



OUR LATEST INFORMATION ON PROTECTION OF US SWINE HERD HEALTH

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SHIC 2025 Plan of Work Focuses on Protection of US Swine Health

Activities of the Swine Health Information Center are guided by its annually updated Plan of Work. The 35 projects included in the recently released 2025 Plan of Work address SHIC's five strategic priorities: 1) improve swine health information, 2) monitor and mitigate risks to swine health, 3) responding to emerging disease, 4) surveillance and discovery of emerging disease, and 5) swine disease matrices. Developed with the input of industry stakeholders, and approved by the SHIC Board of Directors, the 2025 Plan of Work will be implemented by Executive Director Dr. Megan Niederwerder and Associate Director Dr. Lisa Becton with input from the board and SHIC Working Groups. Find the 10th anniversary 2025 SHIC Plan of Work here.

Proposals to address priorities detailed in the 2025 Plan of Work are accepted through targeted RFPs and on a rolling basis for review and funding recommendation. SHIC's activities are guided by the Plan of Work while remaining nimble and responsive to industry needs as they arise. Stakeholder input and ideas are welcomed yearround to inform newly identified industry needs which may necessitate adapting the Plan of Work to fulfill SHIC's mission. In addition to the 2025 Plan of Work priorities, SHIC continues efforts to fill knowledge gaps for H5N1 Risk to Swine through a collaborative research program with FFAR and Pork Checkoff initiated in 2024.

SHIC 2025 Plan of Work Priorities:

Improve Swine Health Information

Domestic disease monitoring through veterinary diagnostic laboratory data collation.

Domestic disease monitoring through voluntary reporting to the Morrison Swine Health Monitoring Project.

Strategic summary of SHIC swine health and disease work-to-date.

Webinars to inform veterinarians and producers about emerging swine health issues.

Maintaining up-to-date swine disease fact sheets.

Ensure timely and valuable communications across all stakeholder audiences.

Monitor and Mitigate Risks to Swine Health

Real-time assessment of high-risk product importation and traveler entry at borders.

Global disease monitoring to identify and inform international swine disease risks.

Foster information sharing with government and allied industry through international animal health organizations.

Transport biosecurity through targeting a regional or production phase approach.

Designing effective cleaning and disinfection tools and practices for swine transport trailers.

Packing plant biocontainment to reduce risk of trailer contamination at the dock.

Packing plant tools for effective cleaning and disinfection of lairage for business continuity.

Personnel movement as a risk of disease spread between farms.

Enhancing biosecurity of mortality management practices to reduce disease transmission back to farm.

Novel ventilation technologies for cost-effective bioexclusion and biocontainment.

Cull sow and secondary market biosecurity and disease surveillance.

Multi-species livestock operations and backyard farms as a risk for emerging disease spillover.

Role of rendering in emerging disease transmission and response.

Responding to Emerging Disease

Emergency disease preparedness and response planning in coordination with state, federal and industry stakeholders.

Monitoring risk of African swine fever recombinant genotype I/II virus to US prevention and preparedness.

Rapid deployment of research funds for a newly emerging disease.

Investigating production and swine health impacts of porcine sapovirus as an emerging pathogen.

Hemorrhagic tracheitis syndrome (HTS) as a potential emerging disease in US swine.

Utilizing Standardized Outbreak Investigations to identify high risk events for pathogen entry.

Identification of early disease outbreak warning signals from industry data.

Surveillance and Discovery of Emerging Disease

Wastewater sampling for emerging disease surveillance.

Tongue tip fluids as a diagnostic sample to target risk-based mortality populations.

Genome-based diagnostic technologies for emerging disease detection and forensic analysis.

Diagnostic fee support to assist in early detection of emerging disease.

Population and environmental surveillance technologies to improve and automate diagnostic testing.

Increasing utility of VDL submissions as an effective surveillance stream for detection of emerging disease.

Investigate the clinical relevance and epidemiology of newly identified agents in VDL submissions associated with swine disease.

Swine Disease Matrix

Updating bacterial and viral swine disease matrices to prioritize swine pathogens.

Using the swine bacterial and viral disease matrices as guidelines for research to enhance swine disease diagnostic capabilities.

SHIC/FFAR/NPB H5N1 Request for Research Proposals Nets 51 Reponses

The Swine Health Information Center partnered with the Foundation for Food & Agriculture Research and the Pork Checkoff to fund a \$4 million research program to enhance prevention, preparedness, mitigation, and response capabilities for H5N1 influenza in the US swine herd. Announced in November 2024, the RFP invited gualified researchers to submit proposals that address the 10 H5N1 Risk to Swine research priorities outlined below. In response to the RFP which closed December 31, 2024, a total of 51 proposals were received from 35 different institutions across six countries. Proposals will undergo competitive review for funding recommendations based on value to US pork producers. This is the largest number of responses to a SHIC RFP to date.

The emergence of H5N1 Influenza A clade 2.3.4.4b in dairy cattle, persistent outbreaks in commercial poultry, and the recent identification of H5N1 in a backyard pig in Oregon highlights the potential threat to the US swine industry. Research priorities for H5N1 Risk to Swine are designed to further strengthen US swine industry prevention and preparedness as well as inform response efforts should H5N1 be introduced into the commercial swine herd.

The 51 proposals are expected to address H5N1 Risk to Swine research priorities described in the detailed Request for Research Proposals found here, including topic areas of 1) vaccines for swine, 2) clinical presentation in pigs, 3) mammary transmission, 4) diagnostic surveillance, 5) introduction and transmission risks, 6) caretakers of pigs, 7) biosecurity practices, 8) safety of pork, 9) mitigating production impact, and 10) pig movements.

Upon completion of the competitive review process, project awards are expected to be announced in spring 2025. Projects demonstrating the most urgent and timeliness of completion, providing the greatest value to US pork producers, and showing efficient use of funds are prioritized for funding. Results will be shared with producers and veterinarians as soon as they become available. Critical research investments are necessary to understand and prevent H5N1 incursion, ensure rapid detection of H5N1 if introduced, protect animal and caretaker health, inform stakeholder response, mitigate production losses on the farm, identify effective control measures, and develop clear messaging to consumers on the safety of pork. Outcomes from the funded proposals will provide critical information that producers, veterinarians, and industry stakeholders can use to better prevent incursion and develop preparedness plans if H5N1 is identified in commercial swine herds within the US.

Foundation for Food & Agriculture Research

The Foundation for Food & Agriculture Research (FFAR) builds public-private partnerships to fund bold research addressing big food and agriculture challenges. FFAR was established in the 2014 Farm Bill to increase public agriculture research investments, fill knowledge gaps and complement the U.S. Department Agriculture's research agenda. FFAR's model matches federal funding from Congress with private funding, delivering a powerful return on taxpayer investment. Through collaboration and partnerships, FFAR advances actionable science benefiting farmers, consumers and the environment.

Swine Health Information Center

The Swine Health Information Center, launched in 2015 with Pork Checkoff funding, protects and enhances the health of the US swine herd by minimizing the impact of emerging disease threats through preparedness, coordinated communications, global disease monitoring, analysis of swine health data, and targeted research investments. As a conduit of information and research, SHIC encourages sharing of its publications and research. Forward, reprint, and quote SHIC material freely. For more information, visit http://www.swinehealth.org or contact Dr. Megan Niederwerder at mniederwerder@ swinehealth.org or Dr. Lisa Becton at Ibecton@ swinehealth.org.

SHIC Monitoring Emerging PRRSV-2 Lineage 1C.5 Clonally Expanded Clade

First reported in the Swine Health Information Center June 2024 domestic disease monitoring report, an emerging PRRSV Lineage 1C.5 subclade has continued to expand, with increased detection through the fall and winter months of 2024. A team of diagnosticians at Iowa State University have led the investigation into the changing diagnostic trends of the detection of an emergent and clinically significant PRRSV-2 Lineage 1C.5 clonally expanded clade. Investigative team members Rabsa Naseer and Drs. Jianqiang Zhang, Phillip Gauger, Giovani Trevisan and Michael Zeller have provided an update on the current situation herein.

Since its emergence in 2020, the PRRSV-2 Lineage 1C.5 has become the dominant lineage in circulation, replacing the prior dominant Lineage 1A in the US. The ISU Veterinary Diagnostic Laboratory has sequenced over 6,000 unique Lineage 1C.5 cases to date, accounting for approximately 72% of the total Lineage 1C cases sequenced at their facility from January 2020 to mid-December 2024. Many of these cases are associated with clinical disease in production systems experiencing PRRS outbreaks. The ISU VDL regularly tracks the diversity of circulating PRRSV strains using both phylogenetic and epidemiological methods, which led to the discovery of an emerging divergent clade within Lineage 1C.5. This clade was notable due to a surge in genetically similar sequences detected over a short period of time and was deemed to be clonally expanding through the swine population. Here, the ISU team has tentatively called it Lineage 1C.5 clonally expanded clade.

From July 2023 to December 2024, 945 cases of PRRSV with ORF5 sequences belonging to this clade have been identified. The ORF5 sequences of this clade exhibit high genetic similarity, with an average nucleotide difference of seven nucleotide bases (98.8% nucleotide similarity), though the entirety of the clade is within 96%. The index case was detected from a grow-finish farm in Iowa on July 20th, 2023, and the majority of subsequent cases have been detected in Iowa swine farms (838), indicating a regional outbreak. This Lineage 1C.5 clonally expanded clade was first detected outside lowa in March 2024, signaling its potential for national spread. To date, this clade has been detected in the states of Minnesota (36 cases), Illinois (17), Missouri (15), Indiana (1), Nebraska (1), South Dakota (1), and Wisconsin (1), highlighting its transmission within the swine population. This clade has been detected primarily in grow-finish farms (464), with fewer cases from breeding farms (101) and nurseries (62); however, this distribution may reflect sampling biases rather than the true prevalence across farm types.

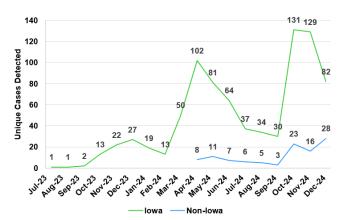
The detection frequency of cases related to this clade of Lineage 1C.5 steadily increased throughout the fall months (Figure 1). After a modest but noticeable rise in cases during November and December of 2023, a significant surge occurred in early 2024. Case numbers climbed from 13 in February to 110 detections by April, nearly a tenfold increase. Although detections declined during the summer months, the strain persisted and resurged in the fall of 2024. By October, case numbers rose to 154, followed by 145 in November, and 110 as of December 26. Notably, an increasing proportion of these detections were reported outside lowa, suggesting the strain's expanding geographic reach.

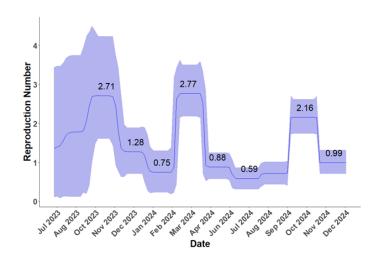
As no swine studies have yet been conducted on this clonally expanded clade of Lineage 1C.5, cycle threshold (Ct) values were used to assess potential differences that might suggest changes in the virus's clinical impact. The Ct value, a diagnostic measure from real-time PCR, indicates whether a sample is positive and semi-quantitatively reflects the amount of virus present. Median Ct values for the entire Lineage 1C.5 are dependent on sample type, with Ct's of approximately 17.3 being observed in lung specimens and 28.9 in oral fluid specimens. The emergent Lineage 1C.5 clonally expanded clade shows a similar pattern, with Ct values of 16.8 for lung and 27.9 for oral fluid. Average Ct values for lung and oral fluid specimens from Lineage 1C.5 as a whole are generally lower than those of Lineage 1A, indicating higher viral loads. The median Ct values for Lineage 1A are 18.4 for lung specimens and 31.4 for oral fluid specimens. This indicates a higher viral load on average in the samples positive for Lineage 1C.5 compared to Lineage 1A.

Bayesian phylodynamic analysis revealed that the genetic diversity of Lineage 1C.5 peaked in February 2023 but declined steadily throughout 2024, with a sharp drop in November 2023. This pattern of decreasing genetic diversity paired with persistent high levels of detection, suggests genetic selection favoring a strain with a transmission advantage. The effective reproduction number, which reflects the expected number of new cases generated from a single positive case, was estimated with phylogenetic methods. During the first wave in November 2023, each detected case led to about 2.7 new cases (point A, Figure 2). The rate dipped temporarily but climbed to 2.7 by March 2024 (point B) and rebounded to around two by October 2024 (point C) after a summer decline.

Ongoing monitoring of PRRSV genetic diversity, including the emergent Lineage 1C.5 and other strains, is crucial for effective management of PRRSV. The emergence of a new, divergent Lineage 1C.5 clonally expanded clade in Iowa, followed by its spread to other states, highlights an outbreak that warrants close attention, particularly regarding its potential to become dominant nationwide. Genetic analysis revealing a clonal expansion within Lineage 1C.5 suggests heightened transmissibility, while lower median Ct values and a higher effective reproduction number emphasize the clade's potential increased virulence and spread; but these features based on sequence analysis remain to be confirmed by experimental inoculation studies. These findings underscore the importance of continued surveillance to mitigate the impact of PRRSV outbreaks on swine health, particularly when new strains are emerging in the swine population.

Questions regarding the information contained in this article can be directed to Dr. Michael Zeller (mazeller@iastate.edu) at the ISU VDL.





SHIC Wean-to-Harvest Biosecurity: Economic and Epidemiologic Benefits of Market Haul Trailer Sanitation (Final Report)

A study funded by the Swine Health Information Center Wean-to-Harvest Biosecurity Research Program, in partnership with the Foundation for Food & Agriculture Research and Pork Checkoff, aimed to understand how different levels of trailer washing impacts the spread of porcine epidemic diarrhea virus. The goals of the study were to determine the best practices that balance disease control and economic feasibility across different swine production scenarios. Led by Drs. Jim Lowe and Ben Blair at the University of Illinois, the study determined that the necessary level of market haul trailer cleaning depends on PEDV prevalence and system connectivity. These insights can help producers develop tailored cleaning protocols that enhance swine health and productivity while effectively managing costs.

The transmission of PEDV within swine production systems poses significant challenges, particularly through market haul trailers transporting pigs between wean-to-finish farms and slaughter facilities. This study aimed to determine the most effective and cost-efficient way to clean market haul trailers transporting these pigs to reduce PEDV transmission while balancing economic feasibility. Two system types were evaluated using computer simulations to model swine production systems under various conditions. The first scenario focused on a single production system with 24,000 sows across eight sites. The second scenario evaluated a region with 24,000 sows divided into four4eographically related systems but operationally independent.

Simulations evaluated how washing different proportions of trailers at a consistent washing efficacy rate would affect the spread of PEDV. Scenarios were conducted with PEDV prevalence levels ranging from low (5%), moderate (10%) and high (20%) to see how PEDV prevalence impacted the effectiveness of trailer washing on disease reduction. Production was set to occur at fixed rates and under fixed time constraints, with weanto-finish farms taking two weeks to fill and six weeks to empty completely, resulting in a 22-week turn. The total costs per scenario included PEDVinfection related expenses and operational costs for truck washing.

Overall results indicated significant reductions in PEDV transmission with increased trailer decontamination. Findings for the single production system scenario showed washing 100% of trailers significantly reduced the number of infected farms, with an average of 23 infected premises. Washing 60% of trailers was identified as a cost-effective strategy for the single production system, achieving a significant reduction in disease spread at a lower cost of about \$32,956 per farm.

In geographically related systems, washing 100% of trailers significantly reduced the number of infected farms, with an average of 10.5 infected premises. Surprisingly, researchers found washing 0% of trailers was found to be the most cost-effective in these segregated systems, costing about \$25,664 per farm. These findings suggest that extensive decontamination might not always be necessary in such segregated systems with dedicated transport.

In addition to the 10% PEDV prevalence rate utilized in the referenced results above, high (20%) and low (5%) PEDV prevalence rates were also evaluated. In scenarios with high PEDV prevalence, it was necessary to wash 80% of trailers to achieve a significant reduction in the number of infected farms at a cost of \$48,957 per farm. In low prevalence scenarios, washing trailers were not required to optimize costs, which dropped to \$26,862 per farm. The study shows that cleaning market haul trailers is crucial for controlling the spread of PEDV, but the extent of washing needed can vary. For interconnected systems or during high PEDV prevalence periods, thorough washing of all trailers is essential. However, in more isolated systems or when PEDV prevalence is low, producers may save costs without compromising biosecurity by washing fewer trailers. These findings offer valuable insights for the swine industry by blending epidemiological and economic analysis techniques.

Additional steps that can enhance biosecurity include performing an assessment of current biosecurity measures with a focus on areas of improvement, tailoring decontamination strategies based on disease prevalence in the area considering efficacy and cost, adjusting strategies as needed depending on emerging data and best practices, and engage with veterinary and biosecurity experts to ensure protocols are sciencebased and specific to farm conditions.

This study provides unique insights into the role of trailer decontamination in mitigating PEDV transmission within the swine industry. By implementing strategic decontamination protocols, producers can significantly reduce disease spread, enhance biosecurity, and improve the overall health and productivity of their herds. While the results offer valuable guidance, producers are encouraged to adapt these strategies to their unique production contexts and continuously refine their practices based on ongoing assessments and expert advice.

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2024 Highlights from SHIC Domestic Swine Disease Monitoring

The Swine Health Information Center recently renewed funding for the Domestic Swine Disease Monitoring Reports through September 2025. Drs. Giovani Trevisan and Daniel Linhares, Iowa State University, lead the program which was initially funded by SHIC in 2017 and continues to focus on the analysis and reporting of collated veterinary diagnostic laboratory data to identify emerging endemic disease trends. Monthly reports provide an early warning system for veterinarians and producers to prompt preventative actions such as increasing monitoring and heightening biosecurity measures. Highlighted from 2024, new analysis tools and additional pathogen data helped enhance the value of the reports to the US swine industry.

The SDRS is the only publicly available source of swine health information from 6 US veterinary diagnostic laboratories representing >96% of all swine samples submitted for testing in the National Animal Health Laboratory Network. With a database containing information for nine endemic porcine pathogens and more than 1.5 million cases, SDRS is one of the largest US and international databases for veterinary diagnostic information. The SDRS has provided science-based spatiotemporal information on pathogen activity in all age categories, from boar studs to breeding herds to finishing with great representation of the US swine industry. Incorporated in 2024, an SDRS Blast tool for PRRSV allows veterinarians, producers, and other users to compare their ORF5 sequences with those in the SDRS database, identify when and where similar sequences in the database have occurred before, and define their genetic nomenclatures by lineage, RFLP, and variant. Further, new SDRS dashboards with revamped information debuted in 2024, improving navigation and providing new tools such as the influenza A virus state-level monitoring. Weekly monitoring of influenza A virus (IAV) PCR detection was added in the PDF reports.

Also added in 2024 is a new PRRSV ORF 5 sequence page in the PDF report. This page includes charts with information about the total number of PRRSV ORF5 sequences performed, the total number of sequences with less than 95% similarity within the SDRS database, the top Lineage and RFLP detected in the US, and the most frequent sequences detected across US states. Implementation of the PRRSV ORF5 variant classification system and display in the SDRS Blast tool also occurred.

PEDV genotype data was included in 2024 to provide new information on variant data that can be classified based on specific genetic characteristics of the spike protein as INDEL and Non-INDEL variants. Moreover, SDRS is one of the sources of information supporting the AASV PEDV Elimination Task Force established in 2024, providing data to aid the US swine industry in tracking PEDV activity in the field.

In 2024, SDRS project website pages including the dashboards and Blast tool had 2,215 unique IP visitors. Across the calendar year, 12 editions of PDF, audio, and video reports were shared via email to 474 registered receivers from 195 organizations from 15 different countries. On the FieldEpi LinkedIn page, the SDRS videos achieved more than 51,395 visualizations. SDRS hosted 12 podcast editions with 11 special guests. The SDRS YouTube channel achieved 5,162 views of video reports and education material. Audio reports were shared through podcast platforms, achieving 3,206 downloads from 23 different countries.

SDRS has shown its utility as a monitoring and early warning system that can identify and track

significant and unexpected changes occurring for swine pathogens. During fall 2024, PRRSV had the highest historical percentage of PCR-positive submissions in the wean-to-market category (42.3% of positive cases) since fall 2020. The weanto-market category represented 56% of the L1C.5 detections, with much of this activity being related to a record detection of PRRSV lineage 1C.5 within a single month (501 in November 2024).

The most frequent wild-type PRRSV-2 strains detected in 2024 were L1C.5 (L1C variant) 1-4-4, L1A 1-7-4, and L1C.2 1-2-4. Of all wild-type strains detected in 2024, over 50% (3,144) were L1C.5, breaking the record of detection within a year since its first emergence in 2020. Most of the sequences were detected in Iowa (1,873), followed by Minnesota (524), Missouri (309), Nebraska (160), and Ohio (40).

During summer 2024, PEDV had the lowest historical percentage of positive submissions in the adult/sow farm category (4.42% of positive cases). March 22, 2021, marked the last field sample received at an SDRS laboratory with a PCR positive result for TGEV. Up to December 2024, more than 165,000 submissions, including more than 400,000 samples, have been tested for TGEV with no TGEVpositive result being detected. M. hyopneumoniae percentage of PCR-positive submissions from breeding herds have decreased substantially from 2021 (21.75%) to 2022 (13.5%) and continued to decrease in 2024 (12%). In contrast, in the weanto-market category, M. hyopneumoniae positivity reached the highest levels (27%) since the fall of 2020. However, using ISU VDL data, the number of cases with a confirmed tissue diagnosis indicating lesions for M. hyopneumoniae decreased over time, reaching a record low number in 2024 (203 cases).

In 2024, PCV3 maintained its detection trend as being the only pathogen with higher positivity in adult/sow farms compared to the wean-to-market category across all months. Yearly average PCV2 positivity in the adult/sow farm category decreased from 39% in 2023 to 33% in 2024. Also, PCV2confirmed tissue diagnosis decreased in 2024 (399 cases) compared with 2023 (540).

Influenza A virus bi-seasonality pattern of PCR detection continued to occur in the spring and fall

of 2024 as expected. However, the peaks of overall positivity were slightly higher in 2024 compared with 2023. In 2023, the peaks of overall IAV positivity occurred in May (34% positivity) and November (33% positivity). In 2024, the peaks of positivity occurred in March (38%) and November (35%).

In 2024, there were fewer influenza A virus subtyping and PEDV genotype tests. The majority of this decrease was attributed to testing strategies by some participant VDLs that started to offer the screening PCR separate from the subtype/genotype PCRs that were previously offered together. Also, some production systems started to test PEDV genotype in-house.

At the ISU VDL, PRRSV had the highest number of confirmed diagnoses (2,566) followed by Streptococcus suis (1,735) and influenza A virus (935) in 2024. Pathogens including PRRSV, influenza A virus, P. multocida, Actinobacillus suis, Streptococcus suis, and Salmonella have given increased signals for diagnosis in October and November 2024.

The information gathered and reported for the SDRS project serves as a vital resource for producers and veterinarians to monitor and identify changes in swine health. Early identification of diagnostic trends in targeted pathogens can support actions geared towards disease prevention such as increased monitoring and increased focus on biosecurity and supports SHIC's mission to reduce the threat and impact of emerging diseases.

SWINE DISEASE MONITORING REPORTS

DOMESTIC

This month's Domestic Swine Disease Monitoring Report brings information about a turning point in the case positivity of PRRSV with a moderate decrease in detection for the wean-to-market category (42% in December compared with 46% in November). The positivity was mainly driven by the PRRSV lineage 1C.5, which represented over 50% of all wild-type detections in 2024. PEDV, PDCoV, Mycoplasma hyopneumoniae, and influenza A positivity ended the year following the overall expected detection curve but with above-forecasted detection levels for some state-specific baselines. In the confirmed tissue diagnoses, there were alarms for increased PRRSV, Streptococcus suis, Pasteurella multocida as the three most frequent diagnoses in November and December. The podcast presented by Dr. Guilherme Cezar, SDRS Coordinator, provides a review of 2024 pathogen activity and SDRS project implementations.

VIEW REPORT

GLOBAL

In the January Global Swine Disease Monitoring Report, read about African swine fever remaining prevalent in Poland, with 44 outbreaks reported in domestic pig herds in 2024. This is 14 more than in 2023 and 30 more than in 2022. ASF has been confirmed in Sri Lanka with 135 outbreaks reported since the initial case on October 25. The Rosalia strain of PRRSV in Spain remains a concern with studies reporting promising results in reducing mortality, improving productivity, and lowering production costs. At the United Kingdom's Dover Port, over six tonnes of illegal meat including pork, was confiscated during a 14-hour operation. The meat was shipped from ASF-affected regions in Romania.

VIEW REPORT

MORRISON SWINE HEALTH MONITORING PROJECT

🗛 MSHMP 🎮 SHC 50 PRRS season 09-10 10-11 -11-12 12-13 -13-14 14-15 -15-16 16-17 -17-18 18-19 -19-20 20-21 21-22 45 40 35 Incidence (%) 30 25 20 15 i 21-22 22-23 23-24 24-25 10 5 0 Jul Aug Sep Oct Nov Dec Jan Feb Mar Apr May Jun PRRS Cumulative Incidence for MSHMP Beginning July 1, 2009

Chart 1 - PRRS cumulative incidence as of November 27, 2024

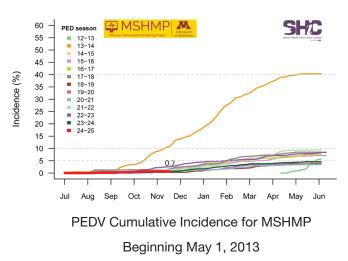


Chart 1 – PED Cumulative incidence as of November 27, 2024