Swine Disease Reporting System
Report # 94 (November 30, 2025)

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

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

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

Collaborators:

Swine Disease Reporting System office: Principal investigators: Daniel Linhares & Giovani Trevisan; Data Analyst: Quyen Thuc Le; Project coordinator: Guilherme Cezar

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

Uni. of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, 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.

Ohio Animal Disease and Diag. Lab. and *The Ohio State University*: 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: Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL.

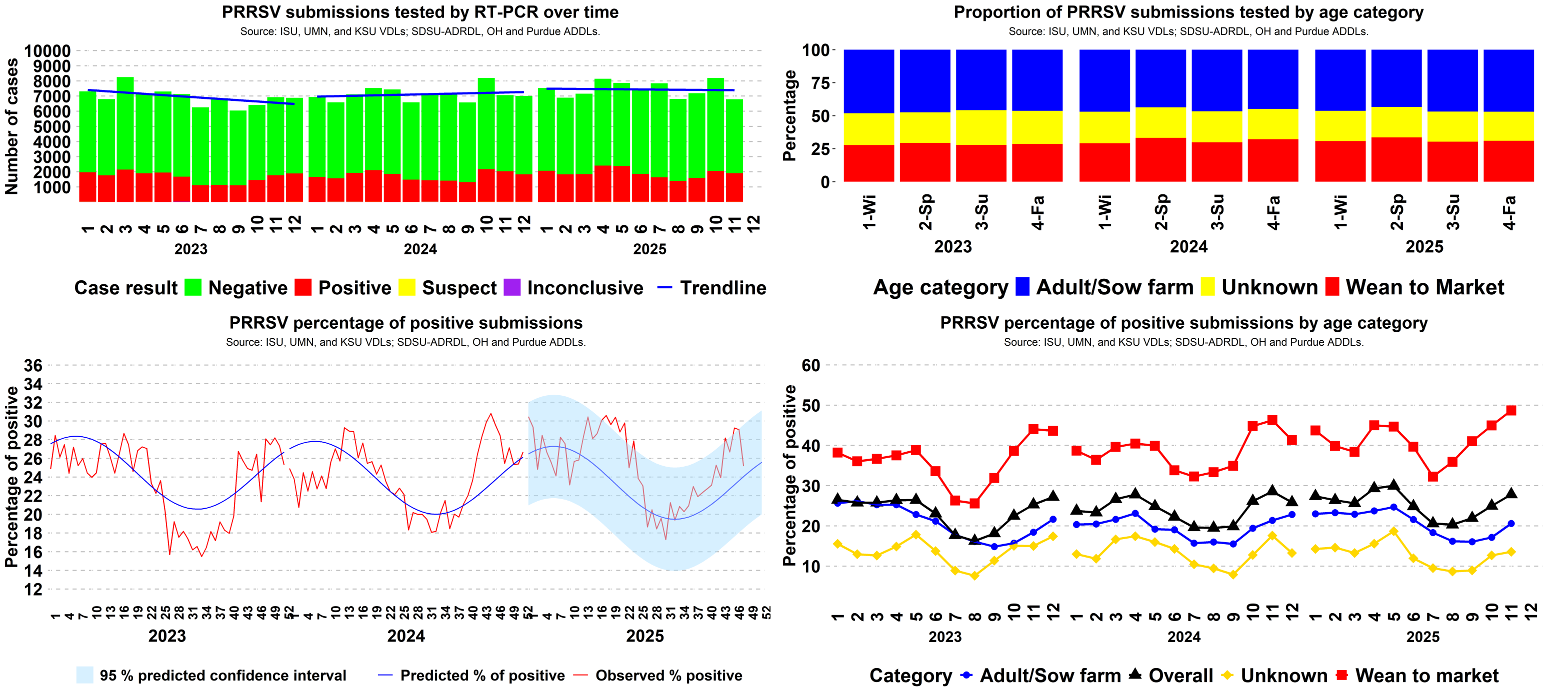
PRRS virus RFLP/Lineage report and BLAST tool: Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

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

Advisory Group: Providing their comments and perspectives monthly: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte 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 November 30, 2025.

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.

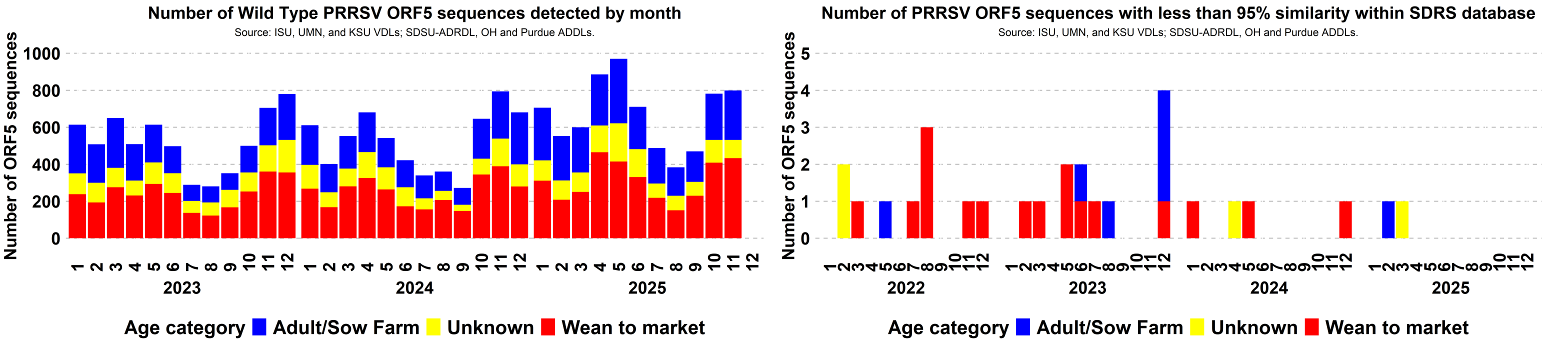
PRRSV percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 27.85% of 6,791 cases tested PRRSV-positive in November, a moderate increase from 24.99% of 8,190 in October;
  - Positivity in the adult/sow category in November was 20.63% (648 of 3,141), a moderate increase from 17.16% (660 of 3,846) in October;
  - Positivity in the wean-to-market category in November was 48.68% (1,036 of 2,128), a moderate increase from 44.96% (1,164 of 2,589) in October;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MN, MO, IN and NC;
- Feedback from some advisors indicated that PRRSV testing has been increasing, with systems appearing relatively stable despite a high percentage of positive unstable sow herds leading to virus leakage in wean-to-market sites and earlier PRRSV activity this year. Severity appears to be mirroring the 2024-2025 Winter/Spring season, being more pronounced than in previous years. PRRSV in grow-finish has risen since late October and is not expected to decline in the coming weeks.
- Some of the advisors also noted that PRRSV activity has increased in the last 30 days across sow farms in multiple states due to new introductions and recirculation of endemic strains. Positivity in wean-to-market sites have been rising over the past two months, with responses ranging from mild to severe outbreaks.

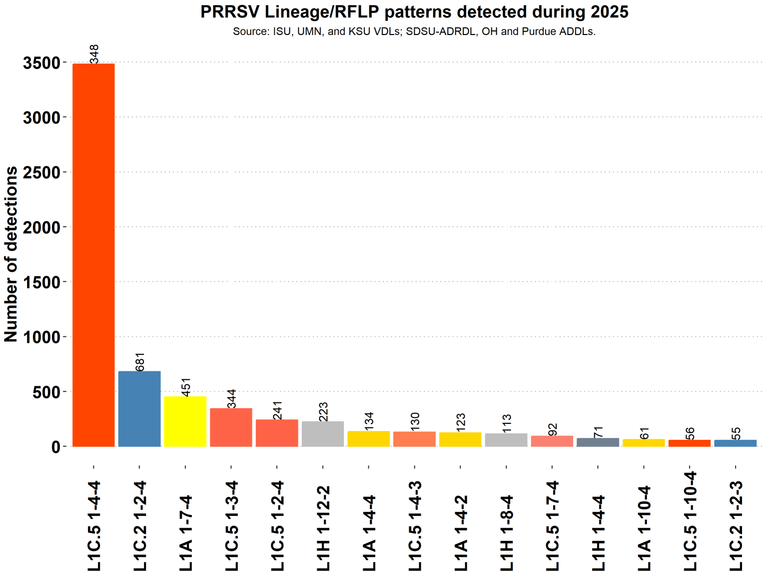
Topic 2 – PRRSV ORF5 sequences detection over time


Number of Wild Type PRRSV ORF5 sequences detected by month

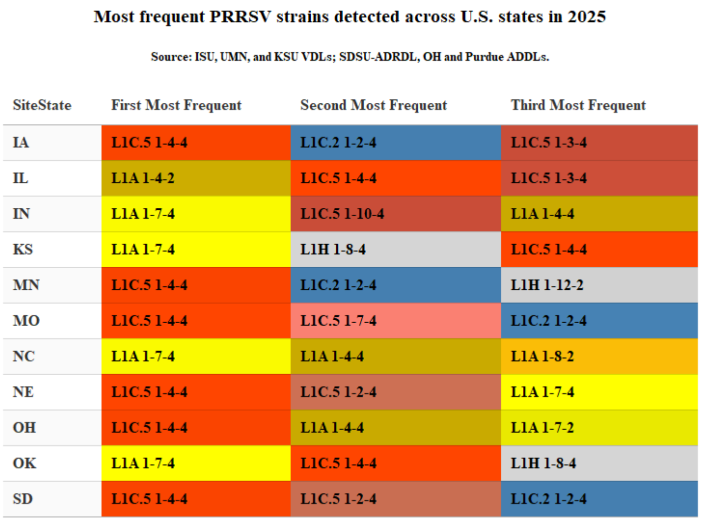
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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 Lineage/RFLP patterns detected during 2025

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


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

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

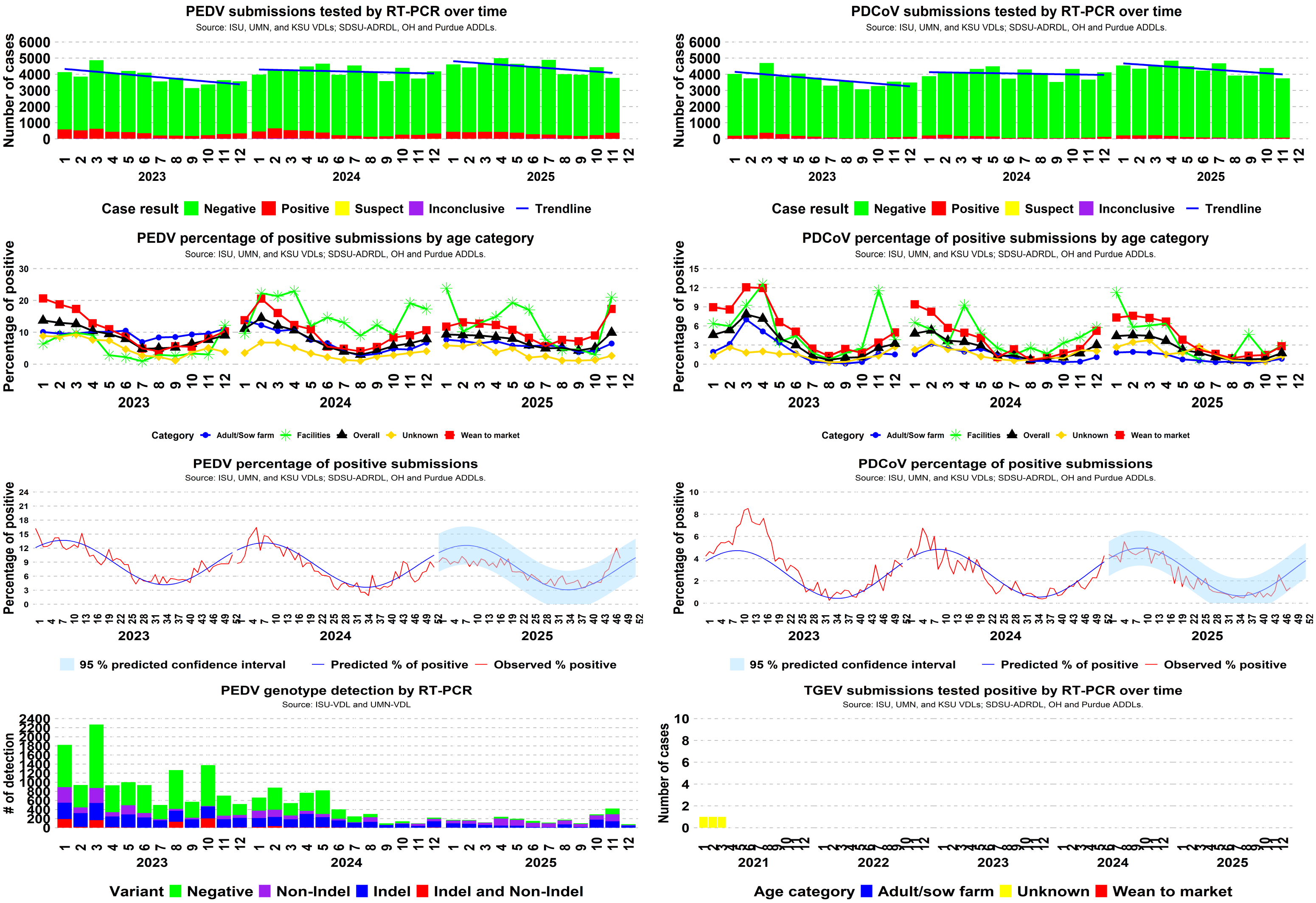
SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	L1C.5 1-4-4	L1C.2 1-2-4	L1C.5 1-3-4
IL	L1A 1-4-2	L1C.5 1-4-4	L1C.5 1-3-4
IN	L1A 1-7-4	L1C.5 1-10-4	L1A 1-4-4
KS	L1A 1-7-4	L1H 1-8-4	L1C.5 1-4-4
MN	L1C.5 1-4-4	L1C.2 1-2-4	L1H 1-12-2
MO	L1C.5 1-4-4	L1C.5 1-7-4	L1C.2 1-2-4
NC	L1A 1-7-4	L1A 1-4-4	L1A 1-8-2
NE	L1C.5 1-4-4	L1C.5 1-2-4	L1A 1-7-4
OH	L1C.5 1-4-4	L1A 1-4-4	L1A 1-7-2
OK	L1A 1-7-4	L1C.5 1-4-4	L1H 1-8-4
SD	L1C.5 1-4-4	L1C.5 1-2-4	L1C.2 1-2-4

Figure 1. **Top**: **Left**: Number of PRRSV ORF5 sequences detected by age category; **Right**: Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher than 606 nucleotides are not included in this analysis); **Bottom** *Left*: 15 PRRSV ORF5 sequences most frequent detected by Lineage and RFLP; *Right*: Most frequent detected PRRSV ORF5 sequences in 2025 by lineage and RFLP at U.S. state level.

SDRS Advisory Group highlights:

- During November 2025, The states with higher number of PRRSV 1C.5 (variant) detections were detected IA, MN, MO, NE, IL, IN, KS, OH, OK, SD (respective number of sequences: 363, 86, 32, 20, 18, 14, 5, 4, 4, 4).
- In November L1C.5 1-4-4 (446) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (50), and L1A 1-7-4 (43);
- 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.
- Increased PRRSV activity in wean-to-market, especially in Iowa/Illinois. The variants 1C.5.32 and 1C.2 have been producing severe clinical signs; some individuals perceive it as worse than it was this past Spring or Summer. The variant 1C.5.32 remains the most predominant one and continues to spread to most US states. There appear to be clusters of varying severity, which motivates veterinarians to sequence the virus to better understand epidemiology and transmission patterns.

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR



PEDV submissions tested by RT-PCR over time

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

PDCoV submissions tested by RT-PCR over time

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

PEDV percentage of positive submissions by age category

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

PDCoV percentage of positive submissions by age category

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

PEDV percentage of positive submissions

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

PDCoV percentage of positive submissions

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

PEDV genotype detection by RT-PCR

Source: ISU-VDL and UMN-VDL

TGEV submissions tested positive by RT-PCR over time

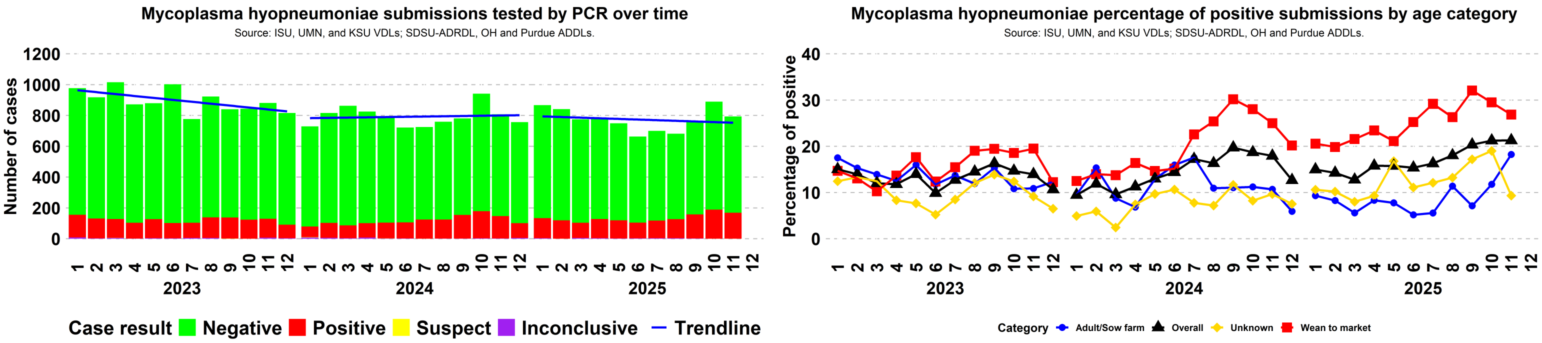
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 9.9% of 3,776 cases tested PEDV-positive in November, a moderate increase from 5.16% of 4,442 in October;
  - Positivity in the adult/sow category in November was 6.48% (84 of 1,297), a moderate increase from 4.18% (65 of 1,554) in October;
  - Positivity in the wean-to-market category in November was 17.33% (235 of 1,356), a substantial increase from 9% (145 of 1,612) in October;
- Positivity in the facilities category in November was 21.01% (29 of 138), a marked increase from 2.99% (4 of 134) in October;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in OK, NC and IN;
  - Overall, 0% of 79 samples had mixed PEDV genotype detection in December, similar to 0% of 422 in November;
- Overall, 1.74% of 3,746 cases tested PDCoV-positive in November, similar to 0.82% of 4,389 in October;
  - Positivity in the adult/sow category in November was 0.86% (11 of 1,282), similar to 0.39% (6 of 1,529) in October;
  - Positivity in the wean-to-market category in November was 2.81% (38 of 1,350), similar to 1.43% (23 of 1,603) in October;
- Positivity in the facilities category in November was 2.9% (4 of 138), similar to 1.49% (2 of 134) in October;
- 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 November, 2025 over a total of 3,626 cases tested. It has been 57 months (with a total of 212,206 cases tested) since the last TGEV PCR-positive result;
- Wean-to-market PEDV positivity ramped up earlier this season compared to last year, with certain systems facing a bigger battle than usual at the sow unit level, largely driven by pit agitation and pumping. In contrast, others reported sow farms remaining stable with no new infections of PEDV/PDCoV, viewing current activity as seasonal and linked to cooler temperatures and manure handling.

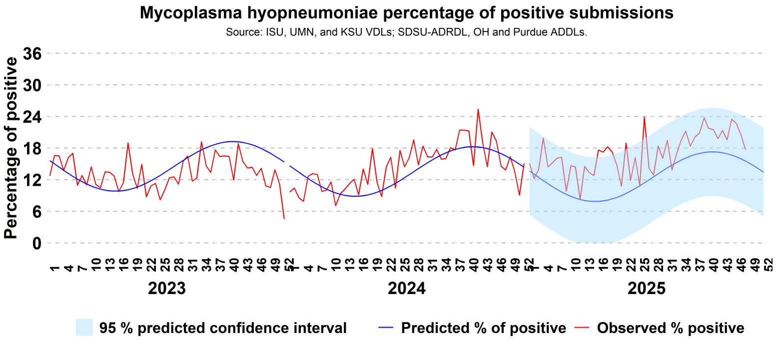
Topic 3 – Detection of *M. hyopneumoniae* DNA by PCR.


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

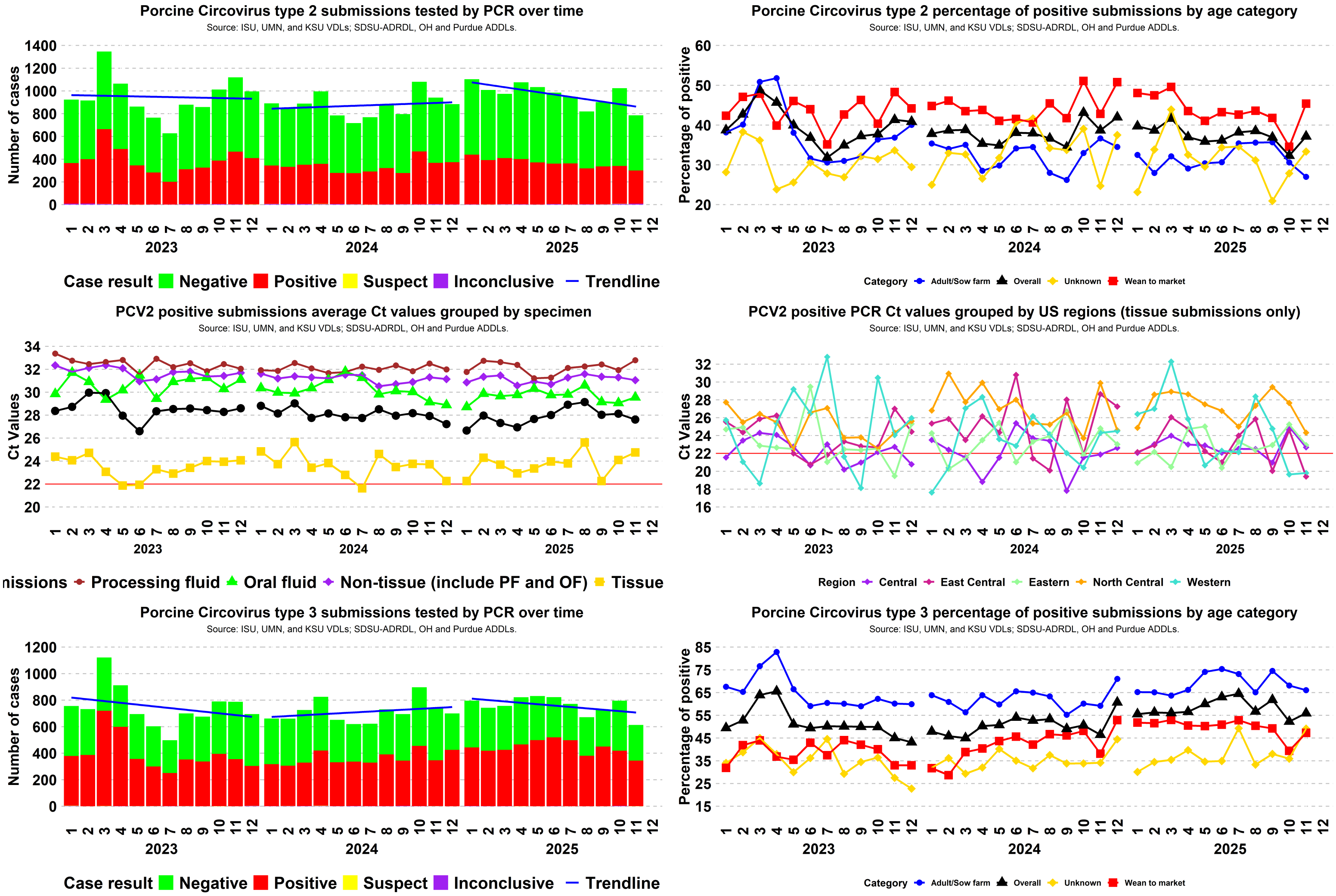
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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 2025 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 21.28% of 794 cases tested *M. hyopneumoniae*-positive cases in November, similar to 21.24% of 890 in October;
  - Positivity in the adult/sow category in November was 18.24% (54 of 296), a substantial increase from 11.78% (39 of 331) in October;
  - Positivity in the wean-to-market category in November was 26.85% (105 of 391), a moderate decrease from 29.5% (123 of 417) in October;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN, NE, IL and NC;
- Some of the advisors reported that *M. hyopneumoniae* remains largely a non-issue, with minimal diagnoses in commercial finishing and no new downstream detections, though a few positives have been noted. With recent medication management updates, clinical severity and subsequent diagnostics are expected to decrease; however, the increase in PRRSV and IAV in flows placed from *M. hyopneumoniae*-positive sow farms is contributing to greater shedding and clinical signs, and may be leading to more *M. hyopneumoniae* being picked up through testing.

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.

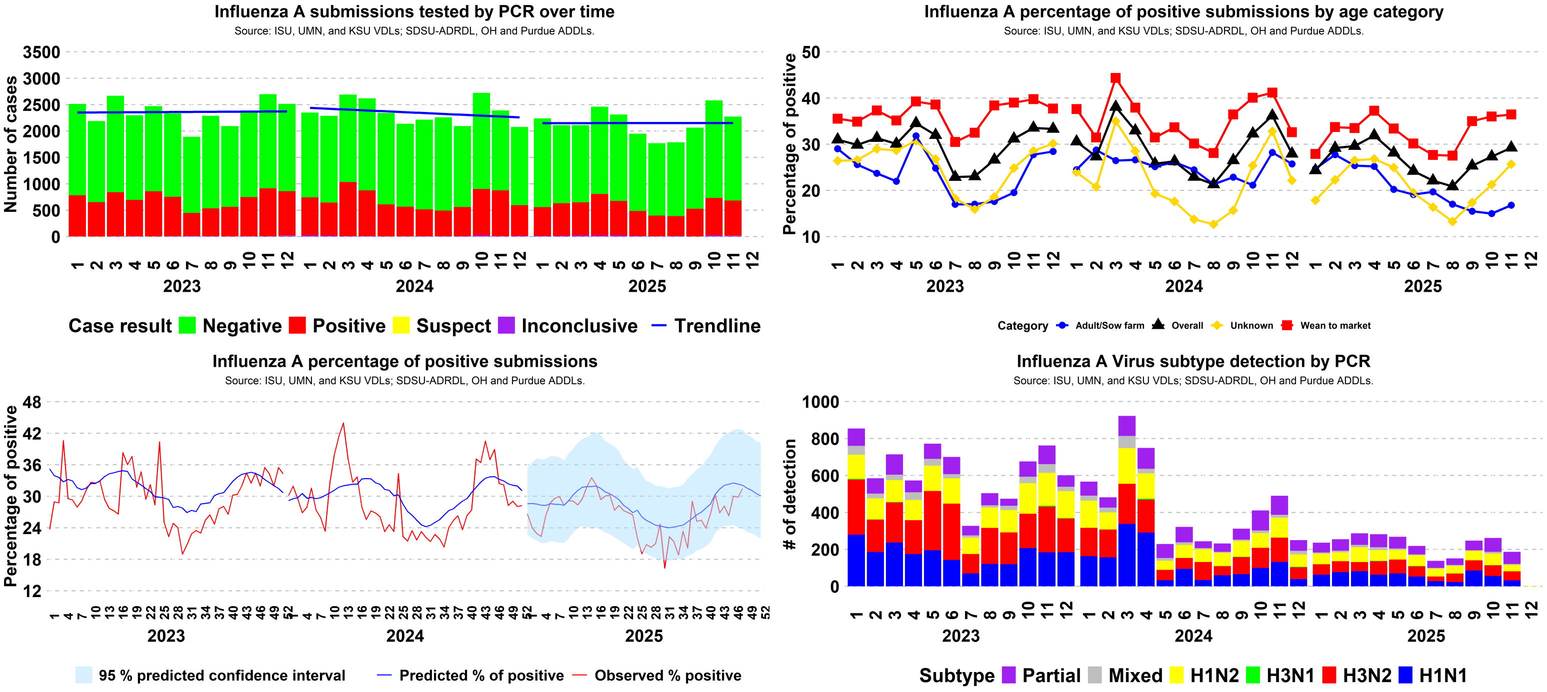
Porcine Circovirus type 3 percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 37.15% of 786 cases tested PCV2-positive in November, a moderate increase from 32.32% of 1,024 in October;
  - Positivity in the adult/sow category in November was 27.01% (84 of 311), a moderate decrease from 30.62% (124 of 405) in October;
  - Positivity in the wean-to-market category in November was 45.39% (187 of 412), a marked increase from 34.56% (178 of 515) in October;
  - In the month of November, the regions with the lowest PCV2 average Ct values in tissue submissions was East Central (18 submissions; average Ct 19.4), Western (6 submissions; average Ct 19.8), Central (58 submissions; average Ct 22.7), Eastern (29 submissions; average Ct 22.9), and North Central (34 submissions; average Ct 24.3);
- Overall, 55.95% of 613 cases tested PCV3-positive in November, a moderate increase from 52.26% of 796 in October;
  - Positivity in the adult/sow category in November was 66.06% (183 of 277), a moderate decrease from 68.12% (250 of 367) in October;
  - Positivity in the wean-to-market category in November was 47.27% (130 of 275), a substantial increase from 39.41% (134 of 340) in October.

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

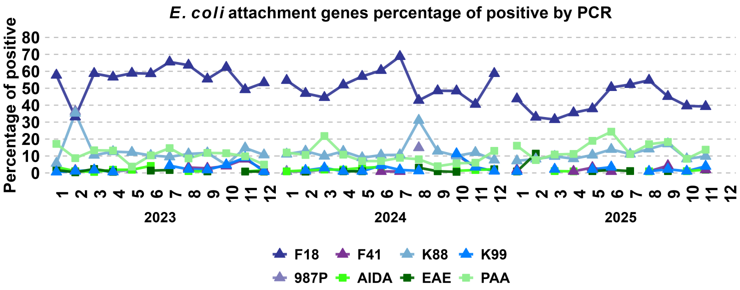
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

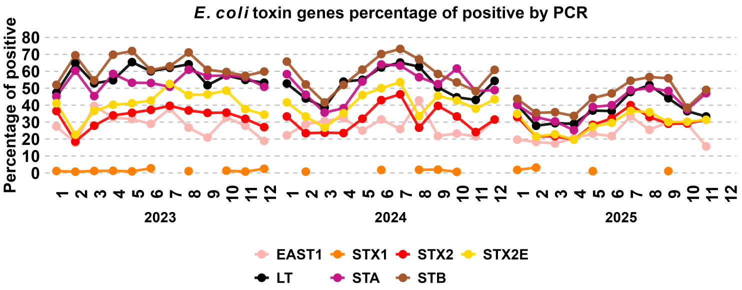
Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.*Right* Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroamnidase regions detected. i.e., “H1 H3 N1”).

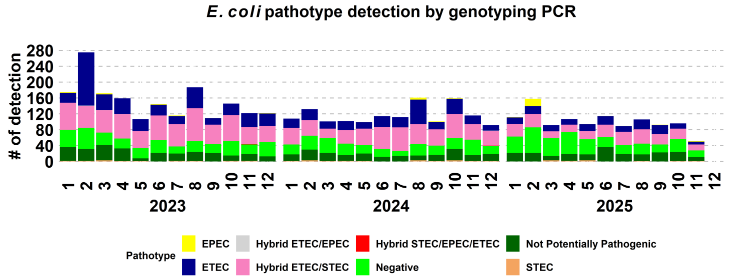
SDRS Advisory Group highlights:

- Overall, 29.24% of 2,274 cases tested IAV-positive cases in November, similar to 27.33% of 2,580 in October;
  - Positivity in the adult/sow category in November was 16.81% (79 of 470), similar to 14.98% (83 of 554) in October;
  - Positivity in the wean-to-market category in November was 36.43% (416 of 1,142), similar to 36.01% (467 of 1,297) in October.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 0% of 2 samples had mixed subtype detection in December, a moderate decrease from 2.67% of 187 in November.
- Some of the advisors reported a sharp increase in wean-to-market IAV and PRRSV-positive submissions, mostly in IA, in mid-October and November, prompting more frequent testing at sites with respiratory issues due to the severity of the cases. Others noted that routine IAV or PRRSV monitoring is not typically conducted in wean-to-market operations, with testing focused on tissue samples from clinical cases to verify either the presence of known strains or identify lateral introductions. Both IAV and PRRSV have been circulating in the same time frame, with activity linked to Fall conditions, pit pumping, and weather swings, contributing to notable respiratory disease activity.

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

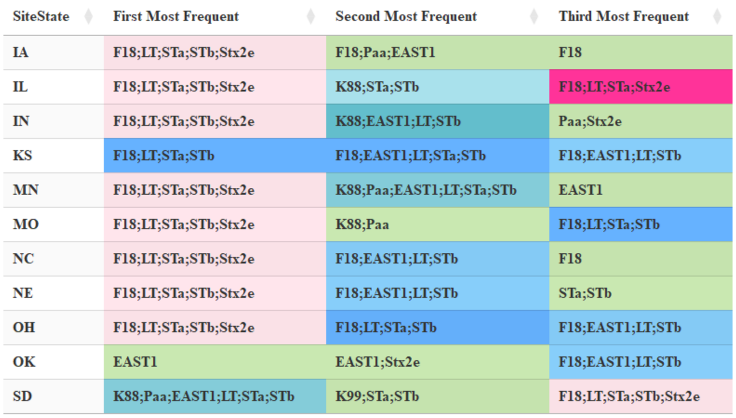






Most frequent *E. coli* virotypes detected by State in 2025

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
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	F18;EAST1;LT;STb	STa;STb
OH	F18;LT;STa;STb;Stx2e	F18;LT;STa;STb	F18;EAST1;LT;STb
OK	EAST1	EAST1;Stx2e	F18;EAST1;LT;STb
SD	K88;Paa;EAST1;LT;STa;STb	K99;STa;STb	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 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, 51 samples were tested for *E. coli* PCR in November;
  - In November the *E. coli* pathotype with higher number of sample detections were Hybrid ETEC/STEC (15 detections), Not Potentially Pathogenic (10 detections), ETEC (7 detections);
  - In November the *E. coli* attachment genes with higher detection rate were F18 (39.22%), PAA (13.73%), K88 (9.80%);
  - In November the *E. coli* toxin genes with higher detection rate were STB (49.02%), STA (47.06%), LT (33.33%).

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

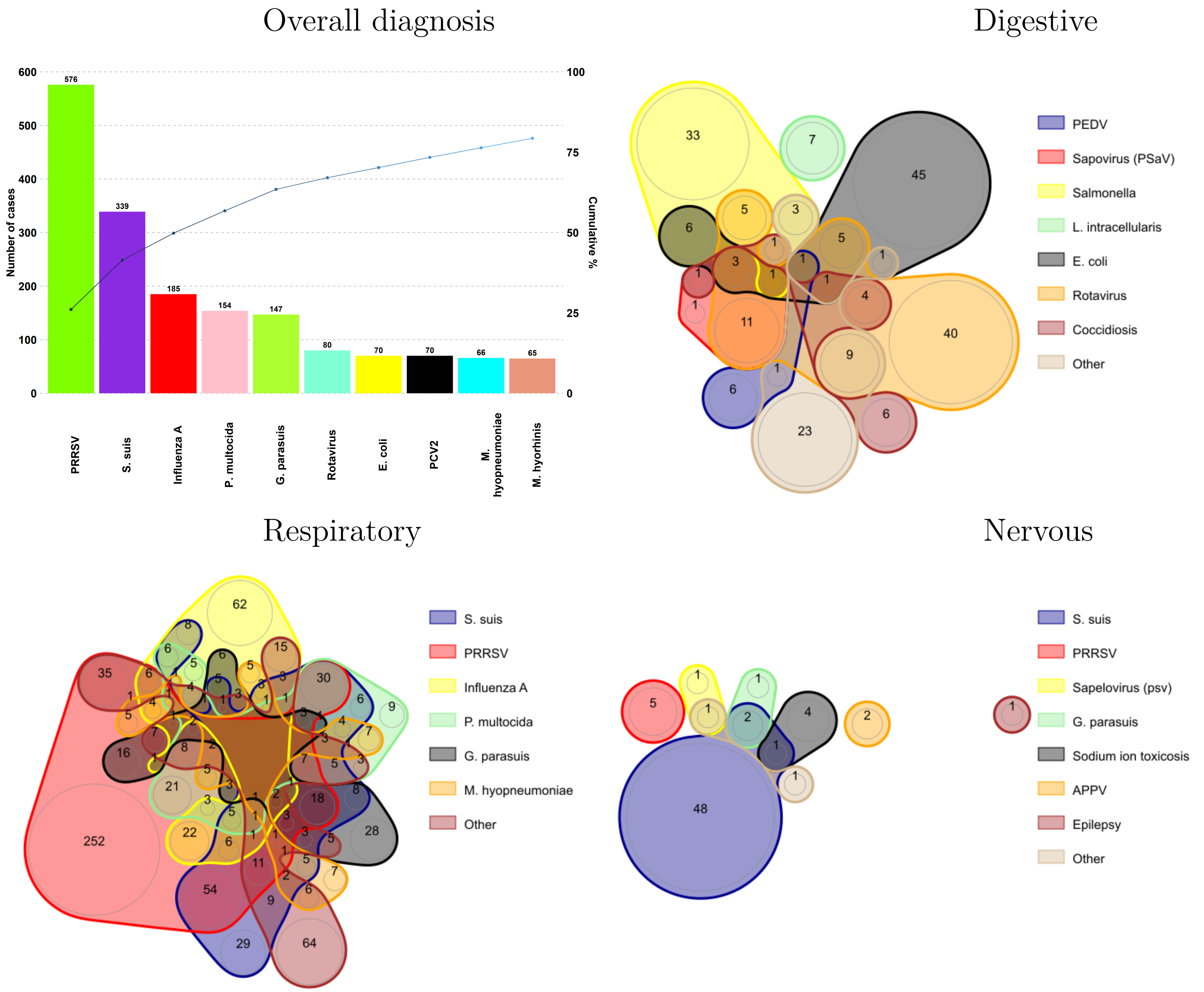


Figure 4. ISU-VDL and OH-ADDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. 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 October. 1 to November. 26, 2025.

SDRS Advisory Group highlights:

- PRRSV (576) led cases with confirmed etiology, followed by *S. suis* (339), and Influenza A (185). PRRSV (540 of 1547) led the number of confirmed respiratory diagnoses, Rotavirus (80 of 274) lead the number of confirmed digestive diagnoses, and *S. suis* (51 of 71) 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.*

Multilaboratory Diagnostic Code Integration with Ohio ADDL

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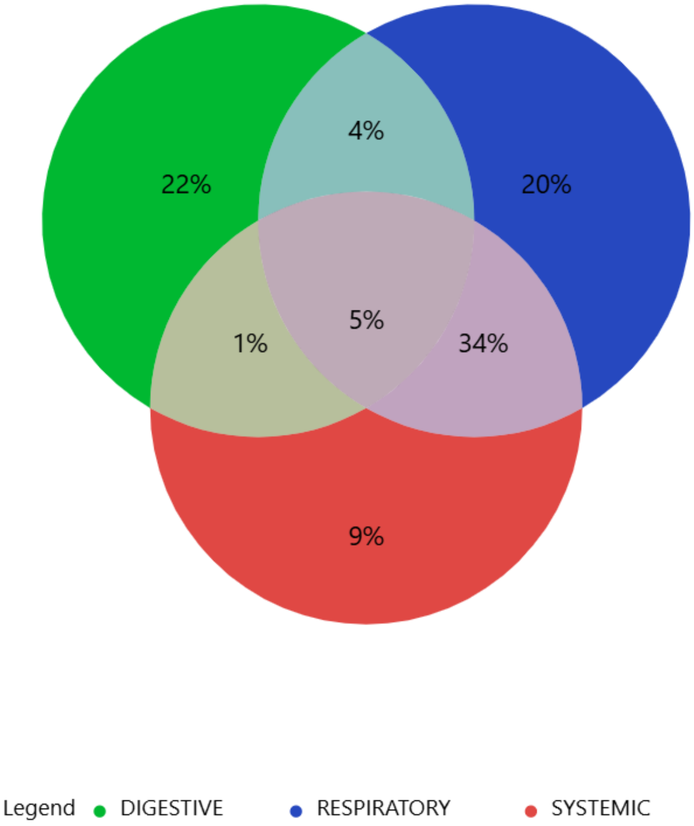
When veterinarians submit tissues for disease diagnostic investigation at veterinary diagnostic laboratories, diagnosticians analyze each case based on clinical history, obtained results from cultures, molecular assays, serology, histopathology, and macroscopic lesions to gather evidence for a diagnosis. When a conclusion is reached, diagnosticians assign a diagnostic code (Dx code) based on a 4-tier level code system, involving: body system, insult type, lesion or tissue affected, and confirmed etiology. The confirmed Dx code system was initially developed by the Iowa State University's Veterinary Diagnostic Laboratory (ISU-VDL), and information for confirmed etiologies/diseases has been shared with the SDRS since 2018. The SDRS worked as a liaison, and the system available at ISU-VDL was transferred and implemented at the Ohio Animal Disease Diagnostic Laboratory (OH-ADDL). The development allowed a full integration of porcine confirmed tissue diagnosis using standardized Dx codes into the SDRS from the two labs.

OH-ADDL confirmed disease diagnosis will be prospectively monitored, along with ISU-VDL data, by the SDRS to understand disease occurrence. Between January 2020 and September 2025, ISU-VDL data alone generated 45,310 eligible cases, revealing that 52.62% (23,846 cases) involved co-diagnoses with 2–9 distinct etiologies. confirmed tissue diseases showed that bacterial and viral insults often overlapped, with 36.62% of cases involving both, compared with 30.12% involving only bacteria and 30.15% involving only viruses. The wean-to-market phase dominated submissions, accounting for 77.05% of all cases and 86.45% of co-diagnoses, while adult/sow farms represented 16.67% (7,557 cases). Notably, 81.77% of co-diagnosis cases (19,501) affected the respiratory system, followed by systemic (61.35%) and digestive (30.88%) systems. It is essential to highlight that cases can involve tissues from multiple animals, which does not necessarily mean that all the etiologies found affecting a system originated from the same animal. Additionally, a case may have had affect multiple anatomic systems affected, which explains why the sum of all systems exceeded the total number of co-diagnosis cases (23,846).

Figure 1. Co-Diagnosis across physiologic systems



- Based on the analysis, only 5% of the co-diagnosis did not affect either the Digestive, Respiratory, or Systemic systems

The value and information generated by the development for veterinarians and producers relies on:

- Recognize that most confirmed tissue diseases have multifactorial causes.
- Highlight that growing animals account for the majority of tissue-based disease investigations.
- Allow, for the first time, integration of confirmed disease diagnoses and monitoring from multiple VDLs, such as ISU-VDL and OH-ADDL.
- Provide a foundation for understanding swine health trends, enabling holistic monitoring and relative assessment of porcine disease occurrence in the field.
- Increase representativeness by capturing regional confirmed disease activity that was previously unavailable, e.g., cases from West Virginia.
- Enable close monitoring of diagnostic trends for the 50 most frequently diagnosed endemic diseases, and track new case counts for less frequent conditions.
- Strengthen early detection of shifts, emergence, and re-emergence of animal health threats.
- Generate actionable information on disease occurrence to support the development of regional or national health strategies.
- Help veterinarians better advise producers on implementing animal health and disease-control strategies.
- Support resource prioritization, such as vaccine development, toward diseases most frequently diagnosed or showing increased occurrence.
- Translate generated information into actionable steps to reduce disease burden in the field.
- Establish a Dx-code monitoring framework that lays the groundwork for future applications across other livestock species (e.g., bovine, avian).

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