Swine Disease Reporting System - Advisory Group Report
Report # 96 (February 3, 2026)

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 https://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: Quyen Thuc Le; Software Developer: Kinath Rupasinghe; Data Analyst: Sajan Kumar Thallapelly and Likhitha Nakka.

Iowa State Uni.: Gustavo Silva, Marcelo Almeida, Bret Crim, Eric Burrough, Phillip Gauger, Christopher Rademacher, Darin Madson, Michael Zeller, Rodger Main.

Uni. of Minnesota: Mary Thurn, Cesar Corzo, Albert Rovira, Matt Sturos, Hemant Naikare.

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

South Dakota State Uni and South Dakota AIB: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings, Eric Nelson, Mendel Miller and Marc Hammrich.

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

Purdue Uni 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 and OH-ADDL.

PRRSView and FLUture and : Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL. PRRSLoom-Variants: PRRSV-2 variant classification from UMN.

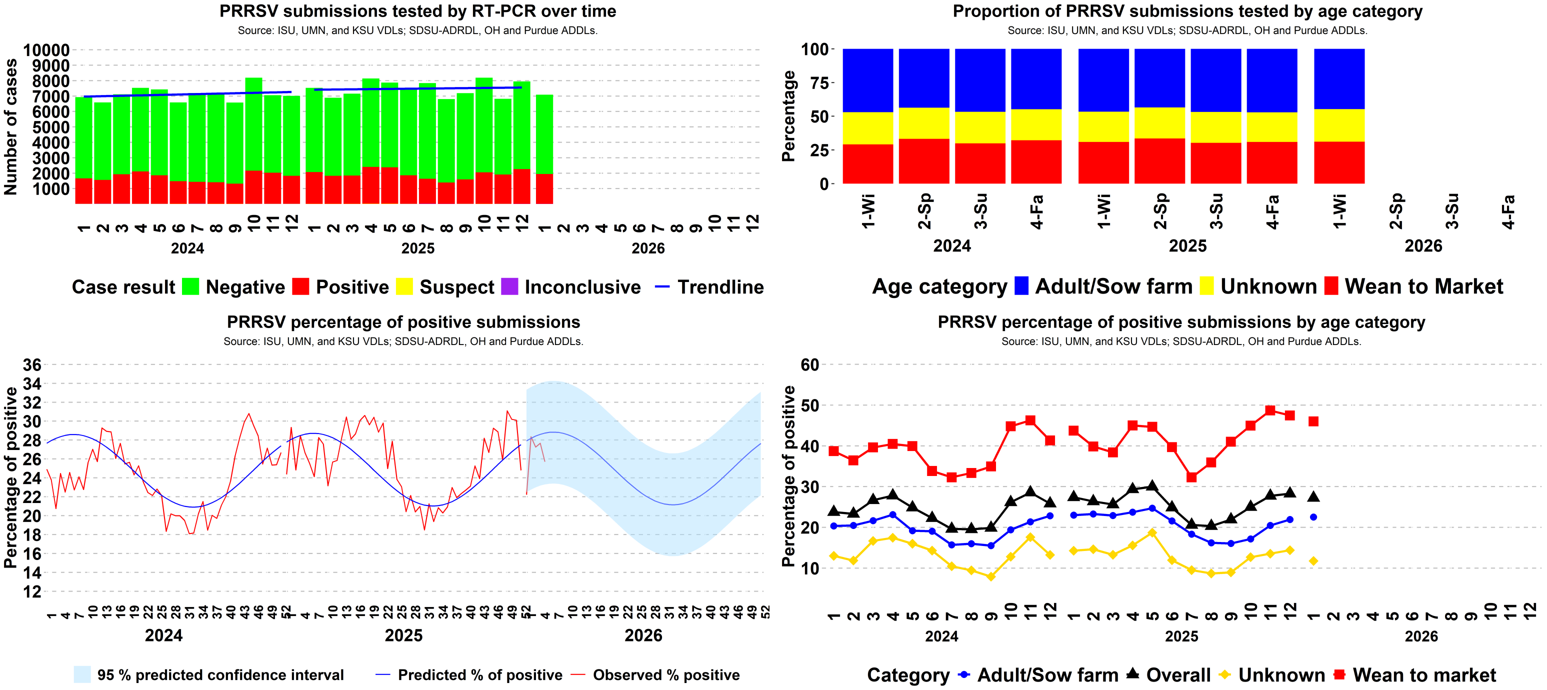
PRRS virus Genotyping report and BLAST tool: Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

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, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

Advisory Group: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Davenport, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, Lauren Glowzenski, Brooke Kitting and Dustin Oedekoven.

Note: This report contains data up to January 31, 2026.

Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.



PRRSV submissions tested by RT-PCR over time

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

Proportion of PRRSV submissions tested by age category

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

PRRSV percentage of positive submissions

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

PRRSV percentage of positive submissions by age category

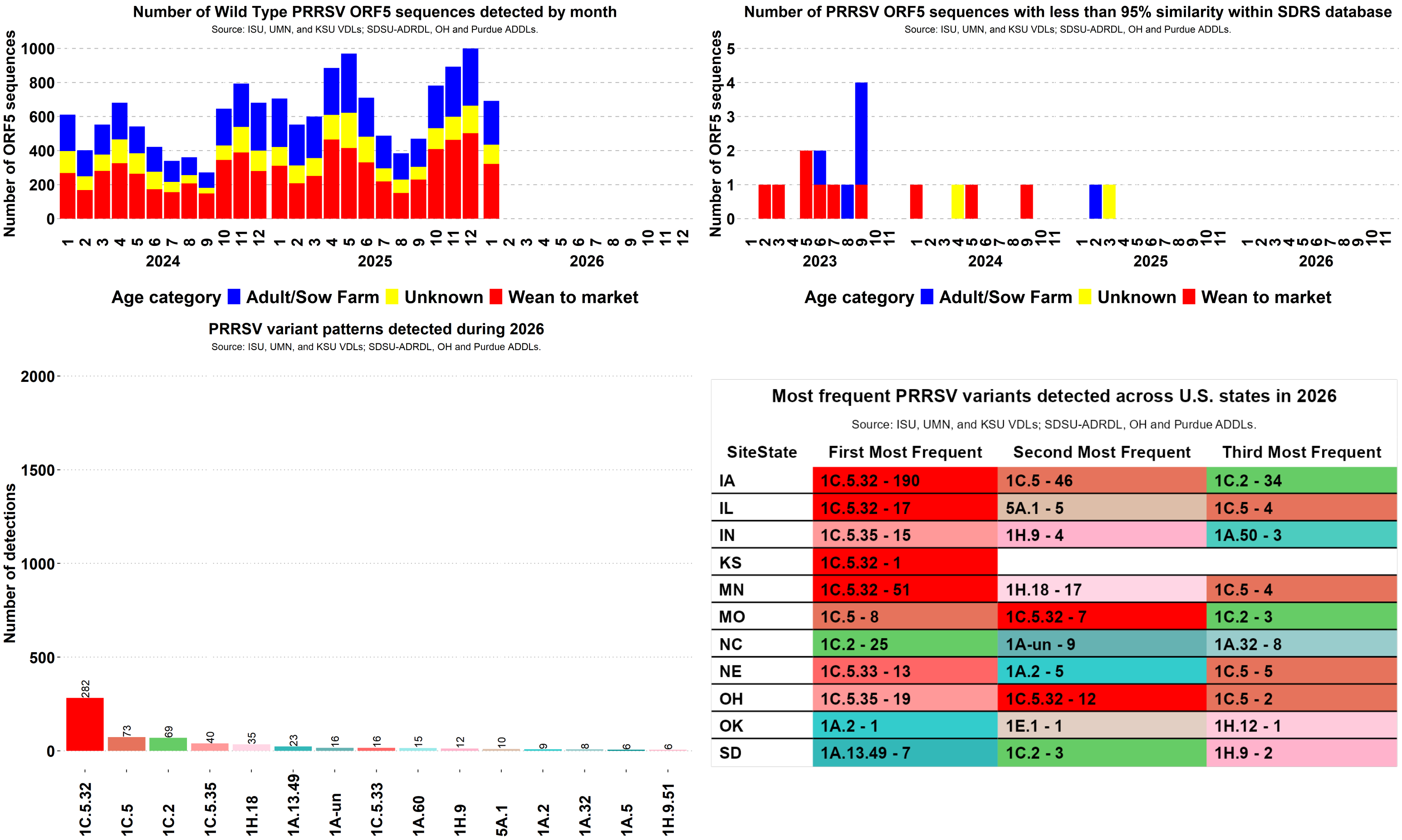
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 27.23% of 7,091 cases tested PRRSV-positive in January, similar to 28.29% of 7,949 in December;
  - Positivity in the adult/sow category in January was 22.53% (714 of 3,169), similar to 21.94% (824 of 3,755) in December;
  - Positivity in the wean-to-market category in January was 46.01% (1,015 of 2,206), similar to 47.46% (1,178 of 2,482) in December;
- Overall PRRSV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Several advisors emphasized that PRRSV remains the most significant endemic disease challenge, with several breeding herd outbreaks occurring through December and January. They have also reported a high incidence of lateral PRRSV transmission in nursery/finishing sites. Others reported PRRSV–IAV combination outbreaks, which they attributed to the ongoing high prevalence of lateral PRRSV in growing sites.

Topic 2 – PRRSV ORF5 sequence detections over time



Number of Wild Type PRRSV ORF5 sequences detected by month

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

Number of PRRSV ORF5 sequences with less than 95% similarity within SDRS database

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

PRRSV variant patterns detected during 2026

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

Most frequent PRRSV variants detected across U.S. states in 2026

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

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	1C.5.32 - 190	1C.5 - 46	1C.2 - 34
IL	1C.5.32 - 17	5A.1 - 5	1C.5 - 4
IN	1C.5.35 - 15	1H.9 - 4	1A.50 - 3
KS	1C.5.32 - 1		
MN	1C.5.32 - 51	1H.18 - 17	1C.5 - 4
MO	1C.5 - 8	1C.5.32 - 7	1C.2 - 3
NC	1C.2 - 25	1A-un - 9	1A.32 - 8
NE	1C.5.33 - 13	1A.2 - 5	1C.5 - 5
OH	1C.5.35 - 19	1C.5.32 - 12	1C.5 - 2
OK	1A.2 - 1	1E.1 - 1	1H.12 - 1
SD	1A.13.49 - 7	1C.2 - 3	1H.9 - 2

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 variant; *Right*: Most frequently detected PRRSV ORF5 sequences in 2026, shown by variant at the U.S. state level along with their respective detection counts **Note: un indicates unclassified**.

SDRS Advisory Group highlights:

- During January, the states with higher number of PRRSV 1C.5.32 detections were detected IA, MN, IL, OH, MO, NE, KS, NC (respective number of sequences: 190, 51, 17, 12, 7, 2, 1, 1).
- In January 1C.5.32 (282) was the PRRSV variant most detected in the U.S., followed by 1C.5 (73), and 1C.2 (69);
- 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.

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

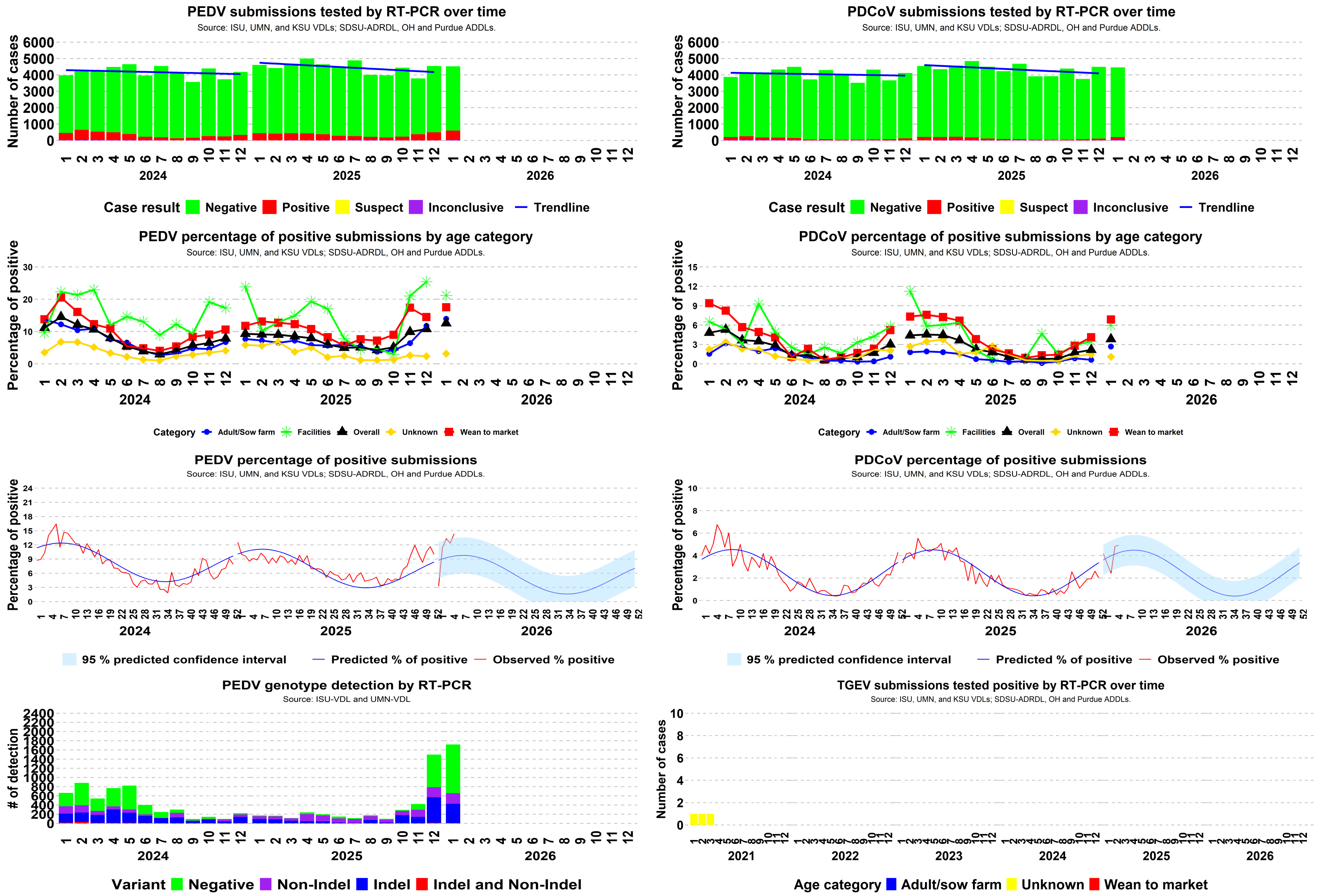
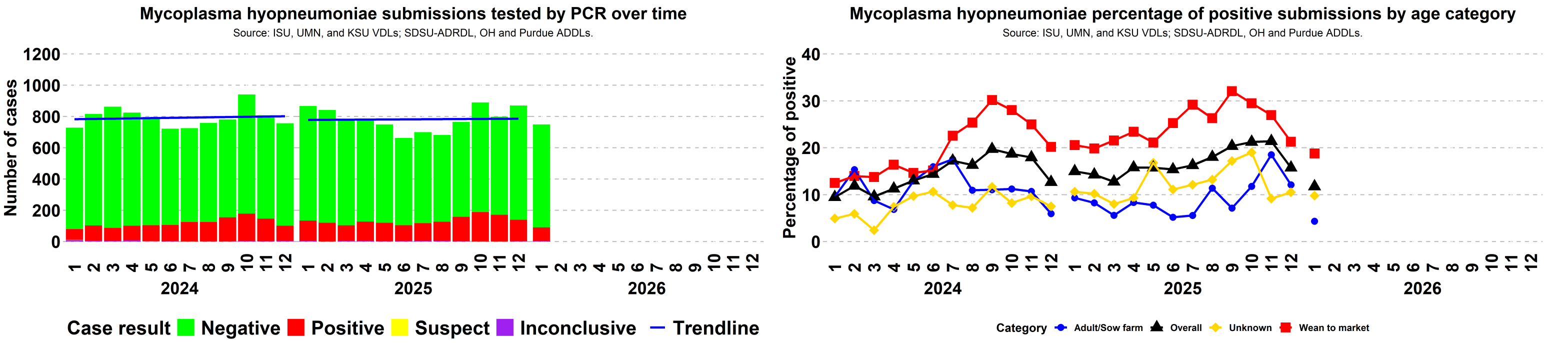


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection over time; Right TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 12.57% of 4,525 cases tested PEDV-positive in January, similar to 10.8% of 4,547 in December.
  - Positivity in the adult/sow category in January was 13.97% (223 of 1,596), a moderate increase from 11.78% (189 of 1,604) in December.
  - Positivity in the wean-to-market category in January was 17.52% (276 of 1,575), a moderate increase from 14.48% (230 of 1,588) in December.
  - Positivity in the facilities category in January was 21.19% (32 of 151), a moderate decrease from 25.43% (44 of 173) in December.
  - Overall PEDV-percentage of positive cases was within state-specific baselines in all 11 monitored states.
  - Overall, 0.29% of 1,718 samples had mixed PEDV genotype detection in January, similar to 0.8% of 1,498 in December.
- Overall, 3.83% of 4,459 cases tested PDCoV-positive in January, similar to 2.18% of 4,495 in December.
  - Positivity in the adult/sow category in January was 2.69% (42 of 1,563), a moderate increase from 0.63% (10 of 1,580) in December.
  - Positivity in the wean-to-market category in January was 6.86% (107 of 1,559), a moderate increase from 4.13% (65 of 1,573) in December.
  - Positivity in the facilities category in January was 5.96% (9 of 151), a moderate increase from 3.47% (6 of 173) in December.
  - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in NC.
- There was 0 positive case for TGEV RNA-PCR in January, 2026 over a total of 4,379 cases tested. It has been 58 months (with a total of 220,665 cases tested) since the last TGEV PCR-positive result.
- Advisors shared that some regions have experienced more PEDV outbreaks than usual for this time of year and increased lateral activity in finishing and nurseries during late 2025. Others noted that PEDV remains relatively quiet in wean-to-market, but recent sow farm positivity in some areas may create additional downstream pressure as the winter season progresses.

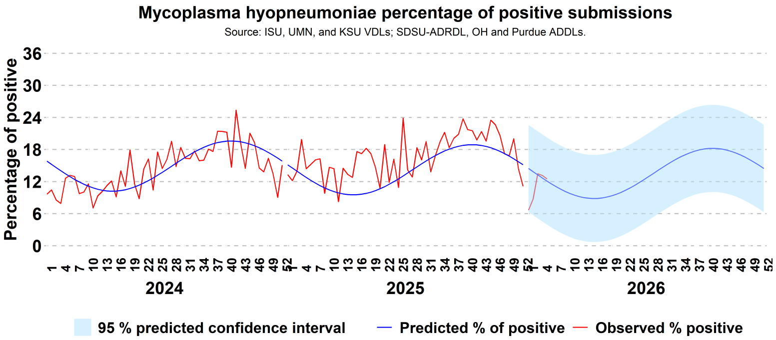
Topic 3 – Detection of *M. hyopneumoniae* DNA by PCR.


Mycoplasma hyopneumoniae submissions tested by PCR over time

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

Mycoplasma hyopneumoniae percentage of positive submissions by age category

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


Mycoplasma hyopneumoniae percentage of positive submissions

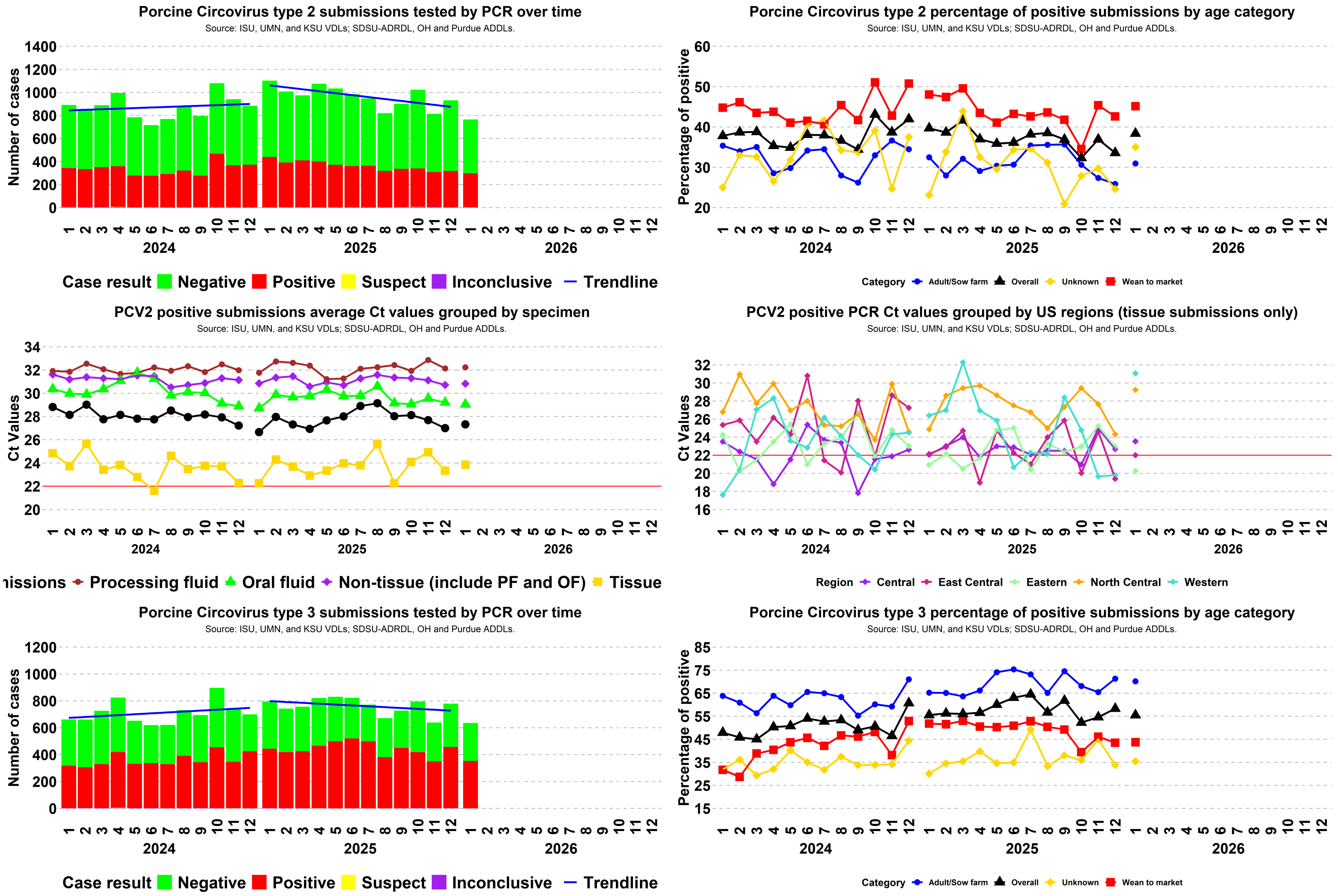
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Figure 1. Top: *Left* 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 2026 predicted value, based on weekly data observed in the previous 10 years.

SDRS Advisory Group highlights:

- Overall, 11.75% of 749 cases tested *M. hyopneumoniae*-positive cases in January, a moderate decrease from 15.75% of 870 in December;
  - Positivity in the adult/sow category in January was 4.35% (12 of 276), a substantial decrease from 12.1% (42 of 347) in December;
  - Positivity in the wean-to-market category in January was 18.79% (62 of 330), a moderate decrease from 21.29% (79 of 371) in December;
- Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states;

Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.


Porcine Circovirus type 2 submissions tested by PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Porcine Circovirus type 2 percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PCV2 positive submissions average Ct values grouped by specimen
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

PCV2 positive PCR Ct values grouped by US regions (tissue submissions only)
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Porcine Circovirus type 3 submissions tested by PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

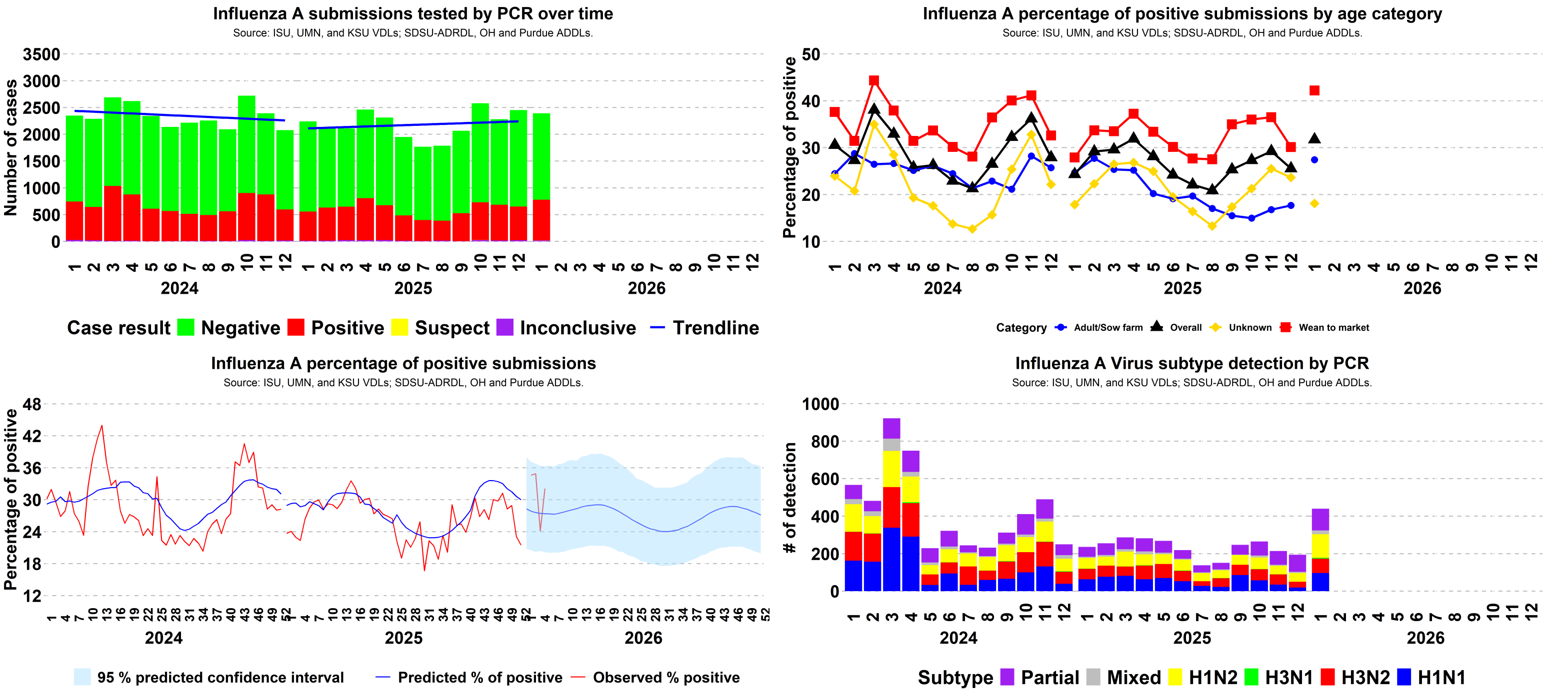
Porcine Circovirus type 3 percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 38.38% of 766 cases tested PCV2-positive in January, a moderate increase from 33.58% of 932 in December;
  - Positivity in the adult/sow category in January was 30.95% (91 of 294), a substantial increase from 25.87% (112 of 433) in December;
  - Positivity in the wean-to-market category in January was 45.16% (168 of 372), a moderate increase from 42.63% (185 of 434) in December;
  - In the month of January, the regions with the lowest PCV2 average Ct values in tissue submissions was Eastern (30 submissions; average Ct 20.3), East Central (23 submissions; average Ct 22), Central (48 submissions; average Ct 23.5), North Central (23 submissions; average Ct 29.2), and Western (5 submissions; average Ct 31.1);
- Overall, 55.5% of 636 cases tested PCV3-positive in January, a moderate decrease from 58.33% of 780 in December;
  - Positivity in the adult/sow category in January was 70.19% (219 of 312), similar to 71.33% (311 of 436) in December;
  - Positivity in the wean-to-market category in January was 43.72% (101 of 231), similar to 43.51% (124 of 285) in December.

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


Influenza A submissions tested by PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Influenza A percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Influenza A percentage of positive submissions
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

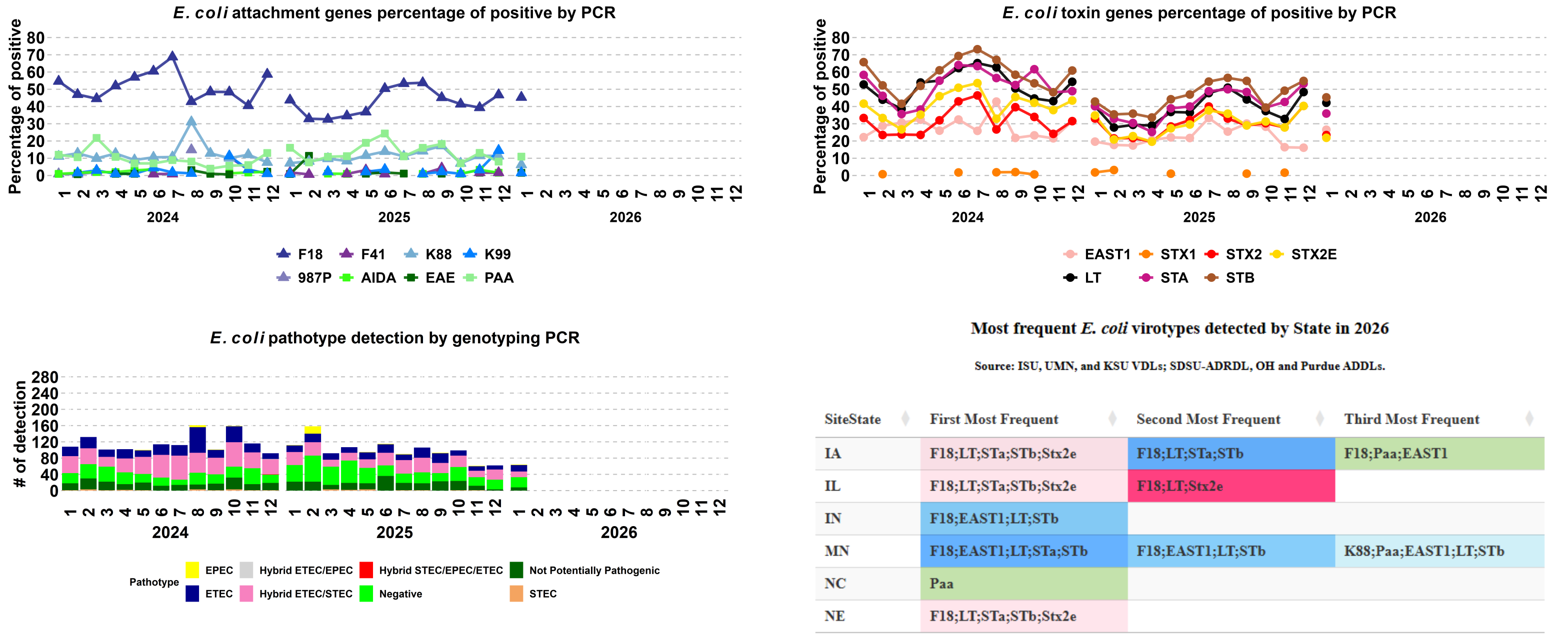
Influenza A Virus subtype detection by PCR
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Figure 1. 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 2026 predicted value, based on weekly data observed in the previous 4 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, 31.73% of 2,392 cases tested IAV-positive cases in January, a substantial increase from 25.57% of 2,452 in December;
  - Positivity in the adult/sow category in January was 27.43% (141 of 514), a substantial increase from 17.69% (89 of 503) in December;
  - Positivity in the wean-to-market category in January was 42.2% (487 of 1,154), a marked increase from 30.12% (359 of 1,192) in December.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 4.55% of 440 samples had mixed subtype detection in January, similar to 3.09% of 194 in December.
- Some advisors noted that IAV activity has generally followed a normal seasonal pattern, with expected levels of circulation and a brief surge of introductions earlier in the winter before things settled down. Others reported that IAV continues to be seen in wean to finish, though prevalence in some areas remains low, and a few reported that IAV activity contributes for PRRSV flare-ups in herds under closure.

Topic 6 – Detection of *E. coli* DNA by Genotyping PCR.


E. coli attachment genes percentage of positive by PCR

E. coli toxin genes percentage of positive by PCR

E. coli pathotype detection by genotyping PCR

Most frequent *E. coli* virotypes detected by State in 2026

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

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	F18;LT;STa;STb;Stx2e	F18;LT;STa;STb	F18;Paa;EAST1
IL	F18;LT;STa;STb;Stx2e	F18;LT;Stx2e	
IN	F18;EAST1;LT;STb		
MN	F18;EAST1;LT;STa;STb	F18;EAST1;LT;STb	K88;Paa;EAST1;LT;STb
NC	Paa		
NE	F18;LT;STa;STb;Stx2e		

Figure 1. Top: *Left E. coli* PCR-Positive results by attachment genes over time. *Right E. coli* PCR-Positive results by toxin genes over time. **Bottom:** *Left E. coli* number of samples tested by PCR genotype and their respective pathotype classification. *Right* Most frequent detected *E. coli* virotype by PCR in 2026 at U.S. state level (color code on table cells associated with the pathotype legend).

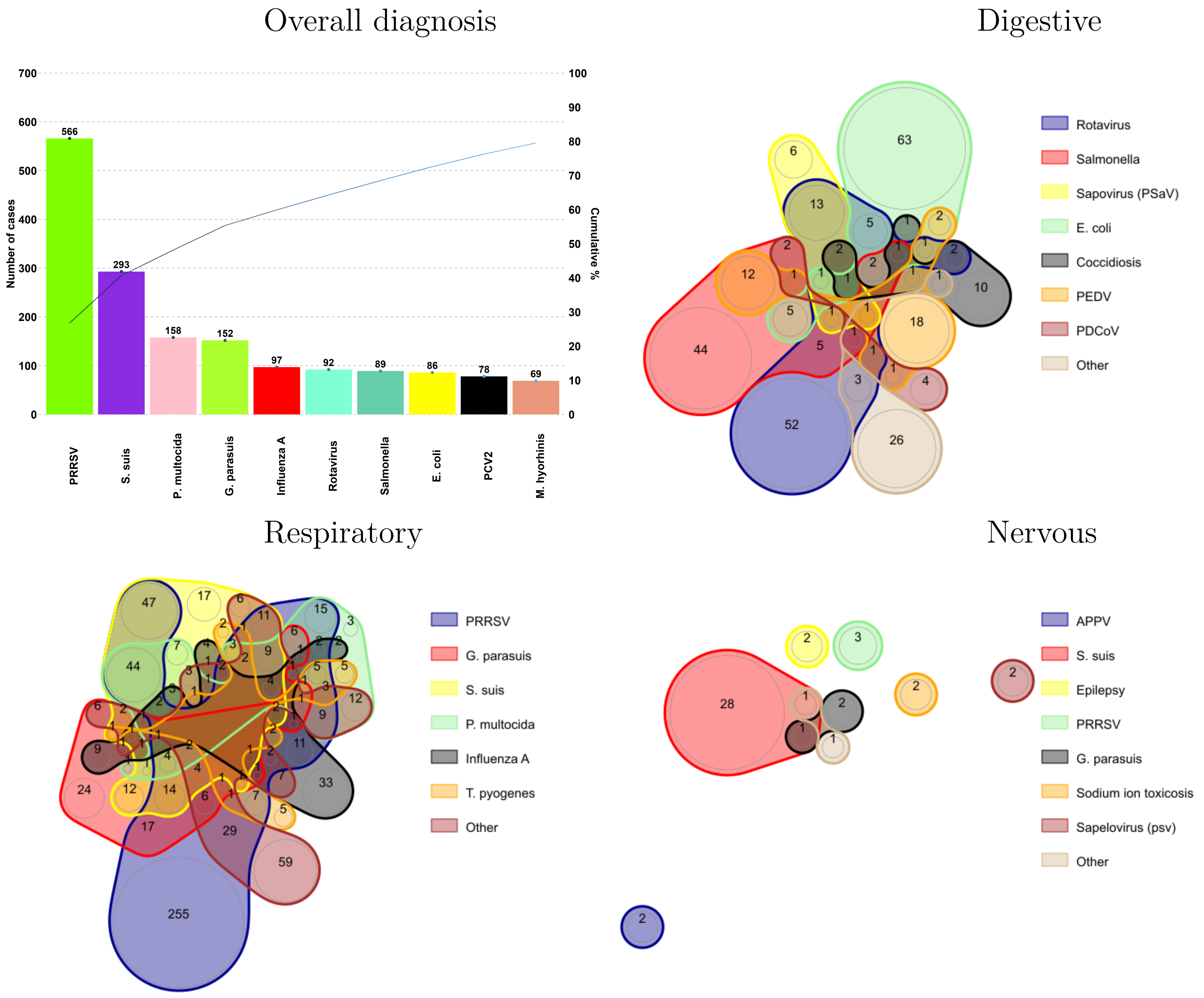
Education Material:

- Click on the links here to access the *E. coli* PCR Genotyping Interpretation Tool
- **Attachment genes: Fimbriae** – F18, K88(F4), K99(F5), 987P(F6), F41; **Adhesins** – EAE (Intimin), PAA, AIDA
- **Toxin genes: Heat-labile** – LT; **Heat-stable** – STa and STb; **Shiga toxins** – Stx1, Stx2 and Stx2e; and EAST1
- **Enterotoxigenic *E. coli* (ETEC):** Has fimbriae and toxin (not Stx2e) genes. Associated with neonatal and post-weaning diarrhea
- **Shiga toxin-producing *E. coli* (STEC):** Has fimbriae (F18) and toxin (must be Stx2e) gene. Associated with edema disease
- **Enteropathogenic *E. coli* (EPEC):** Presence of the EAE (Intimin) adhesin
- **Hybrids (ETEC/STEC, ETEC/EPEC, STEC/EPEC, ETEC/STEC/EPEC):** Combination of characteristics of more than one pathotype

SDRS Advisory Group highlights:

- Overall, 64 samples were tested for *E. coli* PCR in January;
  - In January the *E. coli* pathotype with higher number of sample detections were ETEC (16 detections), Hybrid ETEC/STEC (14 detections), Not Potentially Pathogenic (8 detections);
  - In January the *E. coli* attachment genes with higher detection rate were F18 (45.31%), PAA (10.94%), K88 (6.25%);
  - In January the *E. coli* toxin genes with higher detection rate were STB (45.31%), LT (42.19%), STA (35.94%).

Topic 7 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL and OH-ADDL


Overall diagnosis

Digestive

Respiratory

Nervous

Figure 4. ISU-VDL and OH-ADDL 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, Yanez 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 December. 01, 2025 to January. 26, 2026

SDRS Advisory Group highlights:

- PRRSV (566) led cases with confirmed etiology, followed by *S. suis* (293), and *P. multocida* (158). PRRSV (531 of 1378) led the number of confirmed respiratory diagnoses, Rotavirus (92 of 372) lead the number of confirmed digestive diagnoses, and *S. suis* (30 of 46) 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.*

Disease index based on confirmed tissue diagnosis data to assess endemic swine pathogen activity in the United States of America

Guilherme Cezar[1], Quyen Le[1], Eric Burrough[1], Daniel Linhares[1], Giovani Trevisan[1]

1 - Iowa State University, Ames, IA, USA.

A disease index was developed to evaluate endemic swine pathogen activity in the United States using confirmed tissue diagnosis data from the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL). The dataset included 76,825 porcine tissue cases submitted between January 1, 2020, and December 31, 2025, representing 81 etiologies across bacterial, viral, parasitic, and metabolic/intoxication categories.

The disease index incorporated four epidemiological variables: (1) disease occurrence, defined as the total number of confirmed diagnostic submissions for each etiology per calendar year; (2) disease co diagnosis, representing the frequency of multiple etiologies the same submission; (3) number of Early Aberration Reporting System (EARS) alarms, capturing the frequency of significantly increased diagnostic activity detected through syndromic surveillance; and (4) state occurrence, reflecting the number of U.S. states reporting at least one confirmed diagnosis for each etiology within the evaluated time frame. Each variable contributed to the final index according to predetermined weights: disease occurrence (0.50), EARS alarms (0.26), state occurrence (0.15), and co diagnosis (0.09). The resulting index ranged from 0.01 to 1, with higher values indicating greater pathogen activity.

Across the six year period from 2020 to 2025, porcine reproductive and respiratory syndrome virus (PRRSV) and *Streptococcus suis* (*S. suis*) consistently ranked as the top two pathogens, each maintaining high disease index values and underscoring their persistent impact on U.S. swine health. Several other pathogens remained within the top 10 annually, including *Glaesserella parasuis* (*G. parasuis*), *Pasteurella multocida* (*P. multocida*), influenza A virus (IAV), and rotavirus, while porcine circovirus 2 (PCV2) and *Escherichia coli* (*E. coli*) appeared in the top 10 during four of the six years, indicating stable endemic activity. Additional pathogens entered the top 10 in specific years, such as *Mycoplasma hyorhinis* (*M. hyorhinis*) (2021–2023), *Mycoplasma hyopneumoniae* (*M. hyopneumoniae*) (2020, 2021, 2024), *Salmonella* spp. (2022, 2024), *Trueperella pyogenes* (*T. pyogenes*) (2021, 2023), coccidiosis (2023), and porcine epidemic diarrhea virus (PEDV) (2022). This pattern continued into 2025, when the top 10 pathogens and respective index values were PRRSV (0.90), *S. suis* (0.70), *M. hyorhinis* (0.46), *P. multocida* (0.47), IAV (0.45), *E. coli* (0.45), *G. parasuis* (0.44), PCV2 (0.44), Rotavirus (0.39), and *T. pyogenes* (0.37), reflecting the persistence of many historically high ranking etiologies and reinforcing long term trends observed across the dataset (Figure 1).

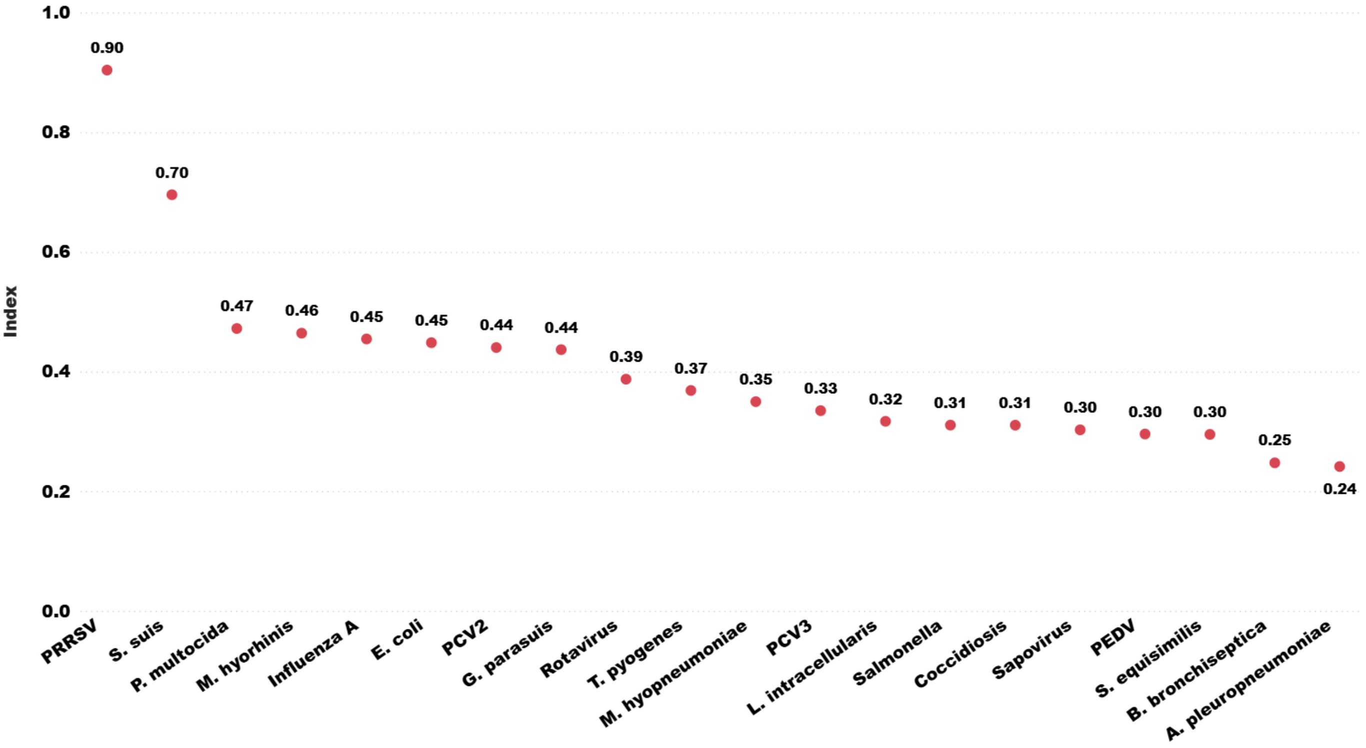


Figure 1. The 20 pathogens with the highest disease index for the year of 2025

This work introduces a novel, data driven framework for monitoring endemic swine diseases using routinely collected diagnostic information. By integrating multiple epidemiological indicators into a single weighted index, the system provides an objective, scalable, and transparent tool for ranking endemic pathogen activity over time in the US swine industry. The generated information will help guiding the swine industry in identify and prioritize animal health resources for the control of most impacting, emerging, or re-emerging endemic pathogens. The methodology here developed is species and region agnostic, allowing for broad application across animal health systems. When paired with a real time data collection and dashboard (available in SDRS dashboard website), the index enhances accessibility for veterinarians, producers, and animal health professionals, supporting evidence based decision making and strategic planning. As animal health challenges continue to evolve, this framework offers a robust foundation for monitoring endemic and re emerging diseases across diverse animal populations.

When interpreting the Disease Index, it is important to recognize that the tool summarizes the pathogens detected in diagnostic submissions without assigning clinical roles to them. Determining whether an agent is acting as a primary cause of disease or as a secondary or opportunistic contributor requires additional context from pathology, case history, and veterinary expertise. As a result, some pathogens may appear prominently in the index because they are detected frequently across diverse submissions, even though they may not be the principal drivers of disease in all situations. Acknowledging this point supports a more accurate interpretation of index rankings within the broader diagnostic and clinical framework.