

Swine Disease Reporting System Report # 85 (March 04, 2025)

What is the Swine Disease Reporting System (SDRS)? SDRS includes multiple projects that aggregate data from participating veterinary diagnostic laboratories (VDLs) in the United States of America, and reports the major findings to the swine industry. Our goal is to share information on activity of endemic and emerging diseases affecting the swine population in the USA, assisting veterinarians and producers in making informed decisions on disease prevention, detection, and management.

After aggregating information from participating VDLs and summarizing the data, we ask for the input of our advisory group, which consists of veterinarians and producers across the US swine industry. The intent is to provide an interpretation of the observed data, and summarize the implications to the industry. Major findings are also discussed in monthly podcasts. All SDRS reports and podcasts are available at www.fieldepi.org/SDRS.

Swine Health Information Center (SHIC)-funded Domestic Swine Disease Surveillance Program: collaborative project among multiple VDLs, with the goal to aggregate swine diagnostic data and report it in an intuitive format, describing dynamics of pathogen detection by PCR-based assays over time, specimen, age group, and geographical area. Data is from the Iowa State University VDL, South Dakota State University ADRDL, University of Minnesota VDL, Kansas State VDL, Ohio ADDL, and Purdue ADDL.

Collaborators:

Swine Disease Reporting System office: Principal investigators: Daniel Linhares & Giovani Trevisan; Project coordinator: Guilherme Cezar

Iowa State University: Edison Magalhães, Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Srijita Chandra, Eric Burrough, Phillip Gauger, Joseph Thomas, Darin Madson, Michael Zeller, Rodger Main.

University of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, Stephanie Rossow, Matt Sturos, Hemant Naikare.

Kansas State University and Kansas Dept. of Agr.: Rob McGaughey, Franco Matias-Ferreyra, Jamie Retallick, Jordan Gebhardt, Sara McReynolds.

South Dakota State University and South Dakota AIB: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings, Beth Thompson.

Ohio Animal Disease and Diag. Lab. and *The Ohio State University*: Melanie Prarat, Dennis Summers, Andréia Arruda.

Purdue University and *Indiana State BOAH*: Craig Bowen, Kenitra Hendrix, Joseph Boyle, James Lyons, Kelli Werling.

Disease Diagnosis System: Consisting of reporting disease diagnosis (not just pathogen detection by PCR), based on diagnostic codes assigned by veterinary diagnosticians from ISU-VDL.

PRRSView and FLUture: Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL.

PRRS virus RFLP/Lineage report and BLAST tool: Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

Audio and video reports: Key findings from SDRS projects are summarized monthly in a conversation between investigators and is available in the Spotify, Apple Podcast, Google podcast, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

Advisory Group: Providing their comments and perspectives monthly: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Mason, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, and Lauren Glowzenski.

Note: This report contains data up to February 28, 2025.



Figure 1. Top: Left: Results of PRRSV RT-PCR cases over time; Right: Proportion of accession ID cases tested for PRRSV by age group per year and season. Bottom: Left Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 4 years; Right: Percentage of PRRSV PCR-positive results, by age category, over time. Wean to market corresponds to nursery and grow-finish. Adult/Sow correspond to Adult, boar stud, breeding herd, replacement, and suckling piglets. Unknown corresponds to not informed site type or farm category.

SDRS Advisory Group highlights:

- Overall, 26.34% of 6,511 cases tested PRRSV-positive in February, similar to 27.71% of 7,431 in January;
 - Positivity in the adult/sow category in February was 23.34% (701 of 3,003), similar to 23.2% (805 of 3,470) in January;
- Positivity in the wean-to-market category in February was 39.73% (801 of 2,016), a moderate decrease from 43.72% (1,010 of 2,310) in January;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA;





Most frequent PRRSV strains detected across U.S. states



Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	L1C.5 1-4-4	L1C.2 1-2-4	L1A 1-7-4
IL	L1A 1-4-2	L1C.2 1-2-4	L1C.5 1-4-4
IN	L1A 1-7-4	L1A 1-7-2	L1H 1-8-4
KS	L1H 1-8-4	L1A 1-7-4	L1H 1-4-4
MN	L1C.5 1-4-4	L1C.2 1-2-4	L1C.5 1-3-4
мо	L1C.5 1-4-4	L1C.5 1-3-4	L1C.5 1-7-4
NC	L1A 1-7-4	L1A 1-4-4	PRRSV-1
NE	L1C.5 1-4-4	L1C.5 1-2-3	L1H 1-8-4
ОН	L1A 1-4-4	L1C.5 1-4-3	L1A 1-7-2
ок	L1A 1-7-4	L5A 2-2-2	L1H 1-4-4
SD	L1C.5 1-4-4	L1C.3 1-4-1	L1A 1-7-4

Figure 1. Top: Left: Number of PRRSV ORF5 sequences detected by age category; Right: Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher than 606 nucleotides are not included in this analysis); Bottom Left: 15 PRRSV ORF5 sequences most frequent detected by Lineage and RFLP; Right: Most frequent detected PRRSV ORF5 sequences by lineage and RFLP at U.S. state level.

SDRS Advisory Group highlights:

• During February 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MO, MN, IL, NE, IN, OH, SD, TX, CA, WI (respective number of sequences: 167, 29, 13, 11, 10, 3, 3, 2, 2, 1, 1).

In February L1C.5 1-4-4 (190) was the PRRSV sequence most detected in the U.S., followed by L1A 1-7-4 (45), and L1C.2 1-2-4 (31);
Click on the links here to access the PRRSV genotype dashboard and the SDRS Blast tool to compare your PRRSV ORF5 sequence with the SDRS database.

• The advisory group highlighted that the higher virulence and more prolonged survival of the L1C.5 virus than other strains contribute to its persistence. The L1C.5 variants are detected at higher viral load, i.e., lower Ct values, what may contributed for additional infections. The movement of these viruses follows pig movements, which may explain the higher activity in areas that predominantly receive pigs, such as the Midwest and, particularly, Iowa.



Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time; Second from top: Left PEDV; Right PDCoV percentage of positive PCR positive results, by age category over time. Facilities are cases submissions from packing plants, truck washes, and vehicles. Third from top: Left PEDV; Right PDCoV expected percentage of positive results for cases tested by RT-PCR and 95% confidence interval for 2025 predicted value. Bottom Left: Number of PEDV genotype detection over time; Right: Number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 9.24% of 4,199 cases tested PEDV-positive in February, similar to 9.33% of 4,609 in January;
 - Positivity in the adult/sow category in February was 7.39% (110 of 1,488), similar to 7.7% (126 of 1,636) in January;
 - Positivity in the wean-to-market category in February was 13.22% (208 of 1,573), similar to 11.78% (204 of 1,732) in January;
- Positivity in the facilities category in February was 8.59% (11 of 128), a marked decrease from 23.84% (36 of 151) in January;
 - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN;
 - Overall, 0% of 158 samples had mixed PEDV genotype detection in February, similar to 1.72% of 174 in January;
- Overall, 4.62% of 4,130 cases tested PDCoV-positive in February, similar to 4.42% of 4,548 in January;
 - Positivity in the adult/sow category in February was 2.02% (29 of 1,439), similar to 1.82% (29 of 1,594) in January;
- Positivity in the wean-to-market category in February was 7.68% (120 of 1,563), similar to 7.32% (126 of 1,722) in January;
- Positivity in the facilities category in February was 5.47% (7 of 128), a substantial decrease from 11.26% (17 of 151) in January;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN;
- There was 0 positive case for TGEV RNA-PCR in February, 2025 over a total of 4,031 cases tested. It has been 48 months (with a total of 173,982 cases tested) since the last TGEV PCR-positive result;
- Advisory group comment on the Bonus page (page 10).



Topic 3 – Detection of M. hyopneumoniae DNA by PCR.





Figure 3. Top: Left MHP; MHP Case results tested by PCR over time. Right MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 14.74% of 787 cases tested *M. hyopneumoniae*-positive cases in February, similar to 14.9% of 866 in January;
 - Positivity in the adult/sow category in February was 8.81% (20 of 227), similar to 9.34% (27 of 289) in January;
 - Positivity in the wean-to-market category in February was 20.16% (76 of 377), similar to 20.43% (85 of 416) in January;
- Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states;



Figure 1. Top: Left: Results of PCV2 PCR cases over time; Right: PCV2 PCR-positive results, by category over time. Middle: Left: Average Ct values of PCV2 submissions by specimen; Right: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and WI), Eastern (AL, AR, CT, DE, FL, GA, KY, LA, MA, ME, MD, MI, MS, NC, NH, NJ, NY, OH, PA, RI, SC, TN VA, VT and WA), North Central (MN, ND and SD), Western (AK, AZ, CA, CO, HI, ID, KS, MT, NM, NV, OK, OR, TX, UT, WA and WY). Red line represent Ct threshold calculated using methodology based on Dx codes. Bottom Left: Results of PCV3 PCR cases over time; Right: PCV3 PCR-positive results, by category over time.

SDRS Advisory Group highlights:

- Overall, 39.13% of 943 cases tested PCV2-positive in February, similar to 39.75% of 1,102 in January;
 - Positivity in the adult/sow category in February was 28.5% (110 of 386), a moderate decrease from 32.5% (143 of 440) in January;
 - Positivity in the wean-to-market category in February was 47.71% (240 of 503), similar to 48.23% (273 of 566) in January;
 - In the month of February, the regions with the lowest PCV2 average Ct values in tissue submissions was Central (66 submissions;

average Ct 22.4), East Central (14 submissions; average Ct 24.2), Eastern (42 submissions; average Ct 24.4), Western (13 submissions; average Ct 26.7), and North Central (19 submissions; average Ct 28.9);

- Overall, 58.01% of 693 cases tested PCV3-positive in February, a moderate increase from 55.6% of 795 in January;
 - Positivity in the adult/sow category in February was 66.35% (207 of 312), similar to 65.25% (231 of 354) in January;
 - Positivity in the wean-to-market category in February was 53.45% (178 of 333), similar to 51.82% (185 of 357) in January.



Topic 5 – Detection of Influenza A Virus (IAV) RNA by RT-PCR.



Figure 3. Top: Left Results of IAV PCR cases over time. Right Percentage of IAV PCR-positive results, by category over time. Bottom: Left expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years. Right Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroamnidase regions detected. i.e., "H1 H3 N1").

SDRS Advisory Group highlights:

- Overall, 29.47% of 1,978 cases tested IAV-positive cases in February, a substantial increase from 24.39% of 2,239 in January;
- Positivity in the adult/sow category in February was 27.95% (116 of 415), a moderate increase from 24.71% (127 of 514) in January;
 Positivity in the wean-to-market category in February was 33.53% (341 of 1,017), a substantial increase from 28.02% (306 of 1,092)

• Fostivity in the wean-to-market category in February was 55.55% (541 of 1,017), a substantial increase from 28.02% (500 of 1,092 in January.

- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 3.83% of 209 samples had mixed subtype detection in February, similar to 2.14% of 234 in January.





Topic 6 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.



Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less frequent etiology/disease are grouped as "other". Non-confirmed diagnoses are not presented. This work is made possible due to the commitment and teamwork from the ISU-VDL diagnosticians who assign standardized diagnostic codes to each case submitted for histopathology: Drs. Almeida, Burrough, Derscheid, Gauger, Magstadt, Piñeyro, Siepker, Madson, Thomas, Gris and previous VDL diagnosticians who have contributed to this process.

Note: Disease diagnosis takes 1 to 2 weeks to be performed. The graphs and analysis contain data from January. 1 to February. 21, 2025.

SDRS Advisory Group highlights:

• PRRSV (456) led cases with confirmed etiology, followed by *S. suis* (247), and *G. parasuis* (116). PRRSV (426 of 1106) led the number of confirmed respiratory diagnoses, Rotavirus (112 of 406) lead the number of confirmed digestive diagnoses, and *S. suis* (27 of 44) led the number of confirmed neurological diagnoses.



Note: The SDRS is a collaborative project among multiple VDLs in the US swine industry. The VDL collaborators and industry partners are all invited to submit content to share on this bonus page related to disease prevention, control, and management. Stay tuned for more content in future editions.

Addition of new age category for enteric coronavirus RT-qPCR detection data: Facilities

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The Swine Disease Reporting System (SDRS) provides valuable insights into both endemic and emerging diseases impacting the swine population in the USA. SDRS has closely monitored nine pathogens' PCR test results in two age categories (adult/Sow farm and wean-to-market). Among these pathogens are three enteric coronaviruses (PEDV, PDCoV, and TGEV). TGEV hasn't had positive cases since March 2021, and PEDV and PDCoV showed trends of decreasing positivity over time. Therefore, one question was raised: "If we decreased positivity in our sow farms and finishing sites, why is it still difficult to eliminate PEDV and PDCoV"? Based on that question, the SDRS could categorize submissions from facilities like packing plants, truck washes, and vehicles and display them as a new-age category: "*Facilities*".

The cases categorized as facilities and tested for PEDV increased in 2020 (Figure 1), with Spring 2020 breaking the 200 case threshold for the first time. Then, Spring of 2021, the number of cases per season doubled compared with 2020, reaching 2024, the historically higher number of submissions within a year (1,842).



Figure 1. Number of PEDV RT-qPCR submitted in the vetrinary diagnostic laboratories since 2015.



Also, the percentage of positive submissions for facilities has been higher than the other age categories, mainly in 2024, where since March, the percentage of positive submissions has been above the wean-to-finish and adult/sow farm age categories (figure 2). This trend was broken in February 2025, when the wean-to-market category demonstrated a higher percentage of positive submissions. This data supports the comments of the advisory group that the industry needs to be aware of truck disinfection where the virus might be circulating until it becomes a biosecurity bridge affecting swine farms.



Figure 2. Percentage of positive submission by age category. Facilities data (green line) represents submissions coming from packing plants, truck washes and vehicles.

From now on, the SDRS will keep monitoring the cases coming from the facility data, which the specimen submitted is more than 99% environmental samples. It is important to highlight that the environmental samples coming from sow farms and wean-to-market are still being categorized as a specimen "*environmental*" within the phases "Adult/sow farm" and "Wean-to-Market" respectively. Therefore, the facility farm type only includes cases coming from vehicles, truck washes, and packing plants. This data will support the swine industry to take better decisions, envisioning eliminating PEDV and PDCoV from the swine industry.

Comment from the Advisory Group: The advisory group highlighted that their approach to PEDV testing involves a combination of strategies to ensure biosecurity and identify the PEDV presence. For breeding stock, they test either pre-shipment or upon arrival, while commercial farms are tested when clinical signs are evident. Non-animal testing has become increasingly important, focusing on truck washes, trailers, service staff vehicles, and various farm facilities. This practice has intensified in recent years to trace lateral infections, particularly in finishers and nurseries. Therefore, the number of PCRs performed for facility data increased since 2020. In addition, the increased monitoring of trucks and other biosecurity practices helped the industry understand the risk areas and maintain site cleanliness, especially during cold weather when cleaning and disinfecting are more challenging. Also, the positive testing at the "facilities" (truck washes, trailers, etc.) shed some light on how some of these lateral breaks may be occurring but also showed that the virus is still circulating in the field, whether identified in a pig or not.