

Swine Disease Reporting System

Report # 103 (September 1, 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 VDL, Purdue ADDL and Illinois VDL.

Collaborators:

Swine Disease Reporting System office: Principal investigators: [Daniel Linhares](#) & [Giovani Trevisan](#); Project coordinator: [Quyen Le](#); Software Developer: Kinath Rupasinghe; Data Analyst: Sajan 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: Cesar Corzo, Albert Rovira, Matt Sturos, Hemant Naikare.

Kansas State Uni. and Kansas Dept. of Agr.: Rob McGaughey, Franco Matias-Ferreira, 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 VDL and The Ohio State Uni: Melanie Prarat, Dennis Summers, Andréia Arruda, Ryan Yanez

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

Illinois VDL: Wes Baumgartner, James Lowe.

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: 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 August 31, 2026.

Topic 1.1 – Detection of PRRSV RNA over time by RT-qPCR.

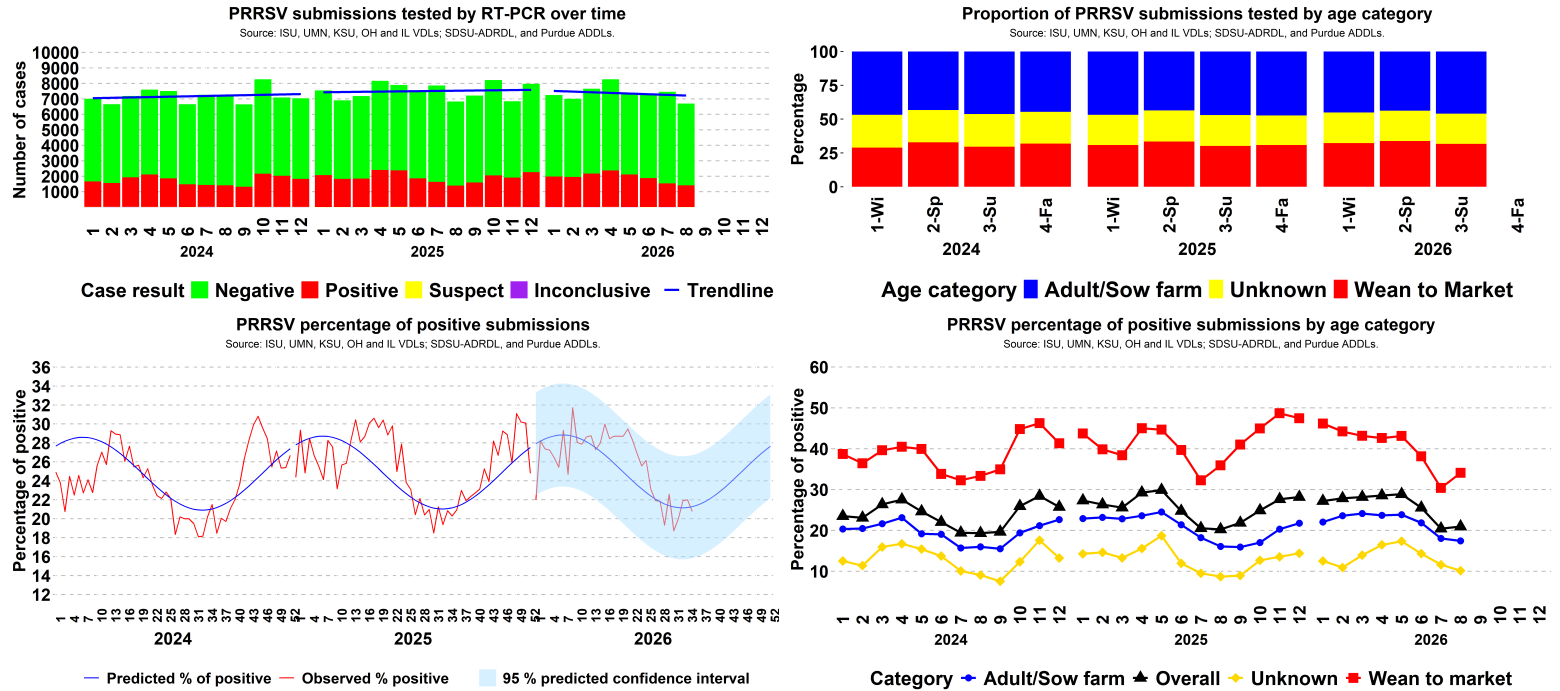


Figure 1. Top: Left: Results of PRRSV RT-PCR cases over time; **Right:** Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom: Left** Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based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

- Overall, 20.96% of 6,694 cases tested PRRSV-positive in August, similar to 20.46% of 7,457 in July.
- Positivity in the adult/sow category in August was 17.47% (538 of 3,079), similar to 18.06% (620 of 3,433) in July.
- Positivity in the wean-to-market category in August was 34.09% (709 of 2,080), a moderate increase from 30.4% (709 of 2,332) in July.
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MO and IL.
- Some Advisors noted that the PRRSV activity observed during summer may reflect continued virus circulation in wean-to-market sites following herd breaks reported during late Spring (May-June).

Topic 1.2 – PRRSV ORF5 sequences detection over time

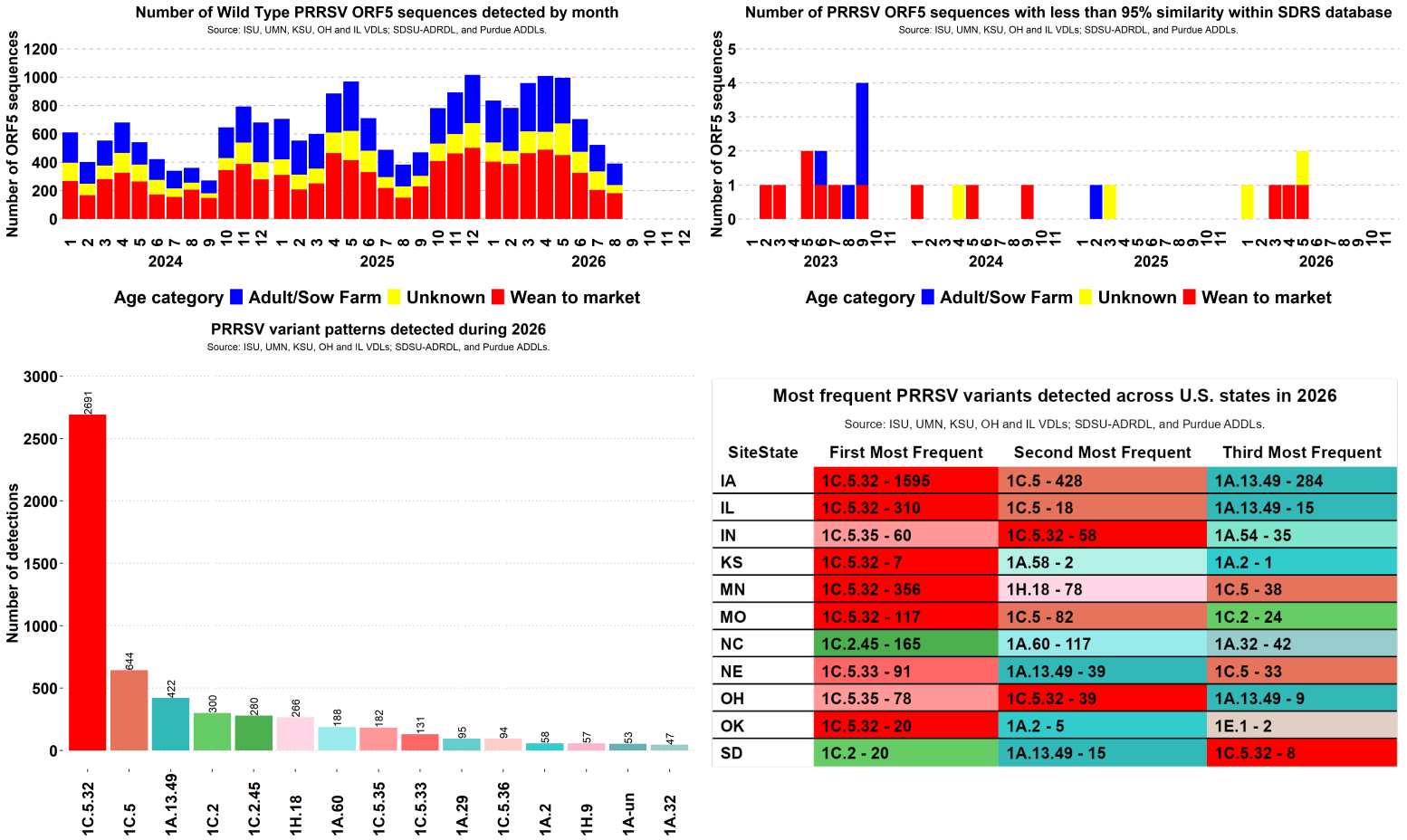


Figure 1. Top: Left: Number of PRRSV ORF5 sequences detected by age category; **Right:** Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher 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**.

Where Does Your PRRSV Sequence Fit?

- Compare your PRRSV ORF5 sequence with the SDRS database using the [SDRS BLAST tool](#). For additional insights, explore the [PRRSV genotype dashboard](#), which summarizes PRRSV genotype trends reported through SDRS;
- SDRS applies prospective variant classification while continuously updating historical records, ensuring that trend analyses reflect the most current data.

SDRS Advisory Group highlights:

- During August, the states with higher number of PRRSV 1C.5.32 detections were detected IA, IL, MN, IN, MO, NC, SD (respective number of sequences: 78, 26, 18, 4, 4, 1, 1);
- In August 1C.5.32 (132) was the PRRSV variant most detected in the U.S., followed by 1C.5 (71), and 1A.13.49 (46);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
 - June 2026: 1K.4 (IN), 1A.29 (MO), 1H.48 (PA)
 - July 2026: 1A.29 (LA), 1C.2 (TN)

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

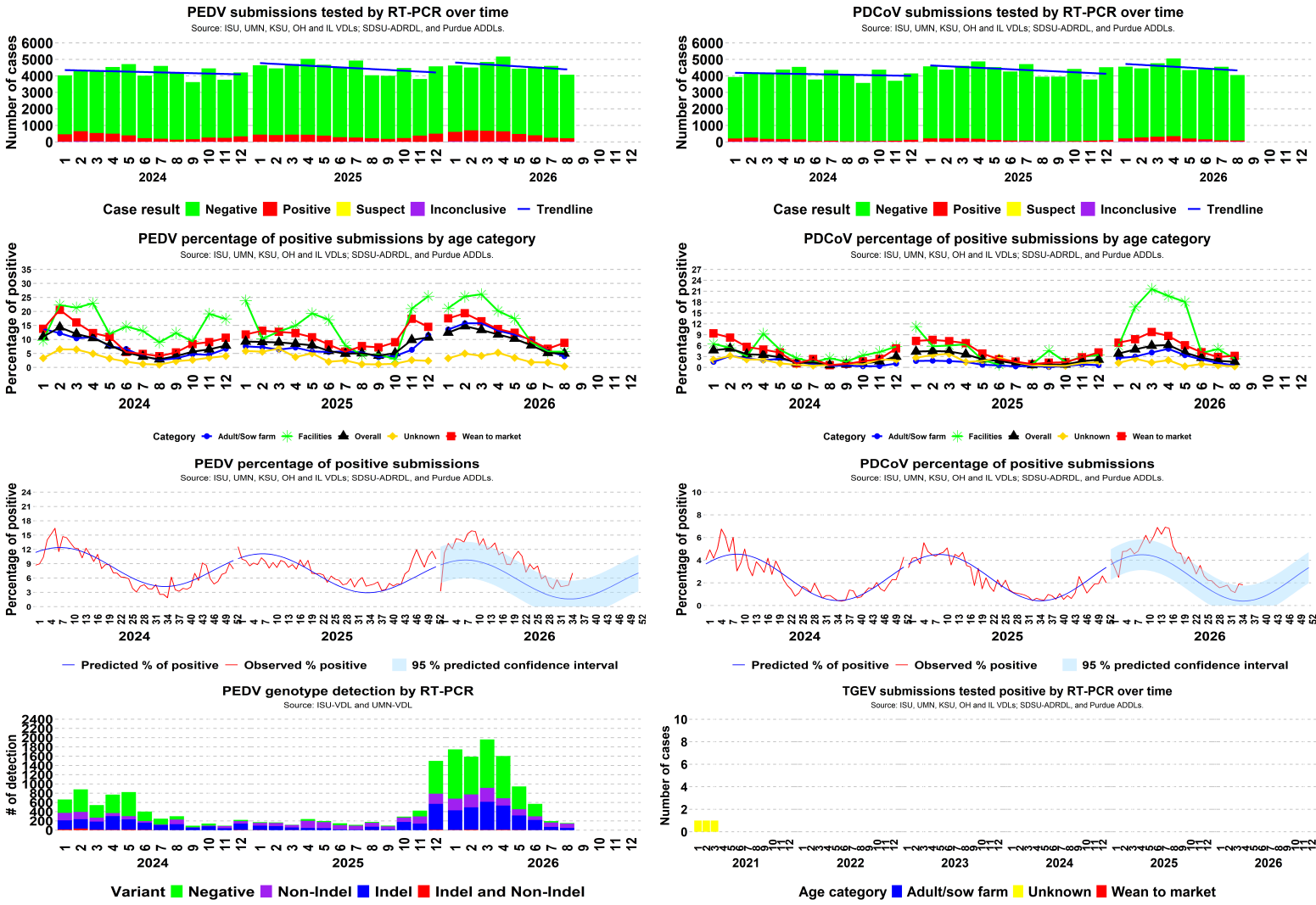


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. **Second from top:** Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. **Third from top:** Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. **Bottom:** Left PEDV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

SDRS Advisory Group highlights:

- Overall, 4.98% of 4,074 cases tested PEDV-positive in August, similar to 5.21% of 4,605 in July.
 - Positivity in the adult/sow category in August was 4.03% (57 of 1,415), similar to 5.86% (96 of 1,639) in July.
 - Positivity in the wean-to-market category in August was 8.79% (135 of 1,536), a moderate increase from 6.69% (116 of 1,734) in July.
 - Positivity in the facilities category in August was 5.6% (7 of 125), similar to 5.7% (9 of 158) in July.
 - Overall PEDV-percentage of positive cases was within state-specific baselines in all 11 monitored states.
 - Overall, 0% of 154 samples had mixed PEDV genotype detection in August, similar to 0.51% of 197 in July.
- Overall, 1.56% of 4,050 cases tested PDCoV-positive in August, similar to 1.84% of 4,555 in July.
 - Positivity in the adult/sow category in August was 0.57% (8 of 1,397), similar to 1.24% (20 of 1,612) in July.
 - Positivity in the wean-to-market category in August was 3.19% (49 of 1,534), similar to 2.9% (50 of 1,723) in July.
 - Positivity in the facilities category in August was 2.4% (3 of 125), a moderate decrease from 5.06% (8 of 158) in July.
 - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in OK.
- There was 0 positive case for TGEV RNA-PCR in August, 2026 over a total of 3,916 cases tested. It has been 65 months (with a total of 254,017 cases tested) since the last TGEV PCR-positive result.

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

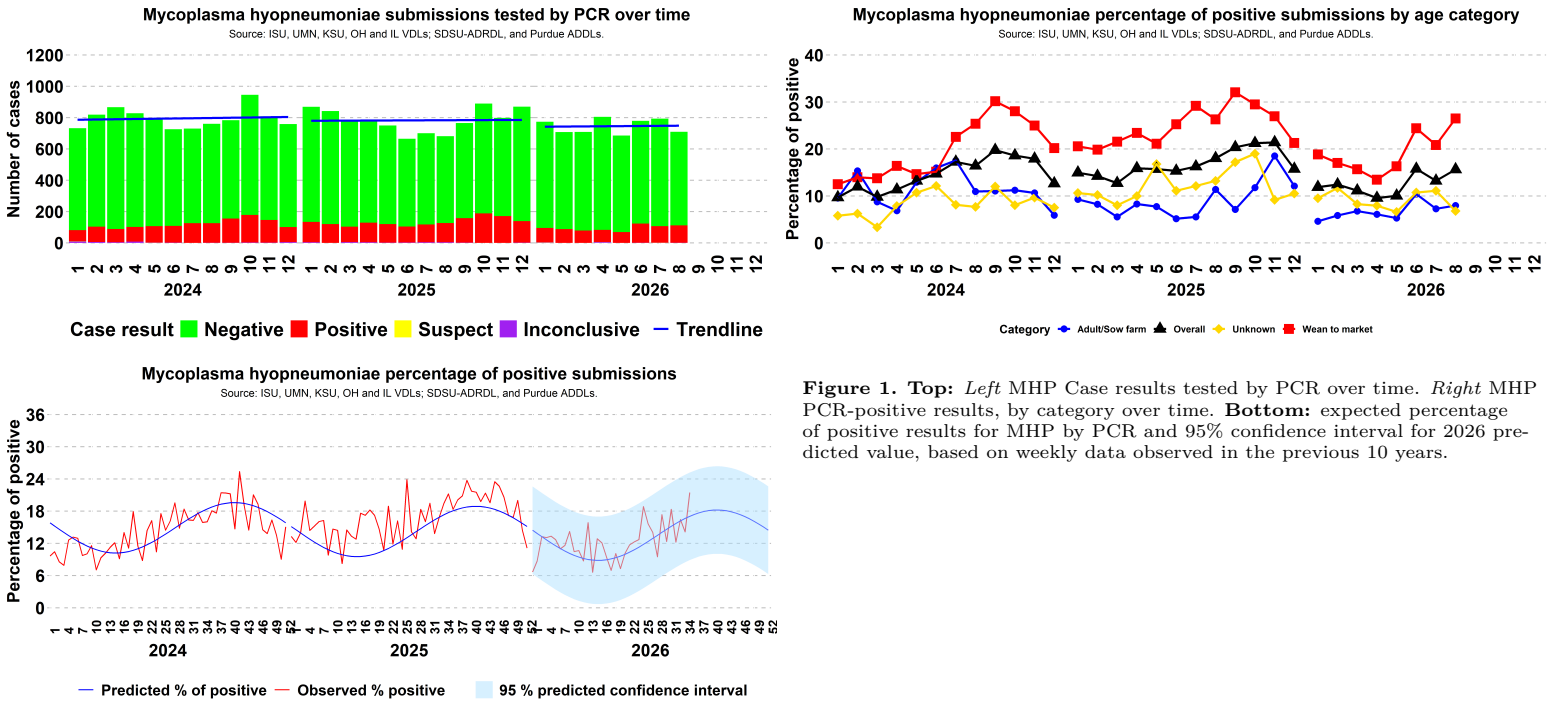


Figure 1. Top: Left MHP Case results tested by PCR over time. Right MHP PCR-positive results, by category over time. Bottom: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

SDRS Advisory Group highlights:

- Overall, 15.63% of 710 cases tested *M. hyopneumoniae*-positive in August, a moderate increase from 13.22% of 794 in July.
 - Positivity in the adult/sow category in August was 7.97% (22 of 276), similar to 7.29% (25 of 343) in July.
 - Positivity in the wean-to-market category in August was 26.49% (80 of 302), a substantial increase from 20.85% (64 of 307) in July.
- 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.

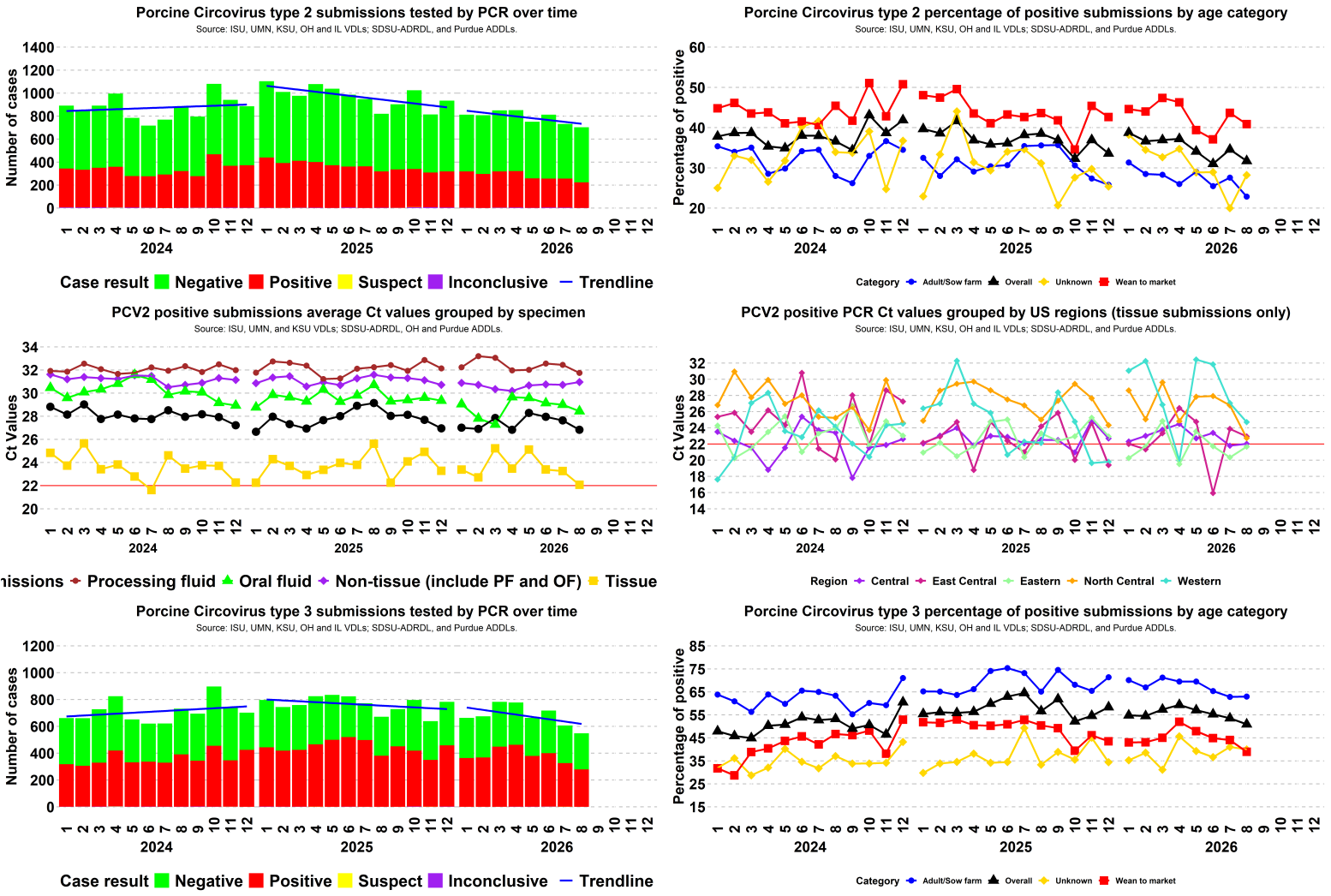


Figure 1. Top: Left: Results of PCV2 PCR cases over time; Right: PCV2 PCR-positive results, by category over time. Middle: Left: Average Ct values of PCV2 submissions by specimen; Right: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and WI), Eastern (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, 31.72% of 703 cases tested PCV2-positive in August, a moderate decrease from 34.56% of 732 in July.
 - Positivity in the adult/sow category in August was 22.85% (69 of 302), a moderate decrease from 27.59% (88 of 319) in July.
 - Positivity in the wean-to-market category in August was 40.87% (132 of 323), a moderate decrease from 43.68% (152 of 348) in July.
 - In the month of August, the regions with the lowest PCV2 average Ct values in tissue submissions were Eastern (21 submissions; average Ct 21.7), Central (39 submissions; average Ct 22), North Central (15 submissions; average Ct 22.7), East Central (8 submissions; average Ct 22.9), and Western (13 submissions; average Ct 24.7).
- Overall, 50.91% of 548 cases tested PCV3-positive in August, a moderate decrease from 53.54% of 607 in July.
 - Positivity in the adult/sow category in August was 62.96% (170 of 270), similar to 62.86% (198 of 315) in July.
 - Positivity in the wean-to-market category in August was 38.94% (81 of 208), a substantial decrease from 44.07% (104 of 236) in July.

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

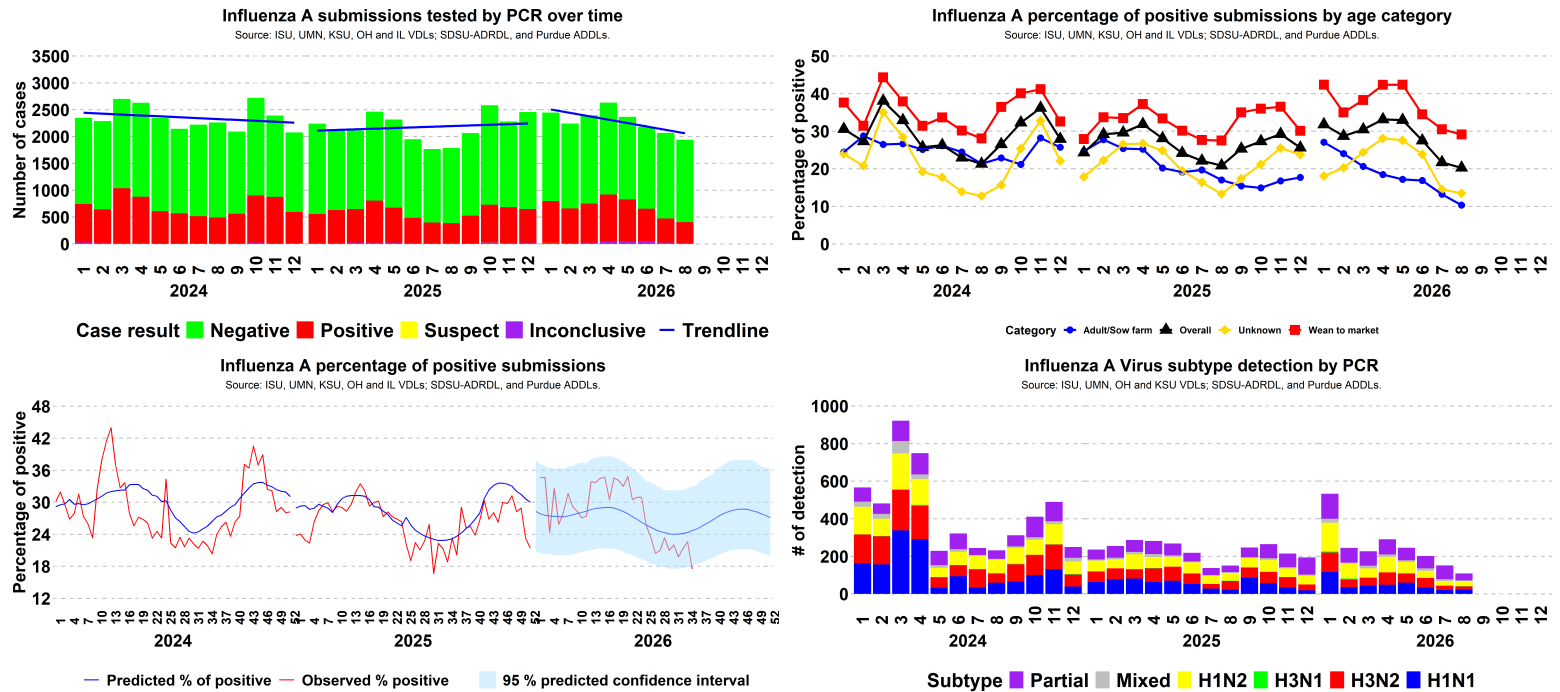


Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 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, 20.26% of 1,940 cases tested IAV-positive in August, similar to 21.72% of 2,067 in July.
 - Positivity in the adult/sow category in August was 10.31% (46 of 446), a moderate decrease from 13.2% (68 of 515) in July.
 - Positivity in the wean-to-market category in August was 29.14% (271 of 930), similar to 30.52% (297 of 973) in July.
 - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, OK, and OH.
- Overall, 2.75% of 109 samples had mixed subtype detection in August, a moderate decrease from 5.92% of 152 in July.

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

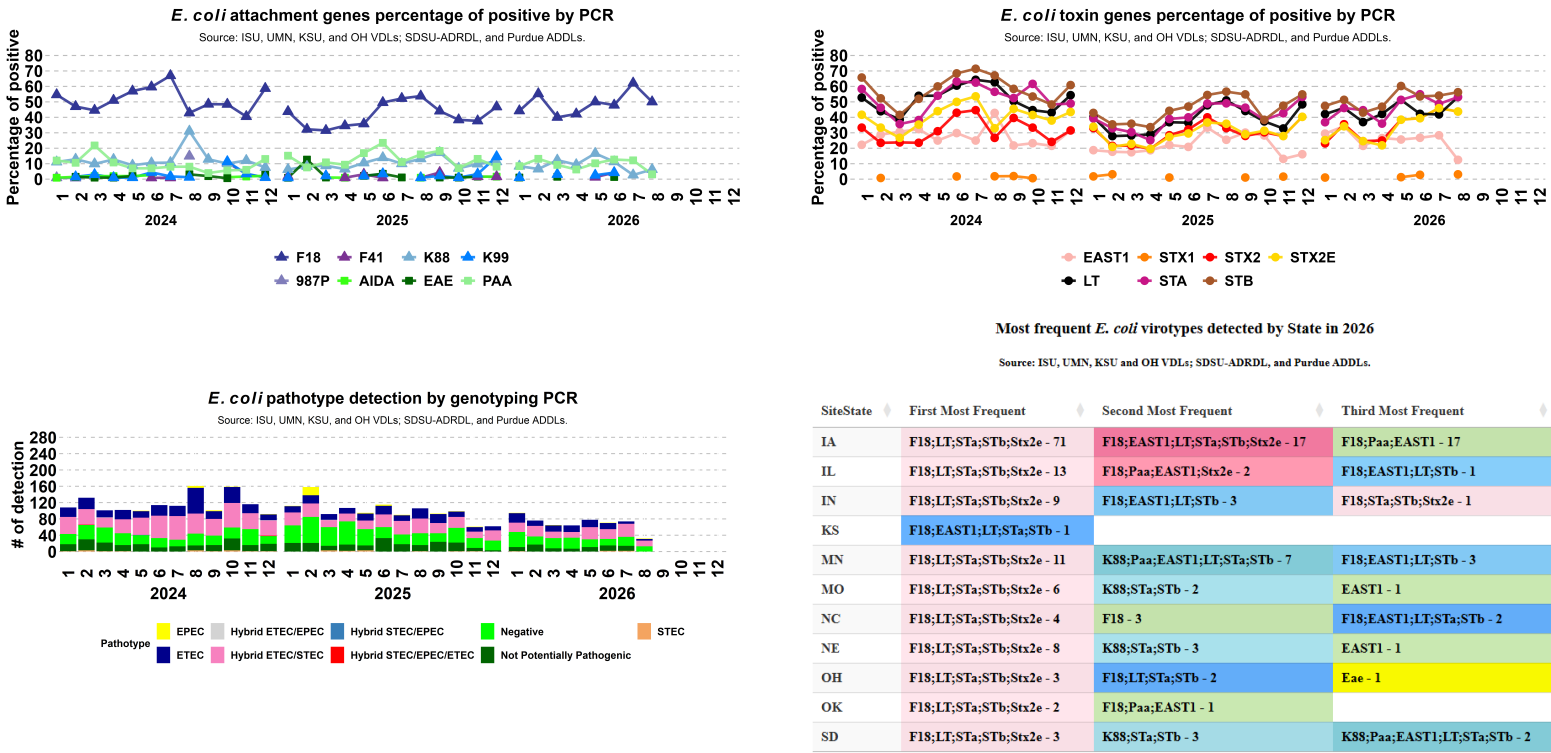


Figure 1. Top: Left *E. coli* PCR-Positive results by attachment genes over time. Right *E. coli* PCR-Positive results by toxin genes over time. Bottom: Left *E. coli* number of samples tested by PCR genotype and their respective pathotype classification. Right Most frequent detected *E. coli* virotype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

Education Material:

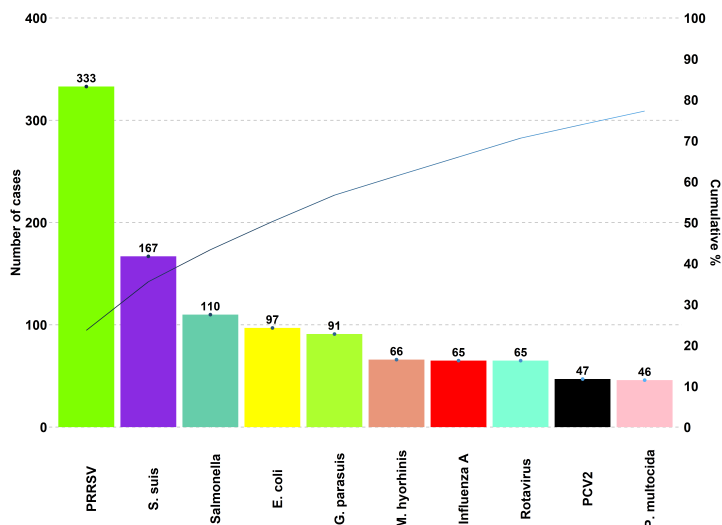
- Click on the links here to access the [E. coli PCR Genotyping Interpretation Tool](#)
- Attachment genes:** Fimbriae – F18, K88(F4), K99(F5), 987P(F6), F41; Adhesins – EAE (Intimin), PAA, AIDA
- Toxin genes:** Heat-labile – LT; Heat-stable – STa and STb; Shiga toxins – Stx1, Stx2 and Stx2e; and EAST1
- 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:

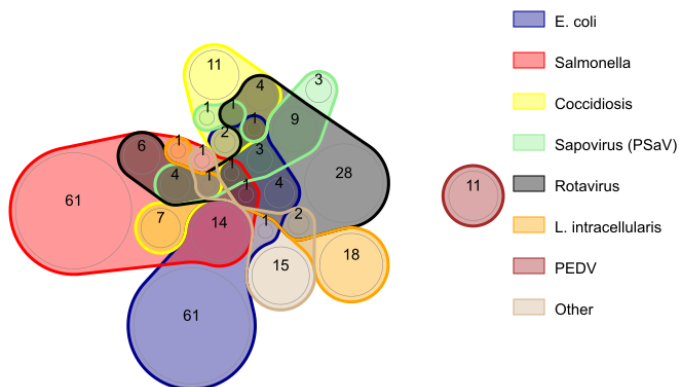
- Overall, 32 samples were tested for *E. coli* PCR in August.
 - In August, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (14 detections), ETEC (4 detections), and EPEC (1 detections).
 - In August, the *E. coli* attachment genes with higher detection rate were F18 (50.00%), K88 (6.25%), and EAE (3.12%).
 - In August, the *E. coli* toxin genes with higher detection rate were STB (56.25%), LT (53.12%), and STA (53.12%).

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

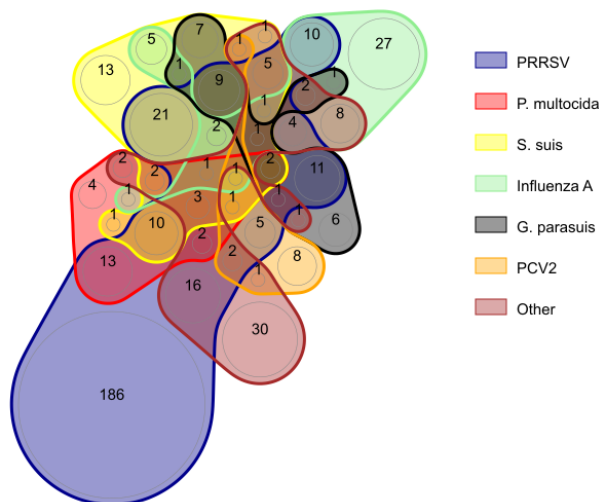
Overall diagnosis



Digestive



Respiratory



Nervous

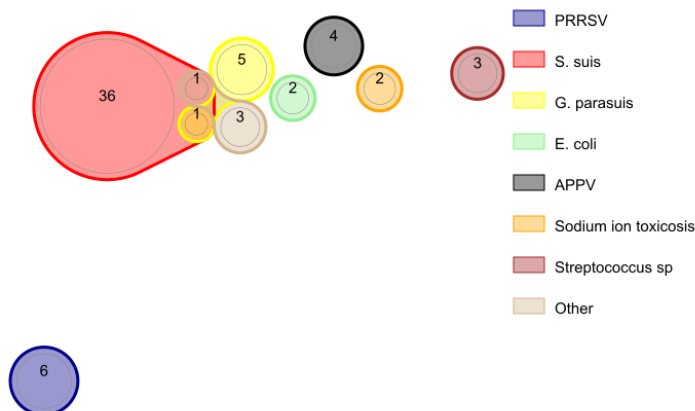


Figure 4. ISU-VDL and OH-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. 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, 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 July 01, 2026 to Aug 26, 2026

SDRS Advisory Group highlights:

- PRRSV (333) led cases with confirmed etiology, followed by *S. suis* (167), and *Salmonella* (110). PRRSV (307 of 652) led the number of confirmed respiratory diagnoses, *Salmonella* (97 of 351) lead the number of confirmed digestive diagnoses, and *S. suis* (38 of 65) led the number of confirmed neurological diagnoses.
- *Salmonella* activity was above expected levels during two weeks in July.

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.

Illinois Veterinary Diagnostic Laboratory Joins the Swine Disease Reporting System Network

Quyen Le¹, Wes Baumgartner², James Lowe², Daniel Linhares¹, Giovanni Trevisan¹

¹Iowa State University; ²University of Illinois Veterinary Diagnostic Laboratory;

The [Illinois Veterinary Diagnostic Laboratory \(IL-VDL\)](#) provides comprehensive diagnostic testing and disease surveillance support for veterinarians, producers, researchers, and animal health officials. The laboratory supports animal health through disease diagnosis, surveillance, and monitoring using a broad range of diagnostic services including molecular diagnostics, bacteriology, virology, serology, pathology, and necropsy examinations.

The IL-VDL is accredited by the **American Association of Veterinary Laboratory Diagnosticians (AAVLD)**, a designation that demonstrates commitment to diagnostic excellence, animal health surveillance, and continuous quality improvement, while its alignment with **ISO 17025 guidelines** provides internationally recognized assurance of laboratory quality, technical competence, and reliability. The IL-VDL is also a **Level 2 laboratory within the U.S. National Animal Health Laboratory Network (NAHLN)**, supporting national animal disease surveillance, preparedness, and response activities, and a member of the **Veterinary Laboratory Investigation and Response Network (Vet-LIRN)**, which enhances laboratory collaboration and capacity for animal health and food safety investigations.

Illinois is one of the nation's leading pork-producing states and an important contributor to U.S. swine production. According to the National Agricultural Statistics Service (USDA-NASS), Illinois maintains a pig inventory of **more than 5.25 million heads**, representing approximately **7.13% of the U.S. swine herd** and **ranking 4th among the top 10 U.S. swine-producing states**. The state's inventory includes approximately **600,000 breeding animals** and **4.65 million growing pigs**, emphasizing the importance of robust animal health surveillance and diagnostic support within the region.

The IL-VDL provides extensive diagnostic support to swine veterinarians and producers throughout Illinois and neighboring states. During 2024, the laboratory performed 6,986 molecular diagnostic tests for major swine pathogens, including **PRRSV, TGEV, PEDV, PDCoV, Senecavirus A, Swine Influenza Virus, Porcine Circovirus, and Mycoplasma hyopneumoniae**. Diagnostic submissions originated from **Illinois (50%), Indiana (40%), and other neighboring states (10%)**, reflecting the laboratory's regional impact and contribution to swine disease monitoring.

As a diagnostic resource serving a large and interconnected swine population, the IL-VDL generates valuable information for disease prevention, biosecurity planning, outbreak investigation, and herd health management. The laboratory's diagnostic capabilities and regional reach provide important insights into pathogen activity and disease trends across the eastern Corn Belt and surrounding swine-producing regions.

The addition of IL-VDL data to the Swine Disease Reporting System (SDRS) will expand surveillance coverage within a key swine-producing region of the United States. By incorporating diagnostic information from Illinois and neighboring states, SDRS gains **additional geographic representation and testing volume**, strengthening its ability to **monitor endemic diseases, identify changes in pathogen activity, detect emerging disease threats, and support informed decision-making by veterinarians and producers**.

The SDRS provides valuable information that supports **disease prevention, biosecurity, disease monitoring, and disease forecasting** throughout the U.S. swine industry. The Illinois Veterinary Diagnostic Laboratory is excited to join the SDRS network (**Figure 1**) and looks forward to collaborating with participating veterinary diagnostic laboratories, veterinarians, producers, and industry partners to further strengthen swine disease surveillance and support the health and sustainability of the U.S. pork industry.

