# SWINE HEALTH INFORMATION CENTER FINAL RESEARCH GRANT REPORT Developing the Swine Health Monitoring Project (SHMP) to build capacity and enable the Swine Health Information Center - SHIC #20-172 Cesar A Corzo (PI) University of Minnesota Year 6 - Final Report February 11, 2022

# **Industry/Research Summary:**

*Objective 1: Monitor trends in pathogens incidence and prevalence* – PRRSv, PEDv, PDCoV, Senecavirus and central nervous system associated viruses continue to be monitored. The 2020-2021 season fortunately ended with the fourth lowest PRRSv breeding herd cumulative incidence (25.8%) during the last 11 years of monitoring. During this year we continued to monitor the emergence and dissemination of a new PRRS variant that caused production losses in the Midwest and changed the seasonality pattern historically observed with PRRS with several associated outbreaks occurring during spring 2020. PEDv continued to be present at a low incidence level as the cumulative incidence remained at 3.5%. Our exploratory data analysis showed that reporting PRRS outbreaks and manure pumping activities are associated as 40% of the breaks occurred within 30 days of this event regardless of type of manure storage.

Objective 2: To conduct prospective monitoring of PRRSv sequence evolution and impact – Throughout the year, we provided outbreak investigation support by comparing sequences to the MSHMP database in nine separate occasions requested by six participants. This allowed us to become a neutral third-party putting systems in contact whenever both parties agree. We also continued to monitor the newly emerged PRRSv variant (L1C144) and offer support to participants and to the industry in understanding the epidemiology of this new variant.

*Objective 3: Develop capacity to capture and analyze movement data* – Transport data is acquired actively and has been analyzed. Movement data can be obtained at a granular level allowing for traceability but most importantly, allows the producer to follow the truck in realtime. Transport biosecurity compliance continues to become an achievable goal including every single step between the truck-wash, loading of pigs, unloading and return to truck-wash. Characterization and description of transport data has shown that few transport vehicles come in contact with 1/3 of the farms of the participating production system indicating an important level of connectivity. Furthermore, transport characterization highlighted the need to monitor vehicle biosecurity protocols towards disease control. Truck traceability (e.g. contact tracing) is possible with the current system which aids in complementing outbreak investigations.

Objective 4: To expand participation of producers to allow for all to be involved – Expansion continues at three levels: sow, boar and growing pig populations. An approximate total of 42 boar studs from 13 participants have been added to our database. The growing pig population continues to grow with 7 companies sharing their growing pig locations. Work is being done towards linking sow and growing pig populations in our database.

### Keywords: Monitoring, Emerging, PRRS, PEDv, Trends

# **Objective 1**

To monitor trends in pathogen incidence and prevalence

- Capacity development to expand capability of SHMP to capture diagnostic data from producers.
- Value for producers to increase representativeness of current reporting trends.
  - 1. Monitoring current pathogen occurrence.
  - 2. Conduct an exploratory analysis to determine whether PRRS outbreaks are related to manure pumping.
  - 3. Include the *Mycoplasma hyopneumoniae* status of SHMP participating sow herds onto our database and estimate breeding herd occurrence and prevalence.

Data provided by participants continues to be translated into trends that are used by the industry as the weekly benchmarking tool.

# PRRS incidence

• The 2020-2021 PRRS season was quite similar when compared with the previous year from a cumulative incidence standpoint as it remained between the lowest at 25.8% by the end of the period. However, this season started with a high EWMA mainly due to continued transmission of the newly emerged L1C144 PRRSv variant since the spring of 2020. The observed increase surpassed the epidemic threshold in May (Figure 1, red arrow), an unprecedented period of higher PRRSv transmission reminding the industry that the virus is equipped with the necessary tools to be transmissible during the warm months.



• Results on the exploratory analysis related to PRRSV outbreaks in breeding herds and its relationship to manure pumping activities continued. A year's worth of PRRSV outbreak data were included in this exploratory analysis. A total of 216 outbreaks were reported during the year, most of these occurring during the fall/winter as expected. Out of the 216 outbreaks that occurred during the MSHMP year, data related to manure pumping activities



was successfully obtained for 69% (149) of the cases from different participants across the nation. Most of the manure pumping events occurred during the months of October, November and April. Out of all the outbreaks in which manure pumping dates were obtained, 25% and 40% of the outbreaks occurred in the first 15- or 30-days post pumping, respectively (Figure 2). This relationship was identified in all seasons except during the winter. When manure storage type (deep pit vs lagoon) was assessed, the incidence rate ratio was similar for both types indicating no difference between manure storage types. These encouraging results motivate the team to continue investigating the potential mechanisms that may be related in the occurrence of this event.

Figure 2. Number of PRRSV outbreaks (OB) in breeding herds according to the days before or after (red line) manure pumping.



• Work has been conducted on creating real-time PRRSv/PEDv outbreak heat maps. The main objective of this effort is to work towards an early warning mechanism for our participants as they have expressed interest in knowing where within a specific state diseases are occurring. Given this interest and their willingness to authorize SHMP to share these maps with participants, we decided to develop the mechanism to create these visuals. We currently have developed the algorithm to create a "static" map but also a short mp4 video clip that will inform participants of current and past breaks (Figure 3). We still have to obtain whole participant approval to make this kind of information available on a regular basis and we plan to make this available through our future SHMP Hub site which will be password protected and only participants will be able to access it.

Figure 3. Example of a "real-time" PRRSv break heat map in the United States.



Active PRRS breaks in this MSHMP year as of 11/10/2020

### PRRS Prevalence

• The 2020-2021 PRRS prevalence continues to remain high as observed in the previous PRRS season with the peculiarity that the apparent cyclicity related to status 1 farms has been lost. We continue to believe that this event may be related to an increased usage of processing fluids as a monitoring tool which has led to improved virus detection and thus decreasing the number of herds being falsely classified as stable. Strain type and population persistence continues to be another potential explanation; however, this needs to be further investigated.





## PEDv incidence

- PEDv incidence during the 2020/2021 season showed no major changes compared to the previous year. Again, this data continues to demonstrate the commitment of the industry and maintains the national elimination conversation relevant.
- We characterized PEDV occurrence amongst SHMP participants in the post-epidemic period (July-2014 and June-2021) from a spatial-temporal perspective. We used data from 1100 breeding farms in 27 states stratified into six regions. A total of 625 PEDV outbreaks were recorded on 373 farms. The total number of farms breaking per year decreased from 95 farms in 32 counties in 11 states between July-2014 and June-2015 to 53 farms in 28 counties in 9 states between July-2020 and June-2021, indicating an overall decrease in occurrence and spatial extent of PEDV.

Outbreaks were seasonal, with most outbreaks occurring during winter (January -March – p = 0.001, relative risk =2.2). However, in some regions, seasonal clusters started in December. Ten spatial-temporal clusters of PEDV cases (p < 0.05), spanning 2.5 km<sup>2</sup> to 833.7 km<sup>2</sup> and 1-5 months, were recorded in four regions (Table 1). Eight of the clusters were observed between 2015 and 2019 in three regions and one in 2021 in one region. The number of companies that owned farms on these clusters varied; however, in the last couple of clusters, one or two companies were involved suggesting that spread may have been occurring within companies. The overall decline in PED cases over the years and the decrease in spatial extent likely reflects ongoing efforts employed by production systems to control and prevent PEDV during the post-epidemic period.

Region	Cluster	Time (month-year)	Area km2	Observed vs expected	# Systems Involved	Total systems in Region
Α	1	Dec-17 to Feb-18	250.8	5.2	3	14
В	1	Jan-16 to Apr-16	833.7	8	6	27
В	2	Dec-15 to Feb-16	205	7.2	7	27
С	1	Feb-21 to Mar-21	149.4	3.1	1	11
D	1	Feb-17 to Mar-17	56.8	19.3	1	7
E	1	Dec-16 to Jan-17	2.5	33.8	1	7
E	2	Jan-15 to Mar-15	30.5	11.7	2	7
E	3	Nov-15 to Dec-15	88.7	11.7	4	7
E	4	Nov-19 to May-20	13.2	10.5	2	7
E	5	Oct-16 to Feb-17	42	14.5	1	7

### Other diseases

 PDCoV continues to be present in the industry in the breeding herd population. Throughout the 2020-2021 season there were a total of 61 breaks reported from 10 systems, totaling approximately 230,239 sows affected. We also assessed PDCoV occurrence between 2015 and 2020 from a spatio-temporal standpoint. We utilized location and outbreak dates to describe and analyze the spatiotemporal trend of PDCoV from reports of more than 1300 farms from 38 systems. There was a total of 163 cases reported in 15 states, with the majority of them (70%) reported in the last couple of years (2019-2021), and over wintertime (93/163), when risk was 3.43 times higher (95%CI: 2.07 – 5.67) related to the lowest incidence season (summer).

A strong (p-value <0.01) spatio-temporal clustering was detected in the study area, with an increased risk (1.5 to 2.5 times) of disease at <5 km distances of farms infected within 35 days (Figure 5). When adjusting for the system, only one cluster (p<0.05) was observed between March and May 2020. Results obtained here highlight a steady increase in cases over the years. The areas and periods of disease aggregation suggest that local transmission from infected to susceptible neighboring farms is happening and likely serving as sources of virus maintaining the disease in the area. Additionally, we assessed whether there was a directionality pattern and after conducting the analysis we were able to determine that outbreaks occurred with a specific pattern. An angle of 105 degrees was determined suggesting that outbreaks were occurring from south-east to north-west or vice versa.

Figure 5. Spatiotemporal clustering within 2km and 7 days showed 2-2.5 more observed cases than expected (turquoise), and within 5km and 35 days indicated 1.5-2.5 observed expected ratio (turquoise and purple).



• *Mycoplasma hyopneumoniae* was successfully added to our database and the system is in place to continue to obtain breeding herd updates from participating companies. Coding was

developed to estimate and chart breeding herd cumulative incidence (Figure 6) and prevalence (Figure 7) and its weekly fluctuations as currently done with PRRS and PED.

Figure 6. SHMP Mycoplasma hyopneumoniae cumulative incidence.



#### Chart 1 - Mycoplasma cumulative incidence beginning July 01, 2009

Figure 7. SHMP Mycoplasma hyopneumoniae cumulative incidence.



### Value to Industry

During the 2020-2021 SHMP year we were able to deliver value to the industry through our weekly reports. Interestingly, our program continues to generate interest as we have had multiple

sources of feedback supporting our efforts but also recognizing SHIC's involvement in this project. Specifically, this year the project led from the beginning the characterization of an emergent strain of an already present pathogen in the industry. Through our processes we rapidly created the epidemiological curve quantifying the number of sequences and sites being affected by this strain. In addition, and as participants felt comfortable, we were able to recreate videos and maps summarizing the current situation. This event allowed us to test our system once again and make sure we can rapidly respond to an industry's emergency by providing quality and reliable data.

Another piece of information shared with the industry and thanks to the nature of the collaborative efforts of this group of producers and practitioners was the exploratory project around manure pumping and disease occurrence. The value brought focuses on the awareness that there seems to be a relationship between this event and PRRS outbreaks. Even though it has not been clarified and understood, it highlights the need to review the practice to make sure processes are being conducted as efficiently and effectively as planned.

Coronavirus research was another area in which through our project we delivered value. Through data analysis we were able to better understand the occurrence of both PEDv/PDCoV in the country. These analysis allowed us to understand that outbreaks tend to be clustered over time and space highlighting again the regional risk. Such information had not been generated before and continues to provide more arguments to an industry that may consider eliminating these viruses.

### **Objective 2- To conduct prospective monitoring of PRRSv sequence evolution and impact.**

- Capacity development to capture diagnostic data from cooperating diagnostic laboratories, production data from producers and develop analytic methods.
- Value for producers to give producers opportunity to respond to emerging highly virulent strains.
  - 1. Develop a prospective methodology to identify PRRSv clusters in time and space as a proxy for real-time warning for producers and practitioners.
  - 2. Conduct sequence analyses to understand PEDv diversity and strain occurrence (e.g. classic vs. INDEL) over-time.

We have been in constant communication with all 4 major veterinary diagnostic laboratories and have been able to understand PRRSv sequence formats from each one of them as this is a vital step for merging data. In addition, this has allowed us to establish a methodology which increases our PRRSv sequence update frequency, which is a step in the right direction to real-time monitoring. We were able to effectively implement automation for sharing sequences and data regarding PRRSv ORF5 sequencing from the UMN VDL. This means that MSHMP participant data is now available in real-time from the UMN VDL.

These frequent updates and virus classification into virus type, RFLP and lineages has opened a great opportunity for the program from an added value standpoint. Maintaining an updated database has allowed us to quickly respond to sequence comparisons requests from participants throughout the year during participants outbreak investigations. We have been involved in nine outbreak investigations from six large production systems throughout this SHMP year (Table 2).

These included remaining investigations associated with the newly emerged PRRSv L1C144 variant. Similar sequences include sequences from the same systems which are conducting the outbreak investigation, in which case we share all the details of the similar sequences including distance to farms. However, in cases where the sequence with the highest similarity includes another system, a distance (e.g. miles to the nearest farm with the highest similar sequence as a range) is provided to preserve anonymity. This not only allows us to give back to the participants, but also stimulates sharing of data, making our dataset more representative. As this process evolves, we have received requests to disclose the name of the participants' whose sequence has the highest similarity to have both parties visit about potential epidemiological links. We have helped get participants in contact after following a process in which anonymity is maintained until both parties agree to meet. No similar sequences were found in four cases, although for one of those the search was limited to 2018 onwards. These sequences are added to the dataset to allow for monitoring.

Data requested	Soguonco #	<pre># of sequences</pre>	<pre># of sequences</pre>	
Date requested	Sequence #	>98%	>99%	
8/25/2021	seq1	308	227	
	seq2	279	1	
	seq3	308	273	
	seq4	308	281	
9/14/2021	seq1	0	0	
10/19/2021	seq1	22	3	
10/25/2021	seq1	0	0	
11/3/2021	seq1	6	0	
11/10/2021	seq1	0	0	
12/2/2021	seq1	3	0	
12/6/2021	seq1	0	0	
12/22/2021	seq1	19	0	

Table 2. Summary of PRRSV sequence comparison requests from SHMP participants.

\* Sequence # – Identifies the number of sequences that were analyzed upon request. For instance, on 8/25/2021 the analysis of sequence #1 yielded 308 or 227 sequences with a similarity of 98% or 99% respectively. If there are more than 1 sequence it is because the participant requested the analysis of multiple sequences.

Two manuscripts were published with this data. The first one comprises a description of genetic diversity and wild-type and vaccine-like PRRSv-2 sequences occurrence. We found that the mean PRRSV ORF5 genetic distance was generally smaller in years in which there was a relative higher frequency of a dominant lineage, that vaccine-like sequences comprised about one fourth of all sequences, that 99% lineage 5 sequences were Ingelvac PRRS MLV-like, and that there was a reduction in the frequency of wild-type lineage 8 sequences from 2012 onwards (Figure 7). The full paper can be found at: <a href="https://doi.org/10.1371/journal.pone.0259531">https://doi.org/10.1371/journal.pone.0259531</a>

Figure 7. Yearly percent nucleotide differences between lineage 5 ORF5 sequences to Ingelvac PRRS MLV; lineage 8 sequences to either Ingelvac PRRS ATP or Fostera PRRS; and lineage 1 sequences to Prevacent PRRS.



Secondly, we have completed an initial assessment of the emergence of the L1C 144 variant that has heavily affected the Midwest and changed the seasonality pattern observed in our exponentially weighted moving average of PRRS incidence. We reported the epidemiological curve of cases of this variant with an unusually high occurrence during spring, that the Midwest continues to be the most heavily affected region, and that no particularly known risk factor for PRRS transmission was associated with the transmission of this variant in comparison to other contemporary variants. Most importantly, we were able to work with producers to make 17 reference ORF5 sequences publicly available to make case ascertainment accessible to anyone (available at GenBank (https://www.ncbi.nlm.nih.gov/genbank/), accession numbers MW525326-MW525341, MW525343). The full description of this investigation is available at https://www.frontiersin.org/articles/10.3389/fvets.2021.752938/full#h6. We continue to monitor this variant and are in close contact with participants to further describe these cases. We are also currently assessing potential methods to identify the emergence of new PRRS virus variants more easily.

Additionally, monitoring of "New" PRRSv sequences continues in North Carolina. The project contrasts sequence submission in the region with sequences detected in previous years in the region on an on-going basis. Since January 2017 we have detected to date 26 new sequences contained to one site and 21 new sequences circulating in a small cluster of sites. We continue to send a periodical report to veterinarians in North Carolina identifying farms with new PRRS strains and monitoring their spread. We plan to follow up with the participating systems to assess if, and to what extent, these monitoring reports have been utilized in their decision-making process.

PEDv has also been another area of focus during 2020-2021 as sequences have also been retrieved from the collaborating VDLs routinely. So far, sequences within this dataset have

originated from 12 states. Most of the sequences belong to the classical strain of the virus with a small proportion belonging to the INDEL strain which clearly highlights the fact that both strains continue to co-circulate (Figure 8). Given the questions from our stakeholders regarding which PEDv strain was the most frequently found, our results clearly show that there is a constant combination of both strains with the classic strain dominating. This finding is important as it clarifies that the INDEL strain, used for herd exposure, is not necessarily responsible for all the sow herd breaks.



Figure 8. PEDv dendogram including sequences according to time of detection from MSHMP participating systems.

### Value to the industry:

An important portion of our stakeholders have demonstrated throughout 2020-2021 that this information brings them value as the outbreak investigation sequence comparisons and estimating distance to highest similar sequence together with us facilitating vet-to-vet conversations. In addition, throughout 2020-2021, the PRRS L1C event led to multiple real-time comparisons and analysis that were connected with location data. If this database and codes had not been in place, sequence analysis would have been hindered and we would not have been able to share information with stakeholders. Along the same lines, monitoring of new strains continues, even though we can identify new strains, determining whether these will be responsible for the next PRRS event needs to be understood.

On the other hand, our analysis on PEDv sequences over time has generated interesting data in that we now have a better understanding on the frequency of the type of circulating strain in the U.S. pig population. Even though there is not a large dataset, it did allow us to characterize frequency of detection over time and confirm that both the classic and INDEL strains are

responsible for current outbreaks with the classic strain dominating. This finding contributes to clarifying whether those that are implementing a controlled exposure may not necessarily be adding complexity to the nature of the occurrence of this disease.

# **Objective 3- Develop capacity to capture and analyze movement data**

- Capacity development To develop capability to capture pig movement.
- Value for producers to supplement veterinarian's outbreak investigations and to provide and organize data that will be made available to applied research projects.
  - 1. Assess the use of the truck movement network currently being studied as an aid for PRRSv outbreak investigation on farms within a system.
  - 2. Define and quantify risky movements within the existent network as a proxy for compliance and risk.

We continued exploring movement patterns within a specific Midwestern system. We reassessed the data including the completeness for the year 2020. Four thousand six hundred and three edges (e.g. trips) were constructed after the removal of the incomplete and incorrect (26% of the records) movements, with 40% (1841/4603) of them occurring in 2020. This marked decrease, although not statistically significant, can be reflecting important changes in pig flow that obey health interventions and perhaps commercial restrictions suffered during the COVID pandemic. Median times spent at the sites remain similar as previously reported, with the longest time spent overall at the truck-wash facilities.

We currently assessed vehicle fidelity across sites to understand the most frequent dyads connected by the tracked vehicles, which can represent the most likely source of infection if an outbreak was associated with vehicle movements. The proportion of movements across site categories overall for 2019, 2020, and the two years respectively are shown in figure 9 and table 3. This initial analysis is the first step to the identification of super spreader sites and their locations together with potential risky movements.

	Destination							
Origin	Finisher	Gilt-Isolat	Nursery	Sow	TruckWash	WeanFinish		
FINISHER	0.0	0.1	0.0	0.0	0.1	0.0		
GILT ISOLATION	0.1	1.6	0.1	1.8	0.1	0.0		
NURSERY	0.0	0.2	1.6	1.3	3.6	0.3		
SOW	0.1	1.3	4.2	5.7	6.1	20.4		
TRUCK WASH	0.0	0.5	0.7	21.5	2.5	2.1		
WEANFINISH	0.0	0.0	0.5	7.6	14.8	1.1		

Table 3: Percentage of in-movements frequency by farm-type. Graded scale colors represent a higher (red) and lower (white) percentage of movements across dyad connections.

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Figure 9: Percentage of movements by the dyad of site category.

With the occurrence of the recent PRRSv breaks during the fall of 2020 with a L1C 1-4-4 strain, we took advantage of this opportunity and used the situation as if it was a FAD emergency. Therefore, we assessed the capabilities to identify movements from and towards the sites breaking with this novel strain with the aim to investigate potential biosecurity breaches while moving animals that could result in the transmission of the disease. While the number of breaking sites was not large enough for testing the hypothesis, it helped us to conduct preliminary evaluations of the data quality as a resource for early response and control of an outbreak. Data including date of event, premises entry/exit times, truck ID, origin of truck, destination was rapidly downloaded from the system and curated. Truck movements were identified and characterized (e.g. origin and destination) in a way that objectively allowed us to see potential connections during specific dates and times. We observed that five and two vehicles respectively entered the infected sow farms sites previous to the onset date, with the majority (96%) of the trips originating from truck wash facilities and two from a wean-to-finish site. The latter and potential risky movements were related to gilt introductions as expected in any sow farm. These results showed that we can conduct contact tracing analysis and assess potential risks for disease introduction represented by unusual movements that can result in breach in biosecurity. Although further outbreak investigation might be needed to conclude the most likely route of pathogen entry to the farms, this proves that transport movement can serve as a tool for outbreak investigations to rule out biosecurity breaches.

# Value to the industry:

Transport vehicle contact tracing is needed as production systems assess their risks and efficiency. Our project has characterized what the distribution of those movements is at a small scale together with the fidelity of trucks and sites. Such datasets exist in an important number of production systems but are not being analyzed from this perspective which certainly draws some questions from a process and biosecurity compliance perspective. In our small dataset, identification of potentially risky movements that warrant more investigation. These types of internal analyses should be conducted at the system level to uncover opportunities. Furthermore, contact tracing of these vehicles before an outbreak will continue to be a tool to complement outbreak investigations. Our data generating system provided high quality data that in real-time can answer questions about the historical routes and length of visits vehicles had before the detection of a pathogen.

# **Objective 4-** To expand participation of producers to allow for all to be involved.

- Capacity In our voluntary program, we ultimately need the capacity to manage data from as many producers as are willing to participate.
- Value for producers As participation expands, power and representativeness of the data increase.
  - 1. Continue to add production systems together with inclusion of growing pig sites of existing participants.
  - 2. Continue to include boar studs together with their historical PRRSv and/or PEDv outbreak data to generate incidence and prevalence estimates.

We continue the expansion of MSHMP on a few different levels: 1) the first area of expansion is made up of non-sow sites. We have continued to expand and track the participating MSHMP boar stud population. Currently we have approximately 9,960 boars in 42 studs located in 28 states belonging to a total of 13 companies; 2) the second area of non-sow site expansion is related to the largest pig population in the U.S., the growing pigs. We currently have 2,270 sites from 7 companies, and 3) we have continued to invite more production systems to join SHMP and we are currently in contact with two Midwest systems that have expressed interest in joining. One of them has already signed all the participation forms whereas the second one is still assessing this opportunity.

As part of the expansion into the growing pig population, it has become clear that it was necessary to pre-address how our database and data management webtool differentiated between breeding and growing site categorization to manage the large number of growing sites. To this end, we have been focusing on database development and webtool functionality. We are now able to link site type (nucleus, multiplication, boar, wean to finish, nursery, etc) to farm category (breeding or growing). This development step allows us to maintain data integrity and organization and to functional work with data both at the current sow/individual farm level and at the large scale required for growing sites. During this process we have identified and implemented bug fixes and numerous other small changes that have improved webtool and database functionality, usability, and quality control.

Work needs to be done on how to track changes in source flows over time, accommodating flows from non-sow sites (nurseries) to other grow sites, and most importantly establishing a low burden method for systems to report changes in flows so that we can maintain accurate and up to date disease statuses.

The boar stud data has allowed us to build the first PRRSV cumulative incidence graph (Figure 10). Interestingly, this graph shows outbreaks occurring during the same window of time that breeding herds usually break. We realize this is a small dataset and more data should be added before any conclusions can be added.



Figure 10. MSHMP boar stud PRRSV cumulative incidence.

#### Value to the industry:

Growth of this project will contribute to solidifying the representativeness of our estimates. As we continue to add growing pig sites specifically, we will enable multiple levels of data analysis. An example of this was portrayed during the PRRSV 144 epidemic in that growing pig sites were plotted on maps and incidence estimations at the breeding and growing pig level by company were obtained. In addition, growth due to boar stud inclusion, although small, is certainly important as it allows us to identify and highlight trends in this important population which interestingly resembles what has been seen in the breeding herd population. As we continue to progress and work with IT capabilities, growing pig sites connected with breeding herds will automatically lead us to build a network of flow with disease status and strain characterization. This will represent tremendous monitoring and risk assessment value to our participants as they will be able to understand strain introductions and origins of strains in a better way.

### **SHMP Related Publications**

1. Kikuti M, Sanhueza J, Vilalta C, Paploski IAD, Vanderwaal K, Corzo CA. Porcine reproductive and respiratory syndrome virus 2 (PRRSV-2) genetic diversity and occurrence of wild type and vaccine-like strains in the United States swine industry. PLoS One, v. 16, p. e0259531, 2021.

- Kikuti M, Paploski IAD, Pamornchainavakul N, Picasso-risso C, Schwartz M, Yeske P, Leuwerke B, Bruner L, Murray D, Roggow BD, Thomas P, Feldmann L, Allerson M, Hensch M, Bauman T, Sexton B, Rovira A, Vanderwaal K, Corzo CA. Emergence of a new Lineage 1C variant of Porcine Reproductive and Respiratory Syndrome Virus 2 in the United States. Front Vet Sci, v. 8, p. 752938, 2021.
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- 5. Makau DN, Alkhamis MA, Paploski IAD, Corzo CA, Lycett S, Vanderwaal K. Integrating Animal Movements With Phylogeography to Model the Spread of PRRS Virus in the U.S.. Virus Evolution, v. 1, p. 1, 2021.
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- 8. Galvis JA, Prada JM, Corzo CA, Machado G. Modeling the transmission and vaccination strategy for porcine reproductive and respiratory syndrome virus. Transbound. Emerg. Dis. 2021. Doi: 10.111/tbed.14007.
- 9. Galvis JA, Prada JM, Corzo CA, Machado G. The between-farm transmission dynamics of Porcine Epidemic Diarrhea Virus: A short-term forecast modeling comparison and the effectiveness of control strategies. Transbound. Emerg. Dis. 2021. Doi: 10.111/tbed.13997.

# **SHMP Related Presentations**

- Paploski, I.; Pamornchainavakul, N.; Makau, D.; Rovira, A.; Corzo, C.; Schroeder, D.; Cheeran, M.; Doeschl-Wilson, A.; Kao, R.; Lycett, S.; VanderWaal, K. Multi-strain dynamics of PRRSV type-2 in U.S. pig populations. Oral presentation. Conference of Research Workers in Animal Disease, Chicago, 2021.
- Pamornchainavakul, N.; Paploski, I.; Makau, D.; Corzo, C.; VanderWaal, K. Revealing invisible links and modes of between-farm PRRSV transmission using genetic-based network analysis. Oral presentation. Conference of Research Workers in Animal Disease, Chicago, 2021.
- 3. Makau, D.; Alkhamis, M.; Paploski, I.; Corzo, C.; Lycett, S.; VanderWaal, K. Integrating animal movements with phylogeography to model the spread of PRRS virus in the U.S. Oral presentation. Conference of Research Workers in Animal Disease, Chicago, 2021.
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occurrence of wild type and vaccine-like strains in the United States swine industry. Poster. North American PRRS Symposium (NAPRRS), Chicago, 2021.

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