# Swine Disease Reporting System
# Report # 92 (September 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, 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 September 30, 2025.

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

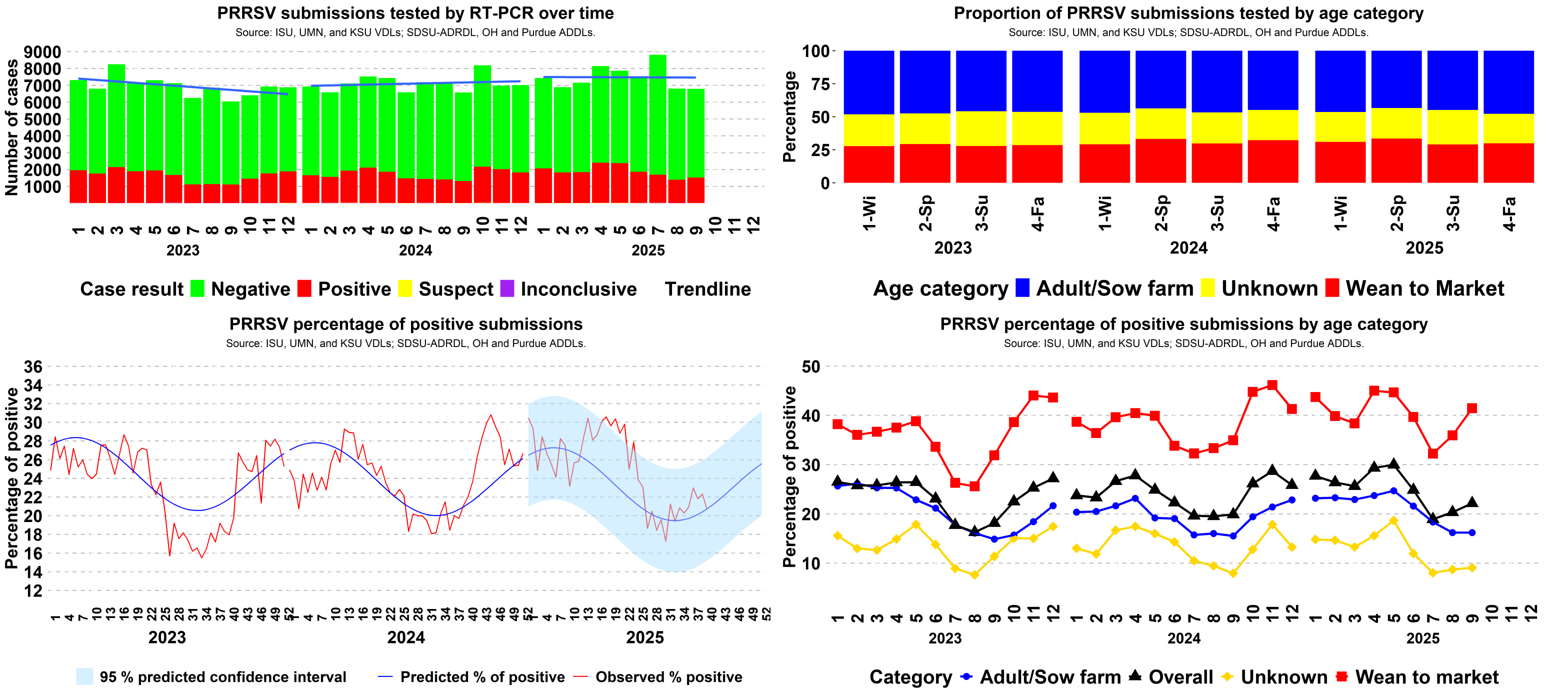
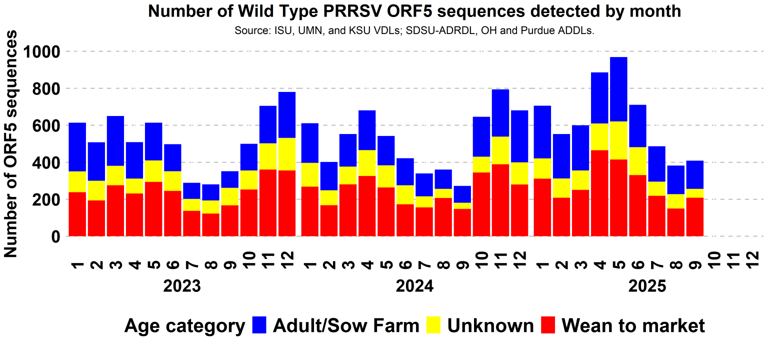


**Figure 1. Top**: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 4 years; *Right*: Percentage of PRRSV PCR-positive results, by age category, over time. Wean to market corresponds to nursery and grow-finish. Adult/Sow correspond to Adult, boar stud, breeding herd, replacement, and suckling piglets. Unknown corresponds to not informed site type or farm category.

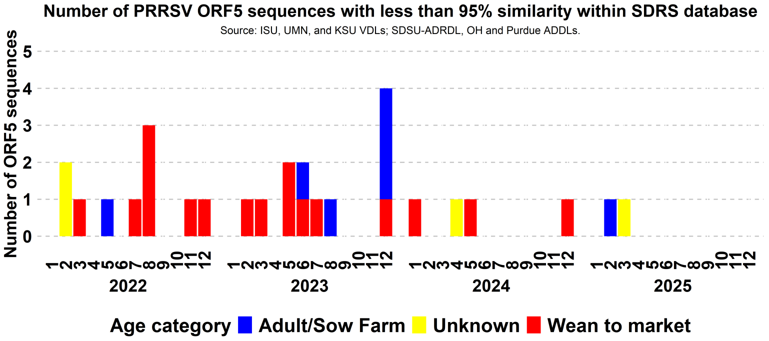
## SDRS Advisory Group highlights:

- Overall, 22.17% of 6,793 cases tested PRRSV-positive in September, similar to 20.34% of 6,808 in August;
  - Positivity in the adult/sow category in September was 16.22% (526 of 3,243), similar to 16.21% (544 of 3,355) in August;
  - Positivity in the wean-to-market category in September was 41.46% (842 of 2,031), a substantial increase from 35.94% (713 of 1,984) in August;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MN, MO and NC;
- The percentage of PRRSV-positive cases in wean-to-market has risen to 41.46%, which is 6.28 percentage points higher than the same period last year. This raises the need to strengthen monitoring and biocontainment at wean-finish sites, and biosecurity in sow herds to minimize the risk of further regional spread.
- Some SDRS advisory members have reported increasingly severe outbreaks, along with a higher frequency of reinfections and lateral transmission in grow-finish sites.

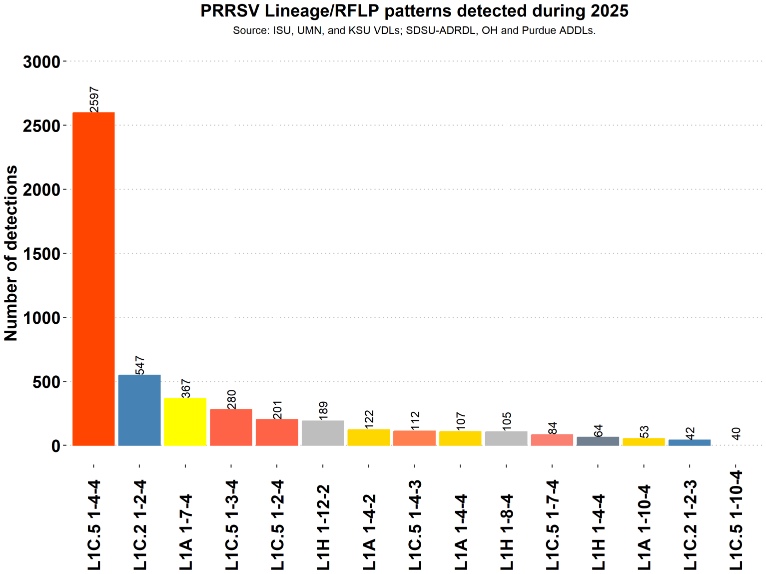
# Topic 2 – PRRSV ORF5 sequences detection over time


Number of Wild Type PRRSV ORF5 sequences detected by month

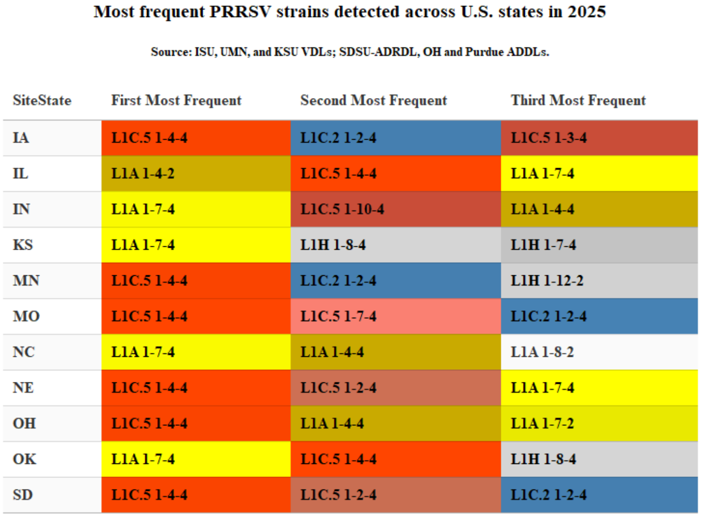
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.


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 | 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 1-7-4 |
| 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 August 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MO, MN, NE, IL, IN, OK, SD (respective number of sequences: 153, 24, 12, 11, 7, 4, 1, 1).
- In August L1C.5 1-4-4 (178) was the PRRSV sequence most detected in the U.S., followed by L1A 1-7-4 (34), and L1C.2 1-2-4 (34);
- 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.
- Lineage 1C.5 continues to dominate PRRSV detections, with 3,347 (48.08% of total) cases reported so far in 2025—surpassing the 2024 total of 3,235, even though 2025 is not yet complete. Iowa alone accounts for 1,182 of these cases. Notably, variant L1C.5.32 is the most prevalent, with 1,745 detections (See Bonus page for more details). Advisory Members have observed that recent outbreaks linked to this lineage tend to be more severe, although mild cases were also reported.
- The first detection of PRRSV ORF5 variant 1C.5.33 was reported in Illinois on September 5, 2025.
- Pennsylvania had its first detection of lineage L1C.2 in 2025, from a sample identified as coming from a wean-to-market site. This lineage had been previously detected in Pennsylvania in 2023 and 2024, but had not been detected in 2025 until now.

# Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

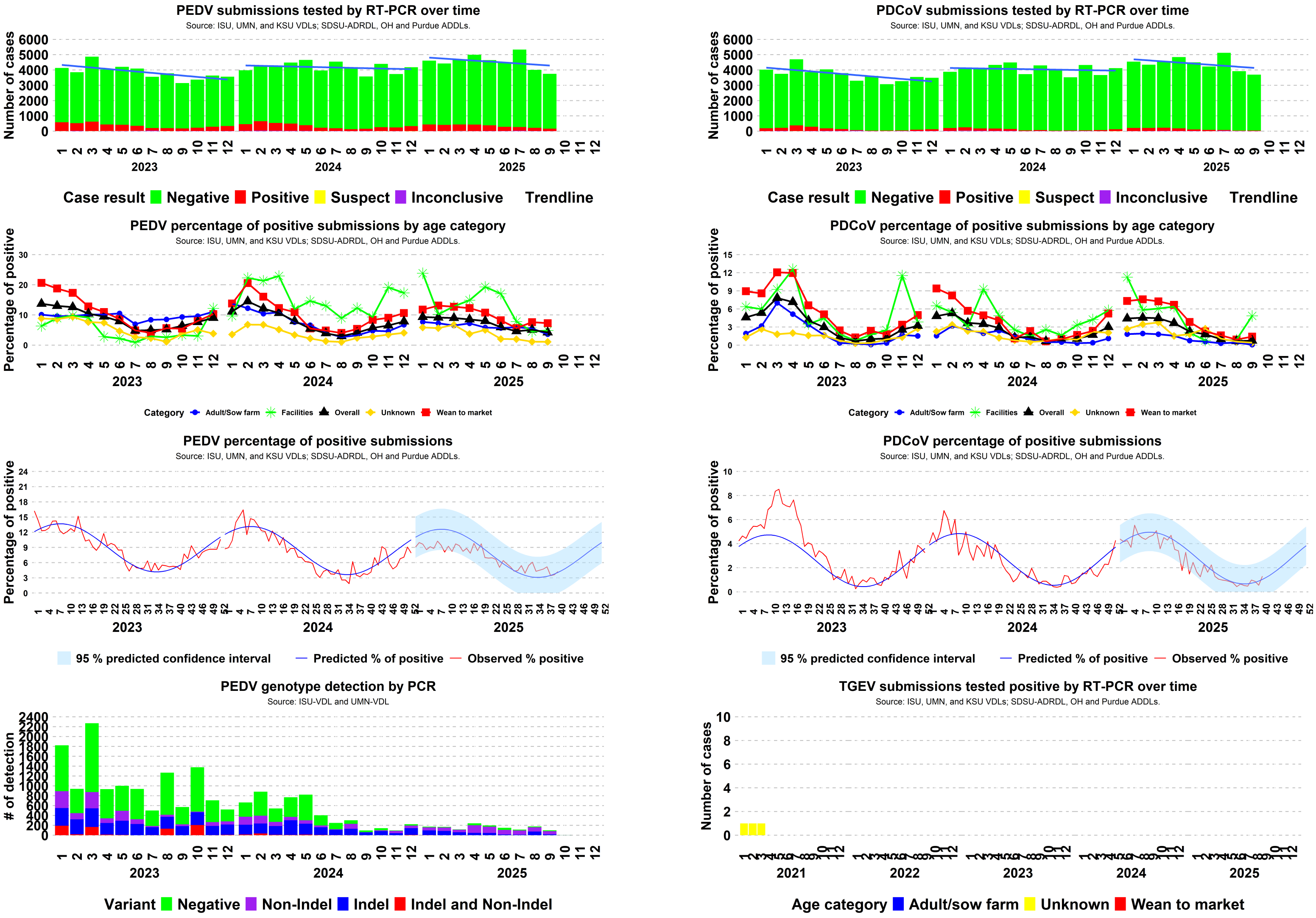
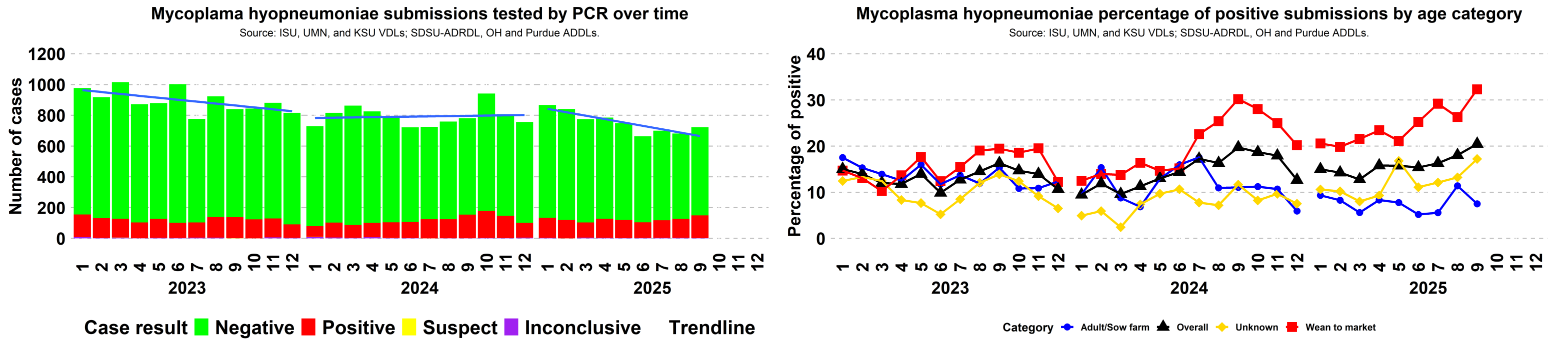


**Figure 1. Top**: *Left PEDV*; *Right PDCoV* cases tested by RT-PCR over time; **Second from top**: *Left PEDV*; *Right PDCoV* percentage of positive PCR positive results, by age category over time. Facilities are cases submissions from packing plants, truck washes, and vehicles. **Third from top**: *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, 4.24% of 3,749 cases tested PEDV-positive in September, similar to 5.11% of 4,010 in August
  - Positivity in the adult/sow category in September was 3.61% (49 of 1,358), similar to 5.5% (79 of 1,436) in August
  - Positivity in the wean-to-market category in September was 7.28% (94 of 1,291), similar to 7.62% (109 of 1,430) in August
  - Positivity in the facilities category in September was 4.85% (5 of 103), similar to 4.5% (5 of 111) in August
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN and OK
  - Overall, 0% of 5 samples had mixed PEDV genotype detection in October, similar to 0% of 99 in September
- Overall, 0.76% of 3,697 cases tested PDCoV-positive in September, similar to 0.66% of 3,918 in August
  - Positivity in the adult/sow category in September was 0.07% of 1,335, similar to 0.43% (6 of 1,392) in August
  - Positivity in the wean-to-market category in September was 1.41% (18 of 1,274), similar to 0.93% (13 of 1,399) in August
  - Positivity in the facilities category in September was 4.85% (5 of 103), a moderate increase from 0.9% (1 of 111) in August
  - 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 September, 2025 over a total of 3,577 cases tested. It has been 55 months (with a total of 204,845 cases tested) since the last TGEV PCR-positive result

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



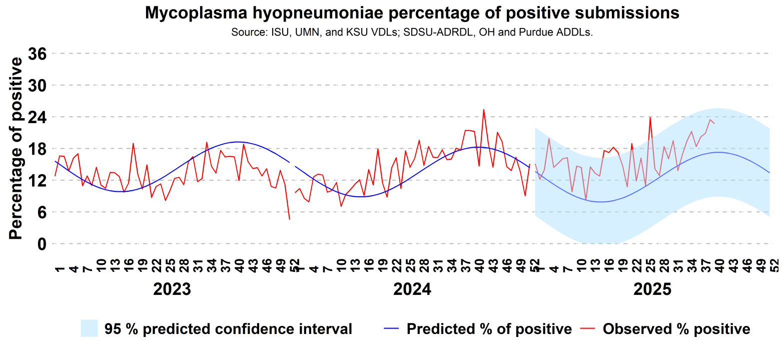


**Figure 1. Top:** *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

## SDRS Advisory Group highlights:

- Overall, 20.47% of 723 cases tested *M. hyopneumoniae*-positive cases in September, a moderate increase from 18.04% of 682 in August;
  - Positivity in the adult/sow category in September was 7.51% (19 of 253), a moderate decrease from 11.4% (31 of 272) in August;
  - Positivity in the wean-to-market category in September was 32.29% (103 of 319), a substantial increase from 26.3% (76 of 289) in August;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN and IL;
- MHP-positive submissions in the wean-to-market category reached the highest recorded rate in 2025 at 32.29%, largely driven by intentional animal exposure for control and elimination projects.

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

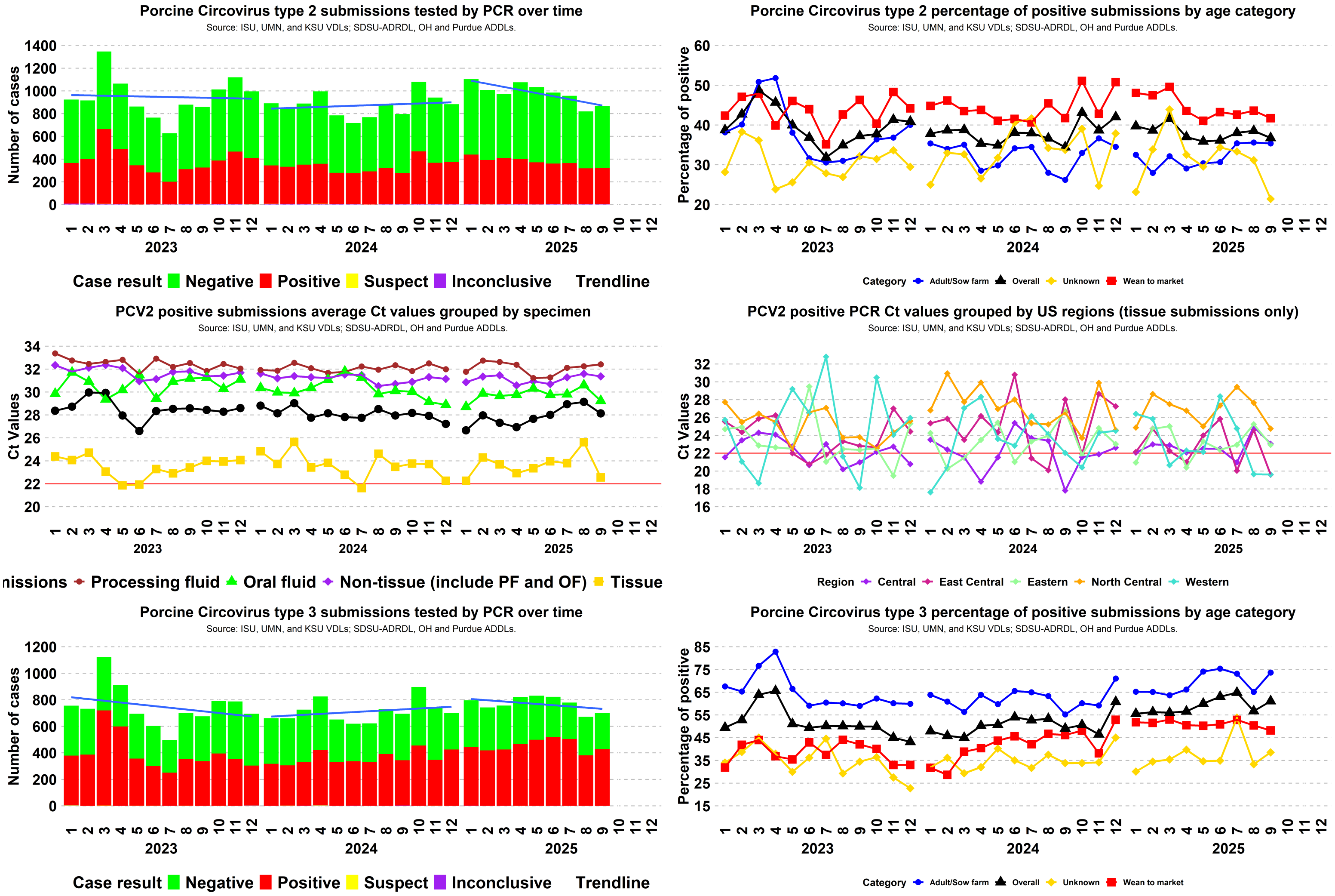


**Figure 1. Top**: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO 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, 36.75% of 868 cases tested PCV2-positive in September, similar to 38.54% of 820 in August;
  - Positivity in the adult/sow category in September was 35.37% (145 of 410), similar to 35.59% (142 of 399) in August;
  - Positivity in the wean-to-market category in September was 41.71% (156 of 374), similar to 43.6% (150 of 344) in August;
  - In the month of September, the regions with the lowest PCV2 average Ct values in tissue submissions was East Central (13 submissions; average Ct 19.6), Western (7 submissions; average Ct 19.6), Eastern (20 submissions; average Ct 22.9), Central (36 submissions; average Ct 23.1), and North Central (27 submissions; average Ct 24.8);
- Overall, 61.09% of 699 cases tested PCV3-positive in September, a moderate increase from 56.7% of 672 in August;
  - Positivity in the adult/sow category in September was 73.68% (280 of 380), a substantial increase from 65.12% (239 of 367) in August;
  - Positivity in the wean-to-market category in September was 48.19% (120 of 249), a moderate decrease from 50.42% (119 of 236) in August.

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

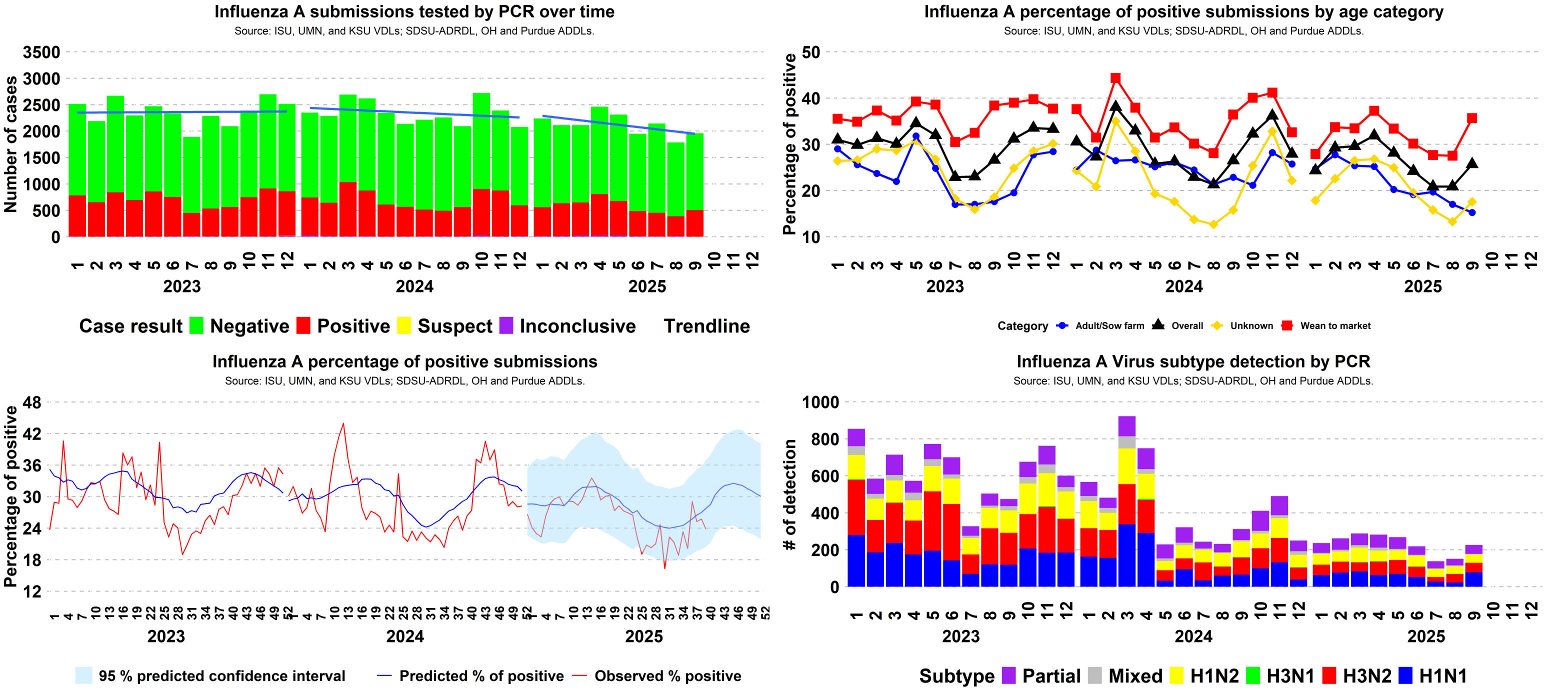
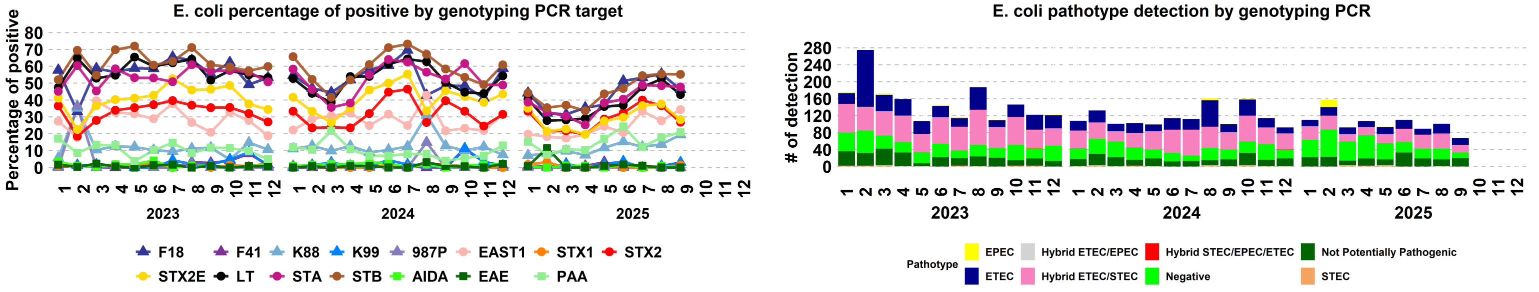


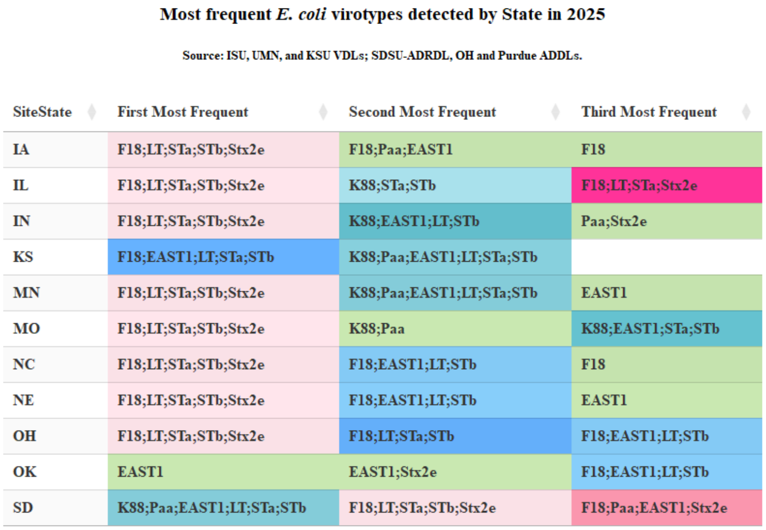
**Figure 1. Top:** *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 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, 25.68% of 1,959 cases tested IAV-positive cases in September, a moderate increase from 20.87% of 1,787 in August;
  - Positivity in the adult/sow category in September was 15.25% (63 of 413), similar to 17.03% (78 of 458) in August;
  - Positivity in the wean-to-market category in September was 35.66% (332 of 931), a substantial increase from 27.52% (229 of 832) in August.
- Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in MN;
- Overall, 1.33% of 226 samples had mixed subtype detection in September, similar to 3.31% of 151 in August.
- From July through September, the positivity rate for cases where IAV and PRRSV were detected within the same case increased from 6% to over 10%.
- The IAV positivity is on the rise particularly in grow-finish sites. Some SDRS advisory group members have noted a concurrent increase in coughing and other respiratory signs among grow-finish pigs, which may be a reflection of increased PRRSV and IAV co-infections.

# 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;EAST1;LT;STa;STb | 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;EAST1;STa;STb |
| NC | F18;LT;STa;STb;Stx2e | F18;EAST1;LT;STb | F18 |
| NE | F18;LT;STa;STb;Stx2e | F18;EAST1;LT;STb | EAST1 |
| 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 | 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, 67 samples were tested for *E. coli* PCR genotyping in September;
  - In September the *E. coli* pathotype with higher number of sample detections were Not Potentially Pathogenic (20 detections), Hybrid ETEC/STEC (18 detections), ETEC (16 detections);
  - In September the *E. coli* genotypes with higher detection rate were STB (55.22%), STA (47.76%), F18 (46.27%);

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

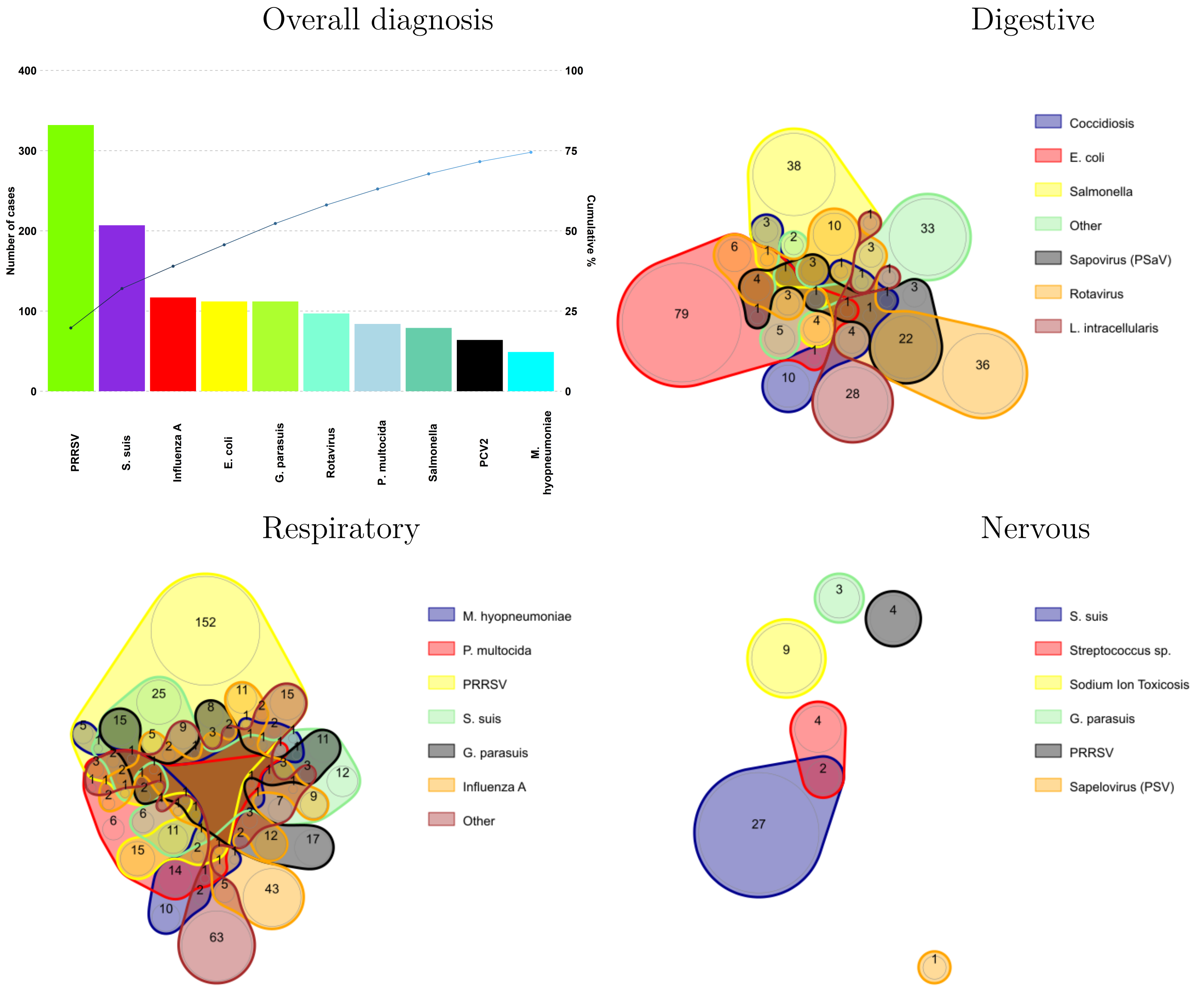


**Figure 4.** ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. 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 (332) led cases with confirmed etiology, followed by *S. suis* (207), and Influenza A (117). PRRSV (306 of 936) led the number of confirmed respiratory diagnoses, *E. coli* (107 of 411) lead the number of confirmed digestive diagnoses, and *S. suis* (29 of 52) 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.*

# Change in the dynamics of PRRSV detection after Lineage 1 C.5 emerging in the United States

Quyen Thuc Le[1], Guilherme Cezar[1], Kinath Rupasinghe[1], Daniel Linhares[1], Giovani Trevisan[1]

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

The SDRS PRRSV Sequencing Database has seen changes in the detection of lineages L1A and L1C.5 from 2020 to 2025, with lineage L1A gradually decreasing in detection, while lineage L1C.5 shows a sharp increase.

Lineage 1A was first detected in the SDRS database in 2006. Since then, it showed a significant increase in the number of detections from 2015 to 2020. However, after 2020, the detections of lineage 1A began to gradually decline. In 2020, a total of 2,481 sequences were recorded, with the majority belonging to the variants 1A – unclassified (n = 1117) and 1A – 2 (n = 363). By 2025, the total number of detections for lineage 1A had decreased to 839, with the main contributing variants still being 1A – unclassified (n = 296) and 1A – 2 (n = 148). As of 2025, lineage 1A has been detected in 16 distinct states. Lineage 1H followed a similar trend to lineage 1A, experiencing a decline over the specified period. There were 1,386 detections of lineage 1H in 2020, which peaked in 2022 with 1,617 sequences, but dropped to 454 detections in 2025. The predominant variant during this time was variant 1H.18, which accounted for 192 sequences and was detected in 8 distinct states in 2025.

Lineage 1C.5 was first detected in 2020 in the SDRS database, with a total of 161 detections across 3 distinct states (Indiana, Iowa, and Michigan). Since then, there has been a sharp increase in detections from 2020 to 2025, reaching 3,347 in 2025. Notably, the variant 1C.5.32 began to surge after its initial detection in 2023, when there were 72 cases reported in Iowa and Missouri. By 2024, the number of sequences for this variant rose to 1,137, with detections across 10 distinct states. In 2025, the count increased to 1,745 sequences, detected in 13 distinct states. Alongside the trend observed in lineage 1C.5, the SDRS database also recorded an increase in detections for lineage 1C.2. The number of detections for lineage 1C.2 grew from 117 in 2020 to 604 in 2025. Notably, the majority of these detections were for variant 1C.2, which accounted for 549 sequences identified across 14 distinct states in 2025.

The recent increases in detections of lineage 1C.5 – particularly the expansion of variant 1C.5.32 – coincide with broader shifts in PRRSV sequence patterns across multiple states. The SDRS will continue to monitor PRRSV sequence dynamics to support timely and informed decision making.

**Figure 1.** Change in the number of the PRRSV lineages detections since the lineage L1C.5 emergence.