

















Swine Disease Reporting System Report # 93 (October 31, 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 October 31, 2025.

















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

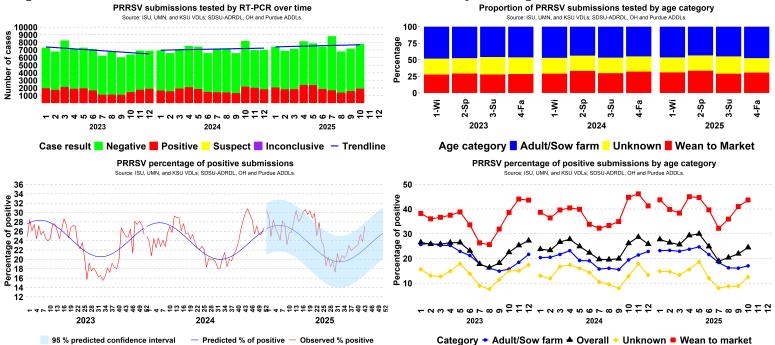


Figure 1. Top: Left: Results of PRRSV RT-PCR cases over time; Right: Proportion of accession ID cases tested for PRRSV by age group per year and season. Bottom: Left Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly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

- Overall, 24.44% of 7,782 cases tested PRRSV-positive in October, a moderate increase from 21.93% of 7,186 in September;
 - Positivity in the adult/sow category in October was 17.03% (626 of 3,676), similar to 16.08% (553 of 3,438) in September;
- Positivity in the wean-to-market category in October was 43.67% (1,069 of 2,448), a moderate increase from 41.03% (880 of 2,145) in September;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MN, MO, IN and NC;
- See highlights in the Bonus page.











SiteState

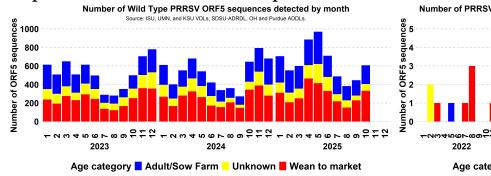


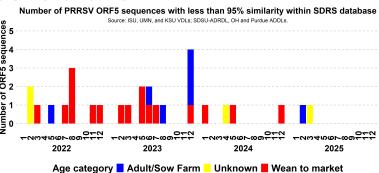


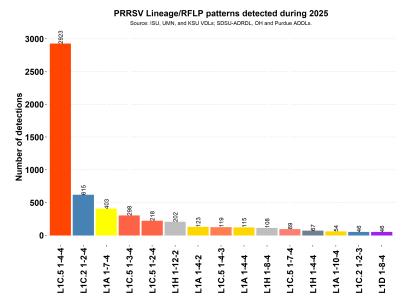




Topic 2 – PRRSV ORF5 sequences detection over time







Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs. First Most Frequent Second Most Frequent Third Most Frequent L1C.5 1-4-4 L1C.2 1-2-4 L1C.5 1-3-4

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

	This Most Trequent	Second Masse Proquent	Initial Mark Trequent
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
мо	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
ОН	L1C.5 1-4-4	L1A 1-7-2	L1A 1-4-4
ок	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.

- During October 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MN, NE, MO, IL, IN, OH, OK, SD (respective number of sequences: 284, 38, 33, 27, 11, 4, 1, 1, 1).
- In October L1C.5 1-4-4 (179) 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.
- See highlights in the Bonus page.

















Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

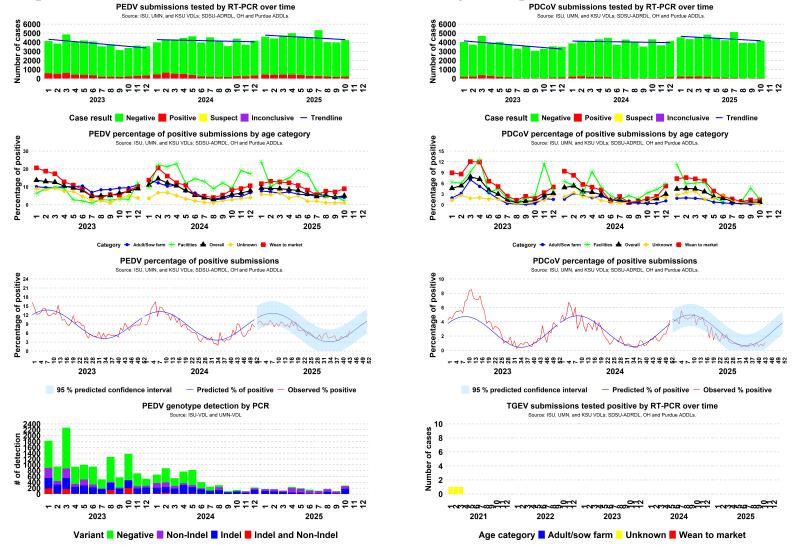


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time; Second from top: Left PEDV; Right PDCoV percentage of positive PCR positive results, by age category over time. Facilities are cases submissions from packing plants, truck washes, and vehicles. Third from top: Left PEDV; Right PDCoV 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.

- Overall, 5.05% of 4,237 cases tested PEDV-positive in October, similar to 4.28% of 3,973 in September
 - Positivity in the adult/sow category in October was 4.11% (61 of 1,484), similar to 3.77% (54 of 1,432) in September
 - Positivity in the wean-to-market category in October was 8.94% (138 of 1.543), similar to 7.18% (99 of 1.378) in September
 - Positivity in the facilities category in October was 2.31% (3 of 130), a moderate decrease from 4.67% (5 of 107) in September
 - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN, OK and NC
 - Overall, 0% of 288 samples had mixed PEDV genotype detection in October, similar to 0% of 99 in September
- Overall, 0.76% of 4,188 cases tested PDCoV-positive in October, similar to 0.77% of 3,917 in September
 - Positivity in the adult/sow category in October was 0.41% (6 of 1,460), similar to 0.14% (2 of 1,407) in September
 - Positivity in the wean-to-market category in October was 1.37% (21 of 1,535), similar to 1.32% (18 of 1,359) in September
 - Positivity in the facilities category in October was 1.54% (2 of 130), a moderate decrease from 4.67% (5 of 107) in September
 - 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 October, 2025 over a total of 4,082 cases tested. It has been 56 months (with a total of 208,690 cases tested) since the last TGEV PCR-positive result
- See highlights in the Bonus page.









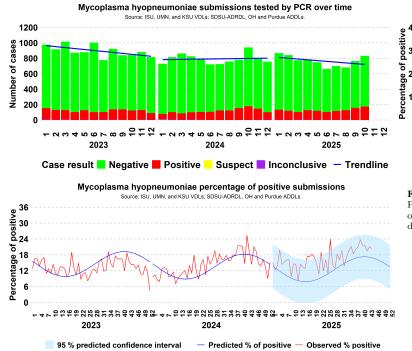








Topic 3 – Detection of M. hyopneumoniae DNA by PCR.



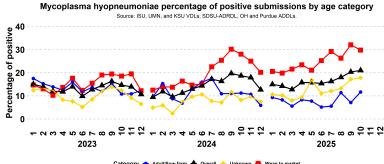


Figure 1. Top: Left MHP Case results tested by PCR over time. Right MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

- Overall, 21.03% of 832 cases tested M. hyopneumoniae-positive cases in October, similar to 20.37% of 766 in September;
 - Positivity in the adult/sow category in October was 11.67% (37 of 317), a moderate increase from 7.14% (19 of 266) in September;
- Positivity in the wean-to-market category in October was 29.79% (115 of 386), a moderate decrease from 32.07% (110 of 343) in September:
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN, SD, IL and IN;
- See highlights in the Bonus page.

















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

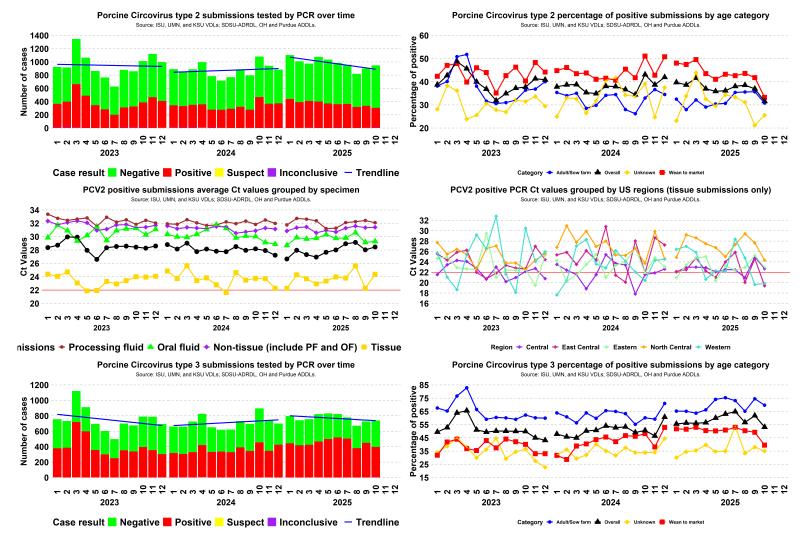


Figure 1. Top: Left: Results of PCV2 PCR cases over time; Right: PCV2 PCR-positive results, by category over time. Middle: Left: Average Ct values of PCV2 submissions by specimen; Right: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (II, IN, MO and WI), Eastern (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.

- Overall, 31.57% of 947 cases tested PCV2-positive in October, a substantial decrease from 36.96% of 901 in September;
- Positivity in the adult/sow category in October was 30.81% (118 of 383), a moderate decrease from 35.68% (152 of 426) in September;
- Positivity in the wean-to-market category in October was 33.26% (159 of 478), a substantial decrease from 41.79% (163 of 390) in September;
- In the month of October, the regions with the lowest PCV2 average Ct values in tissue submissions was East Central (10 submissions; average Ct 19.4), Western (8 submissions; average Ct 19.8), Central (43 submissions; average Ct 22.7), Eastern (24 submissions; average Ct 22.9), and North Central (20 submissions; average Ct 24.3);
- Overall, 53.17% of 741 cases tested PCV3-positive in October, a substantial decrease from 61.81% of 728 in September;
- Positivity in the adult/sow category in October was 69.74% (242 of 347), a moderate decrease from 74.55% (293 of 393) in September:
- Positivity in the wean-to-market category in October was 39.49% (124 of 314), a substantial decrease from 49.24% (130 of 264) in September.

















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

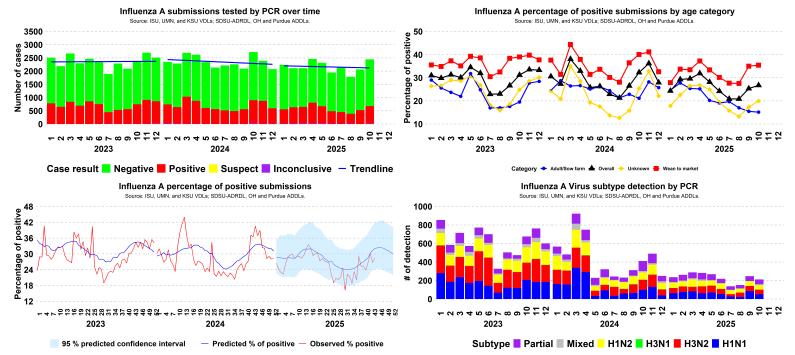


Figure 1. Top: Left Results of IAV PCR cases over time. Right Percentage of IAV PCR-positive results, by category over time. Bottom: Left expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years. 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").

- Overall, 26.75% of 2,445 cases tested IAV-positive cases in October, similar to 25.34% of 2,064 in September;
 - Positivity in the adult/sow category in October was 15.16% (79 of 521), similar to 15.49% (68 of 439) in September;
 - Positivity in the wean-to-market category in October was 35.44% (437 of 1,233), similar to 35% (343 of 980) in September.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 4.72% of 212 samples had mixed subtype detection in October, a moderate increase from 1.21% of 247 in September.
- See highlights in the Bonus page.









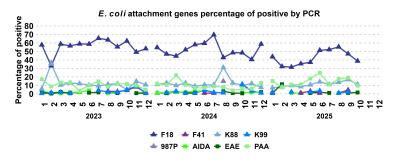


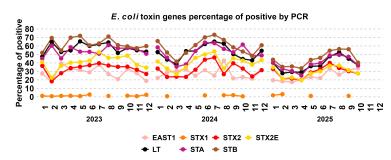






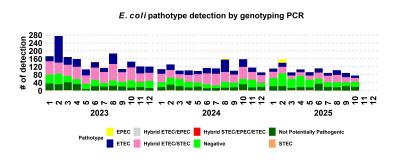
Topic 6 – Detection of $E.\ coli$ DNA by Genotyping PCR.





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	F18;EAST1;LT;STb	F18;LT;STa;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	F18;EAST1;LT;STb
NE	F18;LT;STa;STb;Stx2e	F18;EAST1;LT;STb	F18;STa;STb
ОН	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	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

- Overall, 76 samples were tested for *E. coli* PCR in October;
- In October the *E. coli* pathotype with higher number of sample detections were Hybrid ETEC/STEC (20 detections), Not Potentially Pathogenic (19 detections), ETEC (12 detections);
 - In October the E. coli attachment genes with higher detection rate were F18 (38.71%), K88 (11.29%), PAA (9.68%);
 - In October the E. coli toxin genes with higher detection rate were STB (40.32%), LT (37.10%), STA (37.10%).









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

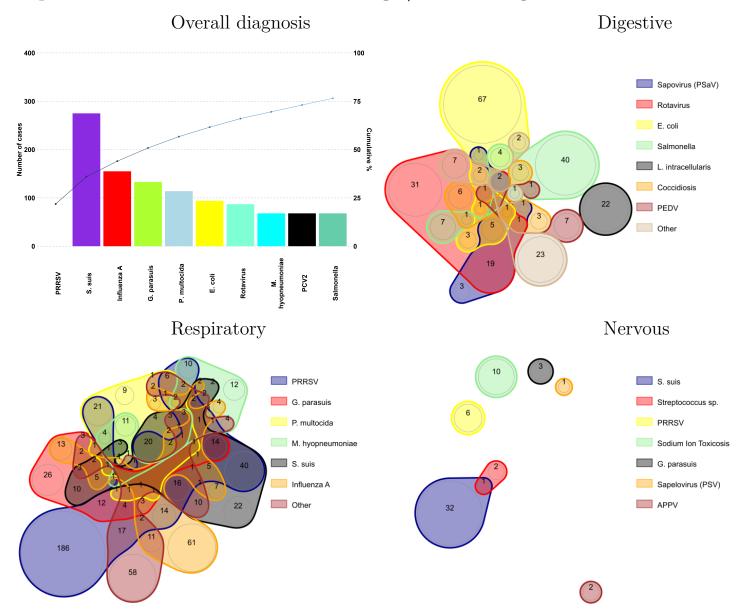


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less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

SDRS Advisory Group highlights:

• PRRSV (424) led cases with confirmed etiology, followed by *S. suis* (275), and *Influenza A* (155). PRRSV (398 of 1214) led the number of confirmed respiratory diagnoses, *E. coli* (87 of 349) lead the number of confirmed digestive diagnoses, and *S. suis* (33 of 58) 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.

SDRS Advisory Group Highlight for Current Pathogen Activity

Guilherme Cezar¹, Quyen Thuc Le¹, Daniel Linhares¹, Giovani Trevisan¹

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

In October the Swine Disease Reporting System Advisory Group gathered for a review of 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 Oct, 2025:

PRRSV

- In 2025, wean-to-market sites reported a historic high level of PRRSV activity during the second quarter, with 43.3% of cases testing positive. This is the highest second-quarter positivity rate since 2013. The previous peak occurred during the summer of 2018, when the positivity rate reached 35%. That same year, there was a sharp increase in sow herd positivity during the winter. Given the current elevated positivity in wean-to-market sites, it is essential to strengthen biocontainment and biosecurity measures to minimize the risk of outbreaks in sow herds. According to the advisory group, PRRSV activity in the field is currently at expected or lower levels, with fewer detections than recent years. Prolonged warmer temperatures and potentially remaining immunity from spring outbreaks may be contributing to this decline.
- PRRSV L1C.5 has been the predominant strain detected, along with multiple new variants. However, the increased detection of L1C.5 may be suppressing the presence of previously dominant strains, as the detections of L1A, L1H, and L1C.3 are declining in 2025. Additionally, another PRRSV lineage, L1C.2, has also seen an increase in detections in 2025, with a rise in the number of sequences and its first detection in new states, including North Carolina.
- Regional data show broad expansion of L1C.5 variants across Iowa, Ohio, South Dakota, Illinois, and Oklahoma.
- The advisory group emphasized the importance of closely monitoring PRRSV L1C.5 due to its aggressive clinical impact and the emergence of new variants within this lineage. Once this variant is introduced into a region, the advisory members noted that they often experience recurrent outbreaks with variants from the original L1C.5 strain, which is reflected in the predominant detections recorded in the SDRS database.

PEDV

- Record high testing volumes in 2025, including >8,000 oral fluid samples per season (spring and summer).
- Overall positivity remains relatively low, and activity on the East Coast is minimal. However, the Southwest U.S. region has experienced persistent outbreaks. It is important to highlight that PEDV cases often resurface in late winter and early spring.
- The advisory group noted that PEDV activity varies by region, with minimal cases reported in the Eastern states but ongoing outbreaks in the Southwest. Advisory Group emphasized that PEDV activity is expected to increase during the upcoming winter months, and that the industry should strengthen biosecurity and biocontainment protocols to prevent the further spread and introduction of the virus. Additionally, the group identified oral fluids as a crucial surveillance tool for monitoring this virus.

TGEV

- In 2025, TGEV completed 4.5 years without positive cases in the U.S. The last positive case detection was in March 2021.
- Over 732,000 samples were tested for TGEV by RT-PCRs since 2021, all negative, projected to surpass 1 million by mid-2026.
- The Advisory Group noted the four years without positive TGEV cases as a milestone, while emphasizing the importance of vigilant monitoring to enable early identification of any resurgence and containment

M. hyopneumoniae

- Sow farm detections remain historically low (<10% positives in summer)
- There has been an increase in positive cases at wean-to-market, mostly the positive cases are primarily a result of intended exposure protocols aimed at maintaining farm stability, with several homogenates and deep tracheal swabs submitted to the VDLs for testing. Iowa cases are more frequently coming from clinical cases, with lung samples collected from finishing animals, which may be a potential reflection of a large growing inventory.
- The advisory group noted a low detection rate on sow farms, but an increase in positive cases on wean-to-market. They identified regional differences in positivity rates, observing more surveillance positives (from intended exposure protocols) in most states. Additionally, there were some confirmed clinical cases resulting from failures in the exposure protocol or lateral introductions, particularly in Iowa.



















IAV

- As expected for the fall season, the positivity rate of IAV spiked in finishing sites at 35%. However, the positivity rate in sow farms remains below the historical average (<20% positives)
- The advisory group noted that the IAV was following its typical seasonal pattern, with peaks in cases observed at finishing sites during the fall. Some regions experienced a quicker recovery and lower mortality rates. However, IAV was occasionally misdiagnosed as PRRSV, and warmer weather has potentially contributed to delayed activity in certain areas.