Swine Disease Reporting System - Advisory Group Report
Report # 91 (September 02, 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, Beth Thompson.

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.

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 Mason, 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 August 31, 2025.

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

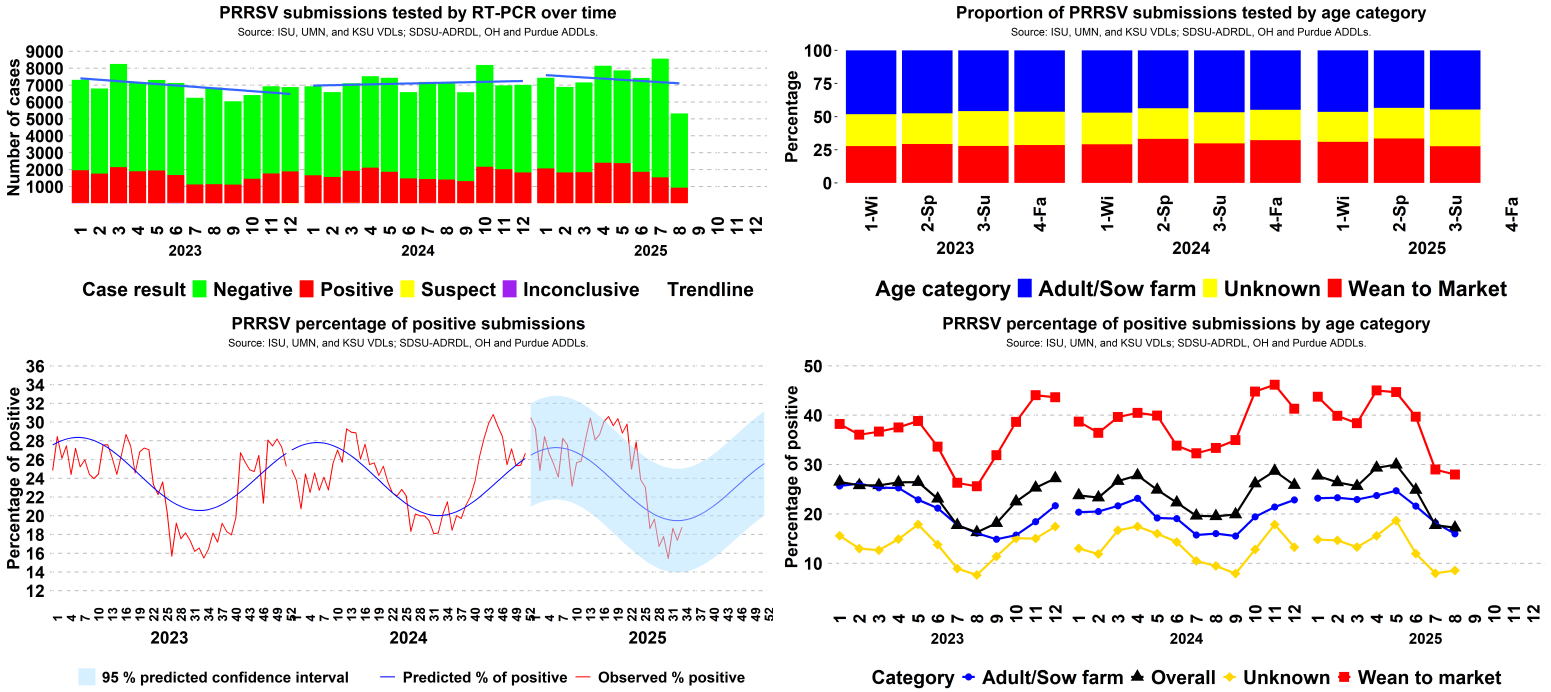
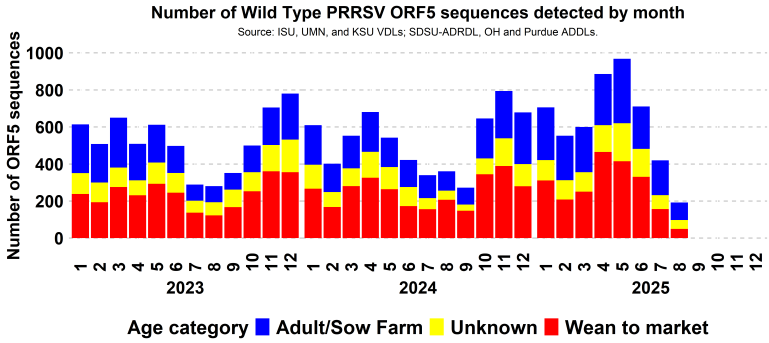


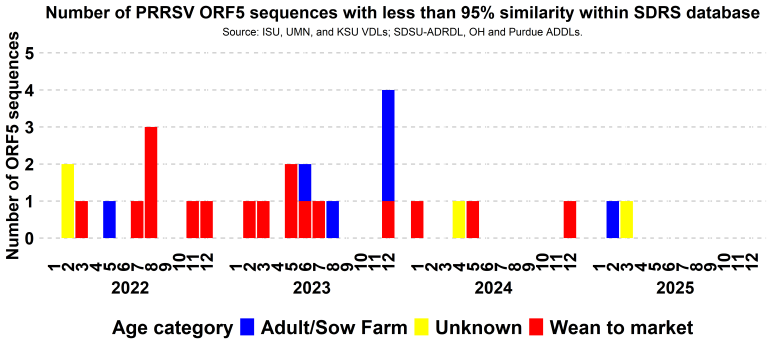
Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based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

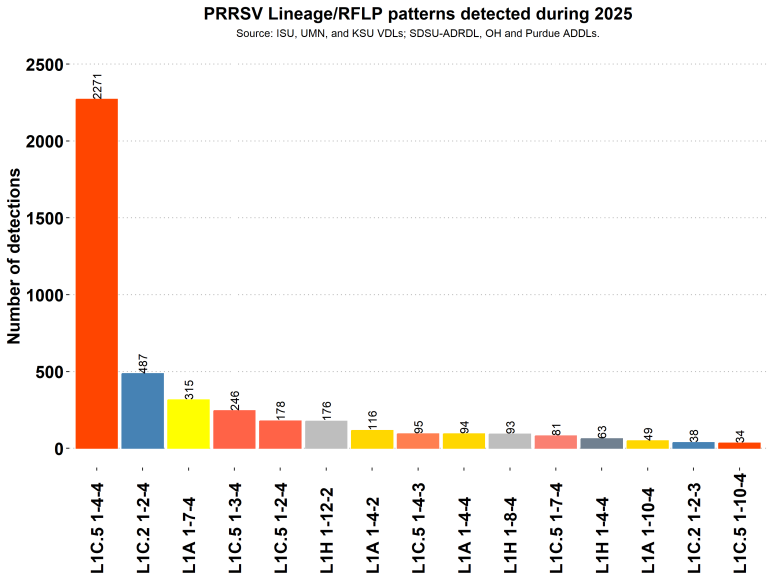
SDRS Advisory Group highlights:

- Overall, 17.22% of 5,326 cases tested PRRSV-positive in August, similar to 17.73% of 8,567 in July;
  - Positivity in the adult/sow category in August was 15.96% (412 of 2,581), a moderate decrease from 18.22% (669 of 3,672) in July;
  - Positivity in the wean-to-market category in August was 27.99% (389 of 1,390), similar to 28.99% (634 of 2,187) in July;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA and MN;

Topic 2 – PRRSV ORF5 sequences detection over time







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	L1A 1-7-4
IN	L1A 1-7-4	L1C.5 1-10-4	L1A 1-4-4
KS	L1A 1-7-4	L1H 1-8-4	L1H 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	L5A 2-1-2
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 August 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MO, NE, MN, IL, IN (respective number of sequences: 83, 17, 7, 6, 5, 1).
- In August L1C.5 1-4-4 (96) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (15), and L1A 1-7-4 (12);
- 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

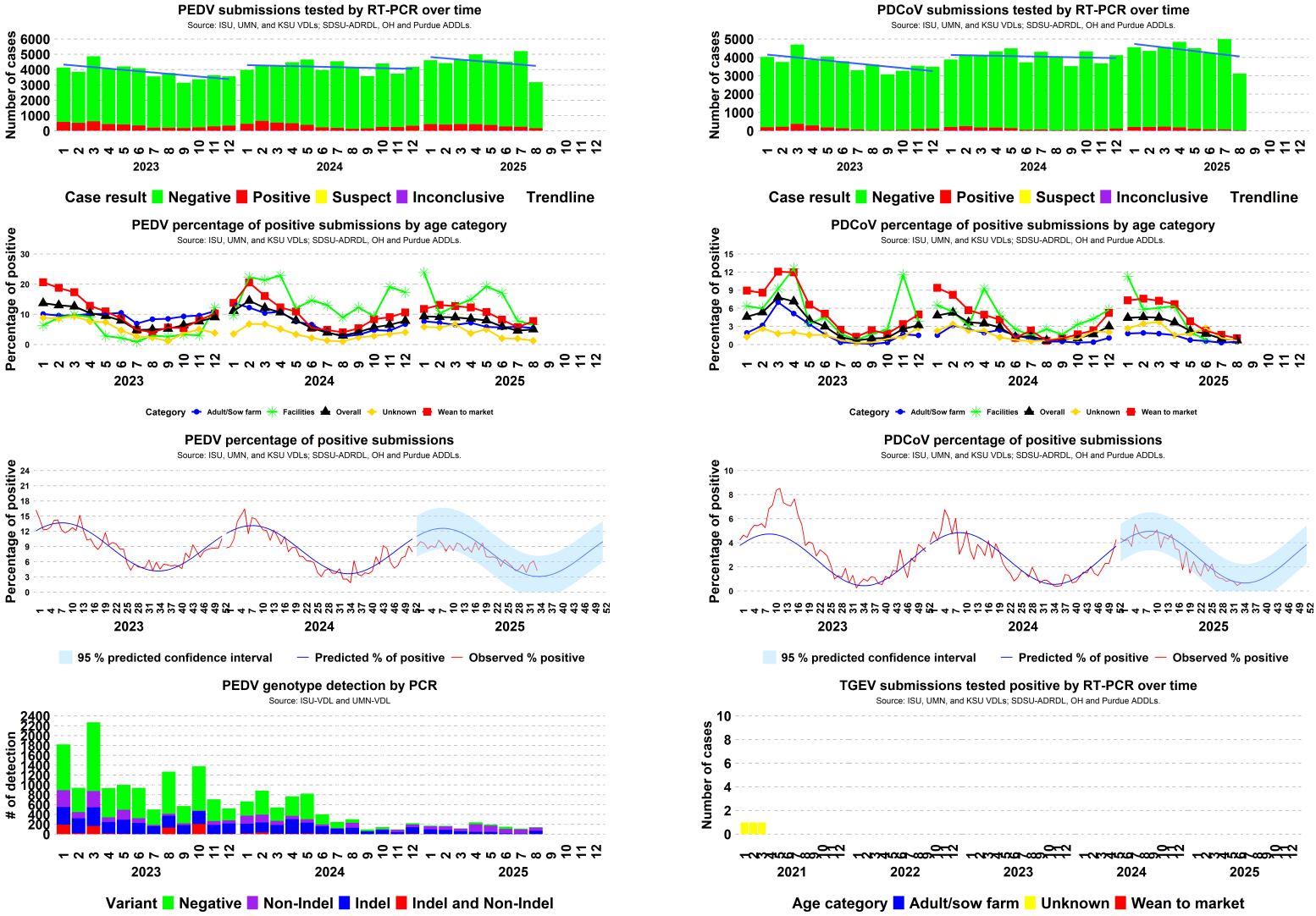


Figure 1. Top: *Left PEDV*; *Right PDCoV* cases tested by RT-PCR over time; **Second from top**: *Left PEDV*; *Right PDCoV* percentage of positive PCR positive results, by age category over time. Facilities are cases submissions from packing plants, truck washes, and vehicles. **Third from top**: *Left PEDV*; *Right PDCoV* expected percentage of positive results for cases tested by RT-PCR and 95% confidence interval for 2025 predicted value. **Bottom** *Left*: Number of PEDV genotype detection over time; *Right*: Number of TGEV positive cases by age category.

SDRS Advisory Group highlights:

- Overall, 5.03% of 3,179 cases tested PEDV-positive in August, similar to 4.61% of 5,207 in July;
  - Positivity in the adult/sow category in August was 5.48% (60 of 1,095), similar to 5.92% (97 of 1,639) in July;
  - Positivity in the wean-to-market category in August was 7.76% (83 of 1,069), a moderate increase from 5.75% (100 of 1,739) in July;
- Positivity in the facilities category in August was 6.58% (5 of 76), similar to 7.83% (9 of 115) in July;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN and OK;
  - Overall, 0.7% of 142 samples had mixed PEDV genotype detection in August, similar to 0% of 114 in July;
- Overall, 0.71% of 3,116 cases tested PDCoV-positive in August, similar to 0.98% of 4,995 in July;
  - Positivity in the adult/sow category in August was 0.47% (5 of 1,063), similar to 0.31% (5 of 1,593) in July;
  - Positivity in the wean-to-market category in August was 1.05% (11 of 1,049), similar to 1.6% (26 of 1,626) in July;
- Positivity in the facilities category in August was 0% (0 of 76), similar to 0% (0 of 115) in July;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN and NC;
- There was 0 positive case for TGEV RNA-PCR in August, 2025 over a total of 3,021 cases tested. It has been 53 months (with a total of 199,692 cases tested) since the last TGEV PCR-positive result;
- The PEDV percentage of positive submissions remained low in August, but the PEDV detection in wean-to-market category increased moderately. The increased in wean-to-market activity prompt a biosecurity alert for sow farms around positive finishing sites.

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

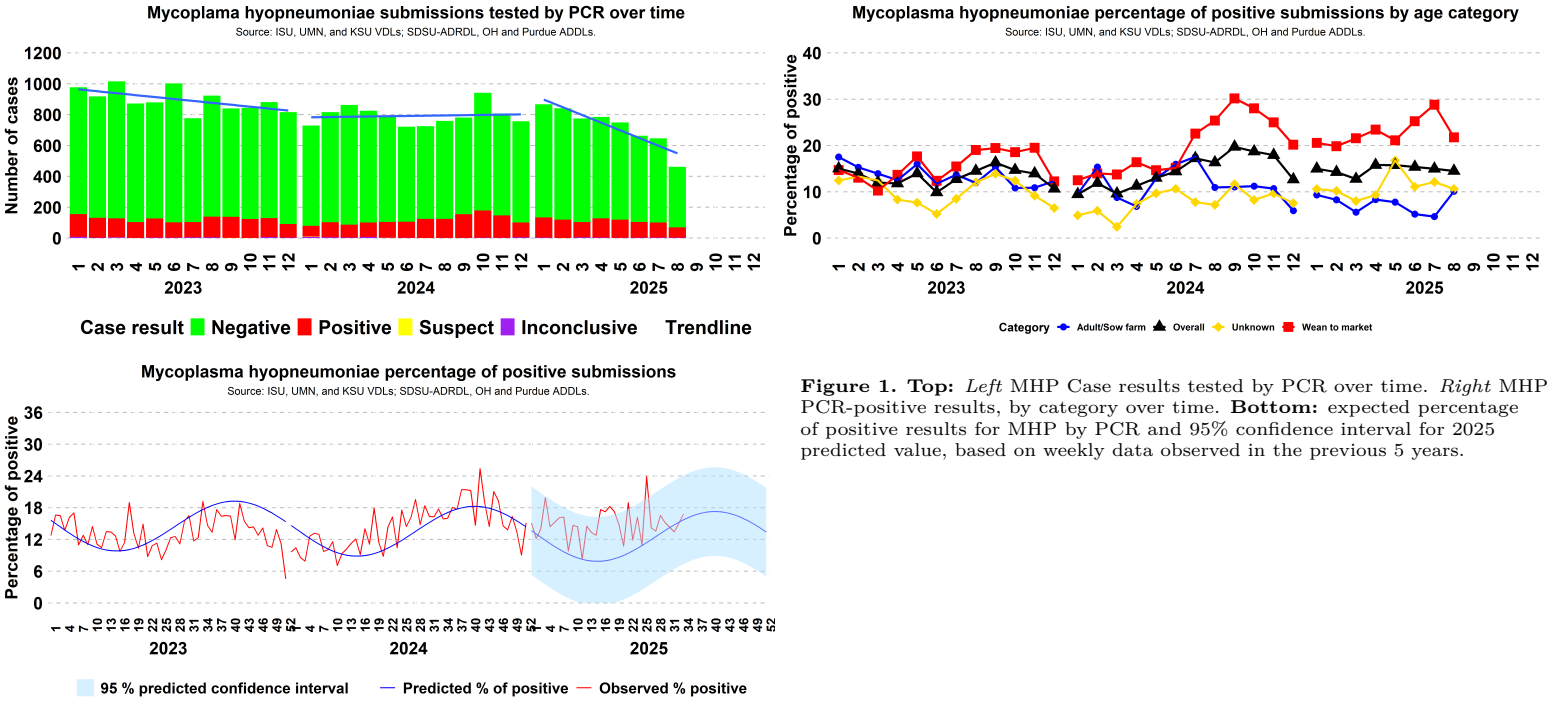
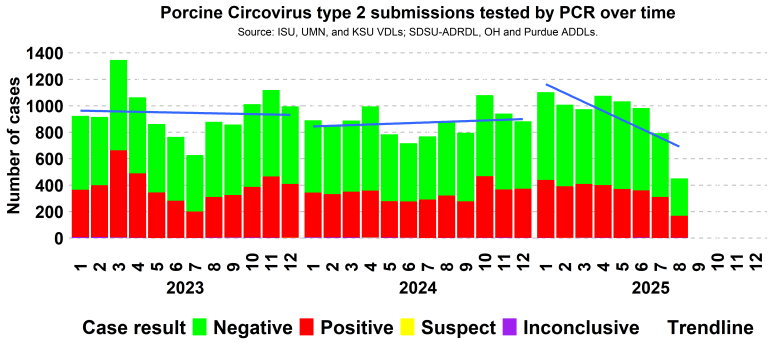


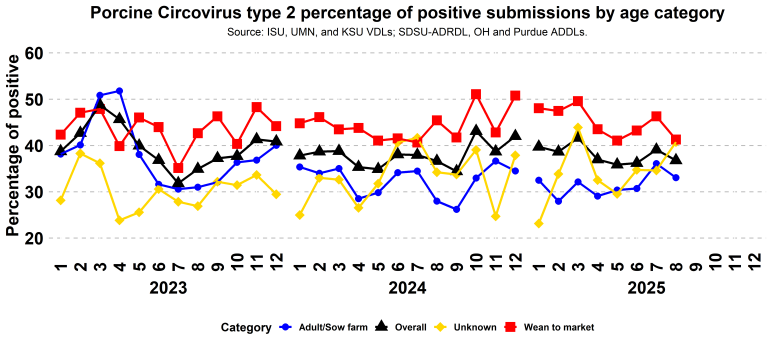
Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

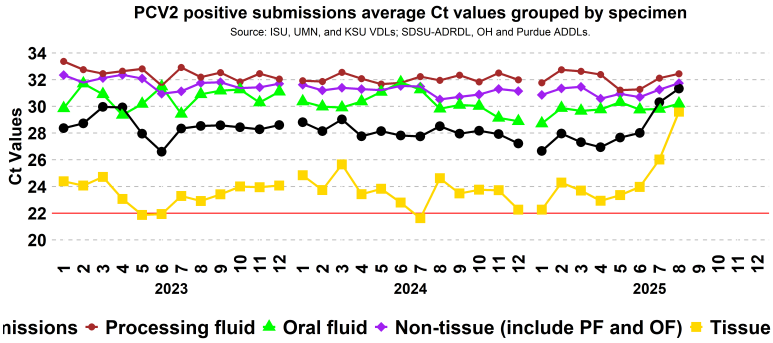
SDRS Advisory Group highlights:

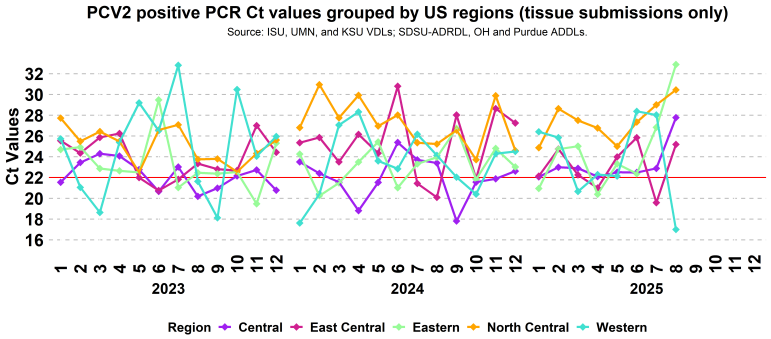
- Overall, 14.5% of 462 cases tested *M. hyopneumoniae*-positive cases in August, similar to 14.99% of 647 in July;
  - Positivity in the adult/sow category in August was 10.1% (20 of 198), a substantial increase from 4.66% (13 of 279) in July;
  - Positivity in the wean-to-market category in August was 21.76% (37 of 170), a substantial decrease from 28.81% (68 of 236) in July;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN;

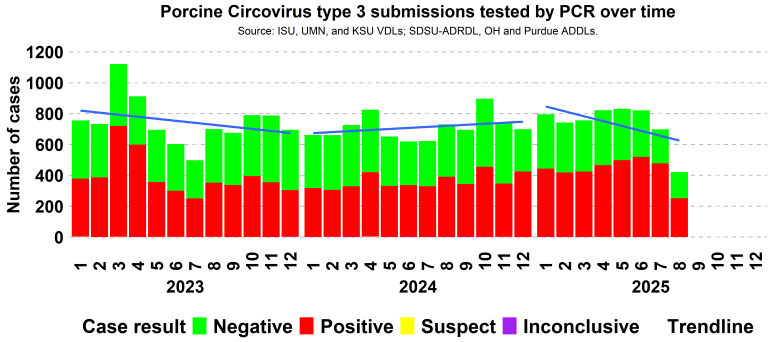
Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.











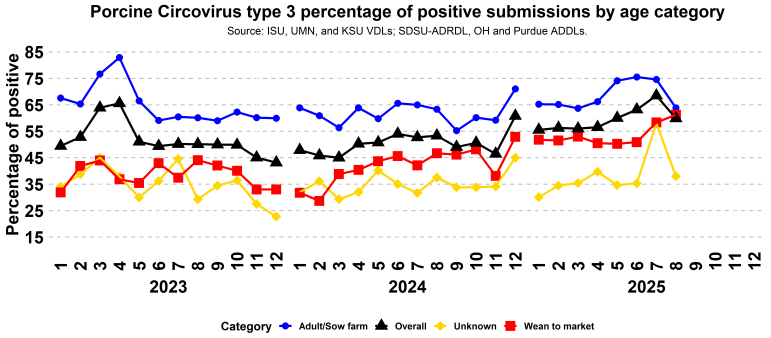


Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 36.81% of 451 cases tested PCV2-positive in August, a moderate decrease from 39.09% of 793 in July;
  - Positivity in the adult/sow category in August was 33.06% (80 of 242), a moderate decrease from 36.09% (170 of 471) in July;
  - Positivity in the wean-to-market category in August was 41.29% (64 of 155), a substantial decrease from 46.31% (113 of 244) in July;
  - In the month of August, the regions with the lowest PCV2 average Ct values in tissue submissions was Western (1 submissions; average Ct 17), East Central (1 submissions; average Ct 25.2), Central (4 submissions; average Ct 27.8), North Central (17 submissions; average Ct 30.4), and Eastern (3 submissions; average Ct 32.9);
- Overall, 59.86% of 421 cases tested PCV3-positive in August, a substantial decrease from 68.48% of 698 in July;
  - Positivity in the adult/sow category in August was 63.84% (143 of 224), a marked decrease from 74.6% (326 of 437) in July;
  - Positivity in the wean-to-market category in August was 61.22% (90 of 147), a moderate increase from 58.33% (112 of 192) in July.
- Tissue-positive PCV2 PCR cases reached an average Ct value of 29, the highest monthly average Ct since 2012, indicating lower viral loads.

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

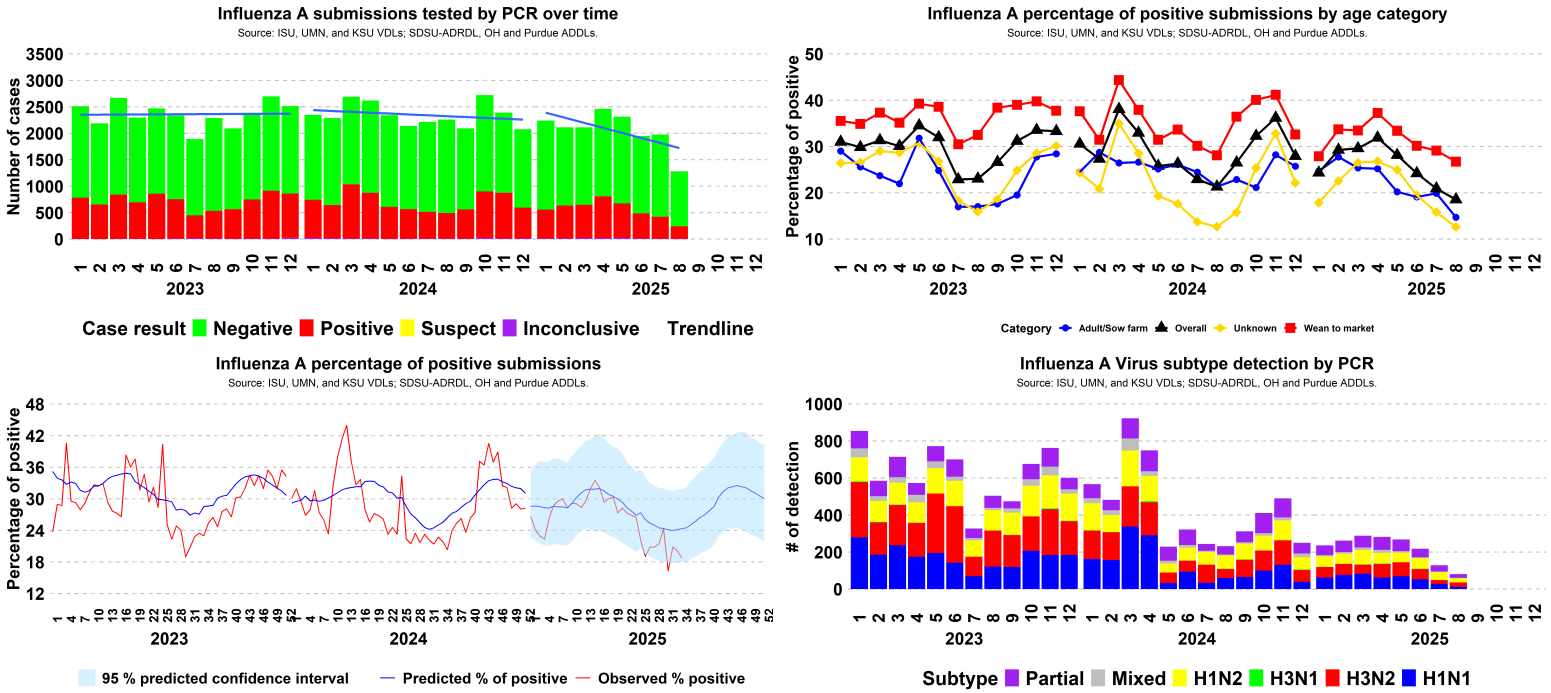
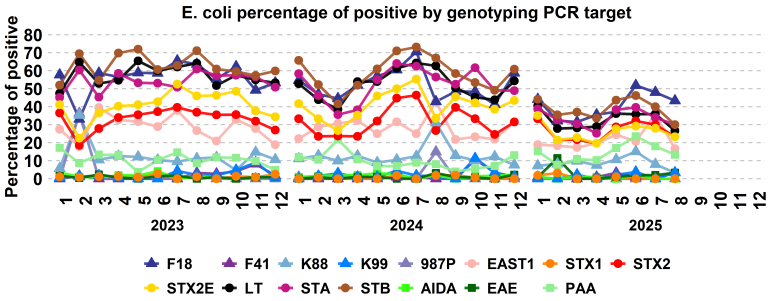


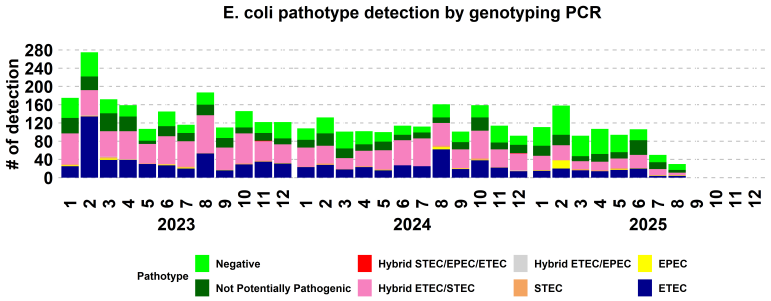
Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 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, 18.55% of 1,283 cases tested IAV-positive cases in August, a moderate decrease from 20.91% of 1,975 in July;
  - Positivity in the adult/sow category in August was 14.72% (48 of 326), a substantial decrease from 19.91% (84 of 422) in July;
  - Positivity in the wean-to-market category in August was 26.73% (131 of 490), a moderate decrease from 29.12% (182 of 625) in July.
- Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in MN;
- Overall, 2.47% of 81 samples had mixed subtype detection in August, similar to 2.33% of 129 in July.
- The overall IAV percentage of positive submissions dropped to 18%, marking the lowest level since 2010, which means an atypical decrease for IAV positive cases.

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	EAE
IL	F18; LT; STA; STB; STX2E	K88; STA; STB	F18; LT; STA; STB
IN	F18; LT; STA; STB; STX2E	PAA; STX2E	K88; EAST1; LT; STB
KS	K88; PAA; EAST1; LT; STA; STB		
MN	F18; LT; STA; STB; STX2E	K88; PAA; EAST1; LT; STA; STB	EAST1
MO	F18; LT; STA; STB; STX2E	K88; PAA	K88; STA; STB
NC	F18; LT; STA; STB; STX2E	F18	F18; EAST1; LT; STB
NE	F18; LT; STA; STB; STX2E	F18; EAST1; LT; STB	EAST1; LT; STA; STB; STX2E
OH	F18; LT; STA; STB; STX2E	F18; LT; STA; STB	EAE
OK	F18; EAST1; LT; STB	F18; EAST1; LT; STB; STX2E	STA; STB
SD	K88; PAA; EAST1; LT; STA; STB	F18; LT; STA; STB; STX2E	F18; PAA; EAST1; STX2E

Figure 1. Top: *Left E.coli* PCR-Positive results by genotype target over time. *Right E.coli* number of samples tested by PCR genotype and their respective pathotype classification (ETEC - Enterotoxigenic *E.coli*; STEC - Shiga toxin-producing *E.coli*; EPEC - Enteropathogenic *E.coli*. **Bottom:** 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-label -**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, and ETEC/STEC/EPEC** - Combination of characteristics of more than one pathotype;

SDRS Advisory Group highlights:

- Overall, 30 samples were tested for *E. coli* PCR genotyping in August;
- In August the *E. coli* pathotype with higher number of sample detections were Not Potentially Pathogenic (6 detections), Hybrid ETEC/STEC (6 detections), ETEC (4 detections);
- In August the *E. coli* genotypes with higher detection rate were F18 (43.33%), STA (30%), STB (30%);
- The advisory group highlighted that the higher detection rates of virulent *E. coli* strains may be due to their increased fitness, antibiotic resistance, and gene sharing among enteric bacteria, which enhances virulence and environmental persistence. According to the advisory, these attributes might explain the highest detection of Hybrid ETEC/STEC strains. Also, the advisory group pointed out that the frequent detection of non-pathogenic virotypes in certain states may be influenced by vaccination practices, microbiome disruption, diagnostic testing, and feed storage conditions.

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

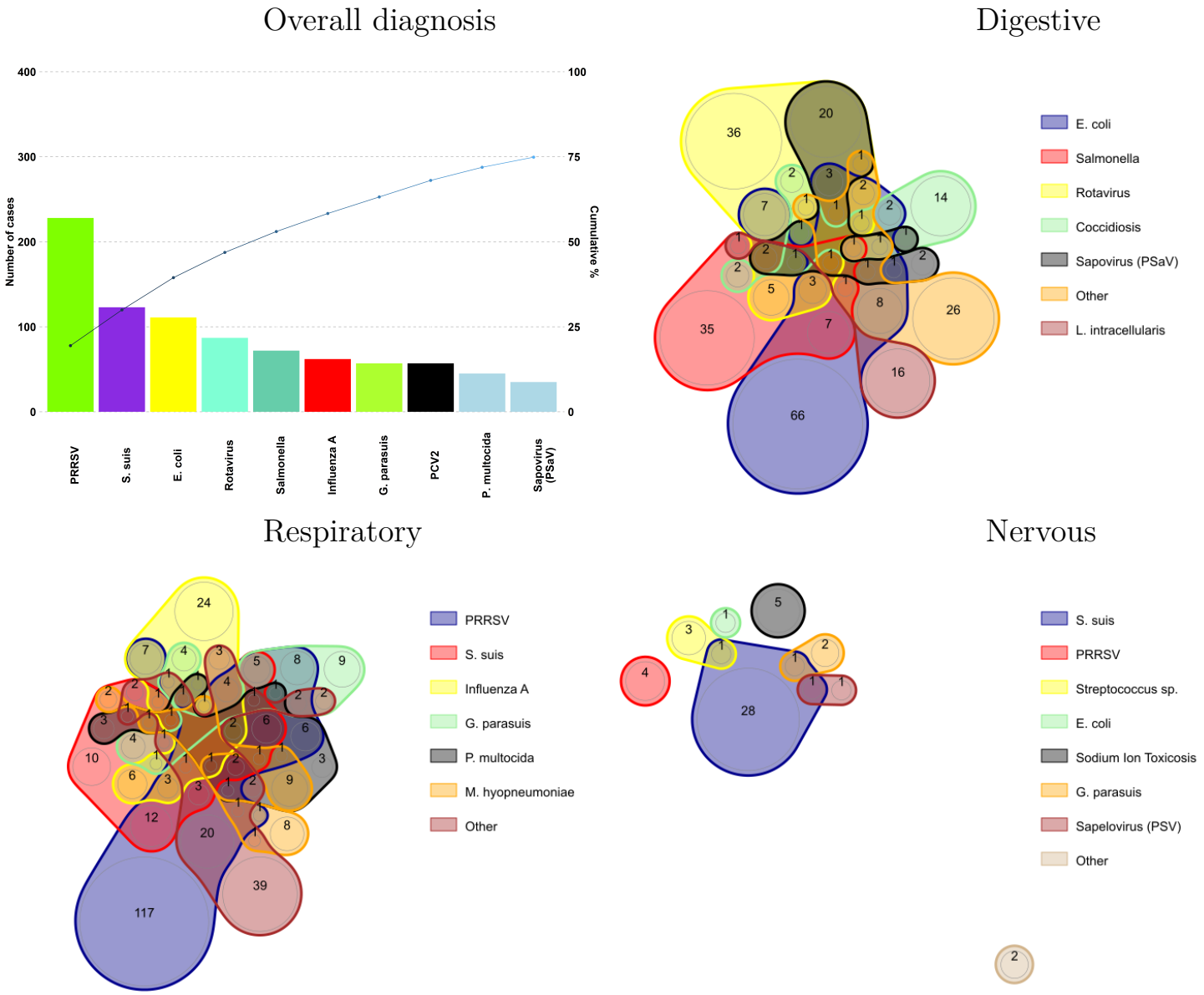


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less 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 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. 1 to August. 25, 2025.

SDRS Advisory Group highlights:

• PRRSV (228) led cases with confirmed etiology, followed by *S. suis* (123), and *E. coli* (111). PRRSV (207 of 547) led the number of confirmed respiratory diagnoses, E. coli (106 of 379) lead the number of confirmed digestive diagnoses, and *S. suis* (31 of 52) led the number of confirmed neurological diagnoses.

• A moderate increase in confirmed tissue diagnosis cases was observed in July and August for Sapovirus, which associated with the decrease of *Mycoplasma hyorhinis* cases, made Sapovirus enter in the top 10 confirmed tissue diagnosis cases in July/August.

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.

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.*

Information for *Escherichia coli* genotype, pathotype and virotype by PCR is now available on the SDRS monthly PDF reports

Elisa De Conti[1], Guilherme Cezar[1], Kinath Rupasinghe[1], Daniel Linhares[1], Giovani Trevisan[1]

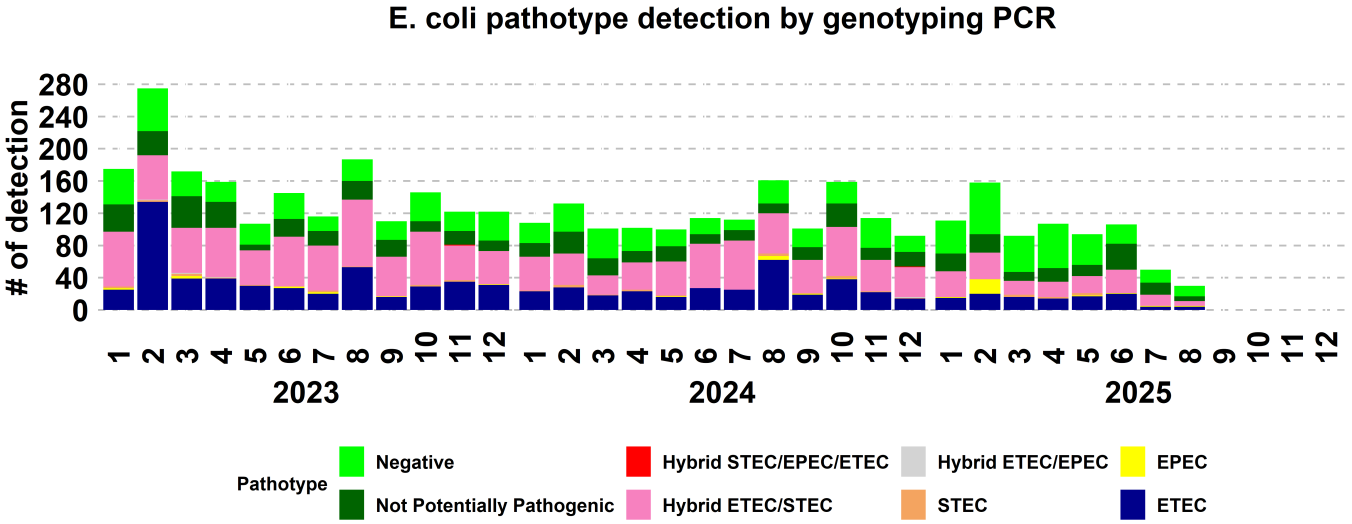
1 - Iowa State University, Ames, IA, USA.

The Swine Disease Reporting System is including a new pathogen on the PDF monthly report: *Eschericia coli. E. coli* infections in pigs, commonly referred to as colibacillosis, are severe conditions that can result in diarrhea, dehydration, and even death. While *E. coli* can be associated with various diseases, it may also be present in healthy pigs, so the characterization of *E. coli* virulence factors has become essential for accurately diagnosing potentially pathogenic strains.

When a clinical sample arrives at the laboratory suspected of *E. coli* infection, the most common approach is initially to process it through general bacteriological culture for pathogen isolation. Once *E. coli* is identified, further diagnostic testing (PCR) is essential to determine whether the isolate harbors specific virulence factors that characterize a strain as pathogenic.

Several types of pathotypes are described in the literature based on PCR genotype, such as enterotoxigenic *E. coli* (ETEC), Shiga toxin-producing *E.coli* (STEC), enteropathogenic *E. coli* (EPEC), and their hybrid versions. Samples not classified as any pathotype were considered not potentially pathogenic (i.e., only a fimbriae gene was detected, with no other gene detection). The samples with negative PCR targets were also classified as not potentially pathogenic. The genotype target genes are associated with the pathotype classification, and depending on the detection and expression of these genes, we can associate them with a potential pathogenic strain (i.e., ETEC pathotype classification because of F18 and STa detection by PCR). The virotypes are identified by collating all positive PCR targets tested within a sample. They can be related to the pathotype classification based on detecting determined genes within a sample. Therefore, the SDRS project incorporated historical and ongoing data *E.coli* genotype PCR from the participant veterinary diagnostic laboratories to report the primary targets detected, the predominant pathotypes in the field, and the main virotypes detected at a state level. All these information are available in the three charts below present in the new *E. coli* page in the SDRS report.

Figure 1. *E. coli* pathotype detection by genotyping PCR.



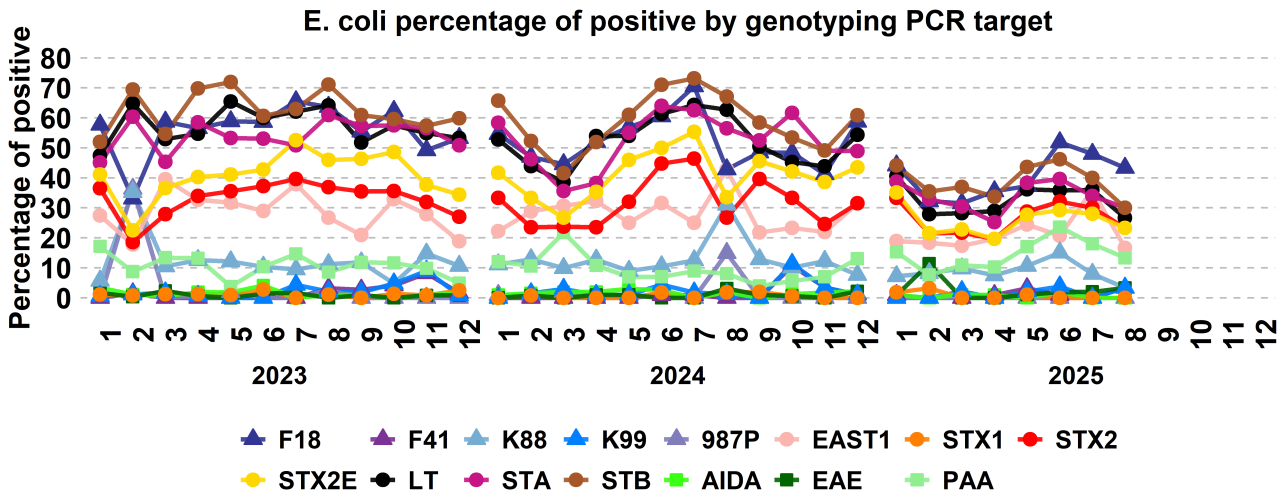
Attachment genes: Fimbriae - F18, K88(F4), K99(F5), 987P(F6), F41; **Adhesins -** EAE (Intimin), PAA, AIDA.

Toxin genes: Heat-label -LT; **Heat-stable -**STa and STb; **Shiga toxins -**Stx1, Stx2 and Stx2e; and EAST1.

Obs: Not all samples have been tested for all targets.

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.

Figure 2. *E. coli* percentage of positive by genotyping PCR target.



Pathotypes: Enterotoxigenic *Escherichia coli* (ETEC) - Has fimbriae and toxin (not Stx2e) genes. Associated with neonatal and post-weaning diarrhea.

Shiga toxin-producing *Escherichia coli* (STEC) - Has fimbriae (F18) and toxin (must be Stx2e) gene. Associated with edema disease.

Enteropathogenic *Escherichia coli* (EPEC) - Presence of the EAE (Intimin) adhesin.

Hybrids ETEC/STEC, ETEC/EPEC, STEC/EPEC, and ETEC/STEC/EPEC - Combination of characteristics of more than one pathotype.

Figure 3. Most frequent *E. coli* virotypes detected by each state in 2025.

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	EAE
IL	F18; LT; STA; STB; STX2E	K88; STA; STB	F18; LT; STA; STB
IN	F18; LT; STA; STB; STX2E	PAA; STX2E	K88; EAST1; LT; STB
KS	K88; PAA; EAST1; LT; STA; STB		
MN	F18; LT; STA; STB; STX2E	K88; PAA; EAST1; LT; STA; STB	EAST1
MO	F18; LT; STA; STB; STX2E	K88; PAA	K88; STA; STB
NC	F18; LT; STA; STB; STX2E	F18	F18; EAST1; LT; STB
NE	F18; LT; STA; STB; STX2E	F18; EAST1; LT; STB	EAST1; LT; STA; STB; STX2E
OH	F18; LT; STA; STB; STX2E	F18; LT; STA; STB	EAE
OK	F18; EAST1; LT; STB	F18; EAST1; LT; STB; STX2E	STA; STB
SD	K88; PAA; EAST1; LT; STA; STB	F18; LT; STA; STB; STX2E	F18; PAA; EAST1; STX2E

Virotypes: Collation of all positive PCR targets tested within a sample. Color code of the table associating the virotype detected with the pathotype classification.