SWINE HEALTH INFORMATION CENTER
FINAL RESEARCH GRANT REPORT FORMAT

Title: Developing the Morrison Swine Health Monitoring Project (MSHMP) to build capacity and enable the Swine Health Information Center –

Project # 25-052 Principal Investigator: Cesar A. Corzo

Institution: University of Minnesota

Date Report Submitted: 4/28/2026

Industry/Research Summary:

Objective 1: Monitor trends in pathogens incidence and prevalence – PRRSv, PEDv, PDCoV, Senecavirus viruses continued to be monitored, each maintaining historical patterns. However, the PEDv cumulative incidence trend was different in that a sharp increase was observed during the fall and into the winter. During 2025 we also explored and developed a method to estimate the breeding herd Influenza A virus (IAV) cumulative incidence. While we confirmed that it is possible to estimate the cumulative incidence based on VDL RT-PCR data, more work needs to be performed to avoid potential underestimation of this metric. Overall, the IAV cumulative incidence ranged between 1% and 5% over the past 10 years.

Objective 2: To conduct prospective monitoring of PRRSv sequence evolution and impact – During 2025 we continued to curate and expand our PRRSv ORF5 database. The representativeness of this database has enabled us to closely monitor throughout the year a newly emerged variant 1H.18. As this variant was monitored, a new system to monitor emerging variants was developed, Variants Under Monitoring (VUM) which is now shared with the public every month. The report is allowing producers to better understand the risk of every single variant that shows rapid dissemination characteristics. Since this report is based on the number of newly infected sites, the industry has an objective measure of variant fitness and thus risk. During 2025, we also assessed the possibility of sharing our weekly maps summarizing disease occurrence. While we believe this would be a great tool for the industry, we need to continue working on pathways to ensure producers and veterinarians feel comfortable with sharing such granular data.

Objective 3: To expand participation of producers to allow for all to be involved – During 2025 we made measurable progress toward broadening participation by successfully onboarding one additional production system, with two additional systems currently in the final stages of enrollment pending submission of required documentation. We have now accounted for 3.9M sows which approximately represents 65% of the U.S. breeding herd. With the goal of better understanding the health profile of the pigs entering the U.S. from Canada, some veterinary clinics and systems were approached to explore whether they would be interested in joining our voluntary project. While there was interest expressed, internal communications needed to occur before them making the decision to join. Fortunately, we did add one system that ships their weaned pig production into the Midwestern United States. On the other hand, we continue to work towards the characterization of each participating breeding herd from a filtration and mortality management perspective.

Keywords: Monitoring, Swine Health, PRRS, PEDv, Senecavirus, Influenza, PRRSv 1H.18, Variants Under Monitoring

Stated Objectives from original proposal

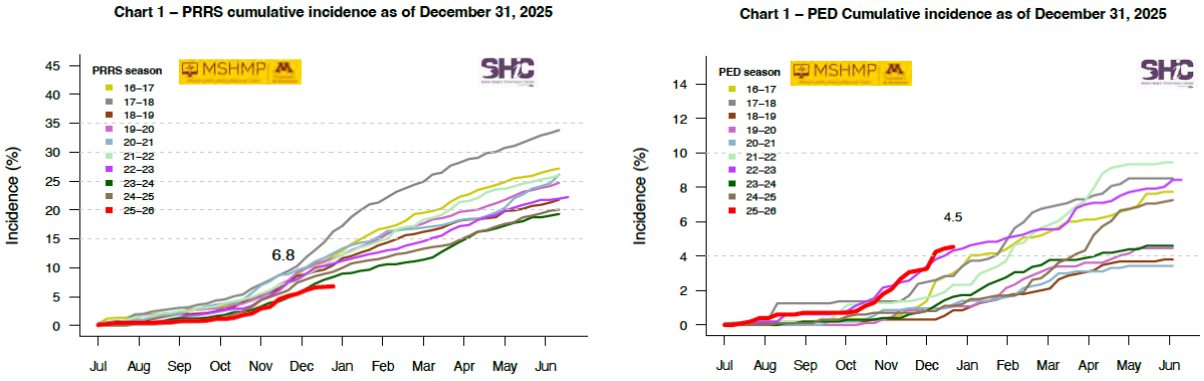
1. To continuously track and analyze trends in the incidence and prevalence of pathogens.
    i. Continue to provide timely and accurate incidence and prevalence charts representative of the US breeding herd.
    ii. Explore ways to classify Influenza A virus status in breeding herds and provide incidence metrics by leveraging data from Veterinary Diagnostic Laboratories (VDL) for more precise estimates.
2. To sustain ongoing surveillance of the PRRS virus sequences impacting the US swine population.
    i. Maintain a comprehensive and up-to-date repository containing PRRS virus sequences from both breeding and grow-finishing pigs.
    ii. Actively monitor the dissemination of the newly emerged PRRSV Lineage 1H.18.
    iii. Explore whether MSHMP participants are ready to publicly share general PRRSV incidence maps at the state and/or county level.
3. To enhance producer engagement, broaden representation, and facilitate access to timely and industry-relevant disease-related information.
    i. Expand participation by continuing to incorporate additional production systems and including growing pig facilities within the existing participant network.
    ii. Determine whether Canadian weaner or feeder pig breeding herd sources could be added to the MSHMP database.
    iii. Expand the competence of the MSHMP database to include filtration status data by ventilation pressure type (positive/negative).

Results and Discussion

Objective 1

Throughout 2025, we consistently delivered timely and accurate incidence and prevalence charts for PRRS and PEDV. We also recently added PDCoV to the list of diseases our project is monitoring. Reports were distributed to participants and the public through our weekly reports, the MSHMP website (https://mshmp.umn.edu), and SHIC's monthly communications. Up until December 2025, The MSHMP has accumulated 17 years' worth of disease monitoring data which clearly highlights the collaborative nature of our participants, the representativeness of the database and the impact of our analysis. Since our cumulative incidence, prevalence and EWMA graphs contain almost two decades worth of data, it was decided together with our participants that specific graphs only contain the most current 10 years of data with the goal of simplifying how data is displayed (Figure 1). This allows readers to more efficiently visualize current disease trends based on nation-wide breeding herd incidence data.

Figure 1. Morrison Swine Health Monitoring Project 10-year PRRSV and PEDV cumulative incidence charts.



In addition, through our participant-only sciences pages, we continue to periodically describe and compare regional disease occurrence and trends, such as PRRS incidence by system and state and PED standardized incidence rate by system, as part of the value-added mission of the project. This detailed data is essential since it enables producers to benchmark and tailor their herd health management strategies to specific regional challenges, enhancing their ability to mitigate the impact of these diseases.

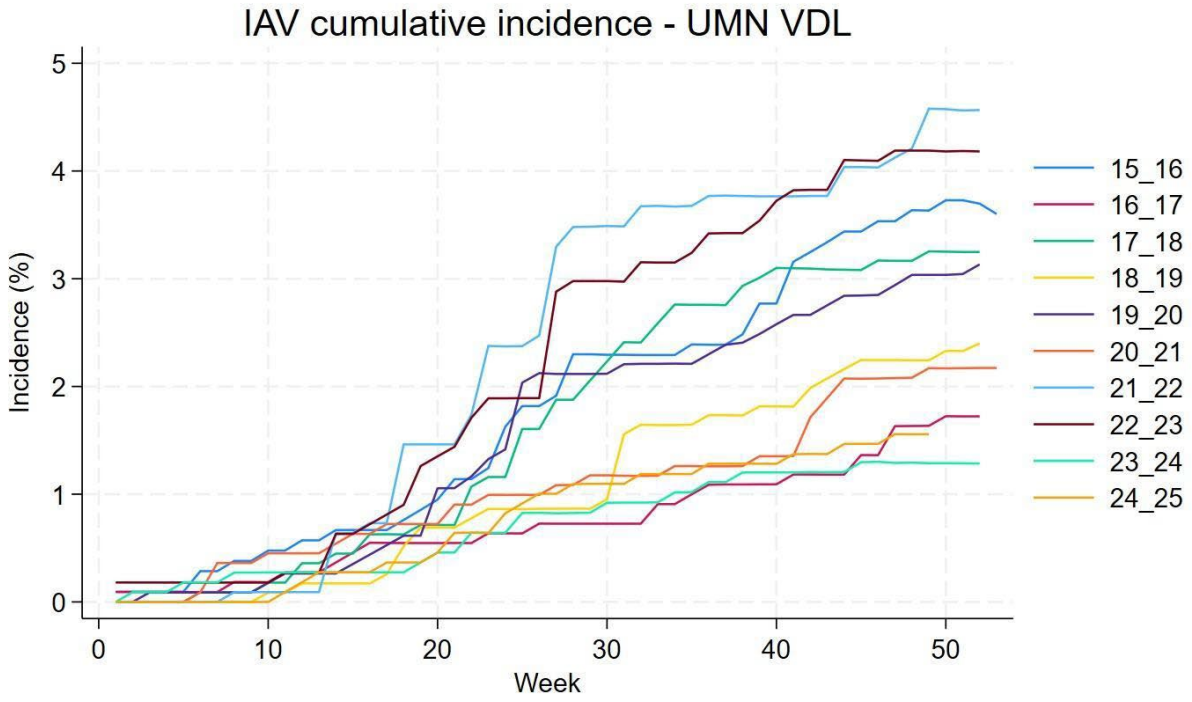
For 2025, we decided to explore whether using University of Minnesota Veterinary Diagnostic Laboratory (UMN VDL) influenza A virus (IAV) RT-PCR data to estimate influenza incidence was possible. We included RT-PCR data from 2015 onwards by mining the VDL dataset and combining data into different categories such as: “blood/serum”, “Oral Fluid/ Processing Fluid” and “Respiratory” indicating all related tissues (e.g., lung, trachea, bronchus, oral, and larynx swabs). By linking molecular data to MSHMP participating breeding sites we were able to assemble an automatable data flow to obtain a denominator and a numerator.

While classification of breeding herds according to IAV is still being discussed at the industry level, we decided to classify farms according to RT-PCR positive results regardless of subtyping and sequencing information as a starting point. We realize that this process requires finetuning; however, our goal was to assess the possibility of classifying herds with current available data. With this preliminary data, we were able to generate a breeding herd cumulative incidence chart (Figure 2) considering a few assumptions regarding sample types and time between same-site submissions. Codes were translated to R to streamline automation and incorporation into the report in the future.

Our results were presented at the MSHMP participant meeting during the 2025 Leman Conference for feedback, where it was proposed that IAV sequencing information would also be added to the case definition. While our first impression is that the graph may be underestimating incidence, we need to remember that IAV monitoring does not occur as frequent as for other diseases such as PRRSV. Potential next steps include the development of a smaller project to enroll a subset of companies and thus implement a monitoring program with an appropriate testing protocol and complementing the data

with additional VDL molecular testing results, as well as procuring agreements to add ISU VDL data.

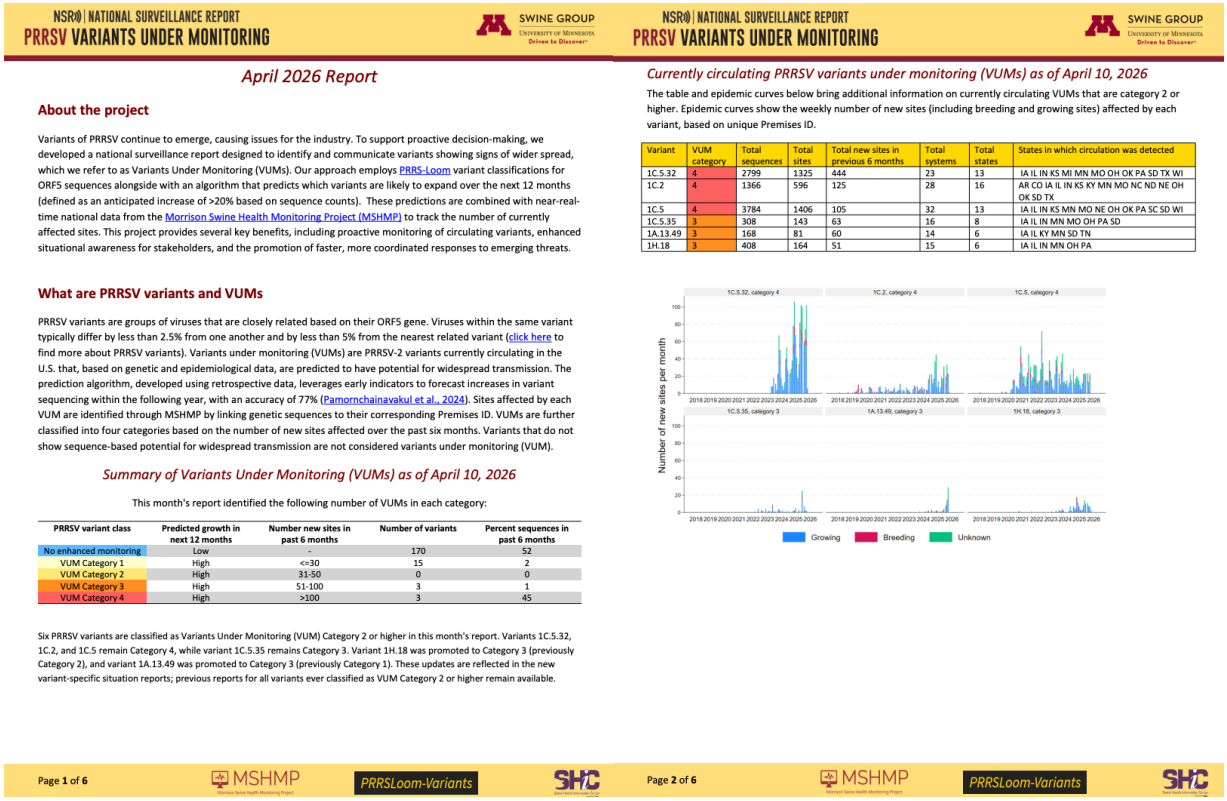
Figure 2. Influenza A virus (IAV) breeding herd cumulative incidence in UMN VDL - MSHMP participating systems.



Objective 2.

The MSHMP participant PRRSV dataset continues to provide significant value to the industry by playing a fundamental role in PRRSV classifications that are scientifically robust and epidemiologically useful. This dataset continues to support the dynamic PRRSV variant classification system through quarterly updates and serves as the basis for the PRRSV Variants Under Monitoring (VUM) monthly report (Figure 3). This report further classifies variants currently circulating in the US into categories based on the number of new sites affected in the previous six months, providing a short list of variants that are currently causing issues in the industry and improving situational awareness. This is possible due to level of data granularity that enables us to link cases to specific sites and locations. Moreover, we continue to support the industry by providing detailed PRRS sequence comparison reports. During 2025, we have aided in 15 outbreak investigations and sequence comparison requests.

Figure 3. PRRSV Variants Under Monitoring report example.



NSRO | NATIONAL SURVEILLANCE REPORT
PRRSV VARIANTS UNDER MONITORING

SWINE GROUP
UNIVERSITY OF MINNESOTA
Driven to Discover

April 2026 Report

About the project

Variants of PRRSV continue to emerge, causing issues for the industry. To support proactive decision-making, we developed a national surveillance report designed to identify and communicate variants showing signs of wider spread, which we refer to as Variants Under Monitoring (VUMs). Our approach employs PRRS-Loom variant classifications for ORF5 sequences alongside with an algorithm that predicts which variants are likely to expand over the next 12 months (defined as an anticipated increase of >20% based on sequence counts). These predictions are combined with near-real-time national data from the Morrison Swine Health Monitoring Project (MSHMP) to track the number of currently affected sites. This project provides several key benefits, including proactive monitoring of circulating variants, enhanced situational awareness for stakeholders, and the promotion of faster, more coordinated responses to emerging threats.

What are PRRSV variants and VUMs

PRRSV variants are groups of viruses that are closely related based on their ORF5 gene. Viruses within the same variant typically differ by less than 2.5% from one another and by less than 5% from the nearest related variant (click here to find more about PRRSV variants). Variants under monitoring (VUMs) are PRRSV-2 variants currently circulating in the U.S. that, based on genetic and epidemiological data, are predicted to have potential for widespread transmission. The prediction algorithm, developed using retrospective data, leverages early indicators to forecast increases in variant sequencing within the following year, with an accuracy of 77% (Pamornchainavakul et al., 2024). Sites affected by each VUM are identified through MSHMP by linking genetic sequences to their corresponding Premises ID. VUMs are further classified into four categories based on the number of new sites affected over the past six months. Variants that do not show sequence-based potential for widespread transmission are not considered variants under monitoring (VUM).

Summary of Variants Under Monitoring (VUMs) as of April 10, 2026

This month's report identified the following number of VUMs in each category:

PRRSV variant class	Predicted growth in next 12 months	Number new sites in past 6 months	Number of variants	Percent sequences in past 6 months
No enhanced monitoring	Low	-	170	52
VUM Category 1	High	<=30	15	2
VUM Category 2	High	31-50	0	0
VUM Category 3	High	51-100	3	1
VUM Category 4	High	>100	3	45

Six PRRSV variants are classified as Variants Under Monitoring (VUM) Category 2 or higher in this month's report. Variants 1C.5.32, 1C.2, and 1C.5 remain Category 4, while variant 1C.5.35 remains Category 3. Variant 1H.18 was promoted to Category 3 (previously Category 2), and variant 1A.13.49 was promoted to Category 3 (previously Category 1). These updates are reflected in the new variant-specific situation reports; previous reports for all variants ever classified as VUM Category 2 or higher remain available.

Page 1 of 6 MSHMP PRRSLoom-Variants SHC

NSRO | NATIONAL SURVEILLANCE REPORT
PRRSV VARIANTS UNDER MONITORING

SWINE GROUP
UNIVERSITY OF MINNESOTA
Driven to Discover

Currently circulating PRRSV variants under monitoring (VUMs) as of April 10, 2026

The table and epidemic curves below bring additional information on currently circulating VUMs that are category 2 or higher. Epidemic curves show the weekly number of new sites (including breeding and growing sites) affected by each variant, based on unique Premises ID.

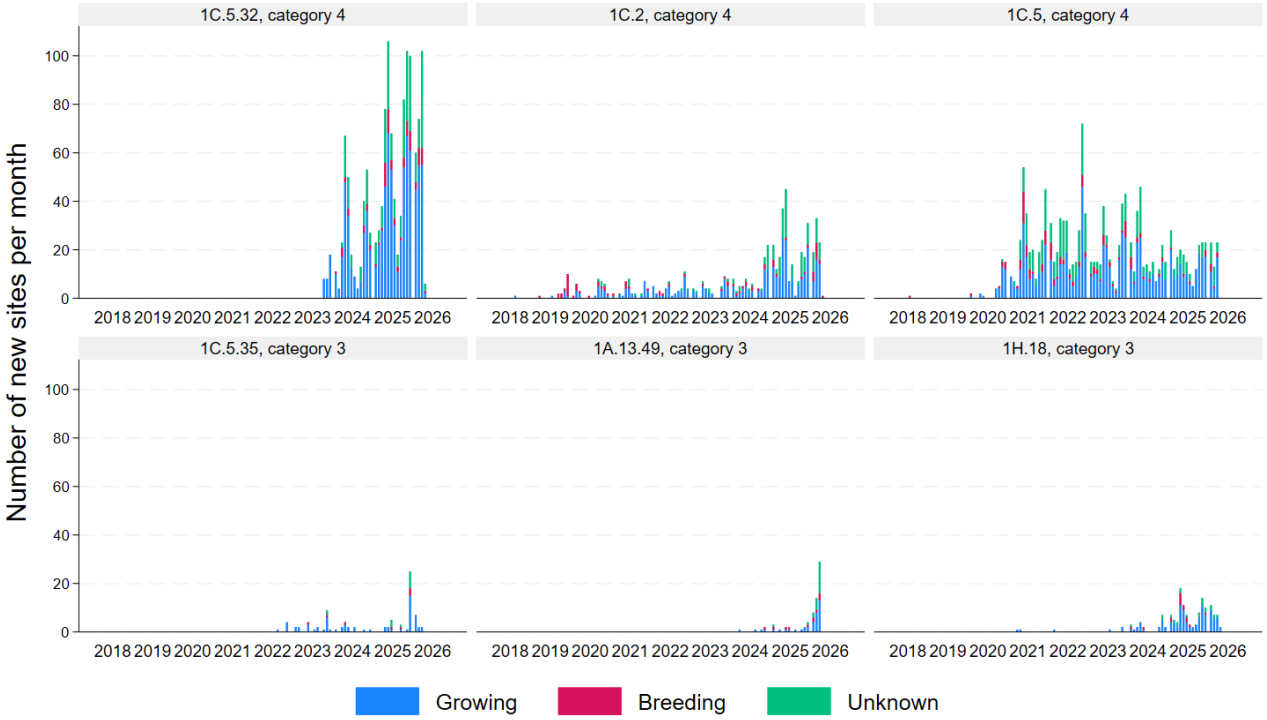
Variant	VUM category	Total sequences	Total sites	Total new sites in previous 6 months	Total systems	Total states	States in which circulation was detected
1C.5.32	4	2799	1325	444	23	13	IA IL IN KS MI MN MO OH OK PA SD TX WI
1C.2	4	1366	596	125	28	16	AR CO IA IL IN KS KY MN MO NC ND NE OH OK SD TX
1C.5	4	3784	1406	105	32	13	IA IL IN KS MN MO NE OH OK PA SC SD WI
1C.5.35	3	308	143	63	16	8	IA IL IN MN MO OH PA SD
1A.13.49	3	168	81	60	14	6	IA IL KY MN SD TN
1H.18	3	408	164	51	15	6	IA IL IN MN OH PA

Page 2 of 6 MSHMP PRRSLoom-Variants SHC

Our second objective for 2025 was related to actively monitor the emergence of a new PRRSV variant classified as 1H.18. PRRSV variant 1H.18 was originally classified as VUM Category 2 (31-50 new sites in the previous 6 months) in August 2025. The variant was moved down to Category 1 (<30 sites) by October 2025, indicating a temporary deceleration on the number of new cases, but went back to Category 2 in December 2025. At the time of writing (April 2026), variant 1H.18 was just reclassified as Category 3 (51-100 sites in the previous 6 months). This system allows us to closely monitor not only variants that have been on the headlines but also those that are circulating at lower levels but have the potential to expand substantially. An example is variant 1A.13.49, which has been monitored since August 2025 when it was classified as Category 1 (<30 new sites in the past 6 months), but that recently showed an exponential increase in transmission and is now Category 3 (Figure 4).

Altogether, the MSHMP collaboration with PRRS-Loom variant classification and PRRSV Variants Under Monitoring allows for a more proactive understanding of viral dynamics in the U.S.

Figure 4. Variants Under Monitoring as of April, 2026. The chart shows a recent reclassification of variant 1H.18 into Category 3 (51-100 new sites).



For our last sub-aim under this objective, we proposed to assess whether our participant network was interested in sharing current farm status through maps. During the last 5 years, we have been generating important pieces of information such as maps containing farm location and their PRRSV/PEDV status in real time. These pieces of information have been shared with our participants during our MSHMP participant meetings to highlight the capacity that today we have generated. We have also used them in specific cases in which we showed viral dissemination trends at the regional level, the most recent example was the L1C.5 virus in which our participants wanted to know the magnitude and rate at which this virus was spreading. Given the interest and willingness of some participants to share data, we consulted with our participant network to assess whether our participants felt comfortable with us making these real-time maps available to the group and potentially to the industry. During our participant-only meeting we surveyed our participants via the Mentimeter.com software regarding the possibility of MSHMP sharing the weekly incidence maps with the network of participants. The group agreed that these maps summarizing disease occurrence are valuable and will provide one more tool for the industry to use when attacking disease. Most (90%) of our meeting attendants agreed with making these maps available to our industry. This is a significant increase compared to five years ago when the half of the group agreed with this initiative.

Objective 3

During 2025 season, we continued to expand producer participation in alignment with our objective of increasing inclusivity and representativeness. One additional production system was fully onboarded, while two others are in the final stages of enrollment pending submission of required documentation. In parallel, we broadened the scope of participation within existing systems by incorporating newly acquired production sites, ensuring that our dataset continues to reflect structural changes within the industry. We are happy to report that our database now accounts for 3.9M sows of the approximately 5.9M sows in our industry.

We also explored opportunities to further extend participation beyond current networks, including engagement with Canadian swine systems that market weaner or feeder pigs to the United States. Given their relevance to foreign animal disease preparedness, especially in the context of PRRSV and SIV variant introduction, we initiated discussions with key veterinary networks to assess interest and feasibility for future inclusion. As of now, three swine veterinary clinics have been approached and while they expressed interest, they need to understand whether their customer base would agree to joining our project. One small Canadian system that sends their weaner pigs into the United States was onboarded.

In addition to expanding participation, we have continued refining and strengthening the dataset by improving key variables of interest, such as air filtration status. This includes ongoing efforts to verify filtration presence and characterize system types (e.g., positive vs. negative pressure), in response to stakeholder interest in biosecurity variables. These updates contribute to creating a more comprehensive and analytically valuable dataset. Air filtration status is available for 60.0% of the MSHMP breeding sites. Of those, 73.7% are not filtered, 20.0% are filtered year-round, while 6.0% are partially filtered. Amongst year-round filtered farms, 79.7% have negative pressure filtration and 20.3% have positive pressure filtration and we are currently working on updating the air filtration status for the remaining 40.0% of the sow herds

Finally, consistent with our commitment to accessibility and transparency, we have maintained regular communication with participating systems and continued enhancing our website to reflect user needs. These efforts have supported sustained engagement and ensured that our reporting remains accurate, relevant, and representative of the industry.

Publications

- Herrera da Silva JP, Paploski IAD, Charette R, Dufresne L, Messier S, Bolduc J, Kikuti M, Pamornchainavakul N, Corzo CA, VanderWaal K. Phylogenetic Lineages of PRRSV-2 from Canada Reveal Patterns of Transboundary Spread and Two Novel Sub-Lineages in North America. Pathogens 2026, 15, 346. https://doi.org/10.3390/pathogens15040346
- VanderWaal K, Pamornchainavakul N, Kikuti M, Zhang J, Zeller M, Trevisan G, Rossow S, Schwartz M, Linhares DCL, Holtkamp DJ, da Silva JPH, Corzo CA, Baker JP, Anderson TK, Makau DN, Paploski IAD. PRRSV-2 variant classification: a

dynamic nomenclature for enhanced monitoring and surveillance. mSphere 0:e00709-24. https://doi.org/10.1128/msphere.00709-24

- Silva, J.P.H.d.; Pamornchainavakul, N.; Kikuti, M.; Yue, X.; Corzo, C.A.; VanderWaal, K. Current Evolutionary Dynamics of Porcine Epidemic Diarrhea Virus (PEDV) in the U.S. a Decade After Introduction. Viruses 2025, 17, 654. https://doi.org/10.3390/v17050654
- Galvis JA, Corzo CA, Machado G. Mitigating between-farm transmission through simulating vehicle rerouting and enhanced cleaning and disinfection protocols. Prev Vet Med. 2025. https://doi.10.1016/j.prevetmed.2025.106650
- Kikuti, M.; Yue, X.; Melini, C.M.; Vadnais, S.; Corzo, C.A. Senecavirus A Incidence in U.S. Breeding Herds: A Decade of Surveillance Data. Animals 2025, 15, 1650. https://doi.org/10.3390/ani15111650
- Herrera da Silva JP, Rossow S, Paploski IAD, Kikuti M, Corzo CA, VanderWaal K. Complete Genome and Recombination Analysis of a Novel Porcine Reproductive and Respiratory Syndrome Virus 2 (Variant 1H.18) Identified in the Midwestern USA. Viruses 2025, 17, 863. https://doi.org/10.3390/v17060863
- Skyes AL,Galvis JA, O'Hara K, Holmstrom L, Corzo C, Machado G. Identifying control strategies to eliminate African swine fever in the United States swine industry in under 12 months. Prev Vet Med. 2025. doi.org/10.1016/j.prevetmed.2025.106598.
- Osemeke O, Silva GS, Corzo CA, Kikuti M, Vadnais S, Yue X, Linhares D, Holtkamp D. Economic Impact of Productivity Losses Attributable to Porcine Reproductive And Respiratory Syndrome Virus in United States Pork Production, 2016 to 2020. Preventive Veterinary Medicine, 2025, 106627, ISSN 0167-5877, https://doi.org/10.1016/j.prevetmed.2025.106627
- Yue X, Leonard M, Tavai-Tuisalo'o M, Malladi S, Kikuti M, Melini CM, Zaabel P, Culhane MR, Corzo CA. Swine Practitioner Practices on Oral Fluid Sampling in U.S. Swine Farms: A Nationwide Survey. Pathogens 2025, 14, 940. https://doi.org/10.3390/pathogens14090940
- Martinez M, Corzo CA, Machado G, Ekiri AB, Deza-Cruz I, Prada JM. Truck cleaning and disinfection and the risk of PRRSV dissemination in multi-site pig production systems in the United States: A network-epidemiological model approach. Prev Vet Med. 2025. doi.org/10.1016/j.prevetmed.2025.106539

Presentations

1. AASV 2025
2. Leman Swine Conference 2025
3. NAPRRS 2025 (NAPRRS/NC229: International Conference of Swine Viral Diseases)

- J.P. Herrera da Silva, I.A.D. Paploski, M. Kikuti, N. Pamornchainavakul, C.A. Corzo, K. VanderWaal. Timing the Regional Dispersal of PRRSV-2 Variants Across the U.S. to Improve Preparedness. 22nd NAPRRS/NC229: International Conference of Swine Viral Diseases. Chicaco, IL. 2026.
- J.P. Herrera da Silva, I.A.D. Paploski, R. Charette, L. Dufresne, S. Messier, J. Bolduc, M. Kikuti, N. Pamornchainavakul, C.A. Corzo, K. VanderWaal. Phylogenetic Lineages of PRRSV-2 from Canada Reveal Patterns of Transboundary Spread and Two Novel Sub-Lineages in North America. 22nd NAPRRS/NC229: International Conference of Swine Viral Diseases. Chicago, IL. 2026.

- C.M. Melini, M. Kikuti, X. Yue, E. Cortus, C. Vilalta, C.A. Corzo. Evaluation of manure pit agitation and pumping as a factor for porcine reproductive and respiratory syndrome (PRRS) virus detection changes through oral fluids. 22nd NAPRRS/NC229: International Conference of Swine Viral Diseases. Chicago, IL. 2026.
- M. Kikuti, N. Pamornchainavakul, I.A.D. Paploski, K VanderWaal, C.A. Corzo. PRRSV Variants Under Monitoring (VUM): An Initiative for Proactive Near Real-Time Surveillance. 22nd NAPRRS/NC229: International Conference of Swine Viral Diseases. Chicago, IL. 2026.
- X. Yue, M. Kikuti, M. Melini, C.A. Corzo. Estimating the effects of negative and positive pressure systems on PRRS occurrence. American Association of Swine Veterinarians., San Francisco, CA. USA. 2025.
- M. Kikuti, M. Melini, X. Yue, S. Vadnais, C.A. Corzo. Refining Senecavirus A disease occurrence estimates in the US breeding herd. American Association of Swine Veterinarians., San Francisco, CA. USA. 2025.
- G. Trevisan, C.A. Corzo, G. Cezar, M. Melini, M. Kikuti, X. Yue, A. Moore, S. Vadnais, H. Naikare, R. Main, M. Prarat, A. Pillatzki, F. Matias Ferreyra, C. Bowen, D. Linhares. PEDV elimination: Estimating prevalence in the U.S. herd. American Association of Swine Veterinarians., San Francisco, CA. USA. 2025.
- M. Kikuti. PRRSV 1C.5.32: A variant with epidemiological indicators of rapid spread across the U.S. Allen D. Leman Swine Conference. St. Paul, MN. 2025.
- J.P. Herrera da Silva, I. Paploski, M. Kikuti, N. Pamornchainavakul, C.A. Corzo, K. VanderWaal. Timing the Regional Dispersal of PRRSV-2 Variants Across the U.S. to Improve Preparedness. Allen D. Leman Swine Conference. St. Paul, MN. 2025.
- J.P. Herrera da Silva, I. Paploski, R. Charette, L. Dufresne, S. Messier, J. Bolduc, M. Kikuti, N. Pamornchainavakul, C. Corzo, K. VanderWaal. Expanding Genetic Landscape of PRRSV-2 in Canada: Cross-Border Spread in North America and the Establishment of Two Novel Sub-Lineages (1K and 1L). Allen D. Leman Swine Conference. St. Paul, MN. 2025.
- M. Kikuti, N. Pamornchainavakul, I.A.D. Paploski, K. VanderWaal, C.A. Corzo. Integrating Swine Diagnostic and Field Data to Detect PRRSV Variants Under Monitoring. Epidemics 10. San Diego, CA. 2025.
- J.P. Herrera da Silva, I. Paploski, R. Charette, M. Kikuti, N. Pamornchainavakul, C. Corzo, Kimberly VanderWaal. Expanding Genetic Landscape of PRRSV-2 in Canada and Cross-Border Spread in North America. Epidemics 10, San Diego, CA. 2025.
- J.P. Herrera da Silva, I. Paploski, M. Kikuti, N. Pamornchainavakul, C.A. Corzo, Kimberly VanderWaal. Timing PRRSV-2 Variant Dispersal across regions in the U.S. Epidemics 10. San Diego, CA. 2025.
- J.P. Herrera da Silva, N. Pamornchainavakul, I. Paploski, A. Rovira, M. Kikuti, X. Yue, C.A. Corzo, K. VanderWaal, Genomic Surveillance of Porcine Epidemic Diarrhea Virus (PEDV) Over a Decade Reveals Ongoing diversification in the U.S. Epidemics 10. San Diego, CA. 2025.

Outreach

- Podcasts

    - Inside PRRSV: Close to Real-Time Variant Tracking (November 12, 2025, The Swine Health Blackbelt Podcast)
    - Eliminating PEDV faster on your farm (July 30, 2025, The Swine Health Blackbelt Podcast)
    - New insights on virus control in swine facilities (July 10, 2025, Feedstuffs)
    - What's Really Happening Inside Pig Farms? (July 9, 2025, The Swine Health Blackbelt Podcast)
- National Hog Farmer
    - PRRSV variants under monitoring: An initiative for proactive near real-time surveillance. Published on National Hog Farmer . 2025.
    - Genetic surveillance of PEDV shows limited spread between U.S. regions. Published on National Hog Farmer. 2025.
    - Senecavirus A: The vesicular disease that continues to challenge swine health. Published on National Hog Farmer. 2025.
- Others
    - New Monthly PRRSV Variant Report Launches with SHIC Support. Published on SHIC
    - University of Minnesota Swine Group Launches PRRSV Variant Monitoring System. Published on AASV
    - SHIC-Funded MSHMP Study Sheds Light on Senecavirus A Incidence in US Swine Herds. Published on SHIC
    - Senecavirus A disease incidence estimates in the U.S. breeding herd. Published on Swineweb