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The Allen D. Leman Swine Conference is an annual educational event for the global swine industry. It is internationally acclaimed for bringing science-driven solutions to the complex challenges facing the industry. Each year hundreds of participants from over 20 countries attend the Leman Swine Conference held in Saint Paul, Minnesota.

Organized by: The University of Minnesota College of Veterinary Medicine and University of Minnesota Extension

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Presenter Name: Fernando P Bortolozzo, *UFRGS - Universidade Federal do Rio Grande do Sul*
Title: Impact of weaning age on pig performance in a commercial multisite production system

In commercial pig production, weaning is an abrupt process, occurring at around 2 to 4 wk of age. It has been demonstrated that success in the nursery phase is highly dependent on the weaning age. However, how weaning age influences performance in the first weeks after weaning is still a question. Thus, this study aimed to evaluate the effects of increasing the weaning age within a range of days on pig performance in the nursery and finishing phases. A total of 1,176 weaned pigs (PIC 337 × Camborough) were individually weighed and placed in nursery pens (14 replications) at 19, 22, 25, or 28 d of age. Pigs were weighed weekly on a pen basis and individually on days 0, 7, and 42 post-weaning. Pigs were fed ad libitum, and feed delivery was recorded on a pen basis throughout the nursery. Average daily gain (ADG), average daily feed intake (ADFI), and feed efficiency (G:F) were calculated using weight and feed disappearance. In the finishing phase (10 replications/weaning age), pigs were weighed on days 40, 80, and 94 after housing and at the 164th day of life. Feed delivery was not recorded in the finishing phase. Thus, BW, ADG, and mortality and removal rates were assessed. In the nursery, as the weaning age increased, initial (5.04, 5.70, 6.52, and 7.26 kg) and final BW (18.2, 19.8, 23.0, and 25.1 kg) increased (linear, $P < 0.001$). The percentage of pigs losing weight during the first week after weaning decreased as weaning age increased (linear, $P < 0.001$). Average daily gain and average daily feed intake increased (linear, $P < 0.001$), and feed efficiency (G:F) tended to increase (linear, $P = 0.081$) with weaning age. Removal rate reduced as weaning age increased (linear, $P = 0.001$), while there was no evidence of a difference in mortality rate ($P = 0.463$). In the finishing period, BW at 136 d post-weaning (114.9, 117.8, 124.7, and 126.5 kg) and ADG improved linearly ($P < 0.001$). There was no evidence of a difference in removal or mortality rates with the increased weaning age ($P > 0.24$). When the performance was analyzed at a common day of life (164 d of age), no effects of weaning age ($P > 0.25$) were found for BW and lifetime ADG. The BW sold per pig weaned increased (linear, $P < 0.001$) with weaning age. Despite the linear response, the magnitude of improvement was high until 25 d, before showing reduced returns from 25 to 28 d. Although lifetime performance was not affected by the weaning age range studied, the consistent effect in the nursery phase and the rise of the number of pigs reaching the market facilitated by the lower removal rate in the nursery phase suggest that 25 d is the optimal weaning age.

Presenter Name: Mariana Boscato Menegat, *Holden Farms*
Title: Phase-feeding: do fewer phases compromise growth performance in grow-finish?

Phase-feeding is the strategy of feeding multiple diets during the grow-finish period to closely meet the changing nutrient requirements of pigs. Phase-feeding strategies with multiple dietary phases and frequent phase changes typically meet more closely the requirements of grow-finish pigs. However, in practice, the within-lot and between-lot variation in pig weight, growth rate, and feed intake represent a challenge for precise multi-phase feeding strategies. Moreover, the manufacture, delivery, and storage logistics for multiple dietary phases are often not feasible in swine production systems. Thus, the objective was to evaluate in a series of commercial research trials whether simplification of phase-feeding strategies to fewer phases is possible without compromising performance and carcass characteristics of grow-finish pigs. Four trials were conducted using 1,100 to 1,188 pigs each (PIC 359 x 1050) from approximately 27 to 127 kg body weight (BW) with different phase-feeding strategies used in each trial. Treatments were based on a combination of three lysine (Lys) specifications at 96, 98, or 100% of estimated requirements and four phase-feeding strategies with 1, 2, 3, or 4 dietary phases. A single-phase feeding strategy reduced ($P < 0.05$) overall growth performance, live BW, and hot carcass weight (HCW) compared to multi-phase feeding strategies with Lys specifications at 98% or 100% of estimated requirements. Multi-phase feeding strategies with 2, 3 or 4 phases led to similar ($P > 0.05$) overall growth rate, live BW, and HCW of grow-finish pigs with Lys specifications at 98% or 100% of estimated requirements. In a 4-phase feeding strategy, Lys specifications at 96% of estimated requirements reduced ($P < 0.05$) overall growth performance compared to feeding strategies with Lys at 100% of estimated requirements, unless Lys specifications were increased to 100% of estimated requirements in the late finishing phase. Compensatory growth was observed on pigs fed 1, 2, or 3-phase feeding strategies or feeding strategies with Lys below the requirements in the early grow-finish phase, as evidenced by improved growth performance driven by improved ($P < 0.05$) feed efficiency in the period following low Lys levels. For carcass characteristics, there was no evidence ($P > 0.10$) for differences in carcass yield, backfat, loin depth, or lean percentage across feeding strategies in any of the trials. In conclusion, phase-feeding strategies provide performance advantages over feeding a single dietary phase throughout the grow-finish period. Simplification of feeding strategies from 4 to 3 or 2 dietary phases with Lys specifications at 98% to 100% of estimated requirements does not compromise overall growth performance and carcass characteristics of grow-finish pigs from 27 to 127 kg BW. However, phase-feeding programs with fewer dietary phases and Lys set slightly below the requirements require more accurate estimates of initial BW and feed intake to avoid severe restrictions in growth rate. Simplification of phase-feeding strategies seems to elicit compensatory growth. Thus, it seems more critical to set Lys closely to the estimated requirements in phase-feeding strategies with fewer dietary phases to allow for compensatory growth to occur.

Presenter Name: Jim Cairns, *Remote Insights*
Title: Improving swine health and productivity and operations with IoT and AI solutions

An overview on how 24x7 remote behavior monitoring using ear tag based accelerometer data can improve sow health and productivity and provide new quantifiable research insights as to the impact of the variables being studied. We will also review our pig counting solution that machine learning models to identify pigs in a video and count them as they cross a virtual threshold resulting in a >99.5% accuracy level.

Presenter Name: Marie Cuhane, *University of Minnesota*
Title: Of Ferrets and Flu; Of Pigs and Pandemics

Comprehensive influenza A virus (flu) surveillance programs with extensive virologic and epidemiologic information are not only needed to detect new influenza strains with epidemic or pandemic potential for preparedness purposes, but are also critical to the pigs and clients under our care as swine veterinarians to provide better prevention, treatment, and control of flu. Effective surveillance programs should target detection of influenza viruses in humans and pigs. Surveillance programs should include detection of viruses distributed throughout the world particularly in high-risk areas where humans, poultry, wild birds and pigs coexist in close proximity. Surveillance in pigs is considered crucial because pigs have receptors for human, swine and avian influenza viruses potentially favoring the emergence of new viral reassortants. There is evidence that the pig may more often be the victim of cross-species transmission from people or birds than they are the source of new viruses. However, any cross-species transmission and the true directionality of virus movement cannot be fully understood without surveillance. Whenever "novel" flu viruses are discovered in humans or pigs, there are implications for pig flu surveillance worldwide. For example, the development of flu candidate vaccine viruses, coordinated by the World Health Organization, is an essential component of overall global flu surveillance strategy and important for pandemic preparedness. Only through international partnerships among human and animal influenza researchers and laboratories can we be sure that there is a process to review swine flu viruses and their potential risk to humans.

Presenter Name: Scott Dee, *Pipestone Applied Research*
Title: 'How can feed mitigation strategies and holding times help eliminate the risk of pathogen introduction via feed',

The role of animal feed as a vehicle for the transport and transmission of viral diseases was first identified during the porcine epidemic diarrhea virus (PEDV) epidemic in North America. Since that time, various feed additives have been evaluated at the laboratory level to measure their effect on viral viability and infectivity in contaminated feed using bioassay piglet models. While a valid first step, the conditions of these studies were not representative of commercial swine production. Therefore, the purpose of this study was to evaluate the ability of feed additives to mitigate the risk of virus-contaminated feed using a model based on real-world conditions. This new model used an "ice-block" challenge, containing equal concentrations of porcine reproductive and respiratory syndrome virus (PRRSV), Seneca-virus A (SVA) and PEDV, larger populations of pigs, representative commercial facilities and environments, along with realistic volumes of complete feed supplemented with selected additives. Following supplementation, the ice block was manually dropped into designated feed bins and pigs consumed feed by natural feeding behavior. After challenge, samples were collected at the pen level (feed troughs, oral fluids) and at the animal level (clinical signs, viral infection, growth rate, and mortality) across five independent experiments involving 15 additives. In 14 of the additives tested, pigs on supplemented diets had significantly greater average daily gain (ADG), significantly lower clinical signs and infection levels, and numerically lower mortality rates compared to non-supplemented controls. In conclusion, the majority of the additives evaluated mitigated the effects of PRRSV 174, PEDV, and SVA in contaminated feed, resulting in improved health and performance.

Presenter Name: Joel DeRouchey, *Kansas State University*
Title: Factsheets, Videos and Other Resources Available Through the Project

Extension and outreach of information developed by the "Improving Pig Survivability Project" project will enable adoption and implementation of strategies that will reduce mortality in pork production. Specifically, the Extension and outreach objectives are to: 1) Increase pork producers' awareness of the factors influencing swine livability and strategies available to achieve improvement, and 2) Ensure the rapid and effective implementation of new technologies to improve swine livability related to their well-being, health and productivity. All information generated by the project can be found at https://piglivability.org/. To receive updates on the latest new information generated, sign up for the notifications at the website. Currently easy to read with specific take-home message factsheets have been or are being developed that focus on very specific aspects, technologies, or practices related to survivability in pork production (https://piglivability.org/fact-sheets). All factsheets are co-developed by project investigators along with undergraduate, graduate and veterinary students. The target audience for the factsheets are producers and farm employees. Current factsheets either published or nearing a publishing release include topics focused on pelvic organ prolapse information (3 total), colostrum management, Fe injections, weaning age, early identification of sick pigs, feeding the sow for pig survivability, along with many more. Visual and audio learning is another aspect of information transfer and this has led to the development of videos that highlight important aspects of swine survivability (https://piglivability.org/videos). Currently 10 short videos have been developed and this will continue to be a focus of outreach. Some of the current videos developed include: whole herd driver of wean-finish mortality, pelvic organ prolapse influencers (5 total on various topics), and a review of post-weaning mortality in commercial production for both infectious and non-infectious factors. For additional audio outreach, a podcast was launched on summer 2020 branded PIGX. The PIGX podcast is focused on discussions with swine industry experts as they engage in conversations aimed to help producers succeed in raising healthy pigs. Our goal with the podcast is to bring together experts in the swine industry to discuss practical, science-based strategies that pork producers can use to reduce mortality in all phases of production. These podcasts will be released monthly on topics influencing swine survivability. PIGX is found on iTunes, Google Play, Spotify, Stitcher, or wherever you find your podcasts. You can also find the podcast at Global Ag Network. Finally, Extension efforts reach numerous stakeholders at state, national and international events where presentations are given by the project investigators.

Presenter Name: Donna Drebes, *Seaboard Foods*
Title: Investigating PEDv Infections and Lessons to Improve Biosecurity in Finishing Pigs

Introduction

Since the initial introduction of PEDv into the U.S. swine herd, acclimation and biosecurity practices to protect sow farms have dramatically improved. This has resulted in low yearly sow farm incidence levels. However, the incidence of PEDv infections in the growing herd has not been established on a national basis. Seaboard Foods initiated a rigorous testing scheme to better understand PEDv infection dynamics in the finishing pig population. The long-term goal was to eliminate PEDv from the finishing pig population and therefore decrease the risk of PEDv breaks system wide.

Materials and Methods

At the outset, PEDv status for all commercial finisher farms operated by Seaboard Foods was unknown; a total of 266 sites located in CO, KS, OK, and TX. To characterize and surveil farms, a three-part testing scheme was initiated to establish health status for each finishing site. All samples were tested by Triplex PDT PCR at ISU VDL (Ames, IA). Farms collected samples as follows: 1 oral fluid per barn, 1 week pre-ship (PST); 1 composite Swiffer, 1 week post placement (PP); and, 1 composite Swiffer, any time scours were observed (CS). All samples with a Ct <30 were considered positive while samples with a Ct ≥30 were considered genetic material. If no scours was present at sites with a Ct ≥ 30, the site was considered negative. Farms were classified as stable (PEDv original, PED indel and PDCoV neg), line 2a (PDCoV or PED indel positive) or line 2b (PED original positive) based off the most recent test submitted. After 30 weeks of sample collection, epidemiological analysis of the surveillance data to was used to describe new introductions in regards to prior status, region and age of pig. PEDv introductions were defined as anytime a site moved from stable to line 2a or line 2b.

Results

Over the 30 weeks of data available 1 site had remained on line 2b the entire time. The virus was introduced into 117 stable sites 123 times. One geographical area had a greater proportion of introductions when compared to the rest of the system. This geographical area is composed of an 800,000 head space finishing complex which shares multiple resources. The highest percentage of introductions (57.4%) occurred from a negative PP test followed by positive CS. The mean time between the negative PP and positive CS was 8.8 weeks.

Conclusions

The high percentage of negative PP to positive CS and high proportion of introductions into one geographical area indicated PEDv virus was being introduced via fomites. This justified investment in multi-site and site specific equipment (ex-dead haul trailers, sort boards). After the segregation of equipment, retesting of sites 8 weeks after initial diagnosis was implemented. The overwhelming majority of them returned to a stable status thus implicating shared equipment as a means of disease transmission. There were status downgrades in sites that never showed any clinical signs. This emphasizes the importance of a robust monitoring scheme. Overall, this process shows that it is possible to dramatically decrease PEDv pressure in a system.

Presenter Name: Beatriz Garcia Morante, *Veterinary Population Medicine Department, College of Veterinary Medicine, University of Minnesota, St. Paul, MN*
Title: North American Mycoplasma hyopneumoniae MICs

Introduction

Mycoplasma hyopneumoniae (M. hyopneumoniae) is recognized as the causative agent of enzootic pneumonia and is a primary contributor to the porcine respiratory disease complex (1). Information about M. hyopneumoniae antimicrobial susceptibility is largely limited, as this species is especially hard to culture and antibiograms are not routinely performed. Indeed, the most current publicly available data on antimicrobial susceptibility for M. hyopneumoniae isolates from the US is dated several decades (2). In this context, the aim of this study was to determine the in vitro susceptibility to different antibiotics of M. hyopneumoniae contemporary isolates originated from field clinical cases in the US.

Materials and Methods

Eleven M. hyopneumoniae isolates were obtained from US swine farm clinical specimens within the most recent six years. Minimum inhibitory concentration values (MICs) of the examined antibiotics against the isolates were determined by a microbroth dilution method (3). Briefly, 100 µL of the appropriate antimicrobial solution was distributed into the corresponding well of microtiter plates, with a final range of antimicrobials from 0.001 to 64 µg/mL. The test was accomplished on 104 CCU/mL of each isolate. All isolates were tested in three independent replicates. For each isolate and plate, two positive (growth) controls were included by adding 100 µL of sterile medium in the wells with no antimicrobial. For negative (uninoculated) controls, four wells were filled with 200 µL of sterile medium. M. hyopneumoniae 11 (ATCC 25095) was used as reference strain for the MIC tests. The range of MICs recorded as well as the concentrations of compounds to which 50% or 90% of the isolates were susceptible (MIC50 or MIC90) were reported.

Results and Discussion

In comparison to the ATCC 25095 reference strain MICs, the M. hyopneumoniae US isolate MIC50/90 values were higher for Enrofloxacin, Marbofloxacin, Tylvalosin, and Oxytetracycline. The highest MIC90 values for M. hyopneumoniae US isolates were found at ≤8 µg/mL for Tilmicosin and Oxytetracycline, whereas the lowest MIC90 value was obtained at ≤0.016 µg/mL for Tylvalosin. Overall, a high in vitro efficacy of the tested agents against M. hyopneumoniae contemporary isolates was observed. Results from this study represent a renewed step towards appropriate and accurate antibiotic treatment of M. hyopneumoniae-driven disease.

References

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2. Williams PP 1978. Antimicrob Agents Chemother 14:210-213.
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Presenter Name: Jordan Gebhardt, *Kansas State University*
Title: Review of Post-Weaning Mortality in Commercial Swine Production

Post-weaning mortality has a complex causal matrix involving animal, environment, and infectious etiologic factors. Despite advances in swine productivity such as total pigs born, growth rate, feed intake, and efficiency, there have been modest to no improvements in post-weaning mortality rates over the last several years. Mortality estimates by phase have been reported to be 3.6% for nursery, 4.1% for grow-finish, and 5.6% of pigs entering the wean-finish phase (USDA, 2015). In order to develop and evaluate strategies to comprehensively manage and reduce post-weaning mortality, addressing the complexity and range of impact that factors have on mortality is necessary to identify and prioritize such contributing factors. Our objective is to describe the current state of knowledge regarding causes of post-weaning mortality by generalizing into non-infectious and infectious contributing factors. Non-infectious factors can be classified into anatomic abnormalities, toxicity, animal factors, facility factors, nutritional inadequacies, season, and management factors. Important non-infectious mortality factors identified through literature review include birth weight, pre-weaning management, weaning age and weight, and season. Additionally, a low incidence but high consequence cause for individual pigs is abdominal organ torsion. Sodium ion or ionophore toxicosis or dietary imbalance due to feed formulation or manufacture error are infrequent, but can be high magnitude. Infectious mortality are often categorized by physiologic body system affected. In an attempt to better understand the complex multifactorial nature of infectious post-weaning mortality, we stratified infectious factors by type of intervention utilized. This stratification method subjectively combines disease pathogenesis knowledge, epidemiology, and economic consequences. These intervention categories included depopulation of affected cohorts of animals, elimination protocols using knowledge of immunity and epidemiology, or less aggressive interventions. The most aggressive approach to control infectious etiologies is through herd depopulation and repopulation. Historically, these protocols were successful for Actinobacillus pleuropneumoniae and swine dysentery, among others. Elimination practices have been successful for Mycoplasma hyopneumoniae, porcine reproductive and respiratory syndrome virus, coronaviruses including transmissible gastroenteritis virus, porcine epidemic diarrhea virus, porcine delta-coronavirus, and swine influenza virus. Many other infectious etiologies present in swine production have not elicited these aggressive control measures because measures such as vaccination or therapeutics are effective, their impact on mortality or productivity is not great enough to warrant, or there is inadequate understanding to employ control procedures efficaciously and efficiently. Non-infectious and infectious mortality causes both need focus to improve wean-to-finish survival. Because of their importance in affecting survival, producers should focus on increasing birth and weaning weight, colostrum intake, and weaning age. Strategies to reduce abdominal organ torsions and gastric ulcers also are important for producers experiencing problems with these low frequency, high magnitude problems. Maintaining and improving herd biosecurity to prevent introduction of pathogens can reduce mortality due to infectious agents. For pathogens already present in the herd, producers must determine if the best management strategy is control (ex. vaccination), elimination (ex. mass exposure and temporary herd closure), or depopulation. Reducing post-weaning mortality remains an opportunity area in the swine industry.

Presenter Name: Douglas Gladue, *Plum Island Animal Disease Center-USDA-ARS*
Title: Development of live-attenuated vaccines for African swine fever virus

African swine fever virus (ASFV) causes a highly contagious disease called African swine fever (ASF), currently causing outbreaks in both Europe and Asia. This disease is often lethal for domestic pigs, causing extensive losses for the swine industry. Currently there is no commercially available treatment or vaccine to prevent this devastating disease, current outbreaks are controlled by culling of infected animals, and have already caused extensive losses to the swine industry in outbreak areas. Very little is known about cross-protection for different isolates of ASFV, making the production of live attenuated vaccines limited to the specific isolate causing an outbreak. Several experimental live vaccine strains have been developed by deleting different genes in ASFV. Here I will discuss a rational approach to developing a vaccine for the current outbreak strain that is rapidly spreading across Asia and Europe and discuss the current status of experimental live attenuated vaccines for ASFV that have been developed worldwide and their effectiveness against the current outbreak strain of ASFV

Presenter Name: Derald Holtkamp, *Veterinary Diagnostic and Production Animal Medicine Department, Iowa State University, Ames, Iowa*
Title: AASV PRRSV classification changes

In 2009, a committee met to discuss terminology to classify swine herds according to their porcine reproductive and respiratory syndrome virus (PRRSV) status. Their work culminated in a peer-reviewed paper entitled "Terminology for classifying swine herds by porcine reproductive and respiratory syndrome virus status" published in the Journal of Swine Health and Production.1 Before publication, the classification system was reviewed and approved by the Board of Directors of the American Association of Swine Veterinarians (AASV). Following the publication of the original classification system, several developments have led to calls for modifications to the system. For example, challenges with consistently weaning groups of pigs that are truly negative for PRRSV from breeding herds classified as Positive Stable (II), have led some to question the criteria and supporting evidence for those herds as some herds may have been falsely classified as stable. The evolution of new isolates that, when present, make it more challenging to stabilize sow farms may have contributed to the challenge of consistently weaning groups of pigs that are truly negative for PRRSV. Development of new sample types, such as oral fluids and processing fluids, and new diagnostic tests have presented opportunities to establish the status of herds more accurately and at a lower cost with less effort.
Because of the new developments and the lessons learned from the adoption of the original classification system, the PRRS Task Force Committee of the AASV voted to revisit the classification guidelines at the AASV annual meeting in March of 2018. A working group was formed to propose modifications to the PRRSV classification system. The modifications to the classification system were reviewed and approved by the Board of Directors of the AASV in the fall of 2019.

Acknowledgements
AASV provided funding to support the work of the working group formed to propose modifications to the PRRSV classification system.

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Presenter Name: Derald Holtkamp, *Veterinary Diagnostic and Production Animal Medicine Department, Iowa State University, Ames, Iowa*
Title: Chronicles of outbreak investigations: How they help us improve our biosecurity programs

The pork industry has changed dramatically in the last half-century. Changes in production practices; the economics of production; science and technology; and disease and health management have increased the need for, and value of, biosecurity. Unfortunately, progress in slowing the transmission of pathogens from herd-to-herd has been slow. This was evident in 2013 and 2014 when PEDV was first introduced into the United States. Within 18 months of the initial case, nearly half of the sow farms in the country became infected. A "ready-fire-aim" approach to biosecurity, guided by experimental research has contributed to the slow progress. When a new study was published demonstrating that, for example, livestock trailers, boots, insects, aerosols, feed or other carrying agents are capable of carrying pathogens from herd-to-herd, the industry has opened fire with only a rudimentary understanding of how much livestock trailers, or boots, or insects or aerosol or feed were contributing to the herd-to-herd transmission of pathogens. Just because they can, does not mean that they frequently do. The better order is "ready-aim-fire" characterized by identifying where farms are most vulnerable to the introduction of pathogens and then prioritizing improvements in biosecurity to address them. This is the aim in “ready-fire-aim.” However, the ad-hoc approaches to biosecurity assessments and outbreak investigations to identify where farms are most vulnerable to the introduction of pathogens have not been very effective for identifying the most frequent ways by which pathogens are being introduced into herds. The result is slow progress on improving biosecurity. While it is true that mistakes are opportunities to learn, the learning part is not guaranteed. Learning faster from our mistakes that result in outbreaks requires a more systematic, comprehensive, and consistent approach.

A systematic, comprehensive, and consistent approach based on the principles of epidemiology and Hazard Analysis Critical Control Points (HACCP), has been developed with funding from the Swine Health Information Center (SHIC). The approach is guided by a form which may be used by veterinarians to conduct outbreak investigations or prospective assessments to identify significant hazards where biosecurity control measures are most urgently needed.
An analysis of nineteen investigations of PRRSV outbreaks conducting using the form revealed that employee entry, removal of culls and repairs done inside the barns were most frequently identified as having a high likelihood of being responsible for the outbreaks. The likelihood of being responsible for the outbreaks was based on an analysis of the hazards associated with these events when the virus was most likely introduced into the herd.
The investigation form is available on-line to producers and veterinarians through SHIC as part of the Rapid Response to Emerging Disease Program (RRP). The purpose of the RRP is to be prepared to rapidly conduct epidemiological investigations when a new swine transboundary or emerging disease threat occurs with a known etiology. The forms and other resources developed for the RRP, are available at www.swinehealth.org.

Acknowledgements
The RRP was funded by the Swine Health Information Center (Project #19-149 SHIC) and the Iowa Pork Producers Association (Project #14-283).

Presenter Name: Cassandra Jones, *Kansas State University*
Title: The role of feed in disease outbreaks: Experiences from Manhattan (KS), VietNam, Brasil, and beyond

Environmental monitoring has been commonly used in food and other facilities manufacturing end-consumer products for years. The potential use of environmental monitoring of viral pathogens within a farm environment has seen an increase in popularity with the growing pressure placed on production systems from diseases. The purpose of this project was to use environmental monitoring to identify biosecurity gaps in production systems experiencing a viral outbreak. In Manhattan, KS, we learned that environmental monitoring for porcine epidemic diarrhea virus (PEDV) was an effective tool to adjust biosecurity procedures, but even more important in employee training. In Brazil, we learned that environmental monitoring for bacterial presence is a direct indicator of feed mill hygiene, and a feed mill audit is helpful to identify these gaps. In Vietnam, we learned that the feed delivery system, as opposed to ingredients, have been the primary source of African swine fever virus transmission throughout the production system. In all cases, environmental monitoring was important to identify root causes and risks for pathogen entry and transmission.

Presenter Name: Bill Kaelin, *McVean Trading & Invesments*
Title: Price Discovery in Today's Hog/Pork Industry

What is price discovery? Do we have it in today's hog/pork industry? Do we need it? If so, can we get it? These questions are some of what I will attempt to address.

Price discovery is the process by which a fair market price is determined through interactions between buyers and sellers, ultimately matching supply and demand. The price that results can be an important reference price for that market/industry.

Historically the market in which price discovery unfolded in the US hog/pork Industry has been the negotiated hog market. For a number of reasons, this market has shrunk to a point that it no longer can serve this function.
I would contend that if the US hog/pork industry is going to continue to be populated by a large number of independent producers selling hogs to independent packers, it is absolutely necessary to have a price that comes from a market that is reliable, well-functioning, transparent and represents transactions by a reasonable number of buyers and sellers. Without it, the industry will slowly become more integrated and independent producers will become contract growers. The negotiated pork cutout should quickly be adopted as the market where price discovery takes place in today's hog/pork industry. The negotiated pork cutout market checks a number of the boxes listed above necessary for a market to serve the price discovery role: mainly there are still many participants that transact regularly in pork market, the amount of negotiated pork traded is still a meaningful amount of total pork traded and has been stable for some time, and its reporting falls under the USDA's mandatory price reporting mandate.

Finally, another requirement for a producer community to stay independent is access to capital. Bankers/investors will likely require risk management as a condition for access to capital. It appears that the CME is actively considering listing a pork cutout contract. If this were to happen, it provides even more motivation for the industry to quickly move to the pork cutout as the primary place where price discovery occurs.

In summary, the US hog industry is at a critical juncture on many fronts. While the shrinking number of negotiated hogs traded is not new, the issue has finally reached a point that it presents an acute problem for the industry. There is increasingly no common measure of value in the industry today which reduces the motivation for the industry to act in concert on important issues, potentially reduces access to capital, and ultimately threatens the ability for the producer community to stay independent. The pork cutout is a viable alternative for the industry to use as its primary price discovery vehicle and should quickly be adopted as such.

Presenter Name: Zoe Kiefer, *Iowa State University*
Title: Identifying Biological Factors Associated with Pelvic Organ Prolapse: Vaginal Microbiome

Sow mortality, as the result of pelvic organ prolapse (POP), has increased in the past five years in the U.S. swine industry and continues to worsen. The vast majority of sows experience POP near the time of parturition although the etiology associated with it remains largely unknown. A perineal scoring (PS) system to assess potential for prolapse during late gestation was developed and 2865 individual sows were scored, (PS1 - a presumed low risk of prolapse; PS2 - a presumed moderate risk; and PS3 - a presumed high risk) while laying. Subsequently, 1.0, 2.7, and 23.4% of sows scored as PS1, PS2, or PS3, respectively, experienced a prolapse. The objective of this study is to identify putative biological factors associated with risk of POP in sows. We hypothesized that sows differing in PS would have differences in vaginal microflora, serum factors, and hormonal profiles. During perineal scoring in late gestation, serum samples and vaginal swabs were collected from sows on different farms. 16S rRNA gene sequences were clustered into operational taxonomic units (OTUs) based on a sequence similarity threshold of 97% using Mothur software. Overall, 89 OTUs differed between PS1 and PS3 for each farm ($P < 0.05$) while whole-community comparisons revealed differences between PS1 and PS3 samples using AMOVA and ANOSIM. Non-targeted metabolite analysis following GC-MS revealed candidate small molecules for POP risk. There were 82 differently abundant molecular features between PS1 and PS3 (> 4-fold change; $P < 0.05$). Whole blood was analyzed and a significant difference in mean platelet value, lymphocytes, and monocytes ($P < 0.05$) was observed between differing perineal scores. Circulating Lipopolysaccharide binding protein was measure via an ELISA and an increase of 24.9% ($P = 0.04$) in PS3 sows compared to PS1 sows was observed. Serum was sent to Biocrates for a 17-panel hormone analysis, changes in Deoxycortisol, Androstenedione, Androsterone, Estrone, β-Estradiol, and Testosterone were significantly different between groups ($P < 0.05$). This project was supported by the National Pork Board and Foundation for Food and Agriculture Research.

Presenter Name: Mariana Kikuti, *University of Minnesota*
Title: Understanding PRRSv diversity at the pig and litter level using whole genome sequencing

Introduction

Although genetic variability has been estimated to be around 3% at both the within herd and individual level using ORF5 sequences, whole genome variability within a naturally infected herd and within individuals is expected to be higher, more informative, and has yet to be documented. Here, we describe preliminary results of overall, within litter, and within piglet PRRSv genetic diversity on a farm undergoing an outbreak.

Methods

A PRRSv naïve 2500-sow farrow-to-wean farm was selected for this study. The farm broke with PRRSv type 2 after maintaining a naïve status for over three years. As part of the PRRS outbreak management protocol, live-virus inoculation was performed in the entire herd nine days after identifying the newly introduced PRRSv. Two weeks after inoculation, all piglets 3-5 days of age (DOA) were individually ear tagged and bled. Surviving piglets were bled again at 17-19 DOA (pre-weaning). Samples were individually tested for PRRSv by RT-PCR, and all positive samples were submitted for MINION sequencing. Consensus whole genome sequences were generated from reads by mapped to the reference MH651739. ORFs 2-7 were analyzed. Samples that were only partially sequenced in any of the ORFs 2-7 were excluded from further analysis.

Results

A total of 127 piglets from 21 litters were sampled at 3-5 DOA and all animals tested PRRSv RT-PCR positive. All 63 surviving piglets at 17-19 DOA were still PRRSv RT-PCR positive. Complete consensus reads were obtained for 101 samples (54 from 3-5 DOA and 47 from 17-19 DOA). Percent identity amongst samples was overall high for most comparisons (>99.0%). The lowest overall and within litter percent nucleotide identity was 95.8% found in ORF4, particularly in litters 10 and 12 at 17-19 DOA. The second lowest percent nucleotide identity was the overall 97.7% identity in ORF5a at 3-5 DOA, and overall and within litter 98.5% in ORF5a at 17-19 DOA. Within animal percent identity between both samplings was also assessed, with lower identity also found in ORFs 4 and 5a at 97.2% and 98.5%, respectively. While most sequences differed less than 1% from the overall ORFs 2-7 consensus, only 30.7% (31/101) of all the sequences were identical to the consensus.

Discussion

Although viral diversity within the piglet population is generally small, higher diversity was found in ORFs 4 and 5a. ORF5a overlaps with the beginning of ORF5, where sites under selective pressure were previously described. PRRSv mutation rate has been estimated at the order of 10-2/site/year, so the high nucleotide difference between the two samples found might represent turnover of a co-circulating virus that was not detected in the first sampling. These animals were also followed at 40-41, 65-66, and 109-110 DOA and will have viral diversity assessed at these stages as well.

Presenter Name: Chong Li, *College of Veterinary Medicine, University of Minnesota, St. Paul, MN, USA*
Title: Genotypic characterization of swine influenza virus reassortants in vaccinated and non-vaccinated pigs

Antigenic shift of influenza A virus (IAV) caused by reassortment can result in abrupt changes in virus phenotype and the virus biological properties, which can result in new viruses with pandemic potential. Pigs can promote virus reassortment due to their ability to replicate IAV from different species, which significantly contributes to the diversity of IAV circulating in pigs. IAV reassortment events not only make vaccination difficult but also pose a significant risk for public health. The 2009 H1N1 pandemic is an excellent example of a novel reassortant virus that emerged in pigs and that then jumped species resulting in a pandemic. Even though vaccination is widely applied in US pig farms to prevent disease and virus shedding, IAV still evolves continuously to escape host immunity and transmit under immune pressure. However, studies that investigate the emergence of reassortant viruses in naïve and vaccinated pigs are lacking. In this study, we collected bronchoalveolar lavage fluid (BALF) samples from pigs vaccinated with a licensed whole inactivated (COM) and/or modified live attenuated influenza (LAIV) vaccine combinations, and then co-infected with an H1N1 and H3N2 virus through nose to nose contact using a seeder pig model, and compared the reassortant viruses with those from non-vaccinated pigs. Two hundred and forty-two purified viral plaques were obtained from 16 pigs and submitted for Nextseq Illumina sequencing. Out of those, 226 plaques were successfully genotyped yielding a single genotype, and 16 plaques were classified as "mixed genotypes" since each of them had more than eight gene segments originating from both viral isolates. Eighteen percent of the plaques (40/226) were identified as reassortant genotypes with at least 21 different gene constellations and out of these, 16 (12.6%) reassortants were identified in vaccinated pigs, 4 (10%) in seeder pigs and 20 (33.9%) in non-vaccinated pigs. Overall, we found that pigs vaccinated with LAIV/COM and COM/COM vaccine combinations not only exhibited decreased viral shedding but also had significantly less frequency of reassortant viruses compared with non-vaccinated pigs ($p=0.015$). Our study provides initial evidence that vaccination can play a role at reducing the emergence of new reassortant viruses in pigs. These results, if confirmed under field conditions, provide insights on the complexity of influenza viral populations in pigs and will be helpful to develop more effective influenza control programs to eliminate IAV from pig farms.

Presenter Name: Steve Little, *University of Melbourne, Australia*
Title: Water medication of growing pigs - Sources of between-animal variability in systemic exposure to antimicrobials

Introduction

Drinking water is well suited for administration of antimicrobials to pigs to control and treat bacterial infections. However, substantial between-animal variability in systemic exposure to antimicrobials occurs when pigs are water medicated. This may lead to many pigs being under-dosed or over-dosed. The three sources of this between-animal variability in systemic exposure are differences in: (1) concentrations of the active antimicrobial in water available to pigs at drinkers in each pen over time, (2) patterns of consumption of medicated water by pigs in each pen over time, and (3) pharmacokinetics (i.e. oral bioavailability, volume of distribution and clearance) between pigs and within pigs over time.

Methods

To further understand the first two sources of between-animal variability in systemic exposure to antimicrobials when pigs are water medicated, the passage of an antimicrobial product through the drinking water distribution system in a commercial grower building during water medication dosing events was studied. Series of water samples were collected from drinkers in four pens in a building housing grower pigs with four differently designed water pipelines, during dosing events of 6-7 hours duration conducted using a proportional dosing pump. Water samples were then analysed for concentration of the antimicrobial administered (amoxicillin). Three alternative dosing regimens designed to administer the same total dose of an antimicrobial were also simulated to assess how the pattern and total quantity of antimicrobial consumed by pigs may differ when using different dosing regimens. A given hourly water consumption pattern was applied and the antimicrobial concentration in the water supply assumed to be constant.

Results

These studies showed the impacts that the design of a drinking water pipeline within a pig building, and other factors associated with water medication, have on the concentration of antimicrobial in water available to pigs in pens distributed across the building over time during a dosing event. Substantial differences were found with differently designed pipelines in the lags from commencement of a water medication dosing event to delivery of medicated water to pigs in pens nearer to the point at which antimicrobial is injected vs. pigs in pens further away from it. Simulations of the three alternative dosing regimens showed that dosing event start time and duration, lags and pigs' hourly water usage pattern can have large impacts on the pattern and total quantity of antimicrobial consumed by pigs.

Conclusion

When water medicating a group of pigs in a given building, the probability that the majority of pigs will attain the systemic exposure to the antimicrobial required to be clinically effective, while also eliminating the pathogen and minimising development of antimicrobial resistance, will depend on many factors. These include the solubility of the antimicrobial used, the design of the building's water pipeline, the hourly water consumption pattern of the pigs and the dosing regimen used. With a better understanding of these factors, we can reduce between-animal variability in systemic exposure to antimicrobials during water medication of pigs and optimise dosage regimens used on pig farms, thereby reducing under-dosing and over-dosing.

Presenter Name: Gustavo Lopez, *University of Minnesota*
Title: Detection of influenza A virus in swine farm workers before and after work

Introduction

Influenza A virus (IAV) affects many hosts, including pigs and people, which represents a public health concern. Bidirectional transmission of IAV leads to both disease morbidity and the potential to generate novel IAV strains. US swine herds experience frequent outbreaks of acute influenza that can impact both swine and human health. Despite the recognition that bidirectional transmission of influenza virus occurs between people and pigs, little is known about how frequently this transmission or exposure takes place. Therefore, the objectives of this study were to implement a surveillance system at the farm worker-swine interface, quantify how frequently farm workers tested positive for IAV and characterize the IAV positive samples to assess risk of interspecies transmission.

Material and methods

Seven sow farms located in the US-Midwest were selected for the study. The farms had a history of IAV infections and 5 of the farms tested IAV positive during the course of the study. We aimed to recruit swine farm workers that worked with pigs at least 2 days a week. After collecting baseline information, we asked each participant to self-collect a nasal swab before entering the farm and at the end of the working day, after completing the daily chores, twice a week for 8 weeks. At each sampling point, participants also collected their body temperature using disposable thermometers and answered a short survey regarding the activities performed during the day, and whether they had influenza-like illness (ILI).

Pigs were also sampled at three time points during the study. Each time 30 nasal swabs were collected from 20 day-old pigs prior to weaning. Farm worker samples were tested individually with an influenza A specific rRT-PCR test that detects both human and swine IAV's. Samples with a cycle threshold <40 were considered positive and positive samples. Pig samples were tested in pools of 3 using an rRT-PCR that targets the conserved matrix gene of IAV.

Results

There were 64 workers enrolled from seven participating farms and a total of 1,815 nasal swabs were obtained from the farm workers. Out of the samples collected, 58 samples (3.2%) tested IAV rRT-PCR positive, 20 (34.4%) of them belonged to samples taken before entering the farm and 38 (65.6%) were collected at the end of the working day. From the 64 enrolled workers, 37 of them tested IAV positive at least once during the study. Pigs from five of the seven participating farms were IAV positive at the three sampling points during the course of the study.

Conclusions and discussion

We were able to establish an IAV surveillance system where workers complied with self-sample collection protocols which indicates our ability to perform studies at the pig-human interface. Our results provide evidence that a number of farm workers can test influenza positive when they report to work at swine farms and at the end of the working day. Results obtained at the end of the day are indicative of IAV exposure while working with pigs at the farms. Further characterization of the samples is needed to understand the implications for virus introduction into farms and risk of bi-directional transmission between pigs and people.

Acknowledgements

This study was funded by the National Pork Board

Presenter Name: Gustavo Machado, *North Carolina State University*
Title: On the ability to predict PRRS outbreaks at the farm-level based on biosecurity practices

Introduction

Biosecurity and immunization have proven success in preventing PRRSV from spreading between farms (1). However, the compliance with biosecurity plans is precluded by its high cost, and more important the lack of quantitative measurements of its impact in reducing risk of PRRSV occurrence. Our goal here was to quantify PRRSV introduction risk and to calculate the contribution of individual biosecurity measures on individual farms PRRSV status.

Materials and Methods

A total of 158 US breeding farms with and without reported cases of PRRSV for the past 5 year, responded to a short biosecurity survey with 44 questions related with biosecurity practices and farm demography (feature) (2). A set of machine learning algorithms were used individually and in combination to: calculate the probability of PRRSV case at each farm, and to quantify how each biosecurity feature played a role in shaping PRRSV risk at farm level calculated by Shapley values (phi) (3). Briefly, Shapley values calculate the importance of a feature by comparing what a model predicts with and without the feature. For example, in a tested positive farm, values greater than 0 identify the contribution of those feature in the risk of a farm to remain positive, while negative values identify those features lowering exposure risk.

Results

Overall individual machine learning algorithms performance varies from 65.42% under gradient boosting machine (4) to 80.23% for random forest (5), while the ensemble of all algorithms performance was 85.54%, which is 5.31% better than the best individual model.

We present each farm predicted probability for PRRSV occurrence driven by biosecurity practices and farm's demography (Fig. 1A). Finally, as an example we selected one PRRSV positive and one PRRSV negative farm to show the contribution of each feature on PRRSV status (Fig. 1B). Further, calculating Shapley values unpacked what each biosecurity practice means in terms of PRRSV exposure risk in an intuitive way that can be used to guide improvements in specific biosecurity practices. For example in figure 1B, when the number downtime hours required for equipment used in manure removal was 72 hours the selected farm was at lower risk of being exposed to PRRSV, on the other hand, in a radius of 3 miles around the selected farm there was 5500 pigs which had a negative impact in this farm ability to remain negative.

A) Shows in the y-axis the calculated probability of a PRRSV case, x-axis the number of reported cases of PRRSV. B) Feature value contributions for each respective biosecurity and farm demography (feature) used to calibrate the models based on Shapley values (phi) for two individual farms (PRRSV positive and PRRSV negative).

Conclusions and Discussion

In summary, we calculated the risk for PRRSV introduction of individual farms, and quantified how each biosecurity feature contributed towards a farm reporting to be positive or negative for PRRSV.

The tool developed in the present study is suitable for identifying where efforts should be focused in biosecurity actions forming part of disease control programs.

Acknowledgments

This work is supported by Critical Agricultural Research and Extension 2019-68008-29910 from the USDA National Institute of Food and Agriculture

Presenter Name: Dominiek Maes, *Faculty of Veterinary Medicine, Ghent University*
Title: Efficacy of three innovative bacterin vaccines against experimental infection with Mycoplasma hyopneumoniae

Introduction

Vaccination with commercial vaccines against Mycoplasma hyopneumoniae (M. hyopneumoniae) reduces clinical symptoms, lung lesions and performance losses. However, vaccination neither prevents colonisation of the pathogen, nor the development of clinical signs and lung lesions. Also, the beneficial effects of vaccination vary between herds. New vaccine formulations that include novel strains of M. hyopneumoniae and innovative adjuvants designed to induce cellular immunity could improve vaccine efficacy against this pathogen.

The aim of this experimental study was to assess the efficacy of three experimental bacterin formulations based on M. hyopneumoniae field strain F7.2C which were able to induce cell-mediated immunity.

Materials and methods

The formulations included a cationic liposome formulation with the Mincle receptor ligand trehalose 6,6-dibehenate (Lipo_DDA:TDB), a squalene-in-water emulsion with Toll-like receptor (TLR) ligands targeting TLR1/2, TLR7/8 and TLR9 (SWE_TLR), and a poly(lactic-co-glycolic acid) microparticle formulation with the same TLR ligands (PLGA_TLR). The liposomal formulation was able to induce strong Th1 and CD8 T cell responses, while the oil-in-water formulation induced a strong Th1 response and a moderate CD8 T cell response. The microparticle formulation had the unique ability of inducing a potent Th17 response.

Four groups of 12 M. hyopneumoniae-free piglets were primo- (day (D) 0; 39 days of age) and booster vaccinated (D14) intramuscularly with either one of the three experimental bacterin formulations or phosphate buffered saline (PBS). The pigs were endotracheally inoculated with a highly and low virulent M. hyopneumoniae strain on D28 and D29, respectively, and euthanized on D56. The main efficacy parameters were: respiratory disease score (RDS; daily), macroscopic and microscopic lung lesion scores (D56) and log copies M. hyopneumoniae DNA determined with qPCR on bronchoalveolar lavage (BAL) fluid (D42, D56).

Results

All formulations were able to reduce clinical symptoms, lung lesions and the M. hyopneumoniae DNA load in the lung, with formulation SWE_TLR being consistently the most effective (RDSD28-D56 -61.9 %, macroscopic lung lesions -88.4 %, microscopic lung lesions -52.3% M. hyopneumoniae DNA load in BAL fluid (D42) -67.3 %).

Conclusions

The improvements obtained with formulation SWE_TLR seemed similar to or sometimes even better than the results obtained with commercial M. hyopneumoniae bacterins under experimental conditions Further research including more animals and raised under field conditions is needed to confirm the present results, and to assess the effects on the reduction of performance losses due to M. hyopneumoniae infections.

Presenter Name: Edison Magalhaes, *Iowa State University*
Title: Measuring the impact of sow farm risk factors on the wean-to-finisht mortality of pigs under field conditions.

Introduction

Sow farm productivity and health status greatly influence the downstream performance1, 2, 3. However, the knowledge concerning this association is originated from studies conducted in experimental environments, not accounting for multiple underlying risk factors occurring under field conditions. Therefore, the objective of this study was to measure the association between sow farm health and productivity on subsequent wean-to-finish (W2F) mortality of weaned cohorts until market.

Materials and Methods

This research describes the development of algorithms to integrate multiple data streams, including 1315 cohorts of pigs marketed from June 2018 to July 2019, which were combined into a single dataset, connecting the pig flow of the groups from breeding to market and accounting for single and multiple sources flows. The variables selected for representing the sow farm productivity parameters were total born, pre-weaning mortality, weaning age, and farrowing rate, which had their averages values estimated in quartiles. Furthermore, sow farm health status for porcine reproductive and respiratory syndrome (PRRS) and Mycoplasma hyopneumoniae (MHP), were classified as negative (absence of the pathogen), endemic (presence, with no clinical signs), and epidemic (clinical cases for the disease). Lastly, the W2F mortality of closeouts with any tissue submitted to veterinary diagnostic laboratory (VDL) for diagnosis (DxCode) was compared with groups without any submission (no DxCode). Thus, generalized linear mixed modeling (PROC GLIMMIX) measured the association between the aforementioned variables with the outcome (W2F mortality).

Results

The W2F mortality geometric mean of the 1315 closeouts was 8.76%. For sow farm productivity parameters, the average productivity for each quartiles and their respective W2F mortality of the downstream cohorts were: (a) the total born quartiles were 14.3, 14.8, 15.1, and 15.6, with the respective W2F mortality of 10.2%a, 8.8%b, 8.3%bc, and 7.8%c;
(b) the pre-weaning mortality quartiles were 10.9%, 13.0%, 14.6%, and 18.2%, with the respective W2F mortality of 8.0%a, 8.1%a, 8.6%a, and 10.3%b;
(c) the weaning age quartiles were 15.3, 16.7, 17.9, 20.3, with the respective W2F mortality of 9.8%a, 8.7%b, 8.1% b, 8.2% b;
(d) the farrowing rate quartiles were 78.4%, 84.3%, 86.7%, and 89.5%, with a W2F mortality of 10.2%a, 8.4%bc, 8.8%b, 7.9%c;
(e) the mean W2F mortality of the closeouts originated from sow farm classified as PRRS negative, PRRS endemic, and PRRS epidemic was 7.6%a, 8.5%b, and 12.3c, respectively;
(f) the mean W2F mortality of the closeouts originated from sow farm classified as MHP negative, MHP endemic, and MHP epidemic was 8.0%a, 8.9%b, and 9.9%b, respectively;
(g) the W2F mortality difference between “DxCode” closeouts compared to “no DXcode” closeouts was 2.22% (10.4%a vs. 8.0%b).

Conclusions and Discussion

This study demonstrated the importance of integrating sow farm data with growing phase information. Overall, the better the sow farm productivity and health status, the lower it was the subsequent W2F mortality. Cohorts with tissue submitted to the VDL were associated with higher W2F mortality. This study revealed a strong association between BTW productivity performance and health status on the subsequent wean-to-finish mortality, demonstrating the significant role that the pre-weaning phase plays in subsequent W2F performance.

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Presenter Name: Victor Martinez Torres, *Schwartz Farms*
Title: Experiences and tips for successful on-boarding programs

Labor shortage has been a challenge for the pork industry in the recent years, companies struggle to fully staff the farms and keep them that way. Modern swine operations require talented employees capable to continuous learning and to acquire new skills day by day if we want to be efficient in the highly competitive environment we operate. In the seek for the right people, we attract individuals with different background, culture, academic level, nationality, and language. Our mission in on-boarding is to make them feel welcomed, to integrate them to our culture and to help them build a career in the industry.

Before starting our on-boarding program we need to think about what do we expect from it and determine if we have the conditions to start and execute it the way we want and what adjustments we need to do.

It is important to review our hiring process, it is common that farm managers (FM) conduct the interviews and communicate to human resources (HR) the decision of hiring an applicant. Including more persons interacting with the candidate before hiring can improve the process.

Having a welcoming strategy is key for every on-boarding, we hire new employees because we need and want them to stay and first impressions are never forgotten. The welcoming strategy needs to be ready before employees get to the farm on their first day of the job.

Probably the oldest on-boarding practice is to assign an experienced employee as a mentor to the new employee, the FM usually chooses the mentor based on who is perceived as the best employee in the department. This option may seem practical but can lead to variations on how the employees are trained. If we choose this on-boarding, we will need one mentor per department in every farm and a training program for them.

An excellent on-boarding option is to have a school farm to on-board new employees in groups. This option requires all new employees in a group start on the same day. This type of on-boarding requires an on-boarding trainer who will ensure the welcoming experience and that the same message is delivered to all the new hires.

If a school farm is not an option, it is possible to have a “traveling” on-boarding specialist. In this case the on-boarding trainer works with new hires at their home farms. In this option it is important to guarantee the training begins on the employee’s first day. The training is enhanced by the one-on-one characteristic of this type of program. This on-boarding offers a special opportunity for the company and the on-boarder: when the right person is hired as trainer, going from one farm to another and being involved in the daily task execution while training allows to detect production improvement opportunities and to give feed back to the FM and supervisors, taking the on-boarder position to more complete functions.

In all cases it is important to have an evaluation-retrain system in place for new hires and continuous training for all employees with a process evaluation and improvement plan.

Presenter Name: Ted Mattthews, *State of Minnesota*
Title: Addressing communication between all players including veterinarians, farm managers and farmers

Addressing communication between all players including veterinarians, farm managers and farmers

Presenter Name: Noelle Noyes, *University of Minnesota*
Title: Fecal microbiome-resistome dynamics of PRRSV-challenged pigs under varying antimicrobial drug exposures'

The association between antimicrobial use and antimicrobial resistance (AMR) is complex, and often impacted by animal health status and herd management factors. The goal of this project was to compare the AMR profiles of growing pigs from wean to market, as they experienced differing health challenges and differing antibiotic exposures. To accomplish this, we randomly allocated weaned piglets to three different treatment groups. Two groups of 36 pigs each were challenged with PRRSV, while a third group of 36 pigs remained unexposed. The challenged pigs were then administered either an "intensive" or a "moderate" antibiotic treatment protocol. The pigs were grown to market weight and then sent to slaughter. Composite fecal samples were collected before weaning and transport; after transport but before vaccination; after vaccination but before PRRSV challenge; after PRRSV challenge but before antibiotic exposures; after antibiotic exposures; and just prior to market. Samples were subjected to total DNA extraction and metagenomic sequencing. Using these data, we identified and counted AMR genes in each sample (N=216), and compared the AMR profile (the "resistome") over time and between treatment groups. Findings indicate that weaning, transport and commingling corresponded to a large shift in the resistome, whereas shifts during PRRSV challenge and subsequent antibiotic exposures were much less pronounced. However, treatment group was a significant source of resistome variation before and during PRRSV challenge and antibiotic exposures, while it did not significantly explain resistome variation at other time points. These findings point to the microbial complexity of AMR, and suggest that antimicrobial use is not the only factor that can drive AMR within hosts. These results also demonstrate the dynamic nature of microbial populations within growing pigs, which may represent an opportunity for both AMR mitigation and promotion of pig health and performance.

Presenter Name: Monique Pairis-Garcia, *North Carolina State University*
Title: Alternative euthanasia techniques for mature sows and boars

Euthanasia is a necessary act for any operation keeping live animals. According to the AVMA Guidelines for Euthanasia (2020), a euthanasia method is appropriate if it safeguards human safety, causes minimal pain and distress, and results in a rapid loss of consciousness and death. Literature validating euthanasia methods and individual pig welfare for immature pigs is well defined. However, there are a limited number of validated euthanasia methods that are safe and reliable that can be implemented in challenging farm settings for mature swine. Therefore, the objective of the present study was to validate the effectiveness of three alternative euthanasia techniques on mature sows and boars.

Euthanasia equipment utilized for this study included:

1) Extra-heavy duty inline, 6 grain captive bolt gun (IL)

2) Extra heavy duty pistol grip, 4 grain captive bolt gun (PG)

3) TBG 96/N electric mobile stunning (ST).

For the captive bolt equipment, three head positions were used and included:

1) Frontal position (bolt placed 2.54 cm superior to top of the eyes at midline; F)

2) Temporal position (bolt placed 3 cm posterior to the lateral canthus of eye; T)

3) Behind the Ear (bolt placed caudal to the pinna of the right ear; B)

The study was conducted over two stages. Stage one enrolled 42 animals (n= 21 sows; n= 21 boars; weight: 292 ± 56kg). Enrolled animals were anesthetized and treatment was administered once a deep plane of anesthesia was reached. Treatment was deemed successful and carried over to Stage 2 if >95% of all animals were rendered unconscious and achieved cardiac arrest by 10 minutes. Stage two enrolled 56 mature sows and boars (n= 35 sows; n=21 boars; weight: 272 ± 43kg). All animals were humanely restrained with a pig snare and treatment was applied.

For stage 1, ST, IL-F and IL-B treatment was 100% effective. IL-F was 100% effective for females but only 33.3% effective for males. The following treatments were carried on to stage 2: ST, IL-F, IL-B, IL-T (female only), PG-B (female only). In stage 2, all treatments were 100% effective. Of the 56 animals anesthetized, six required a second shot due to inaccurate placement of tool (3 stun, 1 IL-B, 1 IL-T, 1 PG-B). This small sample size provides descriptive outcomes for successful alternative euthanasia options for mature sows and boars. Future work is needed to confirm the effectiveness of these tools on a larger population.

Presenter Name: Nakarin Pamornchainavakul, *College of Veterinary Medicine, University of Minnesota*
Title: Estimating farm-level reproduction numbers for PRRSV using sequence-based transmission tree analysis

Introduction

The reproduction number (R) is a fundamental value characterizing a pathogen's ability to spread within populations and is defined as the number of individuals that are infected by a single case. Many disease monitoring programs, however, archive data at the farm-level rather than individual-level, and management interventions are often implemented at the farm level. This creates the need to evaluate a pathogen's transmissibility at the farm-level to better trace disease spread and evaluate the success of control measures. Using transmission tree analysis, we quantify the farm-level R of porcine reproductive and respiratory syndrome (PRRS), which is more compatible with the scale at which disease dynamics are analyzed.

Methods

Utilizing 943 sequences from 651 farms in a single geographic region, we identified three clades of closely related sequences (mean 98.4% nucleotide identity based on ORF5) that were collected from 151 farms between 2014 and 2017. We constructed time-scaled phylogenies for these three clades, all of which belonged to sub-lineage L1A (consisting primarily of RFLP-type 1-7-4). Using the resulting trees, average generation time, and Bayesian inference, transmission networks were built to infer pig-to-pig infection chains, including inference on the number of unsampled individuals within the chain. Farm-level transmission events were inferred for any pair of sequences for which the infection chain transitioned between farms. We then summarized infection chain length according to movement pathlength (how many steps apart farms were in the animal movement network). The median length of infection chains for farms directly connected by movements was then used as a threshold for defining direct farm-to-farm transmission. The number of inferred direct transmission events originating from each source farm was used to calculate farm-level R.

Results

Infection chain length was significantly correlated with movement network pathlength ($rho=0.53$, $p< 0.05$). For farms directly connected by movements, the median infection chain lengths for direct farm-to-farm transmission were 28, 35, and 46 pig-to-pig transmission events for each clade, respectively. Overall farm-level R had a median of 1 and a maximum of 5 (IQR = 1-2). Most of the inferred transmission events (155 out of 174) could not be attributed to direct animal movement, while 3% and 15% of events might occurred via semen and local area spreading, respectively.

Discussion

For these PRRSV variants, a farm is expected to infect a median of one other farm and animal movement was responsible for only 10% of total transmission events. This approach provides supportive information for epidemiologic assessments and a clearer depiction of transmission risk than solely interpreting evolutionary history or animal movement data.

Presenter Name: Jason Ross, *Iowa State University*
Title: An integrated approach to improve whole herd pig survivability

Improving pig survivability rates is a critical component of enabling the U.S. swine industry to meet the growing global demand for animal protein. Faculty and staff programs at Iowa State University, Kansas State University and Purdue University have collaborated with funding agencies, pork producers and allied industry partners to pursue specific objectives focused on improving whole herd survivability in the US swine industry. Overarching objectives of this effort include: 1) Evaluation of the management attitudes and economics associated with improving survivability in U.S. swine production, 2) Identification of putative mortality causes on U.S. sow farms with the development and implementation of targeted strategies to maximize survivability, 3) Reducing wean to finish mortality through the implementation of management strategies founded upon ongoing production research, 4) Developing a nationally effective and sustainable extension, outreach and education resources and strategies to enable adoption and implementation of strategies that will reduce mortality in pork production. These objectives represent an aggressive approach in research, education, extension and human capital development and training and are supported by the Foundation for Food and Agriculture Research and National Pork Board in addition to a vast network of industry collaborators.

Presenter Name: Chelsea Ruston, DVM, *Iowa State University's Veterinary Diagnostic and Production Animal Medicine Department/Swine Medicine Education Center*
Title: Relying on UVC germicidal chambers to safely introduce materials into farms: what you need to know

The disinfecting properties of short-wave ultraviolet-C light (UVC), with wavelengths from 200 to 280nm, are well known and documented (Tseng et al., 2007). UVC's mechanism of action by forming thymine, cytosine, or uracil dimers in DNA or RNA, leading to mutations in the strands and disabling the viruses' ability to replicate (Kowalski, 2009). There are many factors to consider that can affect the efficacy of UVC light, including irradiance, time, distance, microbial susceptibility, humidity, temperature, organic load, surface reflectiveness, surface type (permeable vs. non-permeable surfaces), UVC bulb lifespan, and maintenance.

In the literature, the term irradiance is often used. Irradiance is the UV arriving at a particular surface based on a specified area. As distance increases from the UV source, irradiance decreases. UV Dose is what inactivates the pathogen, and it is a product of irradiance measured in mW/cm2 and exposure time measured in seconds.

Within the past several years, UVC technology has been used increasingly more in the swine industry. However, there is a lack of research available on its efficacy under conditions typically found on swine farms. A study conducted at Iowa State University was done Evaluating the efficacy of UVC for inactivating Senecavirus A (SVA) on three different contaminated surfaces (cardboard, plastic, and cloth) commonly found in swine farms under challenged conditions (top vs. bottom inoculation and in the presence of feces or not). Two UVC devices were used: a commercially available pass-through chamber (PTC) and a simulated supply entry room (SER). The study found that there were no significant statistical differences between the top and bottom inoculated surfaces treated with UVC. Plastic with no feces present was the only group that had over a six log reduction of SVA after UVC treatment in both the SER and PTC. UVC was not efficacious on cloth or cardboard or in the presence of feces on any of the materials studied. This study suggests the need to better understand if current disinfection protocols of materials such as cardboard are effective at the decontamination of these materials.

The on-farm application of UVC is practical for items that cannot be chemically disinfected, such as cell phones, and for small items that would be passed through a UVC chamber that have non-permeable surfaces, such as eyeglasses, cell phones, and plastic bags. It may not be practical in a supply entry room where there are variations in materials that are brought in.

Understanding the limitations of UVC is important when practically applying it on-farm. UVC chambers are not devices that you can purchase and expect to work for years without proper maintenance. Changing and cleaning the bulbs regularly is very important to ensure the device is disinfecting appropriately. Human safety should also be a priority when operating these chambers to reduce the risk of skin burns or eye damage. Overall, UVC can be a useful disinfectant tool to utilize on-farm for surfaces that have no organic material present and have smooth, non-permeable surfaces.

Presenter Name: Joaquim Segalés, *IRTA-CReSA and UAB*
Title: Are pigs susceptible to SARS-CoV-2?

The coronavirus disease 2019 (COVID-19) is an infectious disease that has caused a global pandemic with more than 24 million infected people from around 200 countries or territories, with more than 826,000 deaths to date (World Health Organization, 2020). The causative agent of COVID-19, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is assumed to be originated in bats, but it is believed that the jump from bats to humans included an intermediate host. To date, several animal species have been studied to determine their potential role as intermediate hosts as well as animal models for COVID-19.

The objective of this presentation is to compile existing information regarding susceptibility of pigs to the novel coronavirus. The main rational to test pigs is that the ACE2 receptor of this species is functional either by transfecting swine ACE2 in HeLa cells (which do not express constitutively the human ACE2) or that pseudoparticles with the S protein of SARS-CoV-2 are able to infect swine kidney cells. Furthermore, the ACE2 protein is expressed in all major tissues of pigs as assessed by immunohistochemistry.

To ascertain the susceptibility of pigs to SARS-CoV-2 and set up a putative COVID-19 pig model, the effect of different natural and non-natural routes of SARS-CoV-2 inoculation in domestic pigs (Sus scrofa domesticus) have been investigated in at least five independent experiments. All of them concluded that pig is not susceptible to the novel coronavirus, yielding no evidence of replication and seroconversion when the virus was inoculated through respiratory/oral routes (intranasal, intratracheal and/or per os). However, in two of these studies, non-respiratory inoculation routes were used (intravenous in both trials and intramuscular in one of them) and some of the animals seroconverted against SARS-CoV-2 in apparent absence of replication. It was considered that the parenteral inoculation routes probably exerted a systemic immune response against different epitopes of the virus in absence of infectivity.

In conclusion, the so far performed experimental studies confirm that pigs are not susceptible to the novel virus and, consequently, not a suitable animal model for COVID-19. However, the pig may have a potential usefulness as a model for immunogenicity in preclinical vaccine development studies. The lack of susceptibility of swine to SARS-CoV-2 is an excellent news for the swine industry, since it rules out the potential role of the pig as animal reservoir for the virus or playing a role in the epidemiology of the disease. In spite of such scenario, COVID-19 has had marked effects on the swine industry due to the restrictions caused by lockdowns in most of countries worldwide and the transmission of the virus among workers in farms and meat processing plants.

Presenter Name: Matthew Sturos, *University of Minnesota - Veterinary Diagnostic Laboratory*
Title: FASTA File Manipulation and Interpretation Workshop

Would you like to learn more about genetic sequences or review some of the fundamental methods and tools for genetic sequence analysis? This presentation will provide a mix of lecture-based review of genetic sequencing and analysis as well as opportunities for hands-on sequence file manipulation and interpretation, assisted through step-by-step instructions, demonstration of computer-based and web-based tools, and interactive dialogue. In order to participate in the hands-on portion of this workshop, participants will need to have downloaded and installed a genetics analysis software on their own computers prior to the workshop. Example genetic sequence files will be provided. Contact Dr. Matt Sturos (sturo004@umn.edu) to receive the example sequence files or if you have any questions about software prior to the workshop.

Presenter Name: Matthew Sturos, *University of Minnesota - Veterinary Diagnostic Laboratory*
Title: "Saying hello to our little friend": Streptococcus suis diagnostics

Have your farms been affected by pathogenic Streptococcus suis infections, or do you think that you may be impacted in the future? This presentation will help you to understand some of the basics about S. suis, as well as delve into the advanced diagnostic testing that is currently available. Topics covered will include diagnosing S. suis-associated disease, virulence-associated factors for S. suis, methods of S. suis subtyping such as serotyping and sequence typing, and the use and interpretation of whole genome sequencing data. These topics and tools will help you to feel more comfortable requesting, interpreting and applying S. suis diagnostics to make management decisions on your farms.

Presenter Name: Michael Sweeney, *Zoetis*
Title: Antimicrobial susceptibility of Actinobacillus pleuropneumoniae, Pasteurella multocida, Streptococcus suis, and Bordetella bronchiseptica isolated from pigs in the United States and Canada, 2016 to 2019

Introduction
Antimicrobial surveillance among veterinary bacterial pathogens obtained from clinical specimens provides a platform from which to detect emergence of resistance in animal populations. While veterinary diagnostic laboratories throughout North America provide important antimicrobial susceptibility information for clinical isolates submitted by the attending veterinarian or animal caretaker, the susceptibility results are not typically examined or summarized nationally or regionally. Zoetis has an ongoing swine respiratory disease (SRD) surveillance program in place that first started in 1998. The objective of this study is to report the susceptibility to veterinary antimicrobial agents of Actinobacillus pleuropneumoniae, Pasteurella multocida, Streptococcus suis, and Bordetella bronchiseptica isolated from pigs in the United States and Canada from 2016 to 2019.

Methods
In vitro broth microdilution susceptibility testing for minimal inhibitory concentration values were performed using 10 antimicrobial agents (ampicillin, ceftiofur, danofloxacin, enrofloxacin, florfenicol, penicillin, tetracycline, tilmicosin, trimethoprim-sulfamethoxazole, and tulathromycin) with A. pleuropneumoniae (n = 208), P. multocida (n = 729), S. suis (n = 988), and B. bronchiseptica (n = 499) following methods and susceptibility breakpoints approved by the Clinical and Laboratory Standards Institute.

Results
From 2016 to 2019 A. pleuropneumoniae isolates were 100% susceptible to ceftiofur, florfenicol and tulathromycin while enrofloxacin susceptibility ranged from 82.4-100%, ampicillin ranged from 83-100%, tilmicosin ranged from 96.8-100%, and tetracycline from 0-10.6%. P. multocida isolates were 100% susceptible to ceftiofur while enrofloxacin ranged from 99.3-100%, penicillin from 97.7-100%, ampicillin from 98.3-100%, florfenicol from 98.8-100%, tilmicosin from 97.7-100%, tulathromycin from 99.5-100%, and tetracycline from 23.3-36.1%. S. suis showed high rates of susceptibility with ceftiofur ranging from 91.1-97.9%, enrofloxacin from 89.4-94.1%, penicillin from 79-81.7%, ampicillin from 98.7-99.2%, florfenicol from 96.4-97.8%, and tetracycline from 0.8-1.7%. B. bronchiseptica isolates were 100% susceptible to tulathromycin while florfenicol ranged from 3.6-9.4% and ampicillin showed no susceptibility (100% resistance).

Conclusions
Key antimicrobial agents approved for the treatment of SRD in the United States and Canada show high rates of susceptibility for A. pleuropneumoniae, P. multocida, S. suis, and B. bronchiseptica. Under the conditions of this study, the lowest rates of susceptibility are seen with tetracycline against A. pleuropneumoniae, P. multocida, and S. suis, and with ampicillin and florfenicol against B. bronchiseptica. Additionally, the rates of susceptibility determined in 2016-2019 are similar to what has been observed over the past 21 years of the Zoetis surveillance program. Continuous monitoring of antimicrobial susceptibility among swine pathogens provides up-to-date information about susceptibility trends for commonly used antimicrobial agents and is an important component of responsible use and antimicrobial stewardship.

Presenter Name: Joseph Thomas, *Iowa State University*
Title: My Experience Managing Health and Production in Batch Farrowing Farms

A continuum of production schemes exists in modern sow farms ranging from "continuous flow" production to "4-5 batch" production. This presentation focuses on "5-4" batch production. Specifically, it discusses space considerations, target setting, scheduling/event chain methodology, and logistics in this production scheme.

Presenter Name: Mickie Trudeau, *University of Minnesota*
Title: Methodologies for in-farm evaluation of alternatives to antibiotics

There is evidence that modifications to gut microbiota improves health and productivity of pigs. However, the responses to feed additives on a commercial farm level do not always reflect the response observed on a controlled research farm. The reasons for discrepancy are numerous and point to differences in experimental settings and the incipient state of microbiome research. There is a gap in methodologies between development and application of feed additives in that development of products do not measure the variables that are measured in commercial settings. Likewise, lack of knowledge on the mechanism of action of many potential interventions lead to unknown diet, environment, and pathogen interactions in which products are tested under the biased conditions. For this reason, on farm research is an essential component to further validate the effectiveness of an additive or mechanism of action in a commercial setting. Randomized controlled trials reduce biases when testing the effectiveness of new feed additives. An important component of the process is to identify the unit upon which the treatment is applied (experimental unit) and the unit upon which the effect is measured (measurement unit). It is common to assume that the pen is the experimental unit of a feeding trial. However, our recent research evaluations suggest that the effect of experiment location has greater impact on growth of pigs than the effect of some dietary treatments. These findings suggest that interventions will need to be tested in various groups of pigs using different barns. When conducting this research, cost and facility limitations make it difficult to conduct numerous empirical randomized controlled trials or extensive sample collection to study every new intervention, doses, and interactions. In addition, the goals of industry partners are often financially based and driven by high return on investment in research. Therefore, a logical process should be implemented that funnels information and helps to establish priorities of candidate tests from literature review, in vitro tests, to randomized control trials. Unfortunately, the mode of action for many potential feed additives is poorly understood, especially on a commercial farm setting. For this reason, more advanced analysis including metabolomics and microbiome analysis should be utilized in on-farm research. Fecal samples and serum samples are excellent sample types that do not require special facilities or equipment to collect. Collecting these samples and submitting them for metabolomics or microbiome analysis can produce an abundance of information on how a feed additive is impacting the animal's microbiome, antioxidant status, nutrient status, and general health. This information can even be used to develop a mechanism of action or develop new, novel feed additives. Overall, on-farm trials and in-depth microbiome analyses are economically driven and limited in resources, but with careful considerations in the experimental design, experimental unit, and appropriate technologies, it will be possible to make necessary modifications to gut microbiota to enhance health and productivity of pigs without use of antibiotics.

Presenter Name: Kimberly VanderWaal, *University of Minnesota*
Title: Modeling transmission of SARS-CoV-2 in pork processing plants

Pork processing plants have been hotspots for SARS-Cov2. As a result, the swine industry is facing a major financial and animal welfare crisis due to stalled and backlogged production chains. The objective of this work is to describe the epidemiological situation within processing plants, develop mathematical models to simulate transmission in these plants, and test the effectiveness of worker screening/testing protocols at minimizing SARS-CoV2 circulation. Through collaboration with a prominent multi-company taskforce, we first characterize the epidemic curves and summarize testing data from multiple processing plants. Second, we developed a mathematical model that accounts for asymptomatic, pre-symptomatic, and background "community" transmission. By calibrating this model such that simulated outbreaks resembled the observed epidemiological data, we were able to estimate the initial reproduction number (R) of the virus. Across plants, R generally ranged between 2 and 4 during the initial phase, but subsequently declined to <1 after three weeks, most likely as a result of implementation and compliance with biosecurity measures. Using the calibrated model, we then performed a series of simulations to compare the success of different testing/screening protocols at minimizing SARS-CoV2 circulation. For plants that are in a post-outbreak stage where population immunity is predicted to be high (>60%), the low proportion of susceptible workers means that company-wide PCR screening only reduced the cumulative number of clinical cases by <2%. However, the importance of testing is more profound for workforces using PCR-screening of all employees as a preventive measure or during the early or peak phase of an outbreak, where the use of frequent testing (every 7 days) could reduce clinical cases by 5-10% compared to symptom screening alone, depending on assumptions about the transmissibility of the virus. Even with PCR-screening every three days, >25% of the worker population are predicted to experience clinical disease if community transmission is assumed to be high. While these results are preliminary, this research helps to identify protocols that minimize risk to occupational safety and health and support continuity of business for U.S. processing plants.

Presenter Name: Kimberly VanderWaal, *University of Minnesota*
Title: Machine learning as a tool for animal health and productivity

In the new era of so-called "big data," challenges in veterinary medicine are shifting towards how to translate increasingly abundant and complex data into meaningful insights about animal health and productivity, ultimately allowing for data driven decision-making. The use of big data analytical techniques, such as machine learning, for animal health is a rapidly growing field. The development and refinement of machine learning approaches in veterinary medicine can maximize the utility of data to generate novel insights and significantly improve our ability to identify and respond to evolving animal health concerns. Here, our objective is to provide a broad overview of machine learning concepts and review current trends in their use as tools to improve animal health and productivity. We also highlight examples of the application of machine learning in veterinary epidemiology to predict the risk of PEDV outbreaks in sow farms and in applied virology to improve classification systems for PRRSV sequences.

Presenter Name: Fabio Vannucci, *University of Minnesota*
Title: In situ hybridization (ISH) as a diagnostic and research tool

The U.S. swine industry has evolved over the years from small independent farming operations to integrated large system. Along with this process, the production systems have faced emerging health challenges, particularly regarding virus diseases. In addition, virus-associated syndromes and disease complexes (e.i. porcine respiratory disease) have become more common due to the involvement of multiple pathogens or virus subtypes in the same tissue. While PCR is a highly sensitive tool to detect viral nucleic acid, its interpretation may become uncertain when multiples pathogens or virus subtypes are detected in the same animal. Therefore, the demonstration of antigens within the lesions is critical to determine the actual contribution of a specific pathogen in a disease process. Immunohistochemistry (IHC) is currently the most commonly used method to detect virus protein in infected tissues. However, the availability of specific antibodies is limited, especially for virus subtypes. IHC also requires the development of primary antibodies against a specific pathogen; therefore, it would not be applicable as a rapid diagnostic response to a potential emerging pathogen. For this scenario, PCR-based techniques have been successfully applied due to the quick process for designing RNA or DNA probe. But caution still has to be taken not to automatically interpret virus detection as the cause of disease. In situ hybridization (ISH) is nucleic acid-based method that allows the detection of a particular RNA or DNA sequence within the tissue sections. Using a probe design process similar to the PCR, this technique is able to specifically identify and differentiate virus subtypes within the lesions. Additionally, ISH can be valuable as a rapid diagnostic response, since it does not require the development of specific antibodies. Recently, a novel ISH-RNA platform was validated for detection of emerging swine pathogens and it has been used to study the pathogenesis of endemic viruses and bacteria infections pigs.

Presenter Name: Zhichun Yan, *New Hope Liuhe Co.*
Title: Controlling and Eliminating African Swine Fever Virus from Swine Herd by qPCR-based Test-Removal through Organized Sampling

Introduction
After the first case of African Swine Fever (ASF) outbreak was reported in August 2018, pork producers in China had to cull and destroy many pig herds for following `conventional, standard` ASF control protocols. Mortality of pigs infected by ASFV strain in China, Georgia 2007/1, was reportedly as high as 100%. Production losses was catastrophic during the first six months because entire pig herd on an infected farm and other pigs within three-kilometer radium of the farm had to be completely destroyed if ASFV positive animals were diagnosed on the farm. All large producers had gone into panic at the early stage of ASF pandemic across the industry.

Material and Methods
Attempt to prevent and cease within herd transmission by partially depopulate the animals only based on suspectable clinical signs of ASF in several pig herds was not successful. However, we found that the removal of those animals did slow down the pace of occurrence of animals with the clinical signs. With the early successes, we developed a series of sampling protocol to sample breeding females in crates and pigs in pens, which had been proved effective for diagnostic surveillance. Quantitative Real-time PCR generating numerical Ct values improved the accuracy to precisely determine the number of animals to be removed from a herd when having sporadic infected pigs.

To avoid cross contamination during washing and disinfecting, we gridded entire floor space of a barn into individual cells to ensure surface swap and test were paired before and after disinfection. Each and every animal in the herd or a group of animals where positive were detected as well as all the floor surface cells were sampled by modified swaps for qPCR test by pooling samples based on the Ct values from positive animals. The protocol is known now as `thorough test, precise removal` in contrast to only removing positives with clinical signs that had been proven unsuccessful.

It is crucial to conduct a thorough sampling and testing within a short period of time, normally within one day for any size of herd when positives have been detected. Removal of positive animals and assumingly contacted animals should be based on the Ct values determined from those positive animals – lower Ct indicating the need to remove more animals around infected pigs and any contacted ones as quickly as possible to minimize further transmission. Affected floor `cells` should also be complete swap sampled to avoid contamination although very limited floor contamination had been found in ASFV cases.

Results and Conclusion
`Thorough test and precise removal` had been proven feasible and extremely effective to quickly stop the transmissions within a herd when ASFV DNA were detected from a few of animals by qPCR. Recent practices in China suggested that producers were able to save overwhelm majority of animals if they had conducted thorough sample and test timely and remove all individual infected pigs in a shortest time. A second round of `thorough test` after seven days of the first test is normally required to confirm the ASFV negative status of the herd, otherwise precision removal process should be repeated when positives detected during the second test.

Destroying the entire herd after ASFV detection from some animals is obviously not necessary or applicable with recent development of qPCR and sampling technology. Successes in prevention and control of ASF in Chinese swine industry has been driving significant improvement in facility planning, biosecurity design, pig flow remodeling, as well as a dramatic expansion.

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