Swine Disease Reporting System
Report # 105 (November 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 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-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 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.

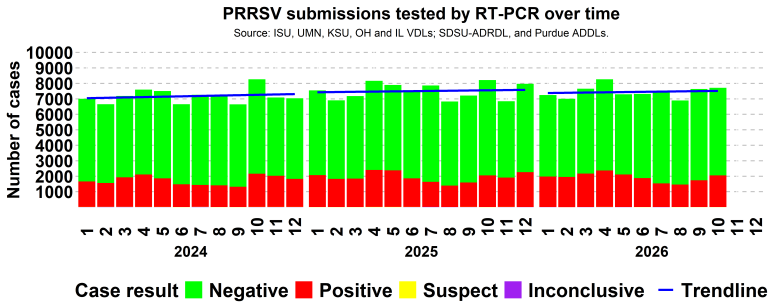
Audio and video reports: Key findings from SDRS projects are summarized monthly in a conversation between investigators and is available in the Spotify, Apple Podcast, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

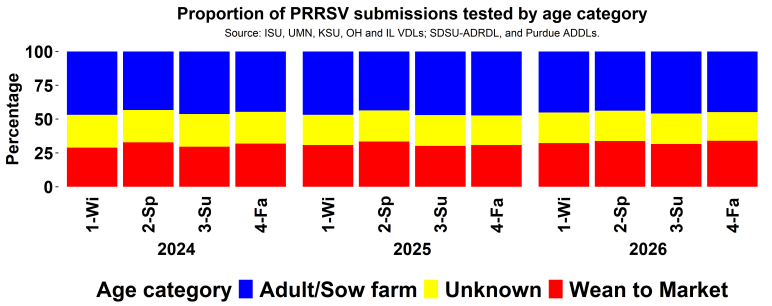
Advisory Group: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Davenport, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, Lauren Glowzenski, Brooke Kitting and Dustin Oedekoven.

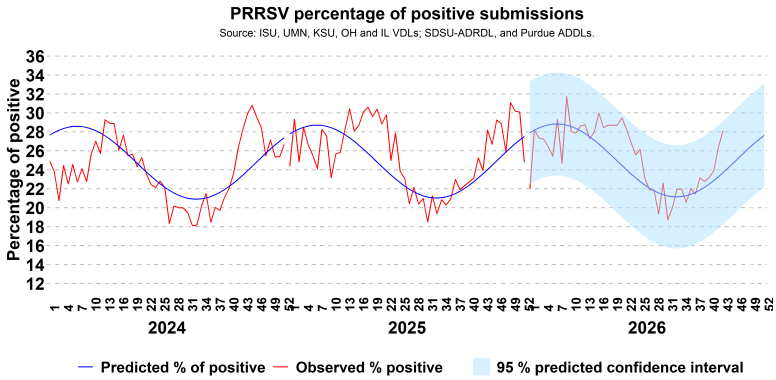
Note: This report contains data up to October 31, 2026.

Communications and information contained in this report are for general informational and educational purposes only and are not to be construed as recommending or advocating a specific course of action.

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







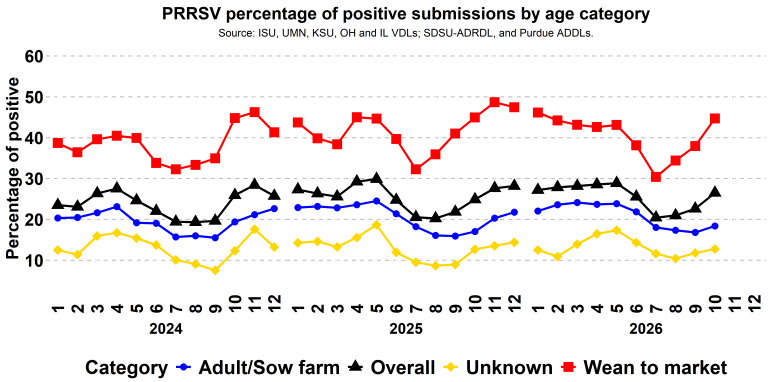
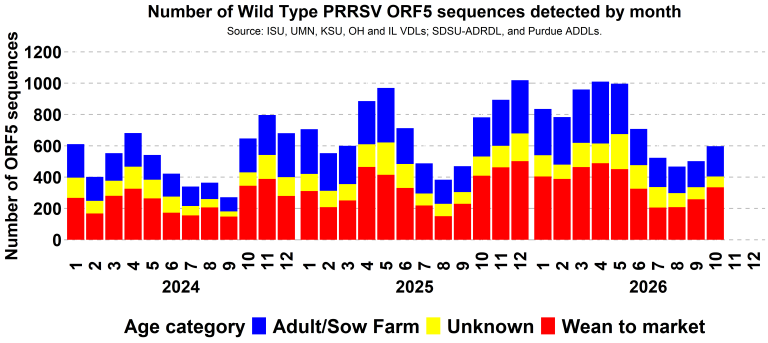


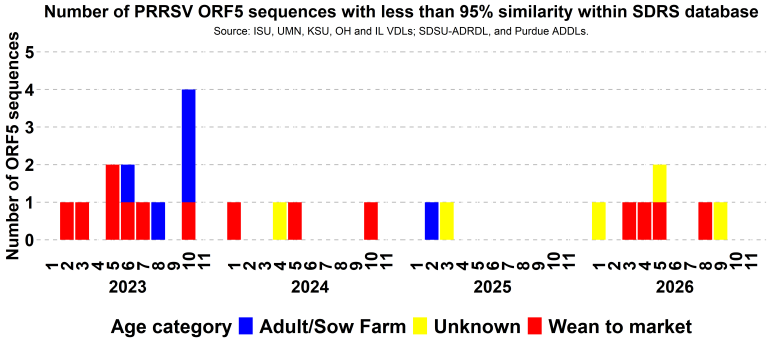
Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based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

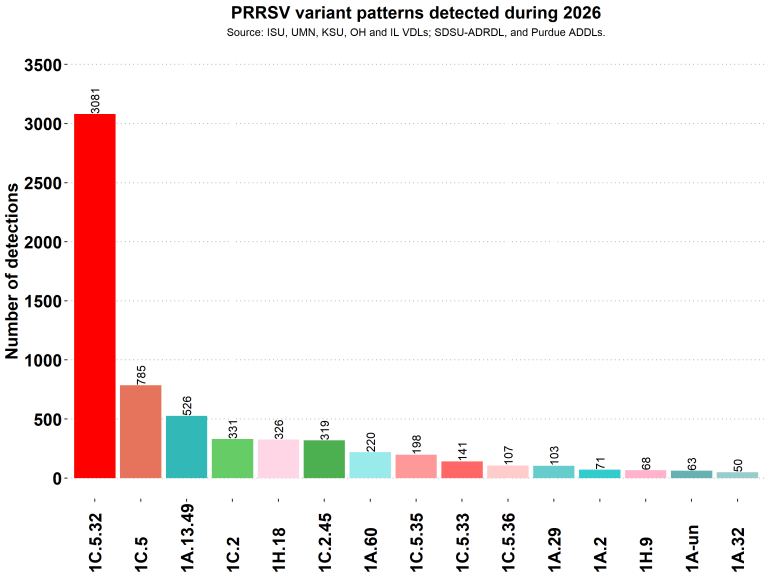
SDRS Advisory Group highlights:

- Overall, 26.51% of 7,718 cases tested PRRSV-positive in October, a moderate increase from 22.65% of 7,639 in September.
  - Positivity in the adult/sow category in October was 18.41% (610 of 3,313), similar to 16.83% (601 of 3,570) in September.
  - Positivity in the wean-to-market category in October was 44.71% (1,222 of 2,733), a substantial increase from 37.96% (941 of 2,479) in September.
  - Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in MO, SD and IL.

Topic 1.2 – PRRSV ORF5 sequences detection over time







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

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

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	1C.5.32 - 1794	1C.5 - 548	1A.13.49 - 360
IL	1C.5.32 - 360	1C.5 - 19	1A.13.49 - 16
IN	1C.5.32 - 68	1C.5.35 - 67	1C.5 - 40
KS	1C.5.32 - 17	1A.2 - 4	1A.58 - 3
MN	1C.5.32 - 459	1H.18 - 94	1A.13.49 - 55
MO	1C.5.32 - 150	1C.5 - 86	1C.2 - 28
NC	1C.2.45 - 190	1A.60 - 138	1C.5.32 - 49
NE	1C.5.33 - 100	1A.13.49 - 43	1C.5 - 34
OH	1C.5.35 - 99	1C.5.32 - 45	1A.13.49 - 16
OK	1C.5.32 - 24	1A.2 - 8	1H-un - 6
SD	1C.2 - 35	1C.5.32 - 25	1A.13.49 - 18

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 October, the states with higher number of PRRSV 1C.5.32 detections were detected IA, IL, MN, MO, IN, NC, NE, OK, KS, OH, SD (respective number of sequences: 78, 23, 21, 10, 5, 4, 4, 3, 2, 1, 1);
- In October 1C.5.32 (152) was the PRRSV variant most detected in the U.S., followed by 1C.5 (57), and 1A.13.49 (44);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
  - September 2026: 1C.2.44 (IL) and 1H.48 (MI)
  - October 2026: 1A.29 (TX) and 1A.13.49 (IN)

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Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

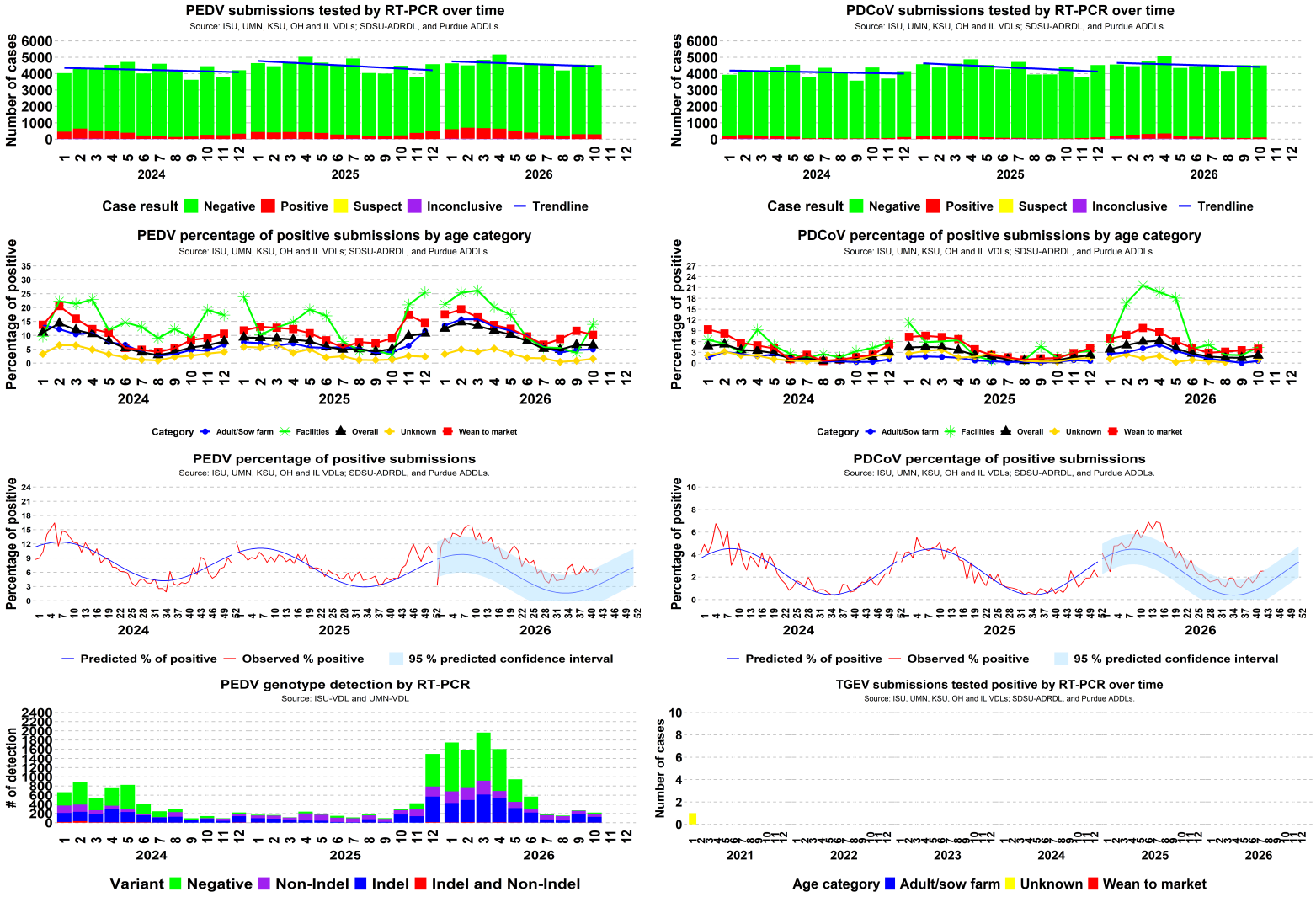


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection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

SDRS Advisory Group highlights:

- Overall, 6.47% of 4,530 cases tested PEDV-positive in October, similar to 6.57% of 4,550 in September.
  - Positivity in the adult/sow category in October was 4.97% (78 of 1,569), similar to 4.78% (78 of 1,633) in September.
  - Positivity in the wean-to-market category in October was 10.22% (179 of 1,752), similar to 11.68% (207 of 1,773) in September.
  - Positivity in the facilities category in October was 13.97% (19 of 136), a marked increase from 3.73% (5 of 134) in September.
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in MO.
  - Overall, 0.91% of 220 samples had mixed PEDV genotype detection in October, similar to 1.12% of 268 in September.
  - Overall, 32.73% of 220 samples had Non-Indel PEDV genotype detection in October, an increase from 26.87% of 268 in September.
  - Overall, 56.82% of 220 samples had Indel PEDV genotype detection in October, a decrease from 68.28% of 268 in September.
- Overall, 2.15% of 4,508 cases tested PDCoV-positive in October, an increase from 1.48% of 4,517 in September.
  - Positivity in the adult/sow category in October was 0.64% (10 of 1,558), an increase from 0.06% (1 of 1,615) in September.
  - Positivity in the wean-to-market category in October was 4% (70 of 1,750), similar to 3.57% (63 of 1,764) in September.
  - Positivity in the facilities category in October was 4.41% (6 of 136), an increase from 2.24% (3 of 134) in September.
  - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA and OK.
- There was 0 positive case for TGEV RNA-PCR in October, 2026 over a total of 4,391 cases tested. It has been 67 months (with a total of 262,820 cases tested) since the last TGEV PCR-positive result.

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

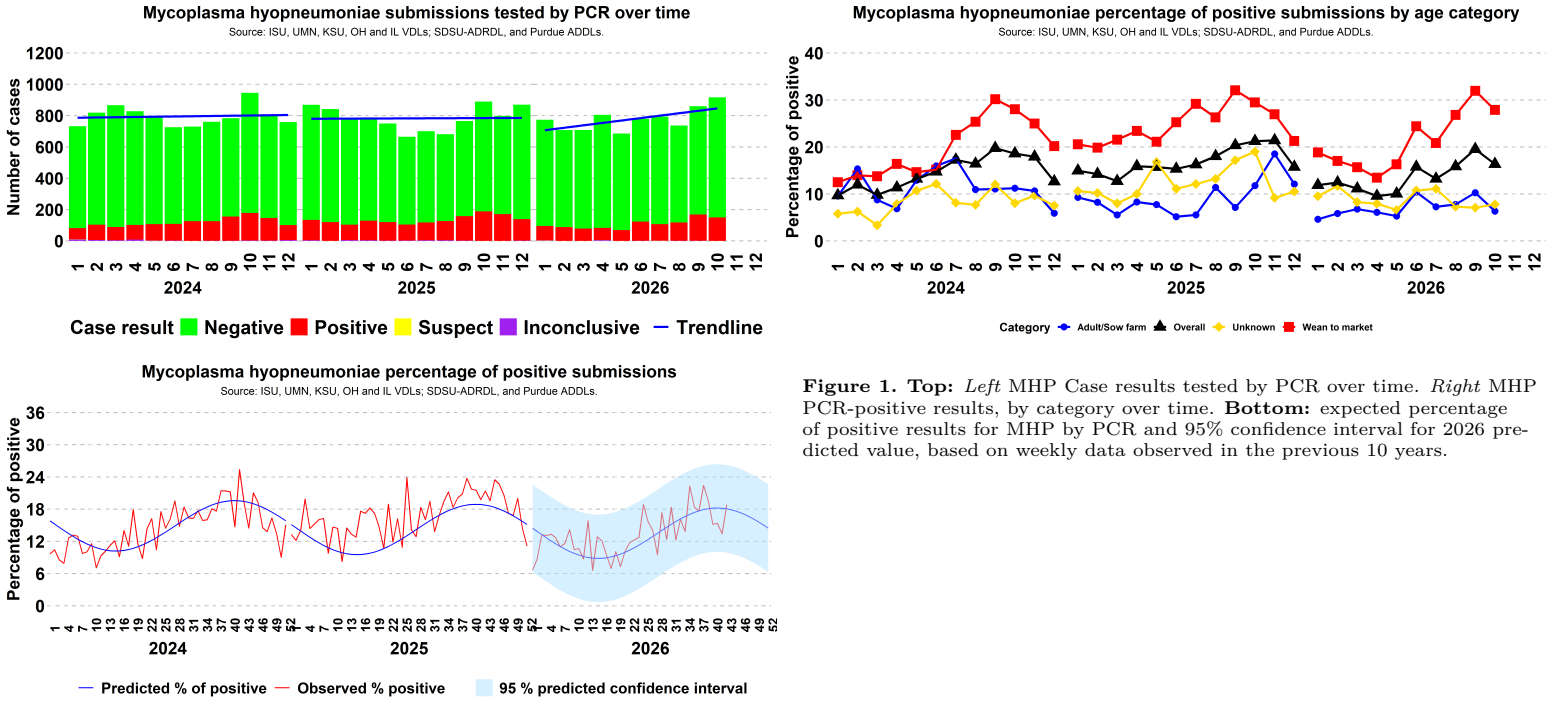
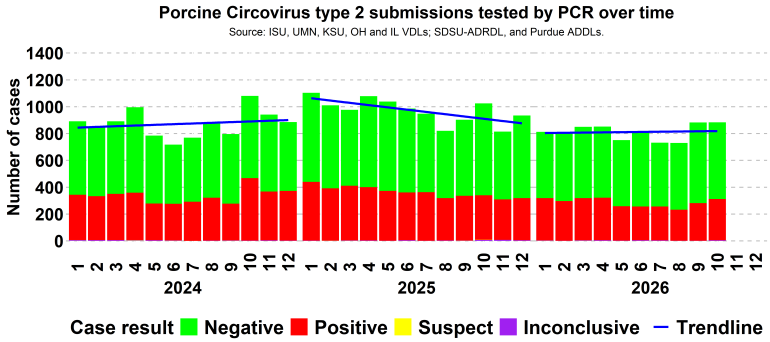


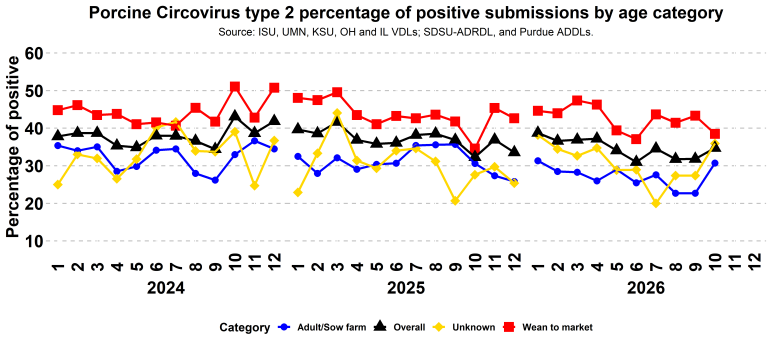
Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

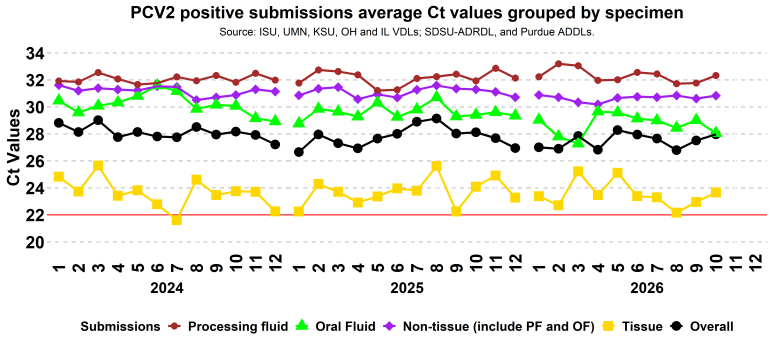
SDRS Advisory Group highlights:

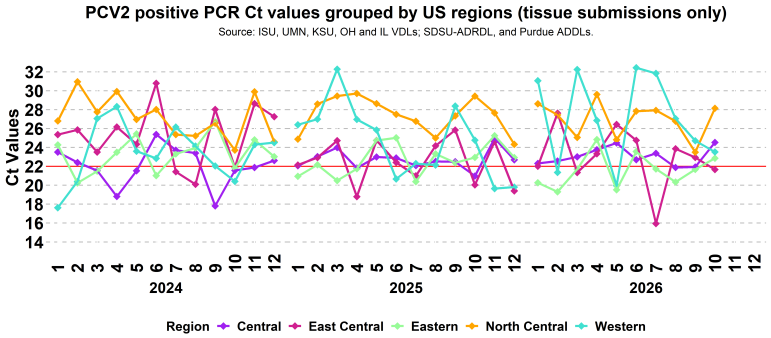
- Overall, 16.36% of 917 cases tested *M. hyopneumoniae*-positive in October, a decrease from 19.53% of 860 in September.
  - Positivity in the adult/sow category in October was 6.34% (22 of 347), a decrease from 10.27% (34 of 331) in September.
  - Positivity in the wean-to-market category in October was 27.88% (116 of 416), a decrease from 31.96% (124 of 388) in September.
  - Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states.

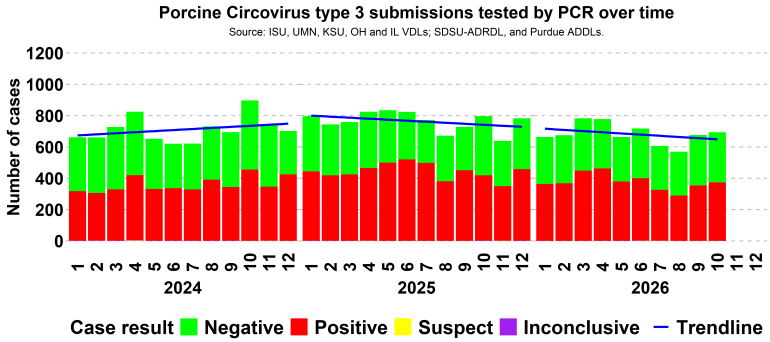
Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.











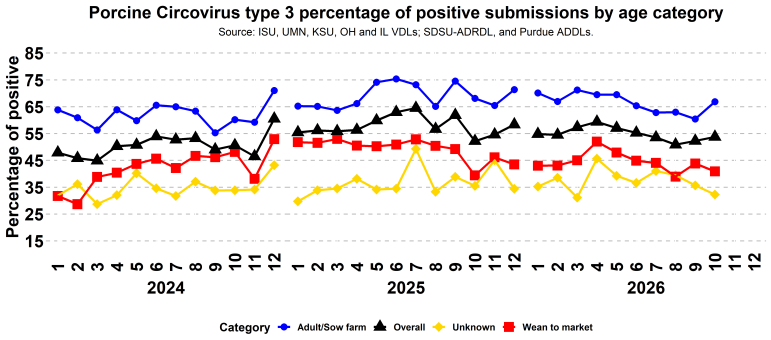


Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 34.73% of 884 cases tested PCV2-positive in October, an increase from 31.82% of 883 in September.
  - Positivity in the adult/sow category in October was 30.71% (125 of 407), an increase from 22.71% (99 of 436) in September.
  - Positivity in the wean-to-market category in October was 38.5% (159 of 413), a decrease from 43.32% (162 of 374) in September.
  - In the month of October, the regions with the lowest PCV2 average Ct values in tissue submissions were East Central (25 submissions; average Ct 21.7), Eastern (15 submissions; average Ct 22.9), Western (20 submissions; average Ct 23.5), Central (38 submissions; average Ct 24.5), and North Central (21 submissions; average Ct 28.1).
- Overall, 53.75% of 694 cases tested PCV3-positive in October, an increase from 52.29% of 677 in September.
  - Positivity in the adult/sow category in October was 66.85% (244 of 365), an increase from 60.42% (229 of 379) in September.
  - Positivity in the wean-to-market category in October was 40.91% (108 of 264), a decrease from 43.86% (100 of 228) in September.

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

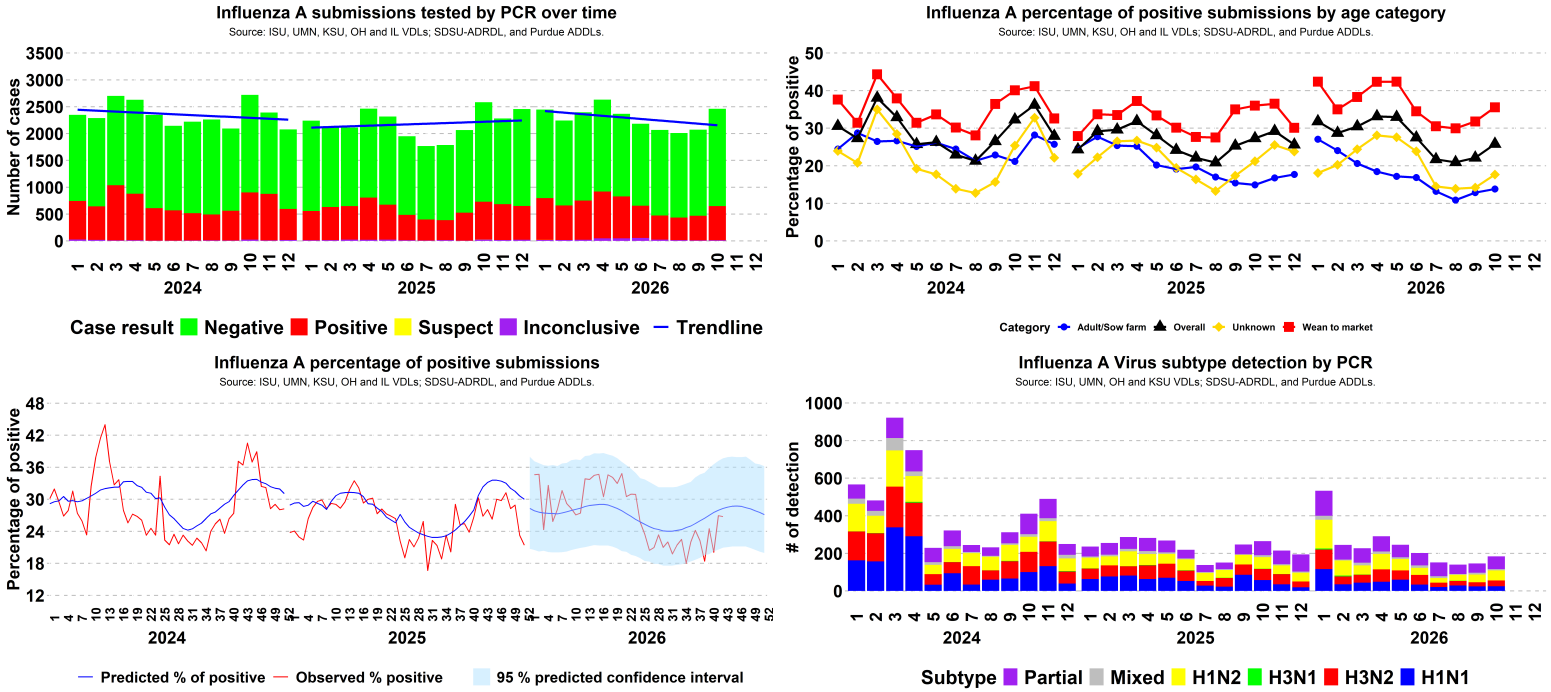
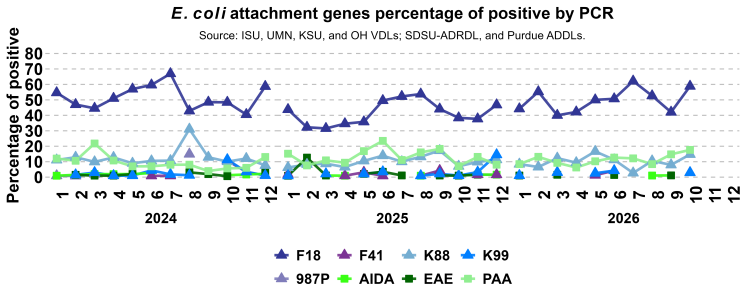


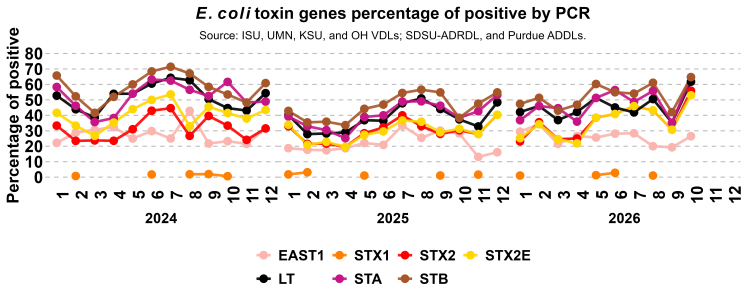
Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 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").

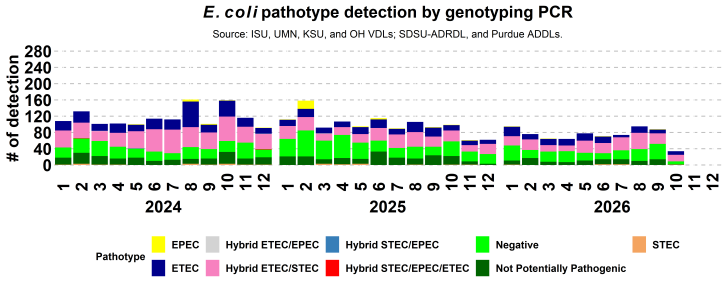
SDRS Advisory Group highlights:

- Overall, 25.79% of 2,462 cases tested IAV-positive in October, an increase from 22.14% of 2,073 in September.
  - Positivity in the adult/sow category in October was 13.82% (80 of 579), an increase from 12.88% (63 of 489) in September.
  - Positivity in the wean-to-market category in October was 35.56% (442 of 1,243), an increase from 31.79% (309 of 972) in September.
  - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in OH.
- Overall, 3.8% of 184 samples had mixed subtype detection in October, a decrease from 6.85% of 146 in September.

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







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

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

SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	F18;LT;STa;STb;Stx2e - 91	F18;EAST1;LT;STa;STb;Stx2e - 20	F18;Paa;EAST1 - 20
IL	F18;LT;STa;STb;Stx2e - 20	F18;EAST1;LT;STb;Stx2e - 2	F18;Paa;EAST1;Stx2e - 2
IN	F18;LT;STa;STb;Stx2e - 14	F18;EAST1;LT;STb - 4	F18;Paa;EAST1 - 3
KS	F18;EAST1;LT;STa;STb - 1	F18;LT;STa;STb - 1	
MN	F18;LT;STa;STb;Stx2e - 17	K88;Paa;EAST1;LT;STa;STb - 9	F18;EAST1;LT;STb - 4
MO	F18;LT;STa;STb;Stx2e - 6	K88;STa;STb - 3	F18;STa;STb - 2
NC	F18;LT;STa;STb;Stx2e - 6	F18 - 4	K88;Paa;EAST1 - 3
NE	F18;LT;STa;STb;Stx2e - 16	K88;STa;STb - 3	F18;Paa;EAST1;Stx2e - 2
OH	F18;LT;STa;STb;Stx2e - 5	F18;LT;STa;STb - 2	K88;STa;STb - 2
OK	F18;LT;STa;STb;Stx2e - 3	F18;Paa;EAST1 - 1	Paa;Stx2e - 1
SD	F18;LT;STa;STb;Stx2e - 5	K88;Paa;EAST1;LT;STa;STb - 3	K88;STa;STb - 3

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, 34 samples were tested for *E. coli* PCR in October.
  - In October, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (16 detections), ETEC (9 detections), and Not Potentially Pathogenic (1 detections).
  - In October, the *E. coli* attachment genes with higher detection rate were F18 (58.82%), PAA (17.65%), and K88 (14.71%).
  - In October, the *E. coli* toxin genes with higher detection rate were STA (64.71%), STB (64.71%), and LT (61.76%).

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

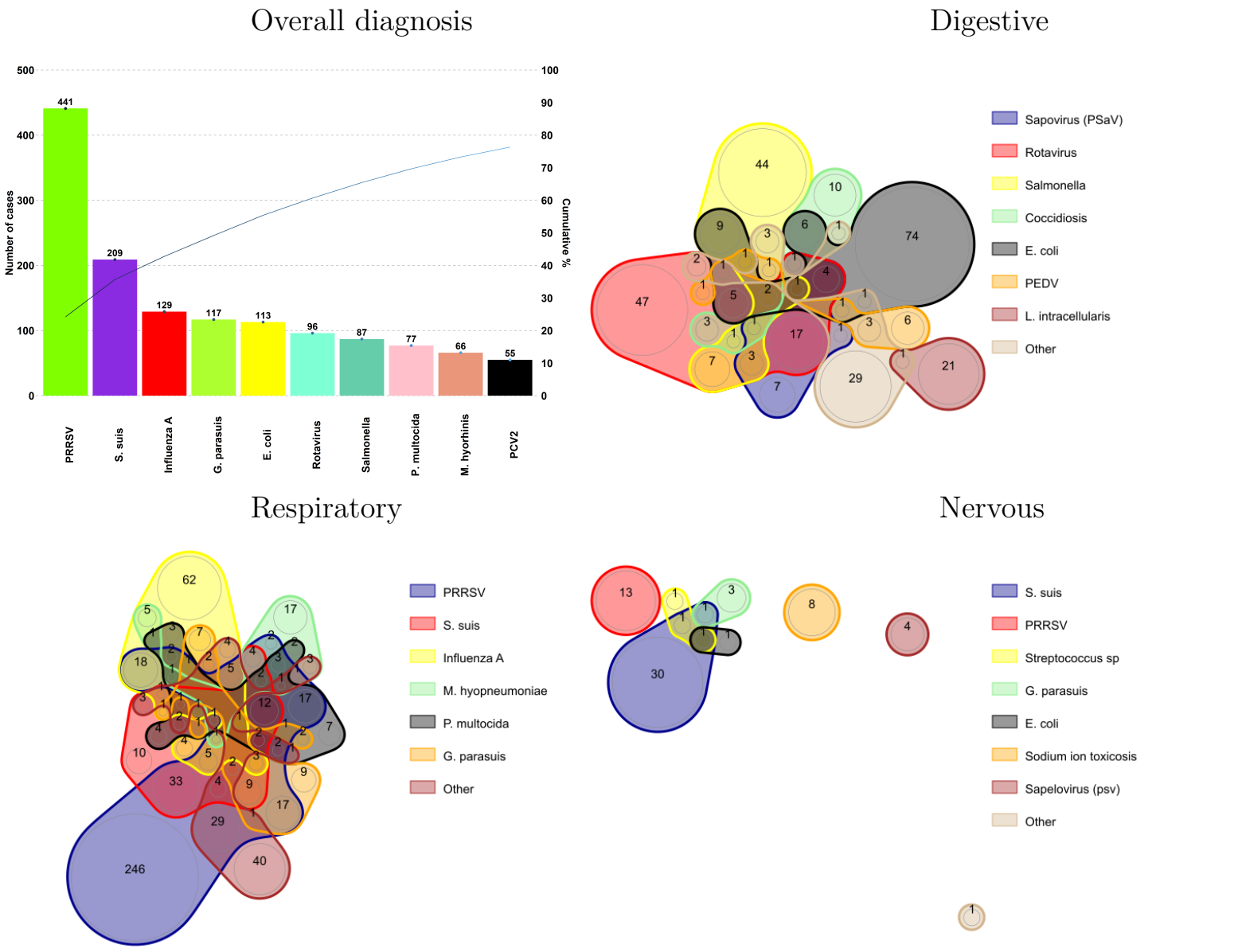


Figure 4. ISU-VDL and OH-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. 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 Sep 01, 2026 to Oct 27, 2026

SDRS Advisory Group highlights:

• PRRSV (441) led cases with confirmed etiology, followed by *S. suis* (209), and Influenza A (129). PRRSV (425 of 948) led the number of confirmed respiratory diagnoses, *E. coli* (105 of 412) lead the number of confirmed digestive diagnoses, and *S. suis* (33 of 68) led the number of confirmed neurological diagnoses.

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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.*

What we're watching this winter: SDRS Advisory Group perspective on swine health trends

Quyen Le[1], Sajan Kumar[1], Thomas Petznick[1], Daniel Linhares[1], Giovani Trevisan[1]
[1]Iowa State University

During October, the Swine Disease Reporting System Advisory Group and participant VDL collaborators gathered to review current pathogen activity detection and trendlines. Here, a summary is provided of the key points about pathogen trends and feedback from the Advisory Group from the Winter Preparedness Call in October 2026:

PEDV

- **PEDV activity increased earlier than typically expected in 2026**. Detections in wean-to-market began increasing during **late August** and remained elevated through September and October. Facilities detections followed a similar pattern during early fall. Overall, PEDV activity remained **above the expected range** for this time of year as the industry entered the fall season.
- Oral fluids continued to account for approximately **two-thirds** of PEDV surveillance submissions in 2026. Regional differences were observed, with Kansas and Oklahoma reporting some of the highest positivity levels among monitored states. Since July PEDV has been active in Missouri and in October activity is also spiking in Indiana and Nebraska.
- Confirmed tissue diagnosis data also indicated increased PEDV-associated enteric disease activity. From January to October 13, 2026, **159 PEDV-confirmed tissue diagnosis cases** had been reported, compared with **139 cases reported during all of 2025**. In addition, **one statistical alert** was generated in September when confirmed PEDV tissue diagnosis activity exceeded levels.
- Advisory members noted that surveillance activities, routine testing, and site clean-up efforts may influence detection trends and should be considered when interpreting positivity data. The group also noted that PEDV activity has historically fluctuated over time and emphasized the importance of continued attention to transportation-related (including truck and trailer biosecurity, and pig movement across regions) biosecurity and biocontainment practices when evaluating opportunities to further reduce PEDV transmission.

PRRSV

- PRRSV activity remained elevated throughout 2026. Positivity during **August and September reached the highest levels observed since 2015**. In addition, PRRSV positivity during **summer 2026 was comparable to levels observed during the summers of 2020 and 2021**. Advisory members discussed widespread circulation of variant **1C.5.32** and increased testing associated with herd monitoring, closure programs, and outbreak investigations as potential contributors to elevated positivity;
- Variant analysis showed broad dominance of PRRSV variants of **L1C.5** and **L1C.2** across monitored states, with notable shifts in dominant variants observed in North Carolina and Illinois. Three variants were identified as accelerating strains in 2026, including **1A.13.49, 1A.29 and 1C.5.32**, all of which more than doubled in detections compared with 2025. Among these, **1A.13.49 increased by more than 700%** since its first emergence in 2024, representing the largest observed among monitored variants;
- Field observations indicate a mixed clinical presentation of variant 1A.13.49, from mild outbreaks to aggressive ones. In general, Advisory members noted the importance of continued monitoring as the variant expands into additional regions;
- SDRS identified **34 interstate first detections** of PRRSV variants during 2026. Variant **1A.13.49, 1A.29, and 1C.5.32** were also among those showing the greatest geographic expansion;
- The continued emergence and spread of PRRSV variants prompted discussion regarding long-term control strategies. Advisory Group members emphasized the importance of continually evaluating biosecurity, biocontainment, pig flow, transportation networks, and regional disease-management approaches as the industry works to reduce the impact of PRRSV.

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Mycoplasma hyopneumoniae (MHP)

- PCR surveillance data indicated increasing MHP detections during 2026, particularly in wean-to-market systems. **The Advisory members** noted that PCR-positive detections are generally linked with testing samples for exposure in elimination programs and should be interpreted with caution to avoid overinterpreting them as pathogen activity in the field;
- Despite increasing PCR detections, tissue diagnosis data showed substantially fewer confirmed MHP cases than historical levels. Data presented during the call indicated an approximately **80% reduction in tissue-confirmed MHP diagnosis**, from 2020 to 2026.

Influenza A Virus (IAV)

- Adult/sow farm IAV positivity remained at **historically low levels** during 2026, representing the lowest activity observed over two decades. In contrast, **IAV-PRRSV PCR co-detection in wean-to-market sites approached 15% during summer 2026**, a level comparable to that observed during summer 2022;
- Confirmed tissue diagnosis data demonstrated increased IAV-associated disease activity during September and early October 2026, as expected for this time of the year;
- Advisory members suggested that improved strain selection and vaccination strategies may have been contributing to reduced IAV activity in sow farms and associated gilt flows. However, the group noted that growing pigs usually remain susceptible to circulating influenza viruses and identified **IAV-PRRSV co-detections** as an area to monitor closely during the upcoming winter season. Members also emphasized that multiple pathogens may contribute to respiratory disease outbreaks in growing pigs, making comprehensive differential diagnostic investigations important.

TGEV

- **TGEV has gone over five and half years without an RT-PCR positive field sample in the United States**. Following a review of historical records, SDRS updated the date of the last confirmed field case to **January 25, 2021**, after determining that a previously reported March 2021 detection was associated with research activities rather than a field case;
- Since the last confirmed field detection, **more than 257,000 RT-PCR diagnostic cases** have been performed without identifying a positive case.