing fiber, vitamins, and enzymes numerically reduced sow mortality when compared to controls (1.3% vs. 4.0%). According to Harshman et al. (2025), administering an antibiotic to sows just before farrowing reduced sow mortality from 2.5% to 1.4%. Other research by Deen and Xue (1999) and Ross (2019) indicates that a younger age at first farrowing and breeding gilts at lighter weights both increase the risk of sow mortality and prolapse, respectively. Deen and Xue (1999) and Ross (2019) further reported a greater number of stillbirths was linked to an increased likelihood of either sow mortality or prolapse. It is suggested that sow farms work to minimize stressors (poor stockmanship, heat, health, etc.) while nutritionists and veterinarians develop solutions to mitigate; oxidative stress, arthritis, cartilage disorders, and improve farrowing kinetics.

**Caught in the Trough: The Interplay Between Mitigants and Feedback**

Rachel Kontz

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Feed is a recognized transmission route for swine disease, as viable viruses can persist in feed under standard storage conditions. To address this, the swine industry has adopted feed additives known as mitigants, which are effective in reducing viral load in feed. Another commonly used strategy is feedback, which involves exposing replacement gilts and gestating sows to pathogens via oral ingestion of contaminated material. This aims to stimulate immunity to pathogens expected to be encountered during production. Feedback material is typically mixed with feed, bringing it into contact with any feed mitigants present.

As both mitigants and feedback are used to manage herd health, it is important to understand their interaction. Specifically, concerns exist that mitigants may inactivate pathogens used in feedback, potentially reducing effectiveness. The objective of this study was to evaluate the effect of feed mitigants on the viability of pathogens used in feedback at three time intervals.

Gestation feed was collected from two commercial sow farms, each using a different type of organic acid-based feed mitigant. From each farm, six 100-gram feed samples were collected and placed in individual bags. Each sample received 200 mL of phosphate-buffered saline (PBS) to simulate moist mixing conditions typical during feedback preparation. To model pathogen exposure, two vaccines were used: Edema Vac F18 (E. coli vaccine) and Ingelvac PRRS MLV (modified live virus vaccine for Porcine Reproductive and Respiratory Syndrome, PRRS). Six bags (three per farm) were each inoculated with 10 doses of Edema Vac F18. Samples were stored at room temperature (72°F) and swabbed at 30 minutes, 2 hours, and 12 hours. Swabs were cultured on 5% bovine blood agar plates. A control plate containing the vaccine alone served as a positive control. Plates were incubated for approximately 12 hours to assess bacterial growth. The remaining six bags (three per farm) were treated with 10 doses each of Ingelvac PRRS MLV. At the same three time intervals, 4 mL of liquid from each bag was collected and transferred into sterile tubes. Samples were frozen and submitted to Iowa State University Veterinary Diagnostic Laboratory for PRRSV RNA detection via quantitative PCR. A sample of the vaccine alone served as a positive control.

All E. coli-treated samples showed strong bacterial growth at all time points, regardless of the mitigant or farm source. These findings suggest that feed mitigants had minimal impact on bacterial viability and did not compromise feedback intended to expose animals to E. coli antigens. All PRRS-treated feed bags tested negative via PCR at all time points. This indicates that the mitigants likely reduced or eliminated PRRSV RNA, potentially enhancing biosecurity but interfering with feedback exposure. These results suggest a dual role for mitigants: reducing pathogen transmission risk while possibly limiting feedback efficacy for viral agents.

**Old Pathogens, New Surprises: Spoiler Alert- You Haven't Seen It All**

Carlos Lopez Figueroa

VDL University of Minnesota

Do you think pathogens don't change? That diseases are static, inflexible? Did you think pathogens always act the same way? Well, I really did, until I came across these two strange clinical-pathological cases. Pathogens are so clever... the older they are, the cleverer they get. My grandmother warned me: you learn with age. Perhaps the PRRSV virus and some serotypes of Actinobacillus pleuropneumonia also know how to keep fighting even years after their appearance. If you thought you knew everything about them, you're wrong. In this talk, I'll show you a new clinical presentation with never-before-seen lesions of both ancient diseases. Come on, you're invited.

**Identifying the experience, skills and professional goals of the TN-visa workers in the U.S. swine industry**

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Due to persistent labor shortages in the U.S. swine industry, many producers are using the Trade NAFTA (TN) visa program to hire foreign workers. Little is known about the backgrounds, education, prior work experience, and motivations of TN-visa workers, despite their critical role in sustaining the swine industry. This study aimed to generate a comprehensive profile of TN-visa swine workers to inform future recruitment, management, and workforce development strategies across the industry.

A collaborative study was led by the University of Missouri, The Ohio State University, North Carolina State University, and the University of Minnesota. A bilingual (Spanish-English) survey instrument was developed to assess seven key areas: (1) general farm information; (2) demographics; (3) academic, professional, and cultural background; (4) personal and professional goals; (5) training opportunities; (6) suggestions for improved working conditions; and (7) retention drivers. Convenience sampling was used to conduct the survey online and in person in 15 states, with a focus on six major pork-producing states (Iowa, Missouri, North Carolina, Minnesota, Ohio, and Illinois). Researchers collected a total of 261 responses—211 from in-person interviews and 50 from online surveys.

Most respondents were young professionals, with 58.8% of them being in the 26–34 age range. All participants have earned a bachelor's degree, and 10% have a master's degree. The breakdown per academic training yielded that they have earned a diploma in agronomy (40.6%), veterinary medicine (36.4%), and animal science (21.8%), coming in second and third, respectively. Even 8.8% of them pursued a dual degree in agronomy and animal sciences. Most farm workers—73.5%—were paid on an hourly basis and worked in barns for farrowing (60.9%), breeding (34.1%), and gestation (32.2%). The survey's participants, who represented various geographic and cultural backgrounds, reported growing up in urban, suburban, and rural settings.

Prior agricultural experience was common, with 68.5% having worked in animal production (dairy, beef, poultry, sheep/goats, etc.). Numerous individuals also possessed expertise in non-animal farming, including greenhouse operations and crop cultivation. Only a small percentage reported prior employment in veterinary clinics, academic institutions, or agricultural consulting. These findings show how well-trained and flexible this workforce is when they come to work for swine employers.

The primary motivations for workers seeking employment in the US on TN visas were financial in nature. Nearly all participants mentioned the potential for higher salaries (96.2%) and the ability to provide for families monetarily in Mexico (90.8%). Other significant factors included improving English literacy (88.1%), addressing Mexico's lack of job opportunities (85.4%), and accumulating professional experience (84.7%).

This study is one of the first to describe TN-visa workers in the U.S. swine industry using direct employee responses. The results offer helpful details about the educational and professional backgrounds of TN-visa holders and highlight the importance of recognizing them as skilled agricultural professionals. These data can inform future industry and extension efforts to improve workforce integration, develop training resources, align job roles with worker experience, and ensure long-term labor sustainability in pork production systems.

**Uncovering the Gaps: Insights from PRRS Outbreak Investigations**

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Pillen Family Farms/DNA Genetics

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) outbreaks remain a significant challenge in commercial swine production. It can be difficult to come up with prevention solutions when the route of introduction is unknown. This presentation will review a series of outbreak investigations with a focus on identifying root causes and implementing targeted mitigation strategies. The primary case study involves a PRRSV outbreak in a geographically remote sow farm, ultimately traced to a contaminated delivery event. Critical to this investigation was the integration of farm-level reporting, geofencing movement data, and ORF 5 sequencing, which together provided the evidence necessary to confirm the source.

Additional investigations will be summarized to illustrate the broader application of geofencing software and sequencing in tracing pathogen introduction pathways. These include a transport-associated break, a gilt-source introduction, and a porcine deltacoronavirus (PDCoV) case in which transport biosecurity failures were suspected but not definitively proven. Across the PRRS cases, ORF 5 sequencing was critical in narrowing down farms to evaluate connections and risk areas.

The discussion will emphasize: investigative details that influenced the accuracy and speed of outbreak source determination, the role of movement data in reconstructing high-risk events, lessons learned from compliance vulnerabilities, and mitigation strategies adopted to reduce future risk

By sharing practical examples and lessons learned from these investigations, this presentation aims to highlight biosecurity gaps. It will also review tools used to more effectively identify, confirm, and prevent biosecurity breaches, particularly those involving supplies and transport, which remain underappreciated but critical risks.

**Effects of High Soybean Meal Inclusion on the Gut Microbiome of Finishing Pigs**

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Soybean meal (SBM) is the primary protein source used in swine diets in the U.S. Midwest region, typically combined with synthetic amino acids to support optimal growth, and performance. While the inclusion rates of SBM typically vary based on market prices, different levels can have significant effects on pig performance and health due to other compounds that are present in SBM, such as polysaccharides and oligosaccharides. These components affect gut health and the microbiome, through metabolic pathways that are not yet fully understood. With new soybean processing facilities in the Midwest, increased production of SBM may reduce its market price, making it a more accessible and economically viable amino acid source. In this context, a better understanding of the effects of higher SBM inclusion compared to low inclusion on the swine gut environment and its microbiome is needed. We hypothesized that distinct populations of bacteria that degrade fiber from complex carbohydrates will be in higher abundance when pigs are fed with high SBM inclusion diets compared to low SBM inclusion diets

546 mixed-sex pigs were used in a 111-day trial to evaluate the effects of diets with 1) low SBM inclusion supplemented with synthetic amino acids (5%; LowSBM) versus 2) high SBM inclusion (28%; HighSBM). All diets were formulated to meet or exceed NRC requirements, with standardized ileal digestible (SID) lysine and net energy (NE) levels kept constant across treatments. Pigs were randomly assigned to treatments and blocked by location, with 26 pigs per pen, 10 pens on the LowSBM treatment, and 11 pens on the HighSBM treatment. To determine fecal bacterial composition and identify candidate gut microbial species, 14 fecal samples per treatment were collected for DNA extraction and 16S rRNA sequencing via PCR amplification of the V1–V3 regions.

A 16S rRNA gene-based analysis of beta diversity, visualized through Principal Coordinate Analysis (PCoA) with Bray-Curtis distances, indicated significant differences in bacterial composition between the two treatments (PERMANOVA, $P < 0.05$). Notably, we found a higher abundance of specific OTUs in the HighSBM samples compared to the LowSBM samples ($P < 0.05$, Kruskal-Wallis test). These included (respective relative abundances in HighSBM and LowSBM samples provided, as well as closest valid relative and nucleotide sequence identity): Ssd-0039 (15.00% vs. 10.00%; Streptococcus alactolyticus, 99%), Ssd-1160, (2.00% vs. 0.10%; Treponema brennaborense, 88%), Ssd-1254 (2.00% vs. 0.03%; Treponema bryantii, 97%), and SBM1-41761 (1.60% vs. 0.22%; Pedobacter nanyangensis, 83%)

With SBM becoming more affordable, this study offers insight into optimizing protein in swine. Results support the hypothesis that HighSBM alters gut microbiome composition, potentially influencing production of short-chain fatty acids and other metabolites. Based on their higher abundance in samples from the highSBM diet, OTUs Ssd-0039, Ssd-1160, Ssd-1254, and SBM1-41761 may be associated with fiber degradation and utilization. These uncultured bacteria may still be undescribed, and further metagenomic analysis is needed to predict their metabolic roles. In the long term, understanding these OTUs may clarify how polysaccharides and oligosaccharides are degraded in the swine gut and their role in short-chain fatty acid production.

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**Optimizing gestation nutrition to mitigate sow anemia, improve farrowing outcomes, and support longevity in the prolific sow**

Katlyn McClellan[1], Eric Weaver[1]

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The nutritional and metabolic demands of modern, highly prolific sows have potentially outpaced the gestation feeding strategies traditionally used in commercial systems. Causes of high replacement and culling rates and increasing sow mortality are often difficult to determine in prolific sow herds. In late gestation, rapid fetal growth, placental expansion, mammary development, and a marked increase in maternal blood volume place considerable demands on the sow, likely elevating her nutrient requirements. Yet, these requirements remain to be determined, leading to probable nutritional shortfalls that heighten the sow's susceptibility to health and reproductive challenges and higher replacement rates.

Among the evidence suggesting that sows are experiencing nutritional deficiencies is the consistently high prevalence of anemia reported across commercial herds, with over 50% of late gestating sows exhibiting hemoglobin concentrations below 10 g/dL. Low hemoglobin levels are strongly associated with prolonged farrowing duration, increased stillbirths, impaired postpartum recovery, and early removal from the herd. Because late gestation is a critical window of vulnerability, maternal hemoglobin concentration may serve as a valuable predictor of farrowing efficiency and sow survivability.

Although anemia is often attributed to inadequate iron intake, its etiology in sows is likely multi factorial. Iron status depends not only on dietary iron supply but also on the availability of other nutrients required for iron absorption, transport, and storage. Because nutrients function in interconnected networks, deficiencies in one can impair the utilization or metabolism of others through shared transport systems, coenzyme activity, or protein synthesis pathways. This interdependence underscores the need for a comprehensive nutritional approach during gestation.

In a controlled longitudinal study involving 70 females (parity 0–5), sows fed a nutrient-enriched late gestation diet, formulated with higher concentrations of amino acids, trace minerals, and vitamins—had improved farrowing outcomes and maternal resilience. In the first reproductive cycle, the sows fed a higher plane of nutrition during late gestation had shorter farrowing durations, reduced stillbirth rates, improved micronutrient status in both sows and piglets, and greater piglet survival to weaning. Additionally, sow removal rates were three times higher in those not receiving the higher plane of nutrition during late gestation in the cycle following the initial phase feeding period. When tracked across two consecutive cycles, sows fed the nutrient-enriched diet in late gestation produced, on average, 2.4 more total pigs born and 2.7 more live born piglets compared with their own prior performance.

As genetic selection continues to drive increases in litter size and fetal growth rate, traditional gestation feeding strategies are no longer adequate to meet the evolving nutrient requirements of modern prolific sows. A phase-based approach to gestation nutrition—prioritizing nutrient bio availability, functional support, and nutrient interrelationships—offers a promising strategy to mitigate anemia, enhance farrowing efficiency, improve neonatal outcomes, and promote long-term sow health and longevity in highly prolific females.

**Experimental comparison of airborne shedding of distinct porcine reproductive and respiratory syndrome virus variants**

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Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) is considered the most economically devastating swine disease in the U.S., with estimated annual losses exceeding $1 billion 1. Given its ability to spread via aerosols2, controlling PRRSV transmission within and between farms is a persistent challenge. The rapid dissemination of variants such as PRRSV L1C1-4-4 has raised questions about whether newly emergent variants exhibit enhanced aerosol transmission compared to older ones. This study aimed to assess the levels and temporal dynamics of virus-laden aerosols from pigs experimentally infected with distinct clinically relevant PRRSV variants.

Methods

Three PRRSV-2 variants were evaluated: L1C.5 1-4-4 and L1A 1-7-4, associated with recent severe outbreaks, and L9A (D99-30100), a historically documented airborne strain and perceived lower virulence.

Fifty PRRSV-naïve, 3-week-old pigs were randomly assigned to four groups (n=14 per variant; n=8 negative control) and inoculated intranasally with 2 mL of virus ($1 \times 10^{5.5}$ $TCID_{50}$/mL) or mock inoculated. Clinical signs, weight, serum, nasal swabs, air, and surface samples were collected over the 20 days. Air samples were obtained using a non-viable Andersen cascade impactor sampler and the AirPrep sampler, while surfaces, specifically aluminum foil sheets placed to capture settling airborne particles, were swabbed using moistened gauze. All samples were collected over 30 minutes and quantified by RT-qPCR targeting ORF62. Viral load was calculated from Ct values using standard curves and expressed as $log_{10}$ RNA copies/$m^3$ for air samples and $log_{10}$ RNA copies/$cm^2$ for surface samples.

Results

All pigs inoculated with PRRSV exhibited clinical signs, with L1C.5 and L1A showing more severe symptoms and reduced growth rates. The variant L1A produced the highest and most sustained viremia, followed by L1C.5, which had a high viremia during the first 7 days post-infection (DPI)., For both variants, the viremia decreased after 15 DPI. Interestingly, variant L9A had the lowest viremia during the first 7 DPI, but remained relatively elevated throughout the study. Similar trends were observed for nasal shedding, with the difference that shedding of L1C.5 was lower after 11 DPI compared to the other two variants.

All three variants were detected consistently in air and surfaces, although with differing patterns. Detection was similar during the first 10 DPI, with L1A showing the highest and most sustained airborne levels. Interestingly, the L1C.5 became undetectable after 13 DPI, coinciding with reduced nasal shedding. Lastly, all strains could be detected in larger particles (>9.0 µm), with less frequent detection in the 9.0 and 4.7 µm range.

Conclusion

This study advanced the understanding of PRRSV transmission through the air and supports the notion that there are differences among PRRSV variants in their ability to become airborne. These results also point to the need to adjust and possibly enhance biosecurity protocols that may be dose-dependent, including protocols for incoming air biosecurity. Ultimately, results from this study should help guide the development of more effective strategies to prevent the introduction of new variants into farms, including variants with a higher propensity to transmit through the air.

**Emergence and dissemination of PRRSV variant 1C.5.32 across Iowa**

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Porcine reproductive and respiratory syndrome virus (PRRSV-2) remains the most economically devastating swine pathogen in the United States (U.S.), with losses exceeding $1 billion annually. The emergence and turnover of dominant PRRSV lineages are well-documented, typically occurring on a 1 to 4-year cycle. Since its emergence in 2020, sublineage 1C.5 has spread rapidly, contributing to more than 45% of U.S. detections. In 2023, an unprecedented clonal expansion within 1C.5, designated as variant 1C.5.32, was identified in Iowa. Within a year, 1C.5.32 accounted for over 38% of all PRRSV-2 sequences in the state. This study aims to characterize the genetic and epidemiological factors underpinning the success of this variant.

PRRSV-2 open reading frame 5 (ORF5) sequences from the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) collected between January 1, 2023, and March 31, 2025, were classified using Nextclade, identifying 1,214 sequences with 1C.5.32 designation over the timespan of the study. Compared to other major lineages, variant 1C.5.32 displays lower reverse transcription quantitative polymerase chain reaction (RT-qPCR) cycle threshold (Ct) values, suggesting higher viral loads. The clonal expansion was characterized by maximum-likelihood phylogenetic inference, with within and between-clade distances calculated for major lineages. This variant demonstrated reduced genetic diversity relative to its parental sublineage 1C.5. Effective population size was inferred using BEAST to assess genetic diversity and evolutionary dynamics. The prior 1C.5 sublineage derived from a recombination event. The 1C.5.32 variant sequences were screened for further recombination with RDP5, but none were detected. Phylogeographic spread was modeled using Markov jumps and log Bayes factor-supported transitions between Iowa quadrants and U.S. states. Bayesian phylogeographic analysis revealed strong transition signals from the northeastern quadrant of Iowa to surrounding regions, illustrating the spatial dynamics of its rapid expansion.

These results highlight evolutionary, epidemiological, and geographic features of an emergent PRRSV-2 clade. By identifying traits associated with enhanced spread and persistence, this study offers valuable insights into surveillance strategies and early warning systems aimed at mitigating future outbreaks of emerging high-impact PRRSV variants.

# Assessing the probability of detection of Salmonella between oral fluids and fecal sample methods under commercial conditions

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## Introduction

Salmonella is a common pathogen found throughout the environment and has been a persistent challenge in swine populations for decades. It affects nearly all swine herds, posing significant issues for pig health, performance, and food safety risks[1]. Traditional bacteriological culture methods of feces remain the primary approach for detecting Salmonella2-4. Oral fluids are a preferred population-based sample for detecting infectious agents under field conditions, as they offer a practical, non-invasive, and pooled collection method that enhances herd-level sensitivity compared to fecal samples5. This study aimed to assess the Salmonella probability of detection between oral fluids (OF) and fecal pool (FP) to enhance surveillance in finisher sites under field conditions.

## Methods

The study was conducted on two commercial grow-to-finish sites located in Iowa, each housing approximately 1,000 pigs in 48 pens. At the time of sampling, pigs were around 11 weeks old, with an average of 22 pigs per pen. From each site, 17 pens were randomly selected, totaling 34 sampled pens. Paired samples, OF and FP, were collected from the pens. For OF collection, ropes were hung for 30–45 minutes. Ropes were then placed in single-use bags, and approximately 10 mL of OF was manually extracted6. FP samples were collected from five different floor locations per pen using sterile 5 mL Whirl-Pak® spoons and combined into a 25 g pooled sample as described by Arnold & Cook (2009)7. All samples were submitted to the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL) for Salmonella culture using RV and TTB enrichment following method v2 described by Love et al. (2008)8. All OF and FP samples were also tested by qPCR9. Statistical analyses included McNemar's test, percent agreement, and relative sensitivity and specificity.

## Results

At both sites, OF sampling detected 14 Salmonella-positive pens, matching FP results at Site 1. However, at Site 2, fecal sampling identified 17 positives. The overall percent agreement between the two sample types was 79.4%, indicating that the tests produced matching results in approximately four out of five cases.

McNemar's test yielded a p-value of 0.450, indicating no statistically significant difference in the discordant pairs between OF and FP results. This suggests that neither method consistently outperformed the other in detecting discordant outcomes.

Relative sensitivity of OF was 83.9%, demonstrating good capability in identifying true positive cases when compared to FP. However, the observed relative specificity was 33.3%, though this likely reflects sampling

variability rather than true diagnostic performance. Regarding PCR results, all samples, OF and FP, were negative (Ct >34).

Conclusion

Overall, culture of OF appears to be a promising, practical tool for Salmonella surveillance, especially in settings where pen-level, non-invasive sampling is preferred. The isolation of Salmonella from OF alone is a notable finding. Additional studies are warranted to further validate its performance under commercial conditions. PCR was not a reliable diagnostic method for detecting Salmonella in either OF or FP under field conditions.

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**Development of a National Swine Health Strategy**

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Introduction

At the March 2025 Pork Industry Forum, the Pork Act Delegate Body passed the following advisement: "The Minnesota Pork Board, Illinois Pork Producers Association, Ohio Pork Council, Indiana Pork, and Missouri Pork Association moves for the development of a producer led National Swine Health Strategy by the National Pork Board. An update regarding the progress in developing the National Swine Health Strategy is to be provided by the National Pork Board to delegates at the 2026 Pork Forum."

Improving the health of the U.S. swine herd remains a top priority for U.S. pork producers. The National Pork Board (NPB) and National Pork Producers Council (NPPC) have long contributed resources to support improvements to swine health. When looking forward to opportunities to improve swine health across the industry, national resources must be allocated strategically to provide the best return on investment.

Advisory Group

NPB and NPPC recognized the need for industry alignment on swine health goals and have established a National Swine Health Strategy advisory group. The advisory group is comprised of board members from the respective organizations, pork producers, and swine veterinarians that represent different geographies, sizes and types of production in the U.S. pork industry. The advisory group will be equipped with comprehensive swine health insights—gathered through surveys, listening sessions, and other sources—to help guide the development of the National Swine Health Strategy. The advisory group is supported by staff from both national organizations, with expected outcomes including a unified approach, prioritized resource allocation, and improved communication among board directors, producers, regulators, and the broader pork supply chain to address the U.S. pork industry's top swine health priorities.

Data Collection

Swine health insights have been collected from pork producers and stakeholder groups throughout the summer of 2025, providing an opportunity to directly impact the scope of swine health work in the pork industry for years to come. The feedback requested from these groups includes insights on 1) What are the top swine health challenges that the industry should work to address? 2) What is a realistic goal for addressing these challenges? and 3) What areas (research, education, policy, etc.) should the industry focus on to meet these goals? Data has been collected through a variety of methods such as online surveys, phone surveys, one-on-one discussions, and listening sessions.

The advisory group's outcomes will be provided to the NPB and NPPC Boards of Directors, state pork associations and other stakeholders. The National Swine Health Strategy and priorities will be shared with the industry to allow all organizations that work on behalf of pork producers to align their efforts with industry-supported priorities.

**Desafios actuales en sitios 1 en Estados Unidos: Una mirada critica**

Juan Orozco[1], Sergio Canavate[1], Jorge Cajamarca[1], Jose Piva[1], Maria Ros[1]

[1]PIC

Swine production in the US has seen significant advancements, particularly in sow productivity driven by improvements in genetic program, nutritional strategies, and management practices. These gains have resulted in larger litter sizes and increased numbers of weaned pigs. However, the industry continues to face significant challenges that threaten sow longevity, including disease outbreaks, the transition to group housing in gestation, labor shortages and high turnover, just to mention some factors.

This presentation outlines practical strategies to improve sow retention and productivity. No doubt that the modern sows are not the same as in the past and they have different requirements. Sows produce more piglets and grow faster than ever before. To maximize their potential and longevity, management practices must evolve accordingly and there is the need of adopting the four-pillar strategy to increase sow longevity and maximize productivity - Genetic Program, Parity 1 Development, Body Condition and Sow Care- is proposed to support sow longevity and maximize productivity.

Other factors to consider that have direct impact on sow longevity are:

Health status is closely tied to performance, and enhanced biosecurity—such as air filtration, stricter transport protocols, and heightened precautions during high-risk periods like manure pumping—plays a critical role. Disease control measures, including herd closures and depopulation-repopulation strategies, are also essential.

People are a key driver of farm success. Employee experience and turnover rates significantly affect performance. As a result, systems are increasingly focused on employee satisfaction, training, and career development. The adoption of new technologies, equipment, and farm design further supports operational efficiency. Well-trained staff directly influence key metrics such as pigs weaned per sow and sow retention.

These findings underscore the need for holistic approaches to balance productivity, welfare, and economic viability in modern swine operations.

**Transforming swine health management via Machine Learning: PRRS monitoring applications**

Nakarin Pamornchainavakul[1], Mariana Kikuti[1], Jing Huang[1], Cesar A. Corzo[1], Maxim C.J. Cheeran[1], Kimberly VanderWaal[1]

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Artificial intelligence (AI) refers to computational tools capable of performing tasks that normally require human expertise, and machine learning (ML) is a branch of AI that learns patterns from data to make predictions. Many people encounter ML every day—whether through email spam filters or credit card fraud detection. In animal health, it is beginning to shape how we forecast disease outbreaks and even assess pain in animals. The Morrison Swine Health Monitoring Project (MSHMP) holds one of the largest swine disease databases in the United States, containing PRRSV genetic sequences alongside epidemiological information from over half of the nation's breeding herds. Despite this resource, PRRSV remains a billion-dollar annual problem in the U.S., with new variants continuing to emerge and immune protection from vaccination or live virus inoculation often proving inconsistent. These challenges call for tools that can turn massive datasets into rapid, actionable insights. By applying ML to MSHMP data, PRRSV variant identification can be achieved in seconds, bypassing the labor-intensive process of building phylogenetic trees. Models trained to recognize nucleotide patterns along the ORF5 gene achieve over 95% accuracy in classifying sequences into nearly 200 known variants. Yet, detecting a variant is only the first step—most variants spread slowly, and only a fraction are likely to become the "next big one." ML models can help distinguish between low-risk and fast-growing variants by analyzing patterns such as deviations from historical sampling trends, the size of the current outbreak, and the amount of genetic diversity within the variant. These predictions have reached up to 77% accuracy in forecasting which variants will grow rapidly over the next year. Identifying high-risk variants naturally raises the question of how best to control them. Virus neutralization (VN) assays provide an experimental measure of how well serum from animals immunized with one variant can protect against another. However, such experimental data are limited and cannot cover every possible combination. Here, ML can fill the gap by predicting likely VN outcomes from sequence data alone, considering amino acid distances, glycosylation patterns, and site-specific differences in protein properties. This approach can classify whether VN titers will be high or low with up to 85% accuracy on internal testing and over 80% on external datasets, enabling more confident selection of vaccines or live virus inoculants tailored to the variant of concern. Together, these advances show how ML—combined with large-scale surveillance—can transform PRRS monitoring from a slow, reactive process into a fast, predictive, and targeted system. For the swine industry, this means earlier warning of emerging threats, more focused monitoring efforts, and better-informed immunization strategies, ultimately moving us closer to controlling one of the industry's most persistent and costly diseases.

**CRISPR Conversations: What Consumers Think About Gene-Edited Pork**

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Based on results from a national survey of U.S. consumers, this presentation will unpack what drives consumer acceptance of CRISPR-edited pork. It will also explore lessons learned from public responses to earlier agri-food technologies, recent trends in consumer research on gene-editing, and implications for effective communication and outreach in the swine industry.

**Hemoglobin in Boars: Impacts on Libido and Sperm Production**

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Background and Objectives

Hemoglobin levels and their effects on production parameters have been studied in piglets, gilts, and sows; however, limited research has focused on boars. The primary objective of this study was to define hemoglobin reference values in commercial boars and evaluate associations between hemoglobin concentration, libido, sperm quantity, and sperm quality. Identifying physiological factors that influence boar performance is essential for improving reproductive efficiency, reducing labor demands, and enhancing stud productivity.

Materials and Methods

Data were collected from 246 boars across four commercial boar studs, representing seven breed lines: Landrace, Large White, Danish Landrace, Meishan, and two Duroc lines. Boar identification, mounting behavior, and hemoglobin concentration (g/dL) were recorded on-site.

Boars were placed individually into a semen collection pen and given five minutes to mount an artificial insemination (AI) dummy. Boars that failed to mount were offered a second and third five-minute opportunity. Depending on farm protocol, Lutalyse was administered after the first or second failed attempt. Once the boar mounted and ejaculation began, a blood sample was collected from the ear or leg vein and hemoglobin concentration was measured using a HemoCue device. Boars failing to mount after three attempts were classified as “failed to mount.”

Additional data, including breed line, total sperm production, percent normal sperm, and age, were obtained from on-farm software (Prism).

For analysis, boars were grouped in two ways: (1) those that mounted on the first attempt versus those that failed to mount on the first attempt, and (2) those that successfully mounted (on any attempt) versus those that failed to mount entirely. Group comparisons were performed using Student’s t-test, one-way ANOVA, and linear regression.

Results

The mean hemoglobin concentration across all boars was 14.15 ± 1.49 g/dL (IQR: 13.13–15.20 g/dL). Hemoglobin concentration was not significantly associated with breed line, total sperm count, percent normal sperm, age, or blood collection site.

Higher hemoglobin levels were significantly associated with improved libido. Boars that mounted on their first attempt had a mean hemoglobin concentration of 14.42 ± 1.42 g/dL, compared to 13.56 ± 1.49 g/dL in boars that failed to mount on the first attempt (mean difference: 0.86 g/dL, $p = 3.22 \times 10^{-5}$). Boars that successfully mounted (on any attempt) had a mean hemoglobin concentration of 14.33 ± 1.18 g/dL, compared to 12.46 ± 1.41 g/dL in boars that failed to mount (mean difference: 1.87 g/dL, $p = 4.57 \times 10^{-8}$).

Discussion

Boars with lower hemoglobin concentrations exhibited reduced libido, potentially due to decreased oxygen delivery and energy availability. Reduced libido increases cull rates and labor requirements, as boars needing multiple mounting attempts extend collection time and raise operational costs. Establishing hemoglobin reference values may help identify boars at risk for poor libido and improve overall stud efficiency.

**Emerging viral threats and mitigation strategies in the swine industry**

Juergen A. Richt

Kansas State University

The global swine industry faces significant challenges from a range of emerging and re-emerging viral diseases, including African Swine Fever, Classical Swine Fever, Foot-and-Mouth Disease, Japanese Encephalitis, Porcine Reproductive and Respiratory Syndrome, and Swine Influenza, among others. These viruses vary in their modes of transmission, virulence, and epidemiological impact but collectively underscore the vulnerability of intensive swine production systems. They not only threaten animal health and welfare, impose major economic losses and disrupt global pork supply chains, but some also pose zoonotic risks to human health. This presentation will highlight recent developments in our understanding of key emerging/re-emerging viral threats to swine populations, and discusses current and prospective mitigation strategies.

Protecting swine populations from viral diseases requires a comprehensive, multi-tiered approach that integrates both conventional and advanced technologies. Biosecurity remains the cornerstone of disease prevention, minimizing pathogen introduction and spread through farm management, hygiene practices, controlled movement, and border protection. Diagnostic tools play a critical role in pathogen detection, enabling timely responses and effective outbreak containment. Point-of-care diagnostic tools, in particular, are field-deployable and facilitate on-site detection, enhancing rapid decision-making in the field. Vaccination continues to be a pivotal strategy, with novel platforms under development to address highly variable or emerging pathogens. Antiviral agents offer therapeutic potential, particularly in cases where vaccines are unavailable or ineffective. Additionally, gene-editing technologies such as CRISPR/Cas offer groundbreaking opportunities to develop pigs with innate resistance or resilience to specific viral infections. Together, these complementary strategies form a robust defense against current and future swine viral threats. Continued innovation and sustained commitment from industry, academia, and regulatory agencies are critical to protect animal and public health, ensure food security, and maintain the resilience of swine production systems worldwide.

**Swine influenza virus introduction in pig farms: a semi-quantitative risk assessment in Northern Italy**

Alessia Rusinà[1], Alessandro Bellato[1], Annalisa Scollo[1], Alessandro Mannelli[1], Laura Tomassone[1]

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Swine influenza (swIA) is a respiratory disease of pigs caused by Influenza A viruses. The predominant strains circulating today result from genetic reassortment of human, avian, and pig strains, as pigs can be infected with both human and avian viruses [1]. Influenza viruses are considered among the priority zoonotic diseases worldwide. Therefore, experts highlight the need to implement research on prevention and control measures and risk assessment to improve surveillance [2].

We conducted a semi-quantitative risk assessment to classify commercial pig farms in terms of the likelihood of introduction and circulation of influenza viruses by evaluating their biosecurity systems. A specific checklist was implemented to assess biosecurity measures and risk factors. Data were collected from 22 commercial pig farms located in Northern Italy, including farrow-to-finish, farrowing, weaning, and fattening sites, through farm visits and interviews with farmers. We used a modified Failure Mode and Effect Analysis (FMEA) [3] to calculate Risk Priority Codes (RPCs), indicating increasing risk levels (from 1 to 5) for six biosecurity criteria: A) personnel, B) animal introduction, C) shelter management, D) animal transport, E) materials management and F) buildings and access control. Importance of biosecurity measures, as assigned by experts, was included in the calculation. An additional RPC captured geographical risk, based on ecological suitability for H5Nx circulation in wild and domestic birds. We then calculated an overall risk index to classify the evaluated farms, from the one at higher risk to the one at lower risk.

The highest risk level for virus introduction (RPC=5) was observed for criterion F (structures and access), across all farms, mostly due to poor control of visitor access. Visitors could enter the farms even when showing influenza-like symptoms, and were not required to wear masks in 86% of the farms. Contact with avian species, which can harbour influenza viruses, was also critical: birds can potentially enter 54% of farms, and personnel in 22% of farms had contact with poultry. For criterion A (personnel), 14 farms had a medium risk level (RPC=3). Although all farms required personnel to change clothing, 22% lacked clear separation between clean and dirty areas, and just 14% required workers to wear masks, which are important for preventing viral exchange between pigs and humans. Conversely, personnel of all farms attended a recent biosecurity training; experts considered this measure the most important. Vaccination and diagnostic practices were limited: no farms tested pigs for SwIAV prior to housing, and only 18% vaccinated animals. However, 10 farms had low risk scores (RPC = 2) for shelter management, indicating good implementation of practices such as quarantine, all-in/all-out systems, and cleaning/disinfection protocols.

Regarding location, 5 farms were located in areas highly suitable for H5Nx circulation in both wild and domestic birds, and thus received the highest risk score.

Given that Europe is endemic for SwIA, risk assessment tools to identify farms at higher risk for virus introduction and circulation could improve early detection of new strains, enhancing surveillance and preparedness strategies.

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**Airborne biosecurity: Comparison of air filtration and an electrostatic precipitator technology**

Mark Schwartz[1], Hasan Al Tarify[1], Bernard Olson[1], My Yang[1], Chris Hogan[1], Montse Torremorell[1]

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Aerosol transmission of porcine reproductive and respiratory syndrome virus (PRRSV) has been identified as one of the modes of virus introduction into swine herds. Mechanical air filtration has been utilized as a means of reducing the incidence of PRRSV introduction into boar studs and sow farms. Factors including limits of particle capture, increased pressure drop and filter maintenance costs have resulted in the desire to explore alternative technologies, including electrostatic precipitation (ESP). Although ESPs have been applied to other areas including power plants and commercial HVAC systems, the application of ESPs to livestock production has not been assessed. A study was conducted to evaluate the efficacy of an ESP in a commercial swine barn, comparing performance metrics such as particle collection efficiency and pressure drop. The efficacy in virus capture was measured by aerosolizing a suspension of PRRSV and utilizing an Andersen cascade impactor to determine the log reduction up and downstream from the ESP unit. Penetration (1 – fractional collection efficiency) with remote optical particle counter sensors (OPC) and pressure drop were measured in real time throughout the study period. Overall, the ESP had a reduced pressure drop, was effective at removing airborne PRRSV and had a high particle removal efficiency comparable to that of a MERV-16 filter. The feasibility of the application of the ESP technology as an alternative to mechanical air filtration, both in terms of the relative costs of installation and operation, as well as the environmental extremes (temperature, dust load, etc) must be considered.

**Comparison of In Vitro and In Vivo Detection Methods for Identification and Discrimination of Infectious African Swine Fever Virus in Heat-treated Samples**

Janine Simmons[1], Lindsay Gabbert[1]

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Introduction

African swine fever virus (ASFV) is a large complex DNA virus and causative agent of the often fatal African swine fever (ASF). Traditional molecular assays such as real-time PCR are highly sensitive for detecting ASFV DNA, but are not capable of differentiating between infectious virions and those which have been inactivated or degraded in the environment. It has been proposed that inclusion of viability dyes, such as propidium monoazide (PMA), in PCR assays allows for discrimination of infectious ASFV from non-infectious virus by preventing amplification of nucleic acids not contained with the intact viral capsid.1,2,3 To better understand the results of these molecular assays, we compared the detection of infectious ASFV by virus isolation in tissue culture to both traditional real-time PCR4 and viability PCR (vPCR). Samples were further analyzed in live swine bioassays to confirm negativity.

Methods

Samples containing wild-type ASFV Georgia 2007 [106.5 HAD50/mL] were incubated at room temperature (23.7˚C), 50˚C, 60˚C, 85˚C, and 100˚C and collected at timepoints from 1 minute – 1 hour depending on the treatment group. All samples were titrated on primary swine monocyte-derived macrophages (MDMs) isolated from whole blood to determine the 50% hemadsorption dose (HAD50). Samples negative for HAD in initial titration tests were further blind passaged 3 times on MDMs to confirm negativity. ASFV DNA was extracted from all heat-treated supernatants and tested by both real-time PCR and vPCR to determine if any correlations exist between ASFV infectivity results established in vitro and results of the molecular methods. Samples negative for HAD in tissue culture, but positive for ASFV DNA by either PCR method, were further analyzed by intramuscular inoculation into pigs in live swine bioassays. Pigs (~13-16 kg) housed in individual pens were injected with 1 mL of each heat-treated ASFV sample. Animals were monitored for clinical signs of ASF disease over a 7-day period prior to collection of blood and spleen tissue for laboratory analysis.

Results

As confirmed by swine bioassay, ASFV wild-type Georgia was heat-inactivated within 1 hour at 50˚C,10 minutes at 60˚C, 5 minutes at 80˚C, and 1 minute at 100˚C. Sample infectivity, as determined in vitro by titration on primary MDMs, demonstrated a 100% correlation with bioassay results, suggesting that tissue culture methods adequately predicted the ability of the heat-inactivated samples to produce clinical disease in swine. PCR tests did not correlate with in vitro or in vivo results, with all samples positive for ASFV DNA—even for treatments not capable of causing disease in animals.

Conclusions

Temperatures at or above 50˚C directly impact time-to-inactivation of ASFV. In-vitro techniques, although time consuming, produced comparable results to swine bioassays. Our data suggest that both standard real-time PCR and vPCR assay were not capable of distinguishing between infectious and non-infectious

ASFV, and often resulted in false-positives. Additional studies are required to further assess dye-based viability PCR methods for ASFV.

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**Key SBM functional compounds reduced pathogen-related mortality in growing pigs infected with PRRSv: Results and clinical description**

Brooke Smith

Cargill Animal Nutrition

Introduction: This presentation will serve as a review of previously published research (Smith et al. 2020) evaluating the effects of dietary soy isoflavones (ISF) on the clinical response and wean-to-market growth performance of pigs infected with porcine reproductive and respiratory syndrome virus (PRRSv) during the early post-weaning period.

Methods: Ninety-six weaned barrows were housed in a biosafety level-2 containment facility and allotted to 1 of 3 experimental treatments that were maintained throughout the entirety of the study: noninfected pigs fed an ISF-devoid control diet (NEG, n = 24), infected pigs fed the control diet (POS, n = 36), and infected pigs fed a diet supplemented with total ISF in excess of 1,600 mg/kg (ISF, n = 36). Following a 7-day adaptation period, pigs were inoculated intranasally with either a sham-control (PBS) or live PRRSv (1 × 10^5 TCID50/mL, strain NADC20). Following inoculation, individual blood samples (n = 8-12/treatment) were routinely collected to monitor viral clearance and hematological parameters, including serum neutralizing anti-PRRSv antibody production. Pen-based oral fluids were utilized to monitor population PRRSv clearance at later growth stages. Comparison of experimental treatments were performed by 1- or 2-way ANOVA depending on whether or not an outcome was repeatedly measured.

Results: Dietary ISF increased ($P < 0.05$) neutrophil cell counts and the relative proportion of peripherally circulating memory T-cells. Dietary ISF also elicited an earlier, more robust anti-PRRSv neutralizing antibody response when compared to POS pigs and decreased the time to full PRRSv clearance from oral fluids. Additionally, and most notably, POS pigs experienced ~50% greater wean-to-market mortality compared to the ISF pigs. Regarding growth performance, as anticipated, PRRSv infection decreased overall growth performance resulting in 5.4% lower average final body weights (BW) for POS vs. NEG pigs ($P < 0.05$), though no difference was observed at the time of harvest for all treatments (Bryan et al. 2020). Dietary ISF resulted in inconsistent effects on growth performance throughout the growth period. Despite variable impacts on growth performance and lack of statistical differences in live body weight between treatments at the time of harvest, when the data were modeled and applied to current packer pricing grids, the lower mortality experienced by the ISF treatment resulted in an approximately 30% increase in projected revenue relative to the POS treatment.

Conclusions: Dietary ISF supported beneficial immune responses and reduced mortality in PRRSv-infected pigs. Decreasing mortality has direct financial implications to producers. While biological mechanisms of these effects remain unclear, these findings suggest that further investigation of soy isoflavones or other soy-derived bioactive components and their application under pathogenic challenge is merited.

**Sudden Death in Sows: Patterns Across Parity and Production Stages**

Laura Solis[1], Chris Rademacher[1], Cesar Moura[2], Gustavo S. Silva[1], Marcelo Almeida[1]

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Introduction

Sow mortality presents significant welfare and economic challenges in commercial swine production. While parity and physiological stage are recognized risk factors, their interaction with timing and pathology remains poorly understood (Supakorn et al., 2019). Sudden death is a leading cause of sow removal, often surpassing reproductive failure or lameness (Friendship & O'Sullivan, 2015). Yet its etiology frequently goes undocumented due to limited necropsy implementation. Previous studies have identified gastrointestinal torsions, gastric ulceration, heart failure, and retained piglets, particularly during the peripartum period, the most vulnerable window for sow mortality (Sanford et al., 1994; Paiva et al., 2023).

Methods

This retrospective study analyzed 150 sudden death cases from two commercial sow farms using systematic on-farm necropsy protocols. Cases were categorized by parity, production stage (breeding, gestation, pre-farrow, farrowed), and death cause. Additional variables included stomach ulcer grade (0–3), gestation day at death, postpartum interval, and age at first service. Data were analyzed using R.

Results

The farrowed period (including farrowing and lactation) accounted for the highest proportion of deaths (56.8%), followed by gestation (days 1–109; 28.1%), pre-farrow (days 110–115; 7.9%), and breeding (open gilts, opportunity sows, and culls; 7.2%). Within the farrowed group, 76% of deaths occurred during the first 7 days postpartum. Among gestating sows, 59% occurred between days 57 and 109, with a peak from days 81 to 109.

Retained piglets were the most common cause of death (29.5%), followed by gastric disorders (including perforated ulcers, acute ulcers, and gastric torsions; 18%), cardiovascular failure (10.8%), and splenic disorders (ruptures and torsions; 9.4%).

Parity 1 and 2 sows represented 49.5% of all deaths. Among parity 1 sows, the average age at first service (AFS) was 264 days (range: 238–313), highlighting variability in gilt development or breeding decisions. Delayed AFS is linked to increased reproductive failure and early removal (Koketsu & Iida, 2020; Malanda et al., 2019), while targeting 220–240 days improves gilt maturity, longevity, and lifetime output (Knauer et al., 2023). AFS is increasingly recognized as a key early-life predictor of sow resilience.

The average gestation length among farrowed sows was 117.5 days. Inducing parturition before a herd's typical gestation length can result in incomplete farrowing, stillbirths, and poor uterine clearance (De Rensis et al., 2012; Nam et al., 2023). Among retained piglet cases, sows had an average of 4.8 fetuses left in the uterus (range: 1–17). These findings underscore the need for herd- and parity-specific induction strategies to reduce fetal retention and associated mortality.

When causes of death were stratified by parity, retained piglets remained the top cause across nearly all groups. Parity 1 showed the most death cause diversity, while older parities (P9–P12) had fewer, more consistent patterns. Nearly two-thirds of necropsied sows had grade 2 or 3 ulcer lesions. Chronic or intermittent stress increases ulcer risk (Kanitz et al., 2018), reinforcing the value of stress-reducing strategies, particularly during late gestation and the peripartum period, to improve sow survivability.

Conclusions

Sudden sow mortality is concentrated in early parities and during the peripartum window, the most vulnerable period for losses. These findings underscore the need for targeted management strategies based on parity, timing, and pathology. Systematic necropsy remains essential to identify preventable causes and guide herd-level interventions.

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**Blind men and the pig: challenging our understanding of sustainable pork systems**

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Modern swine production systems operate within a complex intersection of economic pressure, environmental constraints, animal biology, and social expectations. Yet, much of the discourse surrounding sustainability in pork systems remains narrowly focused on isolated metrics such as feed efficiency, nutrient excretion, or productivity per animal. Drawing on Dr. Carlos Pijoan visionary work we bring the metaphor of the blind men describing different parts of an elephant, this work critically examines the "efficiency paradox" in swine systems—where well-intentioned interventions to reduce environmental impacts may generate unintended consequences across biological, farm, and ecological scales.

This research advances a systems perspective, incorporating insights from our HAPPINESS framework (Health, Animal welfare, Productivity, People, Inputs, Nutrition, Environment, Society, and Scale) to highlight key feedback loops and trade-offs in sustainable nutrition strategies. For example, formulating low-protein diets to reduce nitrogen and phosphorus excretion is a common environmental strategy. However, if these diets limit the animal's metabolic plasticity—its ability to adapt to stressors—this can increase preweaning mortality, sow culling, or disease susceptibility. Consequently, more pigs must be raised to meet production targets, potentially increasing cumulative nutrient output and undermining environmental gains. These dynamics are rarely captured when efficiency is defined solely at the individual animal or barn level.

The analysis also questions common assumptions about system design. Are smaller, diversified, or organic farms inherently more sustainable in nutrient use than large, concentrated animal feeding operations (CAFOs)? While these systems are often perceived as environmentally preferable, few comparative analyses rigorously assess nutrient use efficiency, resilience, or trade-offs at the herd, farm, and watershed levels. We propose that rather than categorizing systems as "good" or "bad," researchers and policymakers should evaluate continuous system attributes—land area, animal density, crop integration—using shared outcome metrics.

Building from recent field trials and productivity data (e.g., MetaFarms, NPB summaries), we developed a simplified system dynamics model in R to simulate sow herd outputs, preweaning mortality, and nutrient excretion under variable dietary and management scenarios. This model illustrates how interventions interact with scale, feedback, and system delays. We also demonstrate how a nutrition-focused intervention (e.g., adaptive protein formulation) can be coupled with agronomic practices (e.g., side-dress manure application) to optimize nutrient use efficiency across the crop-livestock interface.

In doing so, this research aligns with the four sustainability goals of swine feeding programs outlined by Urriola et al. (2022): 1) Improve efficiency of nutrient use, 2) Reduce nutrient losses to air and water, 3) Maintain animal health and performance, and 4) Promote nutrient circularity and recycling. We advocate that nutritionists, veterinarians, agronomists, and policy leaders adopt dynamic systems thinking to better anticipate synergies and trade-offs—moving beyond static performance benchmarks to embrace complexity, blind spots, and the need for integrated solutions.

**The perfect storm: Converging factors that fuel PRRS epidemic waves**

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Over the past 25 years, we have seen the repeated emergence of novel genetic variants of PRRSV-2, including some that exhibit rapid epidemic-like spread that have been catastrophic for the industry (for example, RFLP 1-7-4/L1A, variant 1C.5, and now 1C.5.32). While such patterns are characteristic of multi-strain, rapidly evolving viruses such as PRRSV-2, they raise critical questions: are contemporary epidemic waves worse than previous ones—and if so, what factors underlie these differences, and can we prevent them? In addition, why do some variants spread like wildfire across the industry while others only achieve localized spread? In this talk, we examine how contemporary viruses differ from historic strains through evolutionary, epidemiological, and immunological perspectives. We further discuss how these factors may intersect to create ideal conditions for widespread dissemination of novel genetic variants of PRRSV-2.

**What is Functional Teat?**

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Confirming that each piglet has their own functional teat during lactation enhances piglet survival and reduces competition between piglets (Obermier et. al, 2023). This ensures proper nutrition during early piglet growth, making pre-farrowing assessments critical for piglet survival (Wensley et. al 2022). Prior to farrowing, the stockperson allocates piglets to sows/gilts based on a visual evaluation for accessible teats. However, limited research has validated the accuracy of stockperson pre-farrowing teat assessment compared to a test of teat functionality - the ability to produce colostrum.

Objectives: This pilot study aimed to assess the accuracy of stockperson's visual teat count (GOOD) versus a research definition that includes colostrum production (FUNCTIONAL). A functional teat is one that produces colostrum during parturition. Our second objective was to measure morphological characteristics and changes of the udder and teats.

Methods: Prior to parturition, experienced stockpersons identified the number of GOOD teats on 22 sows. The researcher identified FUNCTIONAL teats within 3 hours of the start of parturition. Teats that did not produce colostrum were considered non-functional. Teat morphology was recorded 2 days prior to farrowing, and on Days 3 and 10 during lactation. Morphological udder and teat measurements included teat spacing (SAMER), teat diameter and length, parenchymal volume (base of the udder to teat distance), and midline udder length (MUL) on Day 0.

Results: Visual assessment of GOOD teats versus FUNCTIONAL was different in 40% (9/22) of the sows/gilts. Nonfunctional teats included blind and injured. Teats identified as nonfunctional at Day 0 did not gain parenchymal volume. Whereas parenchymal volume in trauma-affected teats had variable changes. Interestingly, in 8 sows, nine FUNCTIONAL teats were unused by Day 10.

Multiparous sows had significantly longer MUL than 1st parity sows. The greatest change in udder and teat morphology occurred from Day 0 to Day 3 compared to Day 3 to Day 10. Primarily in parenchymal volume (+19.9% vs. +8.6%) and teat length, while teat diameter and SAMER decreased. First parity sows showed a greater increase in parenchymal volume than multiparous sows over 10 days of lactation.

In conclusion, functional teat predictions were inaccurate in forty percent of the assessments. First parity sows showed greater variability and morphological changes. Integrating objective measures like parenchyma growth and colostrum flow into on-farm farrowing protocols may ensure that each piglet has their own functional teat during lactation.

**Signals and Snags: Leveraging Large Language Models for Near Real-Time Swine Disease Surveillance**

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Introduction

The rising threat of transboundary animal diseases, such as African swine fever (ASF), and foot-and-mouth disease (FMD), underscores the urgent need for robust, near-real-time surveillance systems to guide timely prevention and response1,2. Recent incursions into new regions, including FMD outbreaks in Germany, Hungary, and Slovakia, as well as ASF detections in previously unaffected areas like North Rhine-Westphalia in Germany, highlight the unpredictable and evolving nature of these threats. In this context, the overwhelming volume of publicly available information, which varies greatly in source, quality, and relevance, presents a growing challenge for timely data synthesis and analysis3. To address this, our team has begun exploring the integration of select large language models (LLMs) into our workflow. This research aims to assess the potential of leveraging LLMs to increase the efficiency of data processing, reduce the manual workload for veterinary professionals, and expand the scope of multilingual and geographically diverse swine disease reporting.

Methods

To automate national and regional transboundary swine diseases outbreak identification, Python scripts (Google Colab, Python 3.10) were developed. These scripts used Selenium and BeautifulSoup to extract outbreak information from Google Alert email URLs. Large language models (LLMs) were then used to generate concise summaries (<150 words), which were compared against manually curated reports for accuracy and relevance. Multiple LLMs, namely GPT-4o, Llama-3.2-3B-Instruct, T5-base, and DeepSeek-V3, were evaluated using standardized prompts and formats. Performance was assessed based on factual accuracy, language clarity, and the precision of date filtering to identify the most effective model for streamlining the reporting process.

Results

Among the models tested, GPT-4o demonstrated the strongest overall performance, offering the best balance of factual accuracy, relevance, and reliable metadata extraction. T5-base produced coherent and concise summaries but lacked the prompt adaptability needed for more complex or variable inputs. Llama and DeepSeek delivered acceptable factual accuracy; however, both showed limitations in date recognition and metadata precision, often generating less relevant summaries and struggling to meet length requirements.

Conclusion

The integration of LLM into the swine disease surveillance workflow shows clear potential to improve reporting efficiency, reduce manual workload, and support multilingual, geographically diverse data processing. Among the models evaluated, GPT-4o outperformed the others, demonstrating the most consistent balance between summary quality and metadata extraction. However, its performance still did not meet the standards required for reliable, unsupervised use in disease surveillance. Additionally,

common limitations across all models, such as difficulties with date filtering, disease classification, and summary accuracy, highlight that AI tools, while promising, are not yet capable of operating independently in this context. AI-assisted surveillance can support, but not replace, expert-led efforts in global animal health monitoring. Our experience highlights that while these tools can enhance efficiency, they require close oversight, domain expertise, and continuous evaluation to prevent misinformation and ensure critical signals are not missed. Moving forward, improvements in model performance, access to broader and more localized data sources, and integration with real-time platforms will be key.

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**Blue, Goo and a Tube: A Novel Feedback Delivery System**

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Introduction: Transitioning from individual gestation stalls to group housing creates challenges for swine health management, particularly implementing controlled pathogen exposure ("feedback") programs. While feedback is easily implemented in conventional barns where sows are confined, loose-housed sows present difficulties as animals move freely, making even exposure challenging. Electronic sow feeding (ESF) systems compound these challenges since facilities cannot simultaneously feed all sows. This study investigates dedicated tube-fed feedback protocols with visual monitoring to develop reliable, welfare-conscious methods for controlled pathogen exposure in group-housed sows. We hypothesized 50% of sows would be exposed within 2 hours of delivery.

Materials and Methods: The study was conducted on a 5000-head commercial operation using ESF systems. Eight pens with mixed-parity sows were evaluated, averaging 44.5 animals per pen (range: 35-49). Six pens contained breed group 18 sows (3 weeks pre-farrow) and two contained breed group 16 (1 week pre-farrow). Lesion scoring (0-6 scale) was conducted by trained evaluators before and 24 hours post-feedback to assess welfare. Feedback material from P0-P1 sows and piglet intestinal content was processed with water, Underline Dry Packet, and Reload Pack™ to create a standardized delivery medium. Observations at 30 minutes, 1 hour, 2 hours, and 24 hours quantified animals with blue pigmentation on their snouts.

Results and Discussion: Cumulative exposure rates increased progressively. At 30 minutes, median exposure was 33%, increasing to 46% at 1 hour and 48% at 2 hours. By 24 hours, median exposure reached 73%, with one pen achieving 90%. The 2-hour response rate of 51.4% was not significantly different from the expected 50% (P=0.78, Wilcoxon Signed Rank Test), confirming our hypothesis. Lesion scores showed no significant difference pre- and post-feedback (p=0.30), indicating the delivery method didn't increase fighting. Bland-Altman analysis demonstrated good agreement with minimal systematic bias (mean difference: 0.11). The tube-feeding system effectively delivered feedback to group-housed sows, achieving the targeted 50% exposure within 2 hours without compromising welfare. These results demonstrate that dedicated tube-feeding systems offer advantages over previous methods like ice blocks, providing precise control over timing, dosing, and pathogen viability while maintaining accessibility in commercial ESF operations.