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 #19-235

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Year 5 - Final Report
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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 2019-2020 season fortunately ended with the third lowest PRRSv breeding herd cumulative incidence (24.5%) during the last 11 years of monitoring. During this year we saw a different trend in breeding herd PRRSv prevalence as the proportion of herd staying in category 1 increased and "plateaued" which had not been seen before. PEDv and PDCoV continued to be present at a low incidence level. *Mycoplasma hyopneumoniae* was included into our monitoring program through a convenient sample of 8 systems. We now have the ability to quickly add new pathogens, which allow us to be prepared in the case of a FAD introduction.

Objective 2: To conduct prospective monitoring of PRRSv sequence evolution and impact – PRRSv sequence acquisition has been stabilized and these are being acquired on a monthly basis. Throughout the year, several participants contacted us to provide outbreak investigation support. A total of 29 sequence analysis were conducted with one of the latest being a virulent 1-4-4 virus. This allowed us to become a neutral third-party curating sequence to identify similarities and putting systems in contact whenever both parties agree.

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 real-time. 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 highlighting an important level of connectivity.

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. A new production system joined the SHMP during the year. A total of 30 boar studs from 12 participants have been added to our database. The growing pig population continues to grow with 4 companies sharing their growing pig locations. Work is being done towards linking sow-growing pig populations in our database.

Keywords: Monitoring, Emerging, PRRS, PEDv, Trends

Objective 1

To monitor trends in pathogen incidence and prevalence

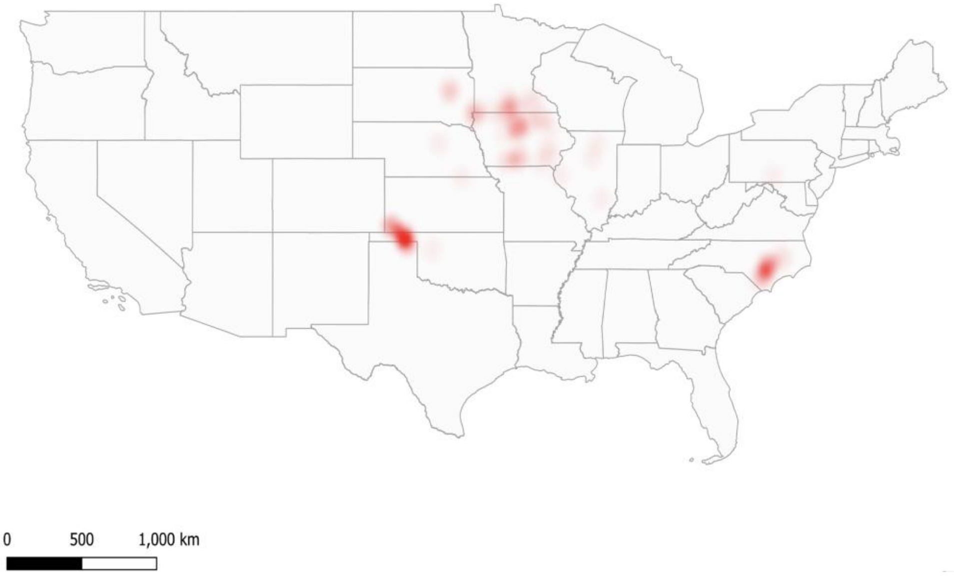
- **Capacity development – to expand capability of SHMP to capture diagnostic data from producers.**
- **Value for producers – to increase representativeness of current reporting trends.**

During 2019-2020, SHMP completed a decade worth of swine infectious disease monitoring. Data provided by participants continues to be translated into trends that are used as a benchmarking tool for the industry.

PRRS incidence

- The 2019-2020 PRRS season was quite similar when compared with the previous year with the cumulative incidence ending at 24.5%?. There was a slight increase compared to the previous year which certainly continues to yield good news in that incidence remained at a "lower" level. Conversations regarding what has changed and how the industry has been able to maintain a low "20's" incidence continue to lead to more questions than answers. Due to COVID-19, systems adopted a restricted farm visit policy which may have contributed to risk reduction. The 2019-2020 cumulative incidence season is the fourth lowest season in the history of the project.
- Work has been conducted on creating real-time PRRSv/PEDv outbreak heat maps. The objective with this is to work towards an early warning mechanism for our participants. 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 1). We still have to obtain whole participant approval to share this kind of information on a regular basis. This topic will be discussed in our next SHMP participant meeting.

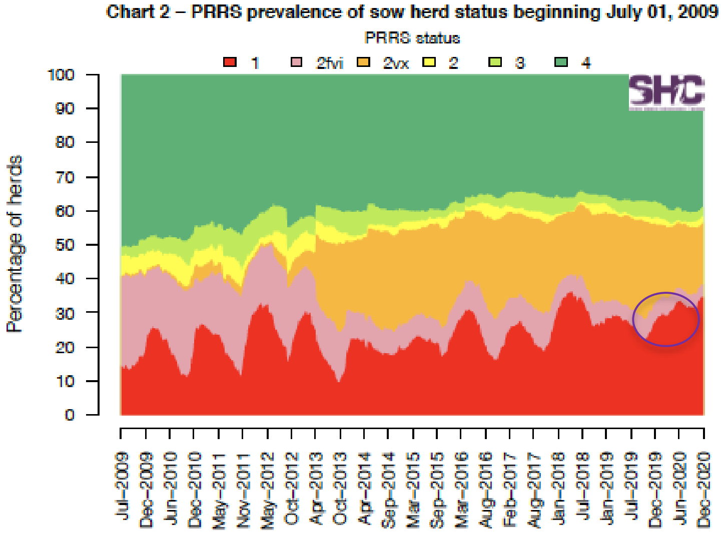
  Figure 1. Example of a "real-time" PRRSv break heat map in the United States.



PRRS Prevalence

- Interestingly, the 2019-2020 PRRS prevalence graph clearly showed us a different pattern compared to previous years. This year herds in category 1 did not follow the historically cyclical pattern, and the proportion of herds plateaued remaining at higher levels (Figure 1). As with previous years, we investigated this event by reviewing the data and asking some of our participants. We continue to believe that this event may be related to an increase usage of adopted processing fluids as a monitoring tool and virus detection has been improved. The fact that this methodology has a higher sensitivity may be driving the "easier" detection of wild type virus. Furthermore, the fact that certain herds may have a multi-strain scenario in the breeding herd together with live-vaccine usage may increase the probability of detection making herds stay in such category for longer periods. Strain persistence continues to be a potential explanation; however, this needs to be further investigated.

Figure 2. PRRS prevalence of SHMP participating sow herds.

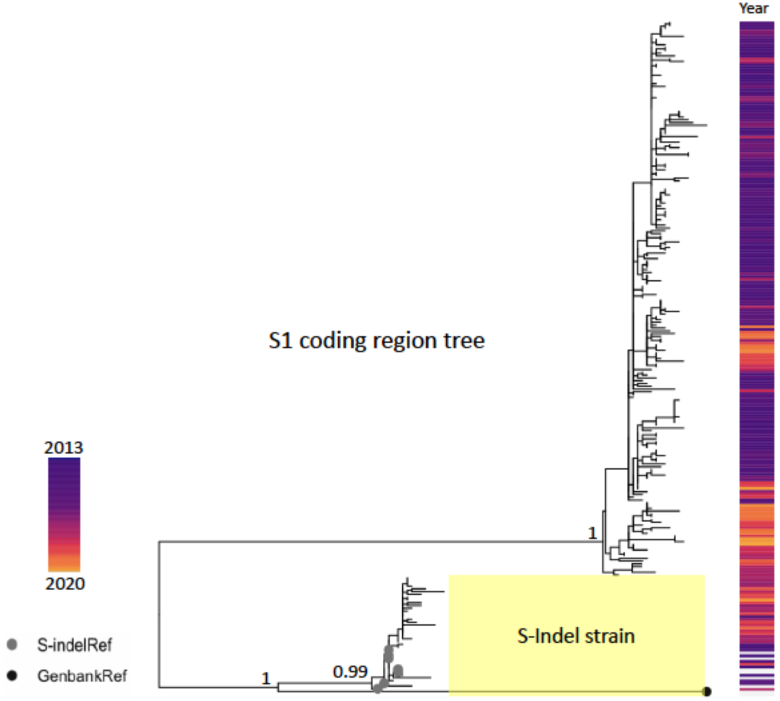


PEDv incidence

- PEDv incidence during the 2019/2020 season showed no major changes compared to the previous year. Of the 41 herds that reported an outbreak during the season, only 1 had reported an outbreak in the previous season (e.g., 2018-2019). Thirteen of those that reported a break in the 2019/2020 season had a break in the 2017-2018 season. This data suggests that the virus does not necessarily circulates among the same regions. The data also also suggests that the incidence in summer and fall are consistently lower than the incidence in winter and spring, suggesting the current endemic transmission of PEDV seems to start in late fall with few new cases reported. The bulk of new cases are being reported during winter and carrying on to spring. As with PRRS, we have also generated the "real-time" PEDv occurrence maps (Figure 1) as a way to continue to support our participants through these informative tools.

During the 2019-2020 season we conducted further analysis on the strain causing these outbreaks in order to understand whether the classic or INDEL strain were responsible for most of the outbreaks. Interestingly there's a mix of both strains occurring at over time as can be seen in the dendogram below (Figure 3). Even though the virus continues to change, it does not seem to be causing major disruptions.

Figure 3. SHMP 2013-2020 PEDv classic and INDEL sequences.



During year 5, MSHMP was involved in a project with a large production system focusing on PEDv control and elimination in the growing pig population. Status data together with testing results at the growing pig level was shared and a descriptive analysis was conducted. The two main conclusions drawn from this study were 1) PEDv was being introduced into growing pig sites approximately 8-10 post weaning; and 2) PEDv can be eliminated from the growing pig population if segregation and monitoring are combined.

Other diseases

- PDCoV continues to be present in the industry but at a lower level in the breeding herd population. Throughout the 2019-2020 season there were a total of 24 breaks reported from 7 breeding herds totaling approximately 82,400 sows affected.
- *Mycoplasma hyopneumoniae* was successfully added to our database and the system is in place to continue to obtain updates from participating companies. Even though not all companies are actively working towards elimination, there has been interest especially from the Midwestern U.S. systems and clinics regarding this initiative as some continue to work towards health improvements. We successfully generated the first cumulative incidence (Figure 4) and prevalence (Figure 5) graphs with available data as historically data is scarce for this bacterium. However, the more information we gather from participants the more interest we see from them in understanding patterns for this pathogen.

Figure 4. SHMP *Mycoplasma hyopneumoniae* cumulative incidence.

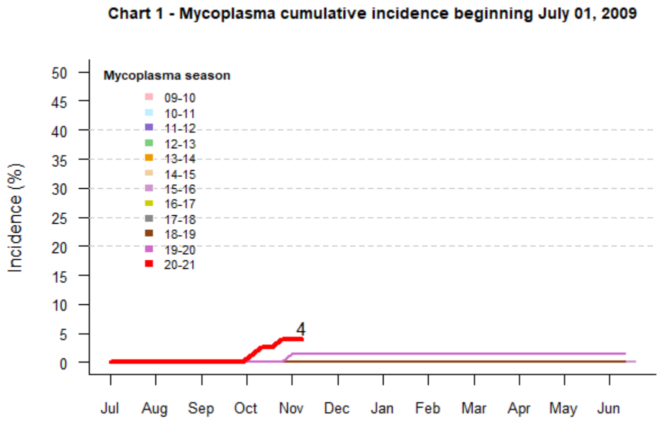
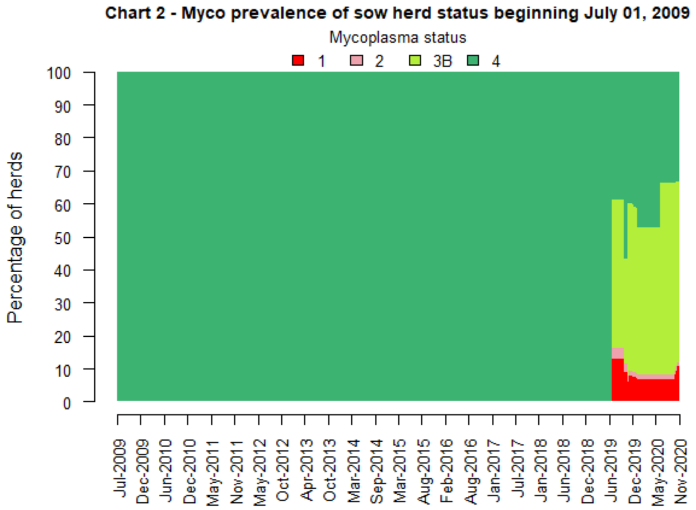


Figure 5. SHMP *Mycoplasma hyopneumoniae* cumulative incidence.



<u>Value to Industry</u>

The industry continues to find the information originating from the SHMP informative as it aids in understanding national trends but most importantly as a risk assessment tool. Furthermore, as our SHMP participant meetings occur, participants continue to appreciate the different types of analyses that they are exposed to and at the same time we receive requests from them to further conduct specific data analyses which altogether makes our participants valued and also active in the project.

Willingness to share and discuss pathogen spread is becoming a natural component in the conversation among certain participants. The disease monitoring data has clearly brought specific groups together in order to further share more data to work towards regional understanding of disease occurrence and even consider elimination of pathogens. All this is starting to lead us into being able to present data to participants in a way that most feel comfortable as locations and maps identifying regions are becoming less of a concern. Still, we have opportunities to bring participants together and further continue such discussions.

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.**

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 on 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. As the monthly updates has been running smoothly for the past quarter, automation of sequence sharing will be assessed starting with 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 25 outbreak investigations from 9 large production systems throughout this SHMP year (Table 1). Out of these, 11 were requested in the current calendar year and corresponded to comparisons of 16 sequences to our dataset. In all these cases, we were able to find similar sequences (>98% nucleotide identity) for all but one case. For this case we also did not find similar sequences stored at GenBank. 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 request to disclose the name of the participants' whose sequence has the highest similarity in order 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.

Table 1. Summary of PRRSV sequence comparison requests from MSHMP participants.

Date requested	Sequence #	# of sequences >98%	# of sequences >99%
2/11/2020	seq1	830	77
3/4/2020	seq1	55	26
3/19/2020	seq1	22	5
4/7/2020	seq1	7	0
4/7/2020	seq1	8	1
	seq2	8	8
	seq3	2155	9
	seq4	1	0
4/14/2020	seq1	201	86
4/30/2020	seq1	345	322
7/13/2020	seq1	18	5
	seq2	18	5
	seq3	18	
7/27/2020	seq1	11	4
9/25/2020	seq1	13	3
	seq2	13	3
	seq3	14	2
	seq4	3	0
9/27/2020	seq1	1	0
11/6/2020	seq1	42	5
11/10/2020	seq1	48	11
11/11/2020	seq1	66	13
	seq2	57	4
11/19/2020	seq1	12	2
11/20/2020	seq1	76	17

* Sequence # – Identifies the number of sequences that were analyzed upon request. For instance, on 2/11/2020 the analysis of sequence #1 yielded 830 or 77 sequences with a similarity of 98% or 99% respectively. If there are more than 1 sequence analysis is because the participant requested the analysis of multiple sequences.

Two manuscripts were prepared with this data. The first one comprises the description of space-time clusters of non-identical sequences in our dataset and the genetic relatedness of sequences inside versus outside those clusters. This analysis showed that several historical space-time clusters were identified in this dataset. However, sequences inside clusters were not always more similar to each other than outside the clusters. An additional spatial analysis to complement data found in this manuscript is still pending. The second manuscript comprises a description of all PRRSv genotype 2 sequences found in our dataset in term of frequency of lineages/sublineages, percent nucleotide difference to the first PRRSv genotype 2 isolated (VR2332) and RFLP type 1-7-4 frequency over time. We expect both papers to be submitted within the first quarter of 2021.

We also assessed how often do we see a lineage/sublineage change by farm according to lab submissions. We assessed only sequences from 2010 onwards, from systems that had ≥1,000 submissions, that belonged to sow farms enrolled at MSHMP, and that we were able to assign a lineage/sublineage. We also excluded all L5 sequences as we are considering those to be vaccine-like, and farms that had only one sequence submission throughout 2010-2020. By looking at 3,557 sequences from 335 sow farms, we found that the average (median) number of sequences submission per farm during this decade of data was 9 submissions (IQR: 5-15, minimum:2, maximum: 58). The average time between submissions was 55 days (IQR: 13-273, minimum:1, maximum: 2,556). We considered a lineage change every time a different lineage than the one from the previous submission from the same farm was found. We found an average of 2 lineage changes per farm during 2010-2020 (IQR: 1-3, minimum:0, maximum: 18). In other words, 20% (19% – 22%) of all sequences submissions from each farm represented lineage changes (80% did not). The average time between submissions that represented lineage changes was 416 days (IQR: 144-898, minimum:1, maximum: 1,983). Although this does not necessarily represent accurately how often a new lineage is introduced into the herds since it uses only laboratory submissions, it give us a general idea of how often to expect a new lineage/sublineage to be detected within a farm. Further steps in this analysis include assessing number and time to lineage changes within different regions and vaccination status.

Additionally, monitoring of "New" PRRSv sequences continues in North Carolina. The project contrast on an on-going basis sequence submission in the region with sequences detected in previous years in the region. Since January 2017 we have detected 21 "New" sequences to date. From those, six have spread to other farms in the region, while 15 have remained contained in a single farm. We continue to send a periodical report to veterinarians in North Carolina identifying farms with new PRRS strains and monitoring their spread. The future of this project is certainly interesting as one of the three main players stopped producing pigs which will certainly decrease the number of pig sites being filled, fewer pigs being moved which may lead to fewer virus strains in the region.

As we were wrapping up the year, one PRRS regional outbreak event was being investigated in which extremely similar sequences were being detected in a short period of time involving 8 different production systems within a region. As we investigate these cases, this allowed us to better understand the strengths and limitations of the different approaches we have been using (space-time clustering and new regional strains) when trying to tackle the goal of comparing newly reported sequences with the MSHMP PRRS library on a semi real-time basis at a participant level. Moving forward, we plan on using a combination of both methods periodically to try to identify these outlier scenarios while allocating efforts to simplify and automate this process as much as possible. Thus, we hope to be able to timely identify and alert producers while we track spread.

Value to the industry:

As the sequence acquisition and data analysis methodology continues to improve, the database becomes more relevant and powerful due to the fact that location, farm type and dates will continue to provide the industry with an opportunity for awareness of newly emergent and rapidly spreading viruses. In addition, by sharing sequences, their dates, locations and farm types allows us to develop methodologies to analyze the data in a manner that is relevant to producers and veterinarians.

Participants continue to rely in molecular data analysis and this year many of our participants appreciated the fact that the MSHMP database provides one more tool for their outbreak investigation process. Furthermore, the fact that participants can request speaking with another participant while maintaining anonymity has clearly provided a safe environment for cooperation.

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.**

During year 5, a great deal of work was invested into understanding recorded data from the trucks being followed. Specifically, we assessed data completeness, data quality, functioning devices, and logistics limitations (e.g. data-recording limitations). This is important as we continue to understand data potential and limitations and find solutions to standardize data collection for the improvement of its quality and completeness. We then proceeded to describe movement patterns and build the network of the system who kindly agreed to work with us by characterizing pig transport movement patterns recorded from a subset of vehicles within one Midwest large swine system representative of modern pig production. This allowed us to obtain preliminary information related to risk assessment of disease dissemination and management practices within the local industry, as well as provide insights for outbreak control and investigation.

We analyzed a sample of vehicles (7 trucks and 5 trailers) and their trajectories between January 2019 and June 2020. When vehicles entered a predetermined area, a signal was captured recording location and time spent in that area. We described 4792 trips over the period (3659 and 1093 in 2019, and 2020 respectively) moving from—and—to 101 sites with different geolocations within the Midwest. These landmarks included different types of farms (sow, GDU, nursery, wean-to-finish, finisher farms) and truck-wash facilities.

Overall, 85.6% (4103/4792) of the movements tracked fulfilled the inclusion criteria for the analysis (Table 2). A total of 101 sites (farms and truck-wash) with different geolocations within the Midwest were part of the network. Interestingly, with the few transport units we are currently following, we rapidly realized that approximately one-third of the sites was coming in contact with these vehicles clearly demonstrating and highlighting once again the importance of transport biosecurity and pig flow.

Table 2: Summary of movements by vehicle type & year in a Midwestern United States pig production system.

	Vehicles	Median (IQR)*	Min-Max	N
2019	Trucks	318 (119.5)	62-648	2409
	Trailers	58 (25)	5-642	806
2020	Trucks	137 (78)	37-207	822
	Trailers	19 (6)	6-24	66

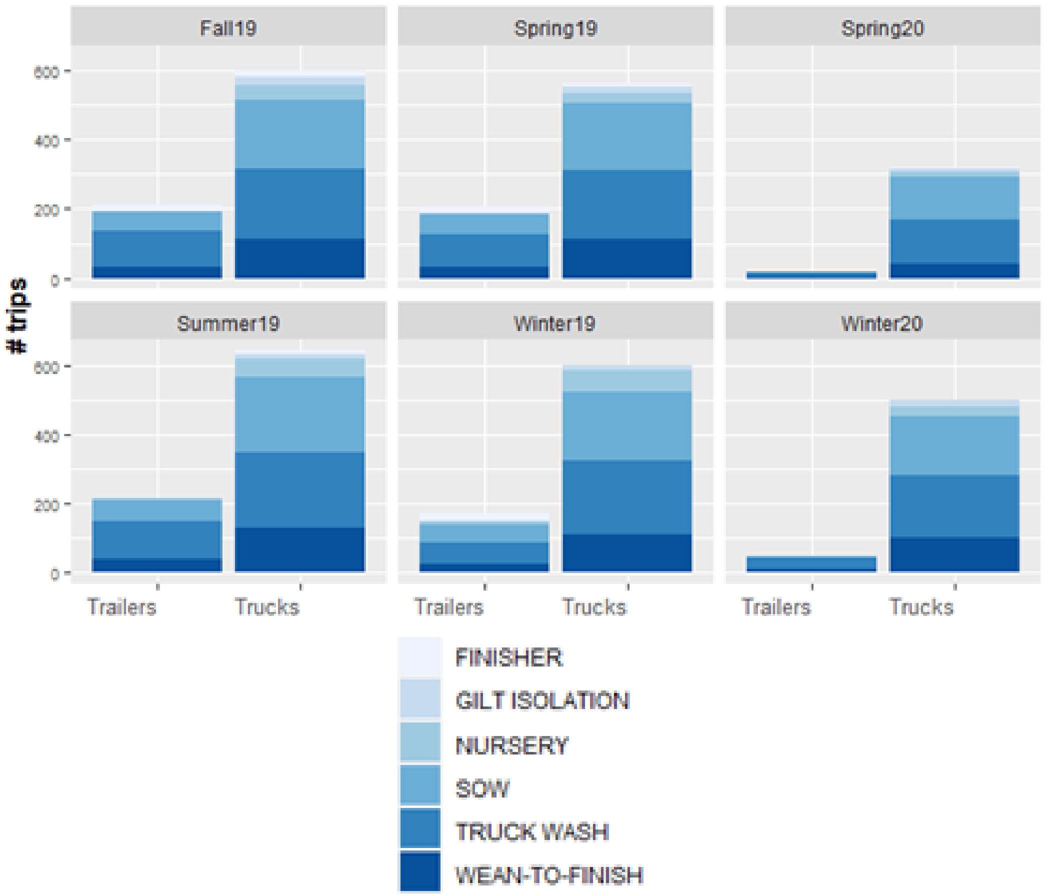
IQR: Inter-quartile range

During this process we identified the following limitations of the data:

1. Time within the landmark - devices recorded groups of observations in which trucks stopped at landmarks for less than 5 minutes, which suggests that polygons created by us delimiting landmarks do not cover the complete area in which trucks circulate within landmarks.
2. Landmark categories (e.g. type of farms/sites) tend to vary according to production needs within weeks/months or season: readjustment and revision of the use of landmarks needs to be considered to understand the potential impact of misclassifying sites.
3. Device batteries: All devices installed were recording data correctly over the period, suggesting long lasting (>1.5 years) data recording.

A second step in the analysis comprised the further characterization and description of movement patterns within a network. This step is key as producers clearly need to understand what options they have should segregation of pig flow/transport/feed mills is required. The seven trucks completed 79% percent of the trips and the rest (21%) by the five trailers analyzed. The proportion of trips among seasons and between years was similar (~25% each season), with most of the trips done to sow farms (32.5%) and truck-wash facilities (37.6%)(Figure 6).

Figure 6: Seasonal patterns by vehicle and landmark category in a Midwestern United States pig production system.



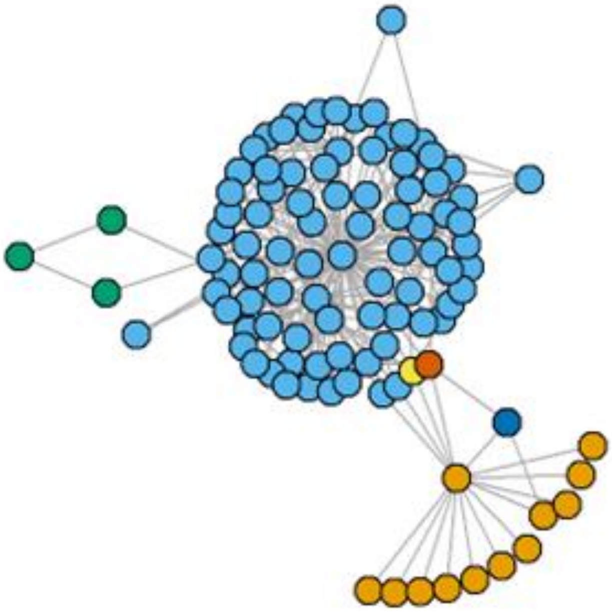
When vehicles parked at landmarks for more than 24 hours were excluded from the analysis, the median overall time spent at the sites was the longest observed, with the median time of washing-&-drying reaching ~2.8hrs (min-Max 17-1440 minutes) (Table 3).

Table 3. Time spent at each landmark across category.

	FINISHER (N=105)	GILT ISOLATION (N=101)	NURSERY (N=248)	SOW (N=1197)	TRUCK WASH (N=827)	WEAN-TO-FINISH (N=727)
Total.Mins						
Mean (SD)	67.8 (237)	115 (117)	50.7 (155)	175 (375)	579 (552)	68.5 (244)
Median [Min, Max]	22.0 [11.0, 1440]	82.0 [10.0, 602]	31.5 [10.0, 1440]	28.0 [10.0, 1290]	171 [17.0, 1440]	22.0 [10.0, 1440]

A preliminary network analysis showed a highly interconnected network (e.g. every farm in the system can be reached through three farms), which represents an important risk for disease spread if cleaning and disinfection are not properly performed. Furthermore, we identified three "communities" in which farm connectivity is strong; however, isolation of these communities can be possible when movements are purposely limited ("social distancing to control disease spread") (Figure 7).

Figure 7: Network of a pig production system connected by pig movement. Each circle represents a landmark within the system, and the lines represent movement of pigs. Each colored group of circles is the community within the system.



Although further analysis needs to be conducted, results showed that swine systems are highly interconnected; however, that connection is not random and some movements (e.g. vehicles) can be targeted when a disease outbreak occurs to reduce the risk of transmission through the whole system. Similarly, time spent at truck-wash facilities suggested that overall, good cleaning practices are performed.

Within the next steps of this analysis, we would like to unravel the movement patterns within network communities and characterize which farms/sites can represent higher risk for disease transmission (superspreaders). We realize sow farms play an important role; however, some other farm types may play an important role. We would also want to create a risk categories framework that can help producers and veterinarians to early identify disease with the optimization of resources by targeting higher risk farms. Finally, we would like to match movement data with retrospective disease-data recorded in MSHMP to validate framework.

Value to the industry:

Unveiling the potential of movement data analysis within a production system has certainly been the most valuable learning from the industry. Today the industry continues to work towards preparedness and by better understanding connectivity among sites, the chances of creating a sound intervention plan with the aim of segregating and "compartmentalizing" will increase as the network is characterized. Furthermore, traceability records are key to outbreak investigation, biosecurity compliance and personnel security. The current data provides such value which is not the case for transport data recorded in paper or based on data driven by farm departures/arrivals.

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

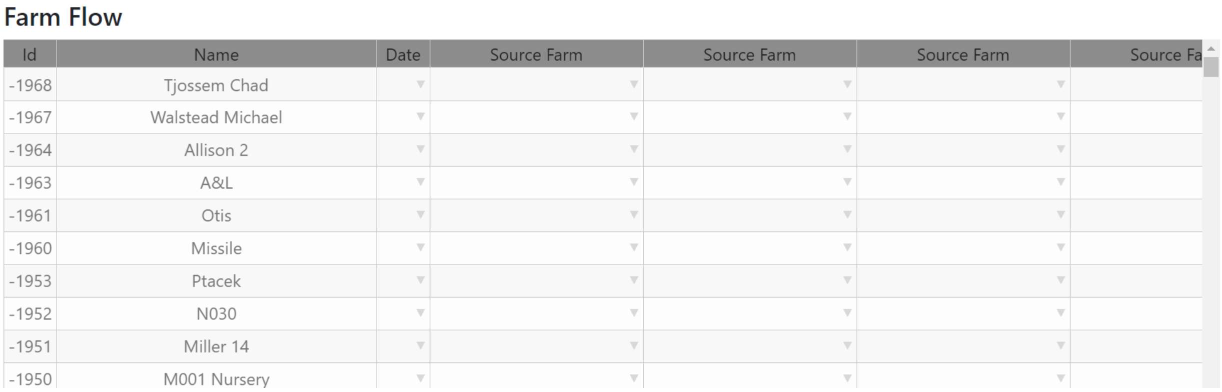
- **Capacity – In our voluntary program, we ultimately need the capacity to manage data from as many producers as are willing to participate.**
- **Value for producers – As participation expands, power and representativeness of the data increase.**

During year 5, SHMP was able continue the expansion 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 9,130 boars in 30 studs located in 15 states belonging to a total of 12 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 over 1,890 sites from 4 companies, 3) we continued to add more production systems as one system joined our program throughout the year.

As part of the expansion into the growing pig population, a prototype function within our own SHMP webtool has been developed, added and tested (Figure 8). This function enables us to connect sow and growing pig sites within a system which allow us to further understand and characterize growing pig status. A single growing site can have multiple tracked source sites, allowing us to partially represent the complexity of pig flows. This new function automatically identifies the disease statuses of the source sites and assigns the finisher with the lowest disease status. For example, if a growing site receives pigs from two different sow farms, 1 PRRS status 4 and another PRRS status 2vx, the growing site would be identified as health status 2vx.

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.

Figure 8. Screenshot of the flow function in the MSHMP webtool.



Farm Flow

Id	Name	Date	Source Farm	Source Farm	Source Farm	Source Fa
-1968	Tjossem Chad					
-1967	Walstead Michael					
-1964	Allison 2					
-1963	A&L					
-1961	Otis					
-1960	Missile					
-1953	Ptacek					
-1952	N030					
-1951	Miller 14					
-1950	M001 Nursery					

During year 5, a new participant system was fully onboarded by including historical data for both PRRS and PED. This system improves our representation in both two states where the project did not have good pig farm representation. At the very end of year 5 another production system requested to be involved in the MSHMP database. Many of the system farms were represented by a participating regional system, but the inclusion of the company as a direct MSHMP participant will improve the timeliness and accuracy of the health statuses.

Unfortunately, a couple of participating company left the project for the first time since it began. Due to financial constraints related to the pandemic, the company closed completely. The pig sites were bought by a current MSHMP participant and the sites have been transferred within the database, while retaining the historical information relevant to the closed system.

Beginning in year 5, a second participant announced that it would be closing for similar reasons in December 2020. This system has sold part of their farms to another SHMP participant and those sites have been transferred within our database.

Out of the 43 breeding herds in these 2 removed systems, 24 were lost which represent approximately 55,800 sows. We were able to store the data of these inactive and transferred farms so that it can be part of future analysis, thereby maintaining the historical accuracy of our information.

Value to the industry:

Representative data continues to be our goal. By expanding our dataset within the sow population but also outside such population will lead us to further connect and understand health events. Today we are before an important PRRSv outbreak that occurred mainly in growing pig sites but because we didn't have these on our database connecting both populations had to be done manually. This clearly shows what the befit of growth into other pig populations is for the industry and it clearly supports our objective to keep working in such direction.

Other SHPM Value Generating Activities

Collaborative Forecasting Projects

A. VanderWaal et al.

Forecasting PEDv and PRRS outbreaks

The ultimate goal of this project is to make real-time farm-level risk predictions for PEDV two-weeks-in-advance to allow for systems to take actions to prevent or mitigate the impact of a disease outbreak. This has been achieved via a server-run machine learning model that takes into account the spatio-temporal distribution of infected farms (from the MSHMP database), animal movements, and environmental characteristics (temperature, humidity, season, land cover, among others). In order to create our machine learning model, we collected retrospective movement and farm status data (2014-2017) from systems representing ~15% of the U.S. sow herd. Based on retrospective data the sensitivity, specificity, positive and negative predictive values for PEDv predictions of our model were 19.9, 99.9, 70.5 and 99.4%, respectively. PRRSv prediction has shown to be more challenging, which we believe might be related to its intense genetic variation that might reflect in immune interactions not present in PEDv. ***In December 2019 we began sending to partnering systems weekly real-time PEDv predictions, and now farm-level predictions have been sent for more than 60 weeks for three different systems.*** A manuscript related to this project has been submitted to *Transboundary and Emerging Infectious Diseases.*

Analysis of animal movements: Data gathered from MSHMP have also been used to understand animal movements and their role in PRRS transmission in the US swine industry. As part of our findings, we have been able to demonstrate that most of PRRS spread is associated with farm contacts through animal movements. Furthermore, the length of potential outgoing infection chains disseminated from some farms can be extremely large, upwards of 650 farms in extreme cases (which was approximately 25% of the farms in the network) in a period of 6 months. This was indicative of the presence of "super-spreader" farms within the network which may contribute to rapid disease spread via animal movements. Overall, the risk of 1-7-4 (Lineage L1A) occurrence in a given farm increased not only as a result of direct contact with an L1A-positive farm, but also increased as a result of indirect connections (contact of a contact) with L1A-positive farms. Moreover, farms that engaged in more outgoing movements also experienced higher risk. This suggests that the risk due to animal movements is not only associated with movements of infected animals to the destination, but also from potential movement-related breaches in biosecurity in the origin farm. This work as so far yielded one published manuscript and two submitted manuscripts.

Role animal movements on the spatial spread of PRRSV

We also integrated the animal movement data and ORF5 PRRSV sequence data into Bayesian phylodynamic models to investigate evolutionary trends and spatial spread of PRRSV Lineage L1A in the U.S. swine industry. Using this novel approach, we stratified the pig movements (wean pig, feeder pig and breeding movements) to assess the contribution of each type of pig movements to the spatial spread of PRRSV.

Movement of feeder pigs played a stronger role in shaping patterns of spatial spread of PRRSV than other types of movements. Our study, therefore, suggests that these types of pig movements ought to be undertaken more cautiously. Additionally, better biosecurity and disease surveillance in nurseries could help with better PRRS management. A manuscript highlighting these findings will be submitted for journal publication in January 2021.

Understanding between-farm transmissibility of PRRSV

We used pig movement data and ORF5 sequence data to estimate the effective farm-level reproduction number (R) of PRRSV (a measure between-farm transmissibility of PRRSV). Based on a phylodynamic reconstruction of the farm-to-farm transmission tree, we concluded that each infected farm transmitted to a median of 1 (IQR 1-2) and a maximum of 5 other farms. We also estimated that a pig-to-pig infection chain length of 28-48 animals was typical for direct farm-to-farm transmission. This knowledge helps to explain the dispersal of PRRSv over time and allows for a clearer depiction of transmission risk. Only a small proportion of inferred farm-to-farm transmission events could be attributed to documented connections between farms (e.g., animal movement or spatial proximity). Quantification of R in pig populations is relevant for tracking the success of mitigation measures at the population level, with the ultimate goal of reducing R to below one.

Temporal dynamics of co-circulating PRRS strains: Using PRRSV genetic data from 2009 - present, we documented the ongoing diversification and temporal dynamics of different PRRSv lineages, including the emergence of specific sub-lineages that appeared to be absent globally pre-2008. We also identified that evidence of positive selection on immunologically important regions of the genome, which supports the hypothesis that immune-mediated selection shapes the evolutionary and epidemiological dynamics for this virus. This work is published on a scientific journal (Frontiers in Microbiology, Impact Factor 4.076) and can be found here (https://www.frontiersin.org/articles/10.3389/fmicb.2019.02486/full).

At a macro-evolutionary level, current research related to PRRS evolution includes analysis of multi-strain PRRS dynamics and emergence of novel variants in an expanded dataset, including an analysis of factors that underpin strain emergence. At the micro-evolutionary level, we are also monitoring the diversification of PRRS viruses over the course of outbreaks in farms with different immunological profiles (that were status 2vx, 2fvi, or 4 pre-outbreak).

We extended our analysis to a larger dataset comprising sequences that began being reported in 2001. We identified a vast diversity of viruses within the most prevalent lineage in the US, and were able to stablish the year of emergence for different strains. Of note, we were able estimate that there is a ***turnover in the most prevalent PRRSv sublineage in the US approximately every 4 years***. This information allows a better understanding PRRS dynamics in the US and may allow for a better preparedness of farms in regards of when to expect a new variant to emerge in the industry. A paper reporting these findings is being written, with an expectation of being submitted in Feb 2021.

Another benefit of building this capacity is on our ability to quickly respond to emerging strains observed in the field. By possessing and being able to work with a vast dataset, we are able to better answer questions that producers might have related to if a specific group of sequences represents an emergence of a new clade or the introduction of a clade circulating elsewhere. ***This information may provide opportunities to better understand the determinants of emergence and diversification of PRRSv in the US***.

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The national incidence of PEDv and PRRSv has been slowly declining over the past years. Our delay in detecting viral circulation as a direct consequence of poor surveillance strategies and the lack of knowledge about the spreading processes continues to challenge pig production systems. In the case of PRRSv, an important roadblock is the deficiency of surveillance in downstream farms, while in breeding herds the “30 samples” still the current industry standard for monitoring, despite its assumption about within-herd prevalence. What we know is that both diseases spread among pig farms mainly by pig and other movements or neighborhood contacts and locally by farm proximity. Thus, the current project used PEDv and PRRSv imperfect occurrence data shared by 3 pig production systems with objective of i) assess the contribution of both transmission routes on the local spread; ii) identify current and future high spatial risk areas, and iii) estimate the impact of disease control interventions in the future spatial spread and use maps to indicate where and which intervention(s) should be deployed.

We built a stochastic susceptible-infectious-susceptible (SIS) epidemic model to mimic how PEDv and PRRSv are transmitted between farms. The transmission between farms can occur by two mechanisms, contact between farms through pig movements and locally by attraction forces between infected uninfected farms. Once the model was parameterized we used the model predicted temporal trends for the next two weeks. For model calibration, we compared the predicted infected sites against the occurrences reported. Finally, we further predicted whether

PEDv and PRRSv target disease control strategies such as vaccination and movement restrictions and/or redirections would have a relevant impact in the future week spreading.

Preliminary results and considerations for PRRSv: We found that pig movements generated the vast majority of the occurrences but mostly driven by sow to nursery movements which was also correlated by proximity with infected farms in a distance range of a maximum of 5 km. We mapped the next week's predictions which showed that PRRSv occurrence could be predicted correctly, however, the model still needs to be improved in regard to its sensitivity of detection. Also, as expected to redirect animal movements shown to be the best intervention in the future incidence scenarios. Thus our research has provided a better understanding of the transmission nature of PRRSv, we still need to improve the uncertainty of some model parameters and adapt this model to PEDv.

Another relevant work is the one related to the evolution and spread of PRRSv strains within and among pig producing companies in North Carolina. Briefly, we examined the local and external dissemination dynamics of PRRSv and the processes facilitating its spread in three production systems. Overall, PRRSv genetic diversity has declined since 2018, while phylodynamic results support frequent external transmission. We found that PRRSv dissemination predominantly occurred mostly through transmission between farms of different production companies for several months, especially from November until May, a timeframe already established as PRRSv season.

SHMP Related Publications

1. Galvis, J.A., J.M. Prada, C.A. Corzo, and G. Machado, 2020: Modeling the transmission and vaccination strategy for porcine reproductive and respiratory syndrome virus. Accepted for publication in the Transboundary and Emerging Diseases - Wiley Online Library
2. Galvis, J.A., J.M. Prada, C.A. Corzo, and G. Machado, 2020: The between-farm transmission dynamics of Porcine Epidemic Diarrhea Virus: A short-term forecast modeling comparison and the effectiveness of control strategies. Accepted for publication in the Transboundary and Emerging Diseases - Wiley Online Library
3. Jara, M., D.A. Rasmussen, C.A. Corzo, and G. Machado, 2020: Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States. *Transbound. Emerg. Dis.*tbed.13728, DOI: 10.1111/tbed.13728.
4. VanderWaal K, Paploski IAD, Makau D, Corzo C. Contrasting animal movement and spatial connectivity networks in shaping transmission pathways of a genetically diverse virus. Preventive Veterinary Medicine. 2020. DOI: 10.1016/j.prevetmed.2020.104977
5. Paploski IAD, Corzo C, Rovira A, Murtaugh MP, Sanhueza JM, Vilalta C, Schroeder DC, VanderWaal K. Temporal dynamics of co-circulating lineages of Porcine Reproductive and Respiratory Syndrome Virus. Front Microbiol. 2019. Nov 1;10:2486. doi: 10.3389/fmicb.2019.02486. eCollection 2019
6. Perez A, Linhares DCL, Goncalves A, VanderWaal K, Machado G, Vilalta C, Sanhueza J, Torrison J, Torremorell M, Corzo C. Individual or common good? Voluntary data sharing to inform disease surveillance systems in food animals. Front Vet S. 2019. Jun 21;6:194. doi: 10.3389/fvets.2019.00194. eCollection 2019.
7. Sanhueza JM, Vilalta C, Corzo C, Arruda, A. Factors affecting Porcine Reproductive and Respiratory Syndrome virus time-to-stability in breeding herds in the Midwestern United

States. Transbound Emerg Dis. 2019 Mar;66(2):823-830. doi: 10.1111/tbed.13091. Epub 2018 Dec 23.

8. Paploski I, Bhojwani R, Kinsley A, Corzo C, Vilalta, C, Perez A, Craft M, Machado G, VanderWaal K. Forecasting outbreaks of PRRS and PEDv in swine movement networks. Conference of Research Workers in Animal Diseases. Dec 2-4, 2018.
9. Machado G, Vilalta C, Recamonde-Mendoza M, Corzo C, Torremorell M, Perez A, VanderWaal K. Identifying outbreaks of Porcine Epidemic Diarrhea virus through animal movements and spatial neighborhoods. Sci Rep. Jan 24;9(1):457. 2019.
10. Kikuti M, Sanhueza J, Vilalta C, VanderWaal K, Corzo C. Genetic and spatio-temporal patterns of porcine reproductive and respiratory syndrome virus in U.S. swine populations. Frontiers in Veterinary Science, v. 6, p. 1, 2019.
11. Sanhueza JM, Stevenson MA, Vilalta Sans C, Kikuti M, Corzo C. Spatial relative risk of PRRS summer outbreaks and factors associated with PRRS incidence during summer. Frontiers in Veterinary Science, v. 6, p. 1, 2019.

MSHMP Related Presentations

1. Paploski IAD, Bhojwani RK, Makau DN, Sanhueza J, Corzo C, VanderWaal, K. Forecasting PEDV outbreaks at the farm-level in the U.S. swine industry. 2020 CRWAD Annual Meeting.
2. Paploski IAD, Pamornchainavakul N, Schroeder D, Rovira A, VanderWaal K. Quantifying sequential dominance of PRRSV strains through classification of sub-lineages. 2020 CRWAD Annual Meeting.
3. Makau DN,Paploski IAD., Corzo C., VanderWaal K. Role of animal movements in PRRS spread in the U.S. swine industry. 2020 CRWAD Annual Meeting.
4. Pamornchainavakul N, Paploski IAD, Makau D, Corzo C, VanderWaal K. Estimating farm-level reproductive numbers for PRRSV using sequence-based transmission tree analysis. 2020 CRWAD Annual Meeting.
5. MSHMP Participant Update – Sept 21, 2020.
6. Kikuti M. Understanding PRRSv diversity at the pig and litter level using whole genome sequencing. 2020. Leman Conference.
7. Paploski IAD, Corzo C, Rovira A, Murtaugh M, Sanhueza J, Vilalta C, Schroeder DC, VanderWaal K. Evolution of PRRSV: lessons from the last 10 years and implications for the future. 2020 AASV Annual Meeting.
8. VanderWaal K, Paploski I, Bhojwani R, Perez A, Corzo C. Forecasting outbreaks of PEDV for near real-time data-informed decision making. 2020 AASV Annual Meeting.
9. Picasso C, Vilalta C, Sanhueza J, Kikuti M, Corzo C. Understanding transport movement patterns within a production system in the Midwest. 2020. Leman Conference.
10. Montoya J, Vilalta C, Sanhueza J, Corzo C. Prevalence of PRRSv, PEDv, PDCoV and TGEv in pig farm manure pits. 2020. Leman Conference.
11. Montoya J, Vilalta C, Sanhueza J, Corzo C. PRRSv prevalence in near-to-market pigs in the United States. 2020. Leman Conference.
12. Paploski IAD, Makau D, Kanankege K, Kikuti M, Pamornchainavakul N, VanderWaal K. Understanding and Predicting Between-Farm Disease Transmission. Workshop at the 2020 Allen D. Leman Swine Conference.

13. Paploski IAD, Makau D, Pamornchainavakul N, Kanankege K, Kikuti M, VanderWaal K. Determinants of between farm disease transmission in swine: the case of PRRSv and PEDv. Infographic presented at the 2020 UMN Research Day.
14. Makau D, Alkhamis M, Paploski I, Corzo C, VanderWaal K. Phylodynamics of PRRSV lineage 1A in the US swine herds. Infographic presented at the 2020 UMN Research Day.
15. Paploski IAD, Bhojwani RK, Makau DN, Sanhueza J, Corzo C, VanderWaal K. Forecasting the spread of viruses in swine in the U.S.: translating movement and environmental data to actionable information. Presented at the EU-FMD conference 2020.
16. PRRS seasonality – perception or reality? National Hog Farmer Webinar. October 6, 2020.
17. MSHMP Update – AASV PRRS Task Force, Orlando Fl. – March 7, 2020.
18. Kikuti M, Vilalta C, Sanhueza J, Kienhe R, VanderWaal K, Schroeder D, Corzo CA. Viremia and mortality in piglets born to sows during a PRRSV outbreak. 2020 AASV Annual Meeting.
19. Vilalta C. PRRS en EEUU y España. Diferentes virus mismos problemas. 1st Gepork swine meeting. Lleida, Spain. Oct 29, 2019