Swine Disease Reporting System - Advisory Group Report
Report # 95 (December 31, 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 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: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings, Eric Nelson.

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, and Brooke Kitting.

Note: This report contains data up to December 31, 2025.

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

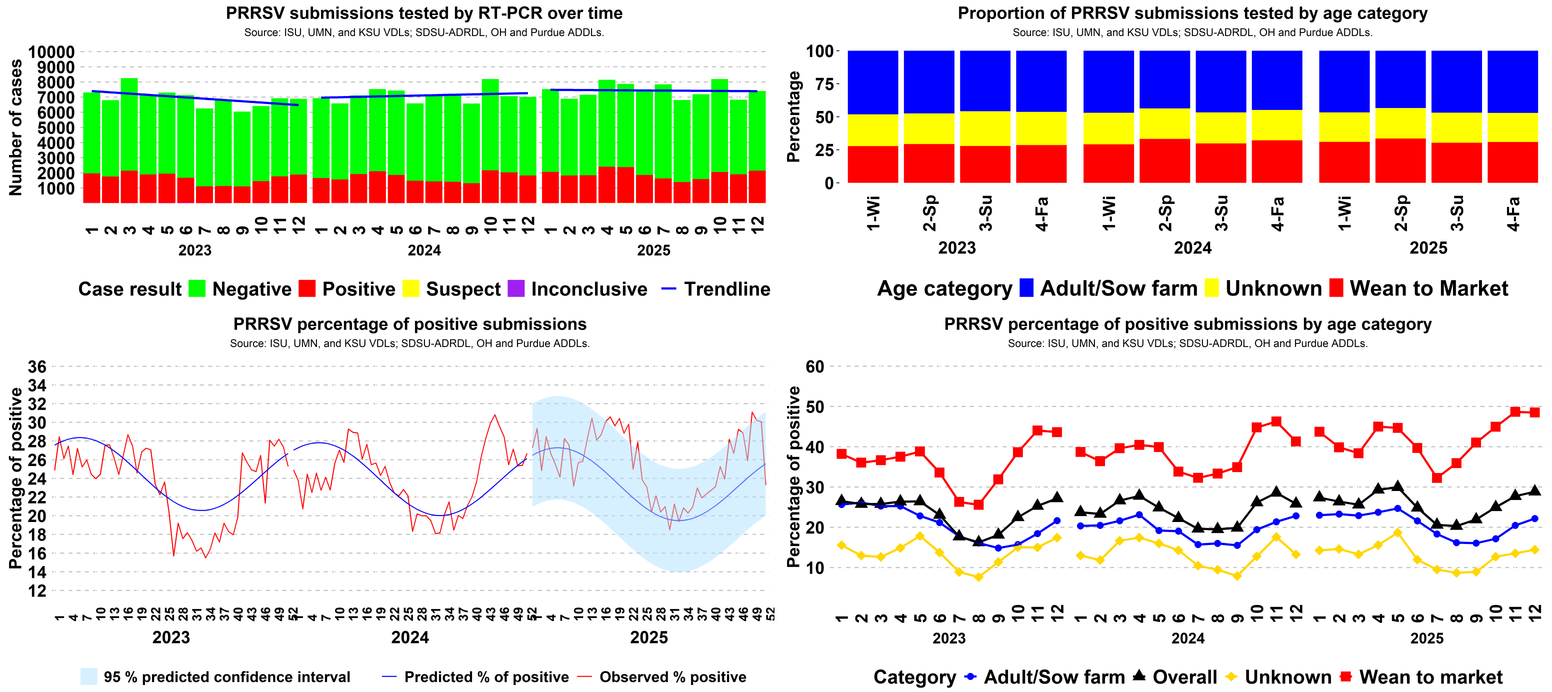
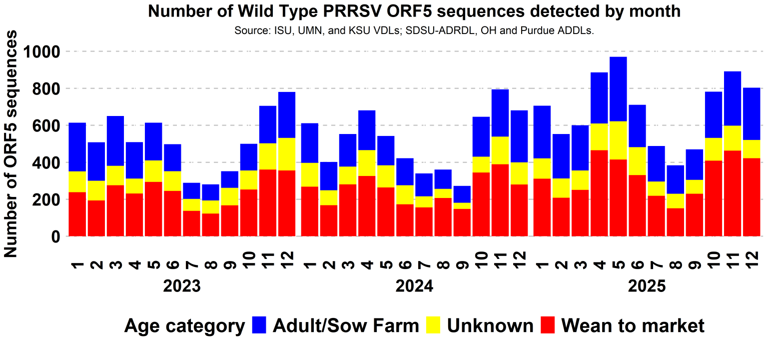


Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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:

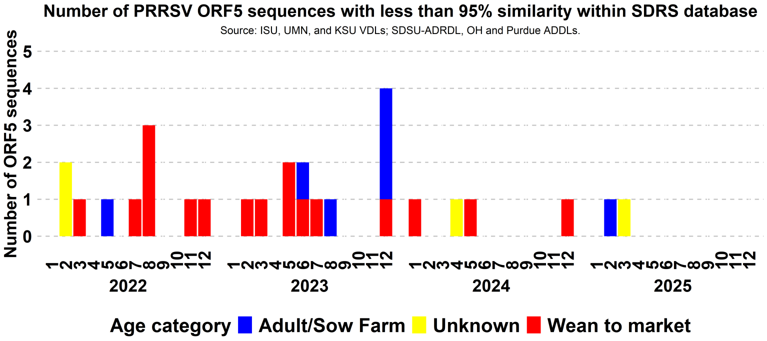
- Overall, 28.85% of 7,407 cases tested PRRSV-positive in December, similar to 27.75% of 6,825 in November;
  - Positivity in the adult/sow category in December was 22.17% (781 of 3,522), similar to 20.5% (649 of 3,166) in November;
  - Positivity in the wean-to-market category in December was 48.5% (1,132 of 2,334), similar to 48.66% (1,038 of 2,133) in November;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MN, MO, IN and NC;
- Some advisory members noted that they are conducting more active surveillance in wean-to-finish sites to better understand the risk these sites may pose to nearby sow units and nurseries. They reported increased sampling compared with previous years, with testing in the wean-to-market category rising 5% in 2025 relative to 2024. The 2025 wean-to-market category also recorded the highest testing volume in the past five years, reaching nearly 28,000 cases. This heightened surveillance was driven by higher mortality linked to the strains currently circulating in the field.

Topic 2 – PRRSV ORF5 sequences detection over time



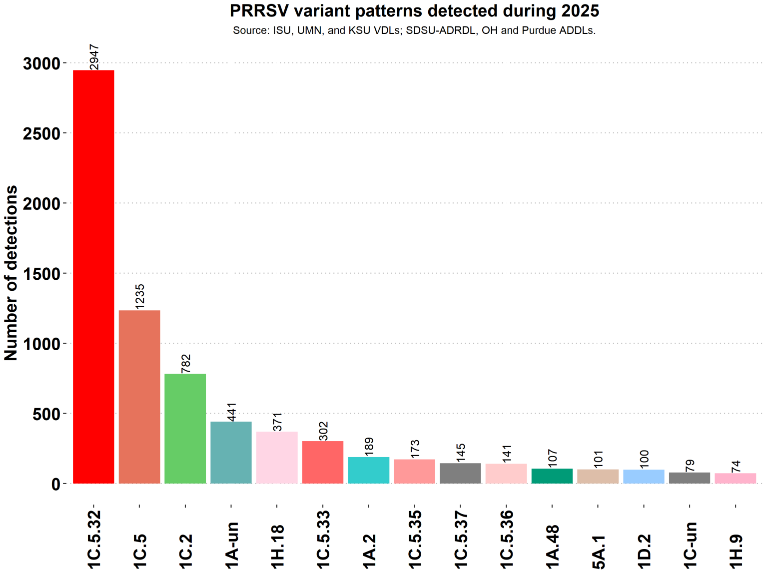
Number of Wild Type PRRSV ORF5 sequences detected by month

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



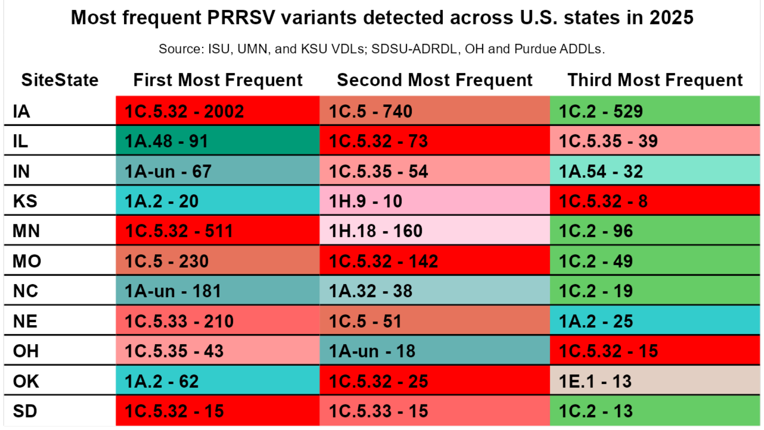
Number of PRRSV ORF5 sequences with less than 95% similarity within SDRS database

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



PRRSV variant patterns detected during 2025

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



Most frequent PRRSV variants detected across U.S. states in 2025

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 - 2002	1C.5 - 740	1C.2 - 529
IL	1A.48 - 91	1C.5.32 - 73	1C.5.35 - 39
IN	1A-un - 67	1C.5.35 - 54	1A.54 - 32
KS	1A.2 - 20	1H.9 - 10	1C.5.32 - 8
MN	1C.5.32 - 511	1H.18 - 160	1C.2 - 96
MO	1C.5 - 230	1C.5.32 - 142	1C.2 - 49
NC	1A-un - 181	1A.32 - 38	1C.2 - 19
NE	1C.5.33 - 210	1C.5 - 51	1A.2 - 25
OH	1C.5.35 - 43	1A-un - 18	1C.5.32 - 15
OK	1A.2 - 62	1C.5.32 - 25	1E.1 - 13
SD	1C.5.32 - 15	1C.5.33 - 15	1C.2 - 13

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 2025, shown by variant at the U.S. state level along with their respective detection counts **Note: un indicates unclassified**.

SDRS Advisory Group highlights:

- During December, the states with higher number of PRRSV 1C.5.32 detections were detected IA, MN, MO, IL, OK, KS, NE, OH, SD (respective number of sequences: 219, 67, 28, 11, 2, 1, 1, 1, 1).
- In December 1C.5.32 (334) was the PRRSV variant most detected in the U.S., followed by 1C.5 (92), and 1C.2 (67);
- 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

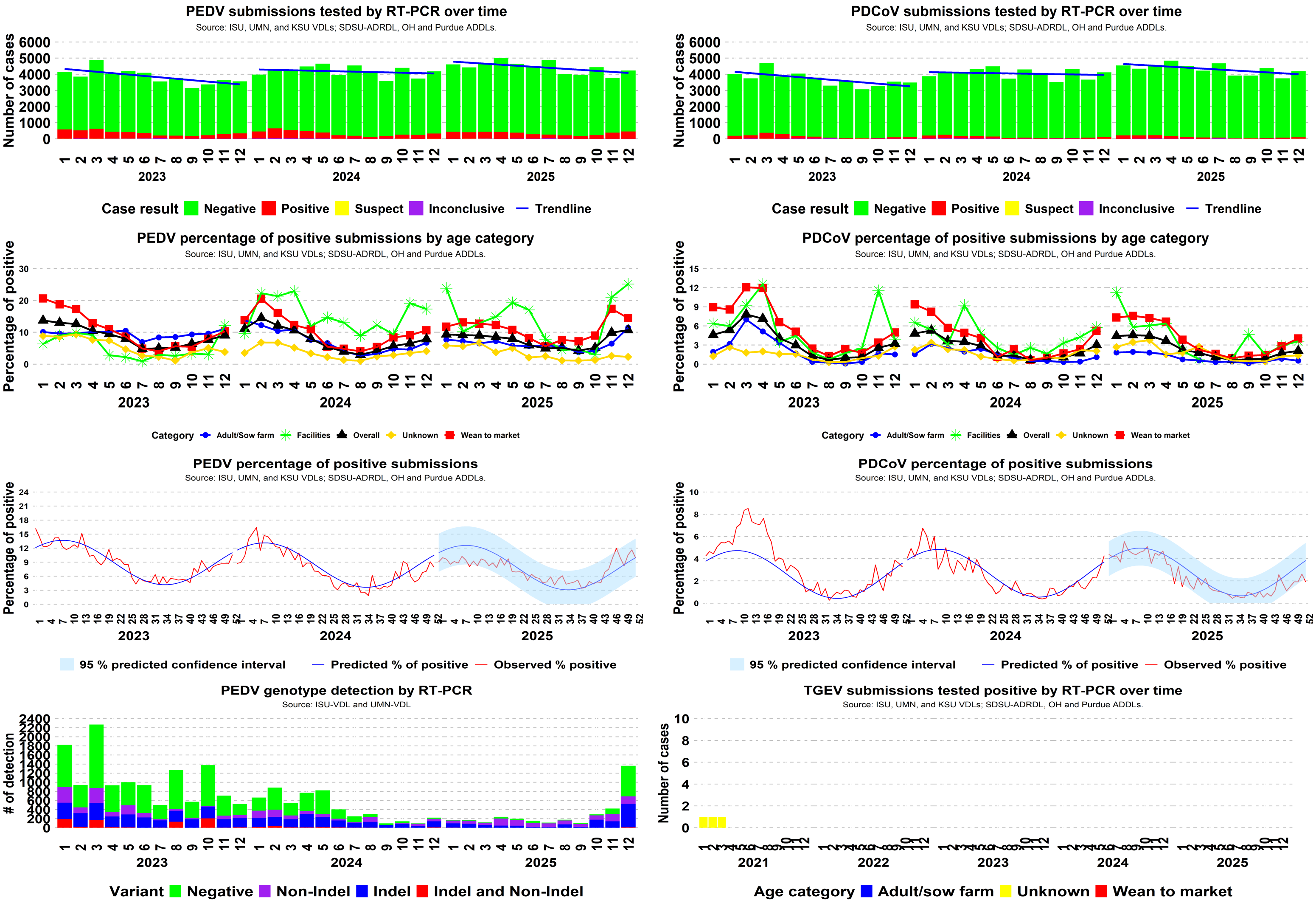
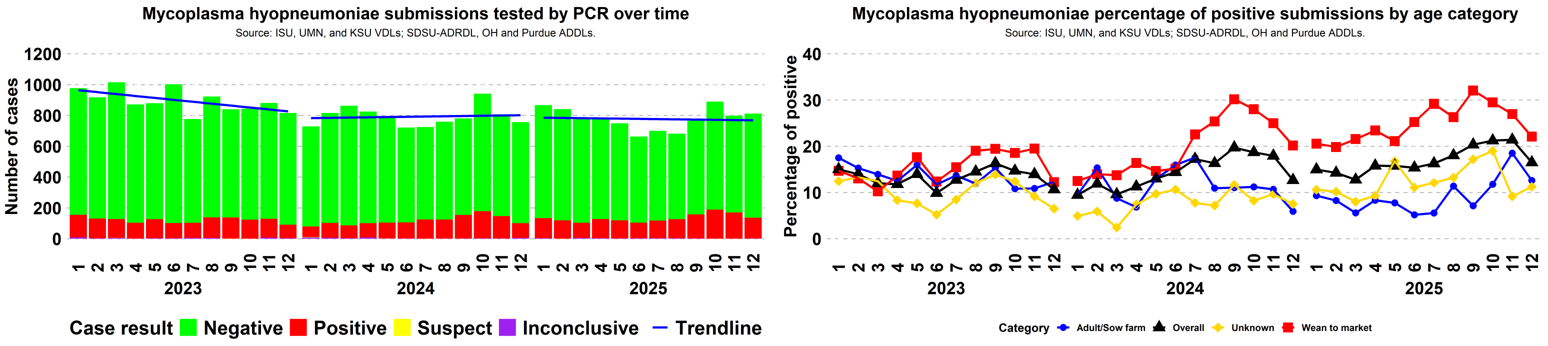


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2025 prediction. Bottom: Left PEDV genotype detection over time; Right TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 10.68% of 4,233 cases tested PEDV-positive in December, similar to 9.91% of 3,785 in November;
  - Positivity in the adult/sow category in December was 11.46% (172 of 1,501), a substantial increase from 6.44% (84 of 1,304) in November;
  - Positivity in the wean-to-market category in December was 14.47% (213 of 1,472), a moderate decrease from 17.38% (236 of 1,358) in November;
- Positivity in the facilities category in December was 25.15% (42 of 167), a moderate increase from 21.01% (29 of 138) in November;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in KS, OK and IN;
  - Overall, 0.59% of 1,362 samples had mixed PEDV genotype detection in December, similar to 0% of 422 in November;
- Overall, 2.1% of 4,187 cases tested PDCoV-positive in December, similar to 1.73% of 3,752 in November;
  - Positivity in the adult/sow category in December was 0.54% (8 of 1,480), similar to 0.86% (11 of 1,286) in November;
  - Positivity in the wean-to-market category in December was 4.04% (59 of 1,459), similar to 2.81% (38 of 1,352) in November;
- Positivity in the facilities category in December was 3.59% (6 of 167), similar to 2.9% (4 of 138) in November;
- 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 December, 2025 over a total of 4,063 cases tested. It has been 57 months (with a total of 215,973 cases tested) since the last TGEV PCR-positive result;
- December recorded the highest PEDV positivity in adult/sow farms in 2025, and a similar pattern of elevated detection was observed for facilities. Some of the advisory members noted that the PEDV detections in sow herds include both PED-Indel and PED Non-S-Indel strains, with some PED Non-S-Indel detections in sow farms representing re-breaks originating from this spring. Several members also reported a highly active PEDV year in their regions.

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



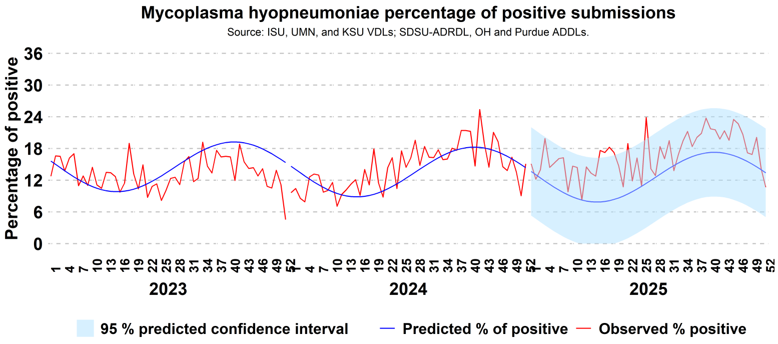
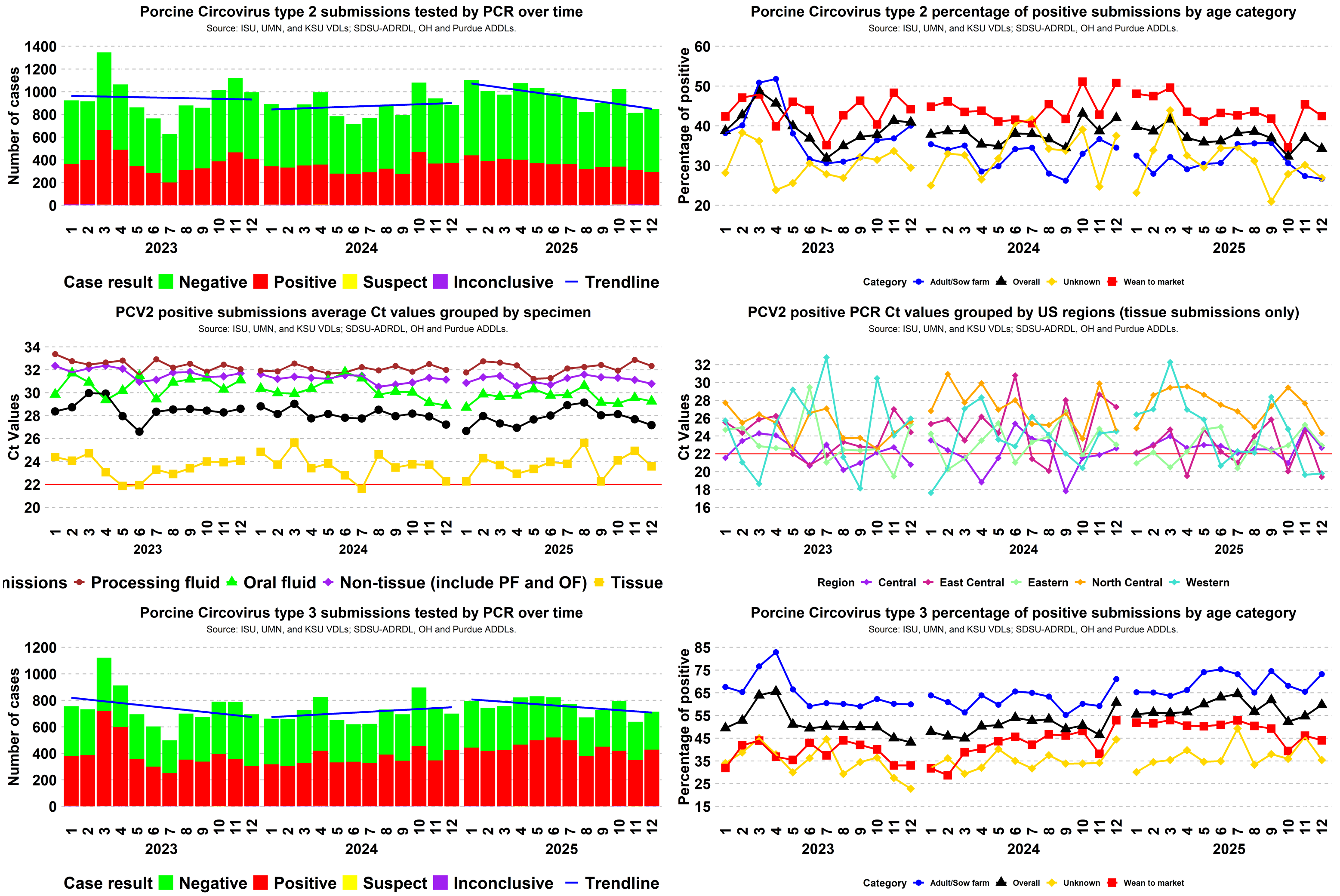


Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 16.5% of 812 cases tested *M. hyopneumoniae*-positive cases in December, a moderate decrease from 21.4% of 799 in November;
  - Positivity in the adult/sow category in December was 12.62% (40 of 317), a substantial decrease from 18.52% (55 of 297) in November;
  - Positivity in the wean-to-market category in December was 22.1% (78 of 353), a moderate decrease from 26.97% (106 of 393) in November;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MN, IN and NC;

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, 34.24% of 847 cases tested PCV2-positive in December, a moderate decrease from 36.98% of 814 in November;
  - Positivity in the adult/sow category in December was 26.67% (104 of 390), similar to 27.36% (87 of 318) in November;
  - Positivity in the wean-to-market category in December was 42.47% (172 of 405), a moderate decrease from 45.39% (192 of 423) in November;
  - In the month of December, the regions with the lowest PCV2 average Ct values in tissue submissions was East Central (14 submissions; average Ct 19.4), Western (9 submissions; average Ct 19.8), Central (44 submissions; average Ct 22.7), Eastern (38 submissions; average Ct 22.9), and North Central (27 submissions; average Ct 24.3);
- Overall, 59.66% of 714 cases tested PCV3-positive in December, a moderate increase from 54.7% of 638 in November;
  - Positivity in the adult/sow category in December was 73.23% (290 of 396), a substantial increase from 65.49% (186 of 284) in November;
  - Positivity in the wean-to-market category in December was 44.07% (119 of 270), a moderate decrease from 46.13% (131 of 284) in November.

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

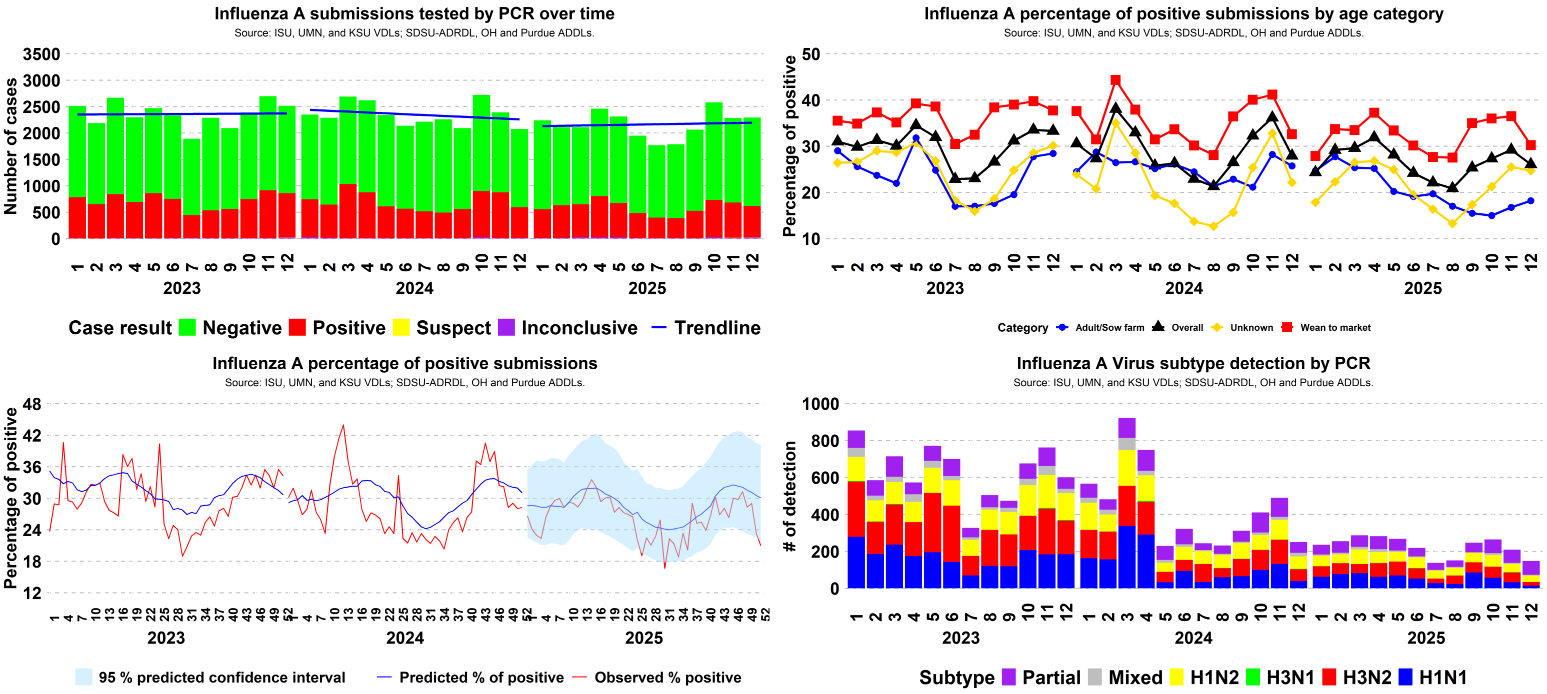
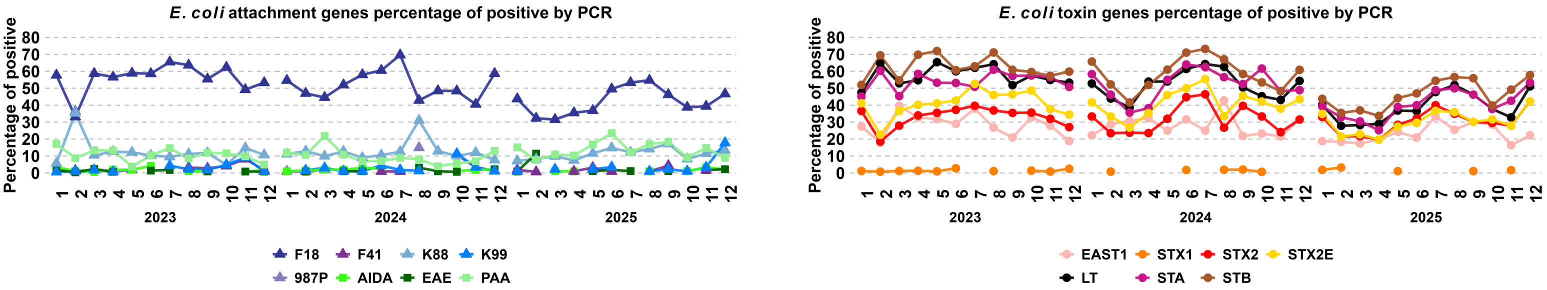


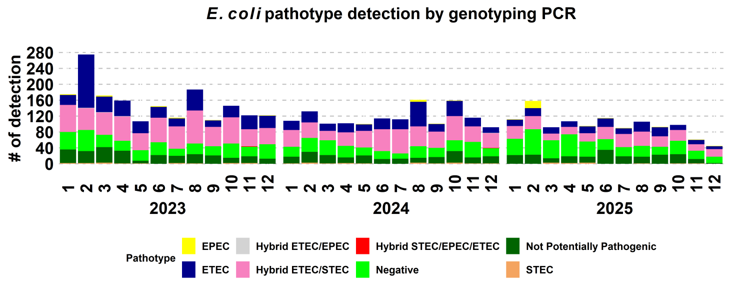
Figure 1. **Top:** *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 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").

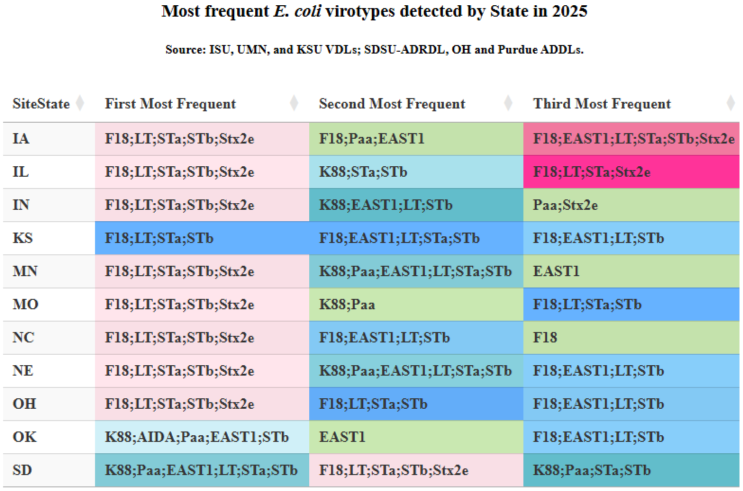
SDRS Advisory Group highlights:

- Overall, 26.08% of 2,293 cases tested IAV-positive cases in December, a moderate decrease from 29.23% of 2,282 in November;
  - Positivity in the adult/sow category in December was 18.2% (87 of 478), similar to 16.77% (79 of 471) in November;
  - Positivity in the wean-to-market category in December was 30.24% (342 of 1,131), a substantial decrease from 36.51% (418 of 1,145) in November.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 2.7% of 148 samples had mixed subtype detection in December, similar to 2.86% of 210 in November.
- Some of the advisors mentioned that they experienced more IAV breaks in the past month than they had during the entire rest of the year.

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






Most frequent *E. coli* virotypes detected by State in 2025

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;Paa;EAST1	F18;EAST1;LT;STa;STb;Stx2e
IL	F18;LT;STa;STb;Stx2e	K88;STa;STb	F18;LT;STa;Stx2e
IN	F18;LT;STa;STb;Stx2e	K88;EAST1;LT;STb	Paa;Stx2e
KS	F18;LT;STa;STb	F18;EAST1;LT;STa;STb	F18;EAST1;LT;STb
MN	F18;LT;STa;STb;Stx2e	K88;Paa;EAST1;LT;STa;STb	EAST1
MO	F18;LT;STa;STb;Stx2e	K88;Paa	F18;LT;STa;STb
NC	F18;LT;STa;STb;Stx2e	F18;EAST1;LT;STb	F18
NE	F18;LT;STa;STb;Stx2e	K88;Paa;EAST1;LT;STa;STb	F18;EAST1;LT;STb
OH	F18;LT;STa;STb;Stx2e	F18;LT;STa;STb	F18;EAST1;LT;STb
OK	K88;AIDA;Paa;EAST1;STb	EAST1	F18;EAST1;LT;STb
SD	K88;Paa;EAST1;LT;STa;STb	F18;LT;STa;STb;Stx2e	K88;Paa;STa;STb

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 2025 at U.S. state level (color code on table cells associated with the pathotype legend).

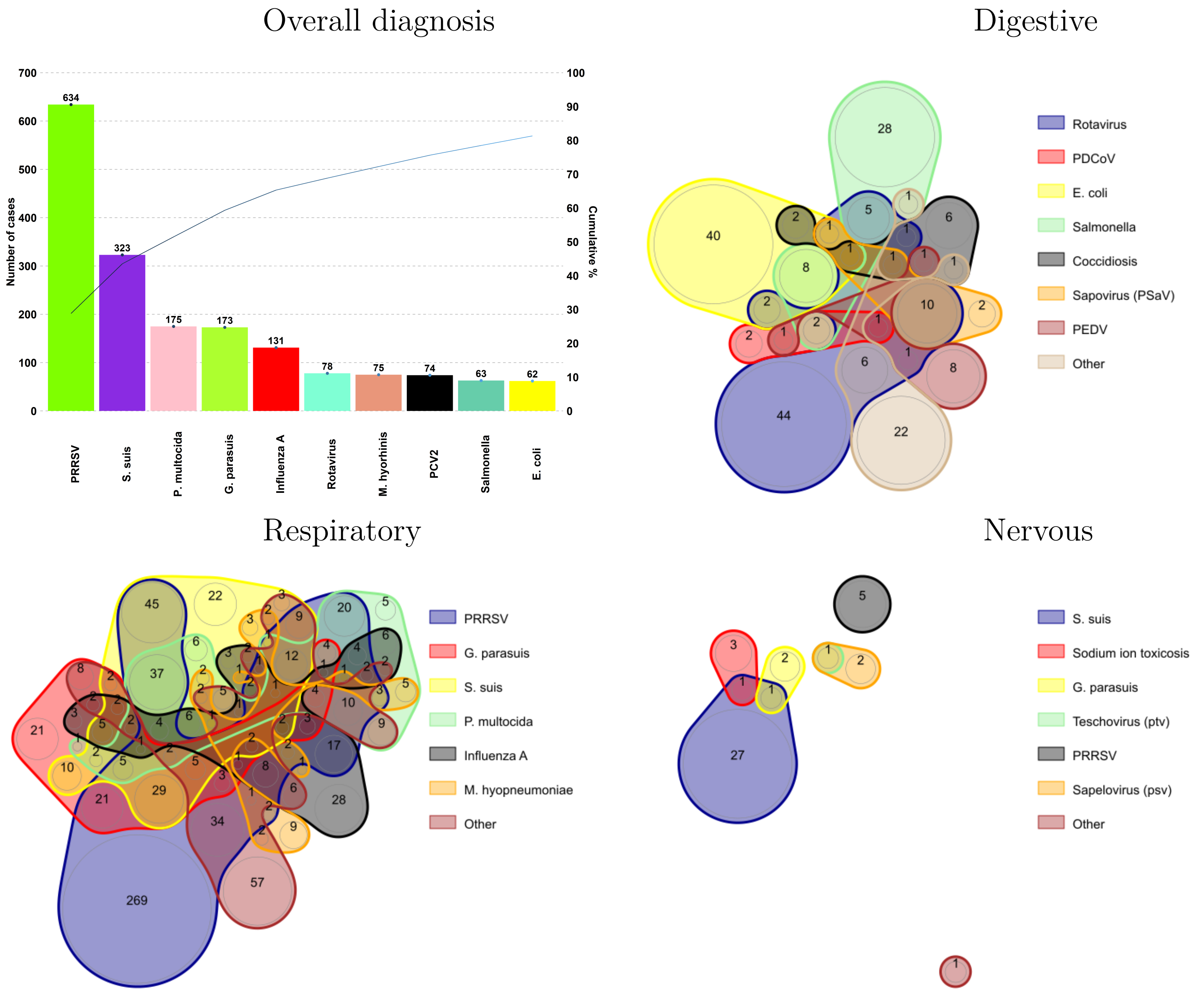
Education Material:

- **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, 45 samples were tested for *E. coli* PCR in December;
  - In December the *E. coli* pathotype with higher number of sample detections were Hybrid ETEC/STEC (19 detections), ETEC (7 detections), Not Potentially Pathogenic (2 detections);
  - In December the *E. coli* attachment genes with higher detection rate were F18 (46.67%), K99 (17.78%), K88 (13.33%);
  - In December the *E. coli* toxin genes with higher detection rate were STB (57.78%), STA (53.33%), LT (51.11%).

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 November. 1 to December. 30, 2025.

SDRS Advisory Group highlights:

- PRRSV (634) led cases with confirmed etiology, followed by *S. suis* (323), and *P. multocida* (175). PRRSV (568 of 1501) led the number of confirmed respiratory diagnoses, Rotavirus (73 of 247) lead the number of confirmed digestive diagnoses, and *S. suis* (29 of 45) 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.*

A 2025 *Swine Disease Reporting System-SDRS* retrospective

Quyen Le[1], Daniel Linhares[1], Giovani Trevisan[1]

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

The SDRS's goal is to share information on the activity of endemic and emerging pathogens affecting the swine population in the U.S., assisting veterinarians and producers in making informed decisions on disease prevention, detection, and management. Currently, SDRS is the only publicly available source of swine health information from U.S. veterinary diagnostic laboratories (VDLs). With a database containing information for ten endemic porcine pathogens and more than 1.5 million cases, SDRS is one of the largest U.S. 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 representativeness of the U.S. swine industry. Thank you to the six VDL partners, SDRS Advisory Board, and collaborators for all of the accomplishments during 2024.

2025 SDRS retrospective includes but is not limited to:

- Addition of *E.coli* PCR genotyping data into the SDRS and a new page in the PDF report and online dashboards, which includes charts with information about *E. coli* PCR-Positive results by attachment genes over time, *E. coli* PCR-Positive results by genes and toxin over time, *E. coli* number of samples tested by PCR genotype and their respective pathotype classification, and the most frequent detected *E. coli* virotype by PCR at U.S. state level;
- Integrating disease diagnosis data from OH-ADDL, along with ISU-VDL, into the confirmed tissues diagnosis page of the monthly PDF report;
- Implemented PRRSV-2 variant classification and PRRSV-1 lineage classifications. Such information can be recovered through the SDRS Blast tool;
- Implemented a disease index dashboard that ranks swine diseases by importance using four key variables: annual disease occurrence, comorbidity with other etiologies, surveillance alarms (cases exceeding baseline expectations), and state occurrence across U.S. regions.
- SDRS has been and will continue to support disease control & elimination programs, including the efforts to eliminated *M.hyopneumoniae*, and the AASV PEDV Elimination Task Force, providing data to aid the U.S. swine industry to keep track of pathogen activity in the field;
- Addition of an ongoing SDRS survey where the audience can make suggestions of new pathogens and improvements on the SDRS project. If you have suggestions for us, click here.

SDRS Extension and Education:

- SDRS project website pages (*https://fieldepi.org/sdrs/*), including the dashboards and Blast tool, had 2,758 unique visitors in 2025, increase 118% compared to 2024, mostly from the US;
- 12 editions of PDF, and audio and video reports hosting 12 talks with subject matter from 12 experts have been shared through e-mail for 688 receivers registered from 292 organizations from 23 different countries and posted on the SDRS webpage;
- Implemented English and Spanish closed captioning on the YouTube videos;
- On the FieldEpi LinkedIn page, the SDRS videos achieved more than 71,765 visualizations;
- Generated 2 open source peer-reviewed manuscripts: Macroepidemiological trends of Influenza A virus detection through reverse transcription real-time polymerase chain reaction (RT-rtPCR) in porcine samples in the United States over the last 20 years; and Harnessing sequencing data for porcine reproductive and respiratory syndrome virus (PRRSV): tracking genetic evolution dynamics and emerging sequences in US swine industry;
- The SDRS YouTube channel achieved 7,451 views on the video reports and education material;
- Audio reports have been shared through podcast platforms, including *Spotify*, *Apple Podcast*, and *Amazon Music*, achieving 4,284 downloads from 27 different countries;
- One MS, two PhD, and one MBA student were trained on the SDRS and concluded their degree in 2025;
- Organized the in-person meeting at AASV and the Winter preparedness call with the SDRS Advisory Board, where emerging disease pressures were discussed, and recommendations were made in SDRS reports regarding strategic prevention/control actions to be taken by the US swine industry.

Pathogen activity highlights:

PRRSV

- PRRSV had the historically highest percentage of PCR-positive submissions in the wean-to-market category (48.5% of positive cases) since 2018;
- Change in PRRSV lineage detections: lineage L1C.5 emerged in 2020, and expanded rapidly from 161 detections in 2020 to 5,080 in 2025, driven primarily by variant 1C.5.32, firstly detected in 2023, which alone accounted for 28% of the detections within the 1C.5 lineage (58% of the detections within this lineage in 2025), making its appearance in 14 states, and became the predominant in IA (3009), MN (648), MO (160) and IL (93). Lineage 1C.2 also increased steadily, reaching 848 detections in 2025; and became the fourth most frequent detected in recent five years. The Lineage 1A and Lineage 1H are still active in the field, but L1A declined to 1,131 detections by 2025, representing 14% of detections, and Lineage 1H showed a similar pattern, peaking at 1,617 detections in 2022 with 16% of all detection before decreasing to 620 detections with 6% of total detection in 2025;
- In 2025, several PRRSV variants were detected for the first time across states: variant 1C.2 in ND and NC; variant 1C.5.32 in KS, OH, OK, PA, and TX; variant 1C.5.33 in IL; and variant 1C.5.38 in MO;

PEDV/PDCoV/TGEV

- During the winter of 2024-2025 (December–February), PEDV recorded its lowest percentage of positive submissions in the adult/sow farm category, at 7% compared to all winters since 2015. In the fall of 2025, positivity in this category was similarly low at 5%, marking the lowest level relative to fall seasons since 2015. However, November-December 2025 showed a notable increase, with positivity rising to 11.46%, the highest rate observed in 2025. In contrast, PEDV detections in the wean-to-market category rose to 11% in fall 2025—the highest for that season since 2023. The positivity rate of PEDV in facilities in December 2025 was 25.15%, highest since 2023. Overall, PEDV positivity in 2025 remained within expected ranges, except during the weeks of November 2nd and 16th, when rates exceeded expectations.
- For PDCoV, overall percentage of positive cases was within forecasted expected ranges for 2025 following a trend for decreased detection in the last 2 years. In the weeks of April 14th and May 5th it was below expected.
- On March 22, 2021, the SDRS laboratory network received its last field sample testing RT-PCR positive for TGEV. From that date through December 2025, more than 215,973 submissions, including over 855,221 samples, were tested by RT-PCR assays for TGEV RNA, with no additional positive results detected;

M. hyopneumoniae

- Sow farm detections remain historically low (<10% positives in winter, spring, and summer);
- However, in the wean-to-market category *M. hyopneumoniae* positivity reached the highest levels (29.04%) since the fall of 2019. Mostly, the positive cases are primarily a result of intended exposure protocols aimed at maintaining farm stability, with several homogenates and deep tracheal swabs submitted to the VDLs for testing. Iowa cases are more frequently coming from clinical cases, with lung samples collected from finishing animals, which may be a potential reflection of a large growing inventory. In addition, using ISU VDL data, the number of cases with a confirmed tissue diagnosis for *M. hyopneumoniae* (cases where diagnosticians gather available data including clinical history, tests performed, and microscopic and macroscopic lesions) decreased over time, reaching a record low number in 2025 (235 cases) decreasing 50% when compared with 475 cases in 2020;

PCV2/PCV3

- PCV3 kept its trend of detection being the only pathogen monitored by the SDRS, having positivity in the age category Adult/sow farm above the positivity in the wean-to-market category in all seasons since 2018;
- PCV2 positivity in wean-to-market reached its lowest detection (40%) since spring 2022;

IAV

- In Fall 2025, Influenza A virus recorded its lowest positivity in the adult/sow farm category across all seasons since 2015, at 15%. Meanwhile, the wean-to-market category marked its lowest fall-specific positivity in 2025, at 35% compared to other fall seasons since 2015;

E.coli

- In 2025, *E. coli* detections dropped to their lowest level since 2008, with 1,012 samples recorded. The most common pathotypes were Hybrid ETEC/STEC (26%), Not Potentially Pathogenic (18%), and ETEC (16%). Among attachment genes (554 detections), F18 was dominant at 43%, followed by Paa (14%) and K88 (11%). For toxin genes (484 detections), the leading ones were Stb (45%), Sta (39%), and LT (38%).

Highlights for disease diagnosis from *Iowa State University Veterinary Diagnostic Laboratory* and *The Ohio Animal Disease Diagnostic Laboratory*:

- PRRSV had the highest number of porcine-confirmed diagnoses (3,242) followed by *S. suis* (1,844), IAV (818), *P.multocida* (795) and Rotavirus (660) in 2025;
- The top five diseases with the highest index in 2025 were PRRSV (0.76), *S. suis* (0.54), IAV (0.44), *P. multocida* (0.37), and *G. parasuis* (0.36).

Happy 2026!!! and stay tuned for new SDRS developments in 2026.

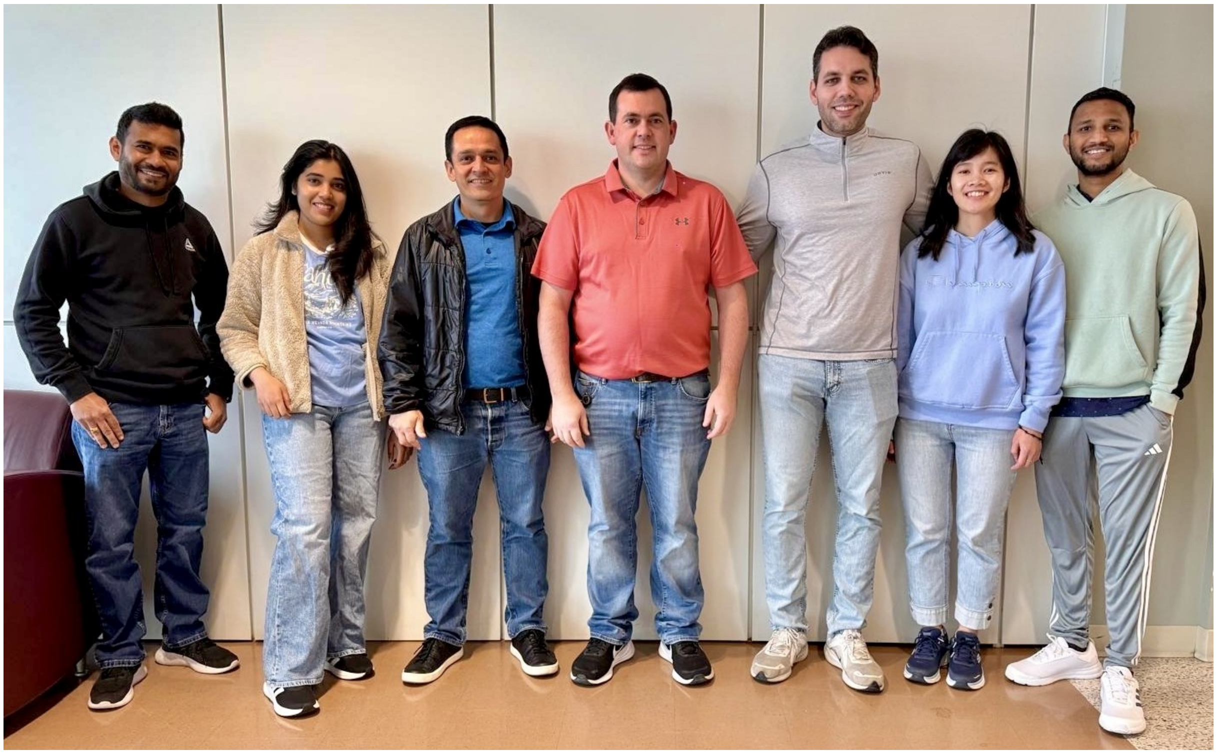


Figure 1. The Swine Disease Reporting System Team: *from left to right: Kinath Rupasinghe, Likhitha Nakka, Daniel Linhares, Giovani Trevisan, Guilherme Cezar, Quyen Le and Sajan Thallapelly*