Swine Disease Reporting System - Advisory Group Report
Report # 99 (May 5, 2026)

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

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

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

Collaborators:

Swine Disease Reporting System office: Principal investigators: Daniel Linhares & Giovani Trevisan; Project coordinator: Quyen Thuc Le; Software Developer: Kinath Rupasinghe; Data Analyst: Sajan Kumar Thallapelly and Likhitha Nakka.

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

Uni. of Minnesota: Cesar Corzo, Albert Rovira, Matt Sturos, Hemant Naikare.

Kansas State Uni. and Kansas Dept. of Agr.: Rob McGaughey, Franco Matias-Ferreyra, Jamie Retallick, Jordan Gebhardt, Sara McReynolds.

South Dakota State Uni and South Dakota AIB: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings, Eric Nelson, Mendel Miller and Marc Hammrich.

Ohio Veterinary Diagnostic Laboratory and *The Ohio State Uni*: 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-VDL.

PRRSView and FLUture and : Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL. PRRSLoom-Variants: PRRSV-2 variant classification from UMN.

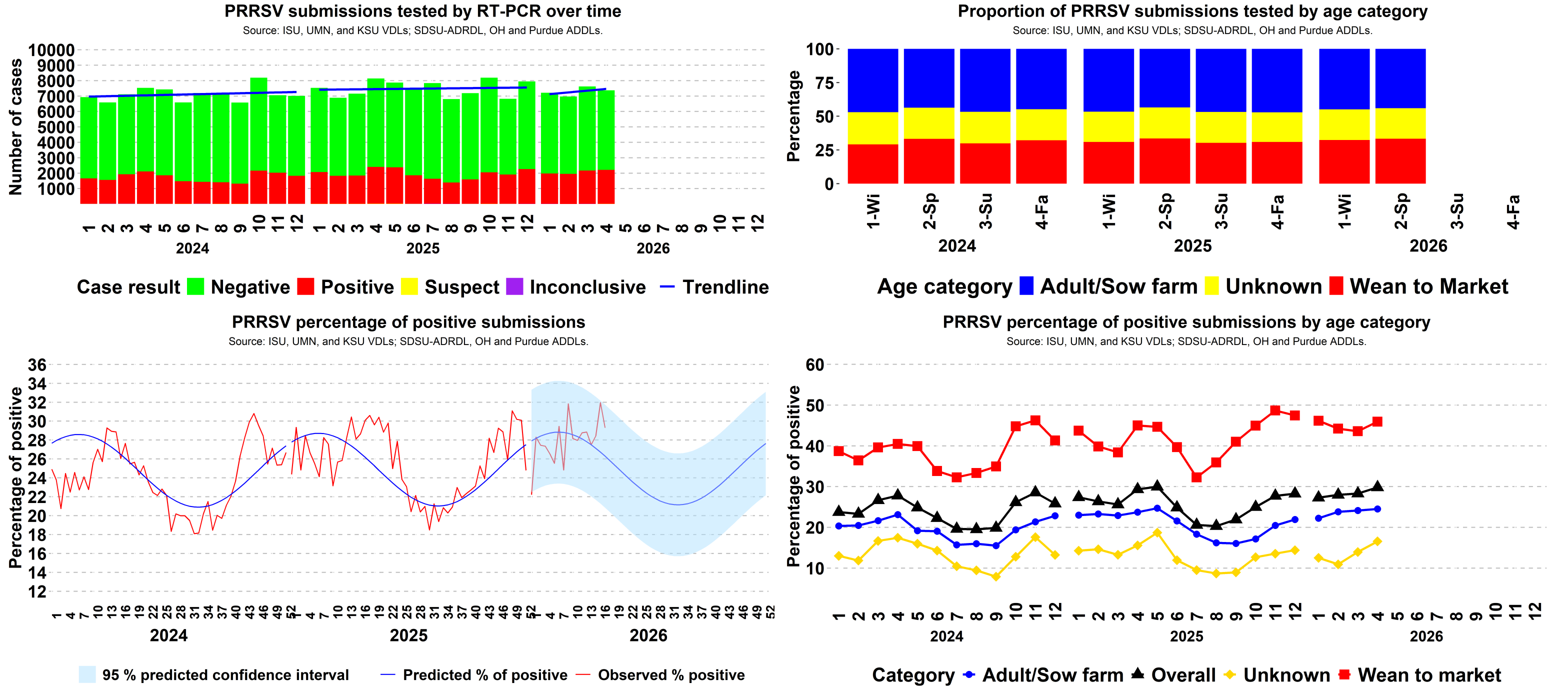
PRRS virus Genotyping report and BLAST tool: Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

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

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

Note: This report contains data up to April 30, 2026.

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.

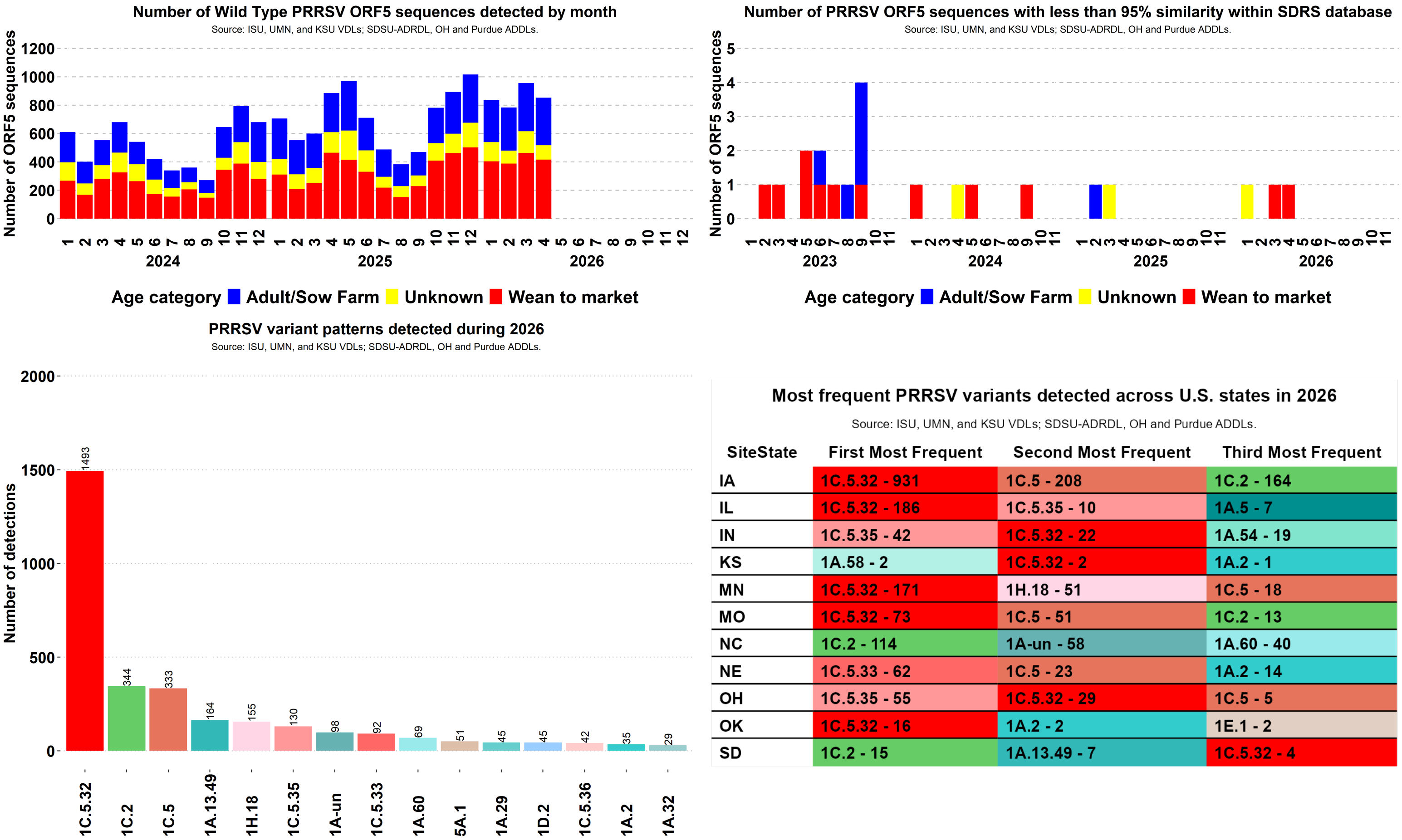
PRRSV percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 29.83% of 7,374 cases tested PRRSV-positive in April, similar to 28.31% of 7,625 in March.
  - Positivity in the adult/sow category in April was 24.52% (810 of 3,304), similar to 24.16% (798 of 3,303) in March.
  - Positivity in the wean-to-market category in April was 45.94% (1,119 of 2,436), a moderate increase from 43.58% (1,114 of 2,556) in March.
  - Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA and IL.
  - Some of the Advisors reported that clinical respiratory disease is primarily associated with PRRSV through both vertical and lateral transmission. They noted that emerging PRRSV variants may be contributing to ongoing challenges with persistence and control, with PRRSV remaining the primary concern. Several Advisors indicated that break severity has remained elevated, most commonly associated with the 1C.5.32 variant, with other variants reported less frequently. It was further noted that characteristics of this variant may be contributing to slower site stabilization compared with historical expectations, resulting in multiple breaks within a single production cycle.

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 variant patterns detected during 2026

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

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

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

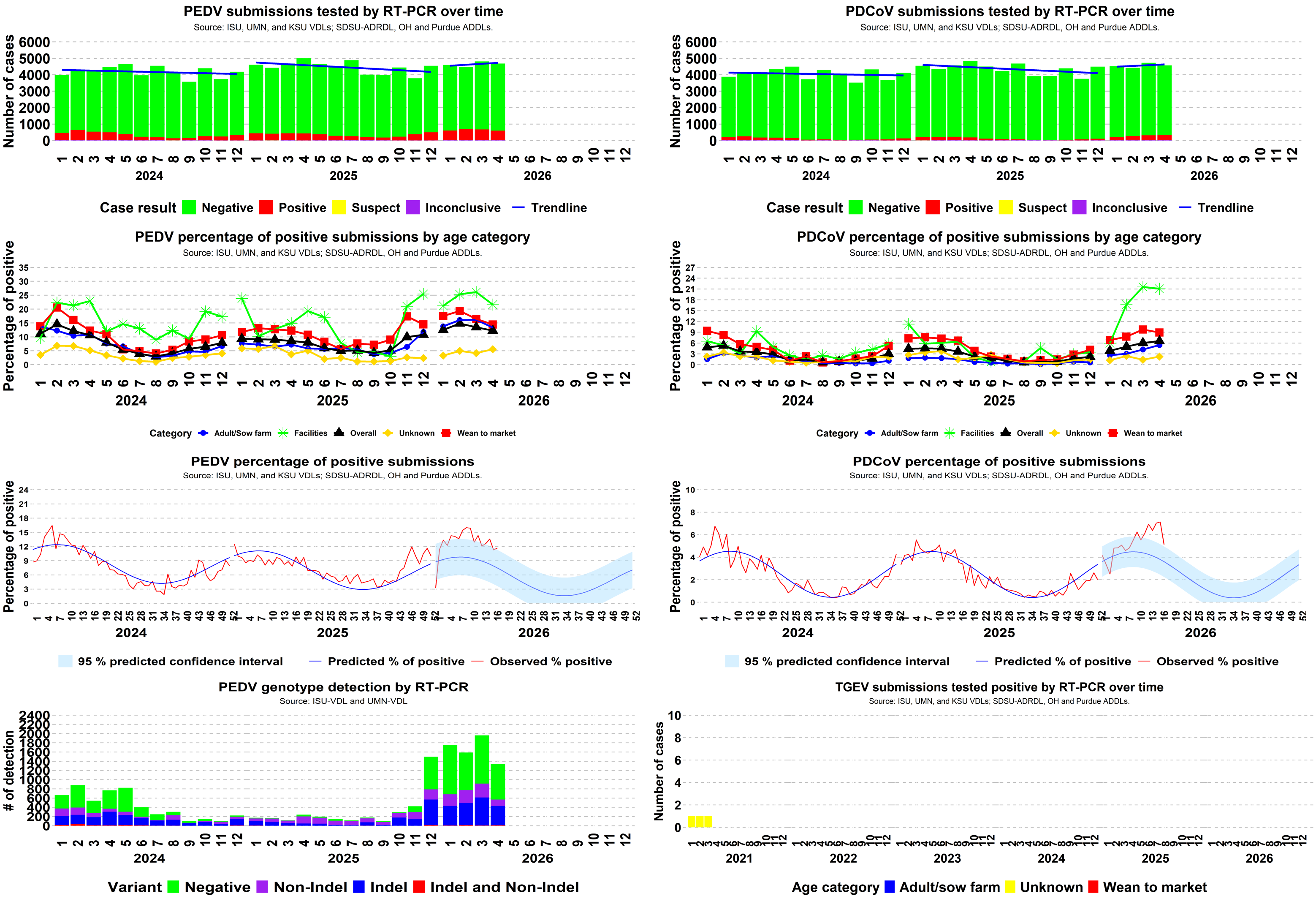
SiteState	First Most Frequent	Second Most Frequent	Third Most Frequent
IA	1C.5.32 - 931	1C.5 - 208	1C.2 - 164
IL	1C.5.32 - 186	1C.5.35 - 10	1A.5 - 7
IN	1C.5.35 - 42	1C.5.32 - 22	1A.54 - 19
KS	1A.58 - 2	1C.5.32 - 2	1A.2 - 1
MN	1C.5.32 - 171	1H.18 - 51	1C.5 - 18
MO	1C.5.32 - 73	1C.5 - 51	1C.2 - 13
NC	1C.2 - 114	1A-un - 58	1A.60 - 40
NE	1C.5.33 - 62	1C.5 - 23	1A.2 - 14
OH	1C.5.35 - 55	1C.5.32 - 29	1C.5 - 5
OK	1C.5.32 - 16	1A.2 - 2	1E.1 - 2
SD	1C.2 - 15	1A.13.49 - 7	1C.5.32 - 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 variant; *Right*: Most frequently detected PRRSV ORF5 sequences in 2026, shown by variant at the U.S. state level along with their respective detection counts **Note: un indicates unclassified**.

SDRS Advisory Group highlights:

- During April, the states with higher number of PRRSV 1C.5.32 detections were detected in IA, IL, MN, MO, OK, IN, NC, OH, NE (respective number of sequences: 271, 68, 40, 22, 7, 6, 5, 3, 1);
- In April, 1C.5.32 (439) was the PRRSV variant most detected in the U.S., followed by 1C.5 (92), and 1C.2 (90);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
  - March 2026: 1C.2 (NV, VA), 1A.13.49 (NE, MO), 1C.2.39 (OK, NE), 1C.5.35 (MI)
  - April 2026: 1C.5.33 (KS), 1A.29 (CO)
- Click on the links below 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


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

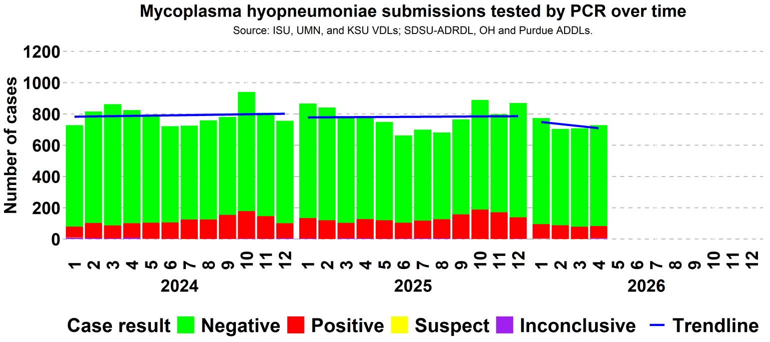
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

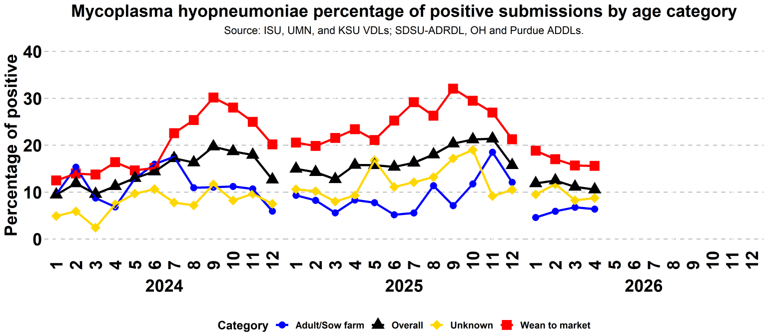
Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection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

SDRS Advisory Group highlights:

- Overall, 12.27% of 4,679 cases tested PEDV-positive in April, similar to 13.49% of 4,810 in March.
  - Positivity in the adult/sow category in April was 13.36% (239 of 1,789), a moderate decrease from 16.13% (278 of 1,723) in March.
  - Positivity in the wean-to-market category in April was 14.45% (235 of 1,626), a moderate decrease from 16.49% (273 of 1,656) in March.
  - Positivity in the facilities category in April was 21.62% (40 of 185), a moderate decrease from 26.14% (46 of 176) in March.
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN and SD.
  - Overall, 0.67% of 1,343 samples had mixed PEDV genotype detection in April, similar to 0.25% of 1,962 in March.
- Overall, 6.54% of 4,573 cases tested PDCoV-positive in April, similar to 6.03% of 4,729 in March.
  - Positivity in the adult/sow category in April was 5.46% (96 of 1,758), similar to 4.22% (72 of 1,705) in March.
  - Positivity in the wean-to-market category in April was 8.93% (140 of 1,567), similar to 9.77% (158 of 1,618) in March.
  - Positivity in the facilities category in April was 21.08% (39 of 185), similar to 21.59% (38 of 176) in March.
  - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in KS, OK, and OH.
- There was 0 positive case for TGEV RNA-PCR in April, 2026 over a total of 4,524 cases tested. It has been 61 months (with a total of 234,088 cases tested) since the last TGEV PCR-positive result.
- Some of the Advisors reported that PDCoV cases are typically very mild and can be eliminated from sow herds without depopulation when enhanced cleaning, internal biosecurity, and removal or euthanasia of scouring litters are implemented, with overall production losses remaining low.
- The Advisors also noted that PEDV activity was especially high toward the end of winter (February–March) but has calmed significantly over the past month. These challenges at sow farms were associated with more growing pigs becoming infected, although there was no indication that lateral spread among growing pigs exceeded typical levels.

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





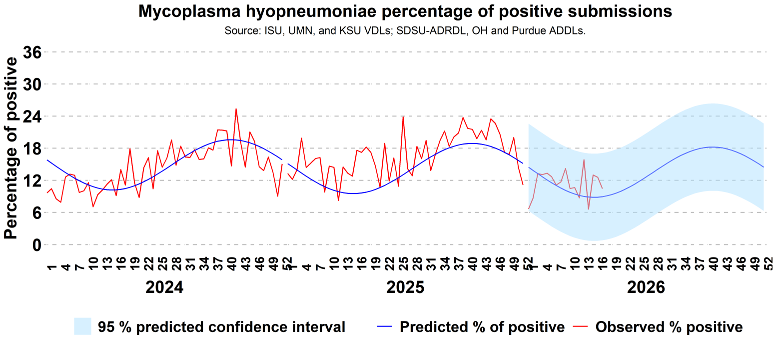
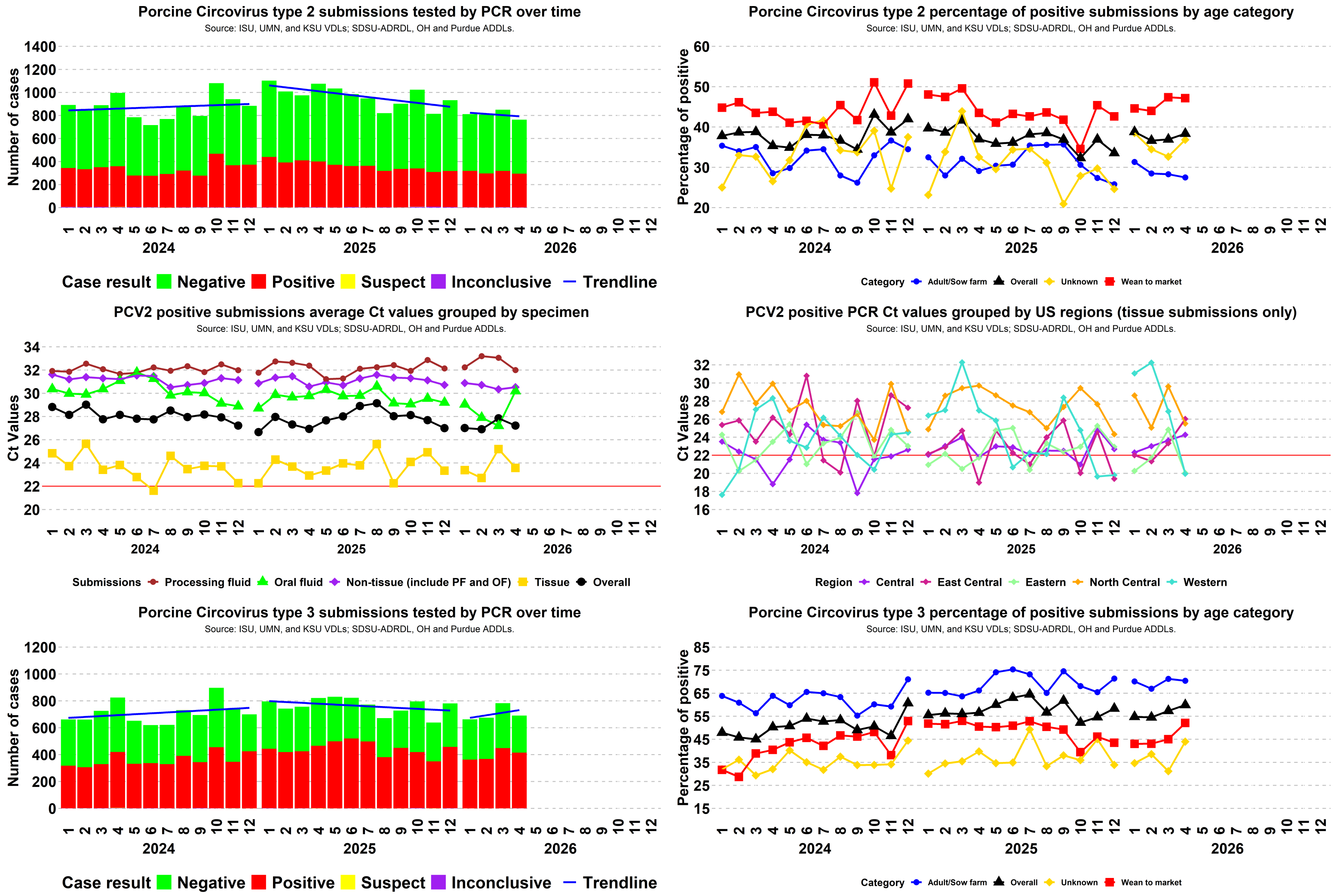


Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

SDRS Advisory Group highlights:

- Overall, 10.56% of 729 cases tested *M. hyopneumoniae*-positive in April, similar to 11.14% of 709 in March.
    - Positivity in the adult/sow category in April was 6.4% (19 of 297), similar to 6.77% (17 of 251) in March.
    - Positivity in the wean-to-market category in April was 15.59% (46 of 295), similar to 15.69% (51 of 325) in March.
    - Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states.

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


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

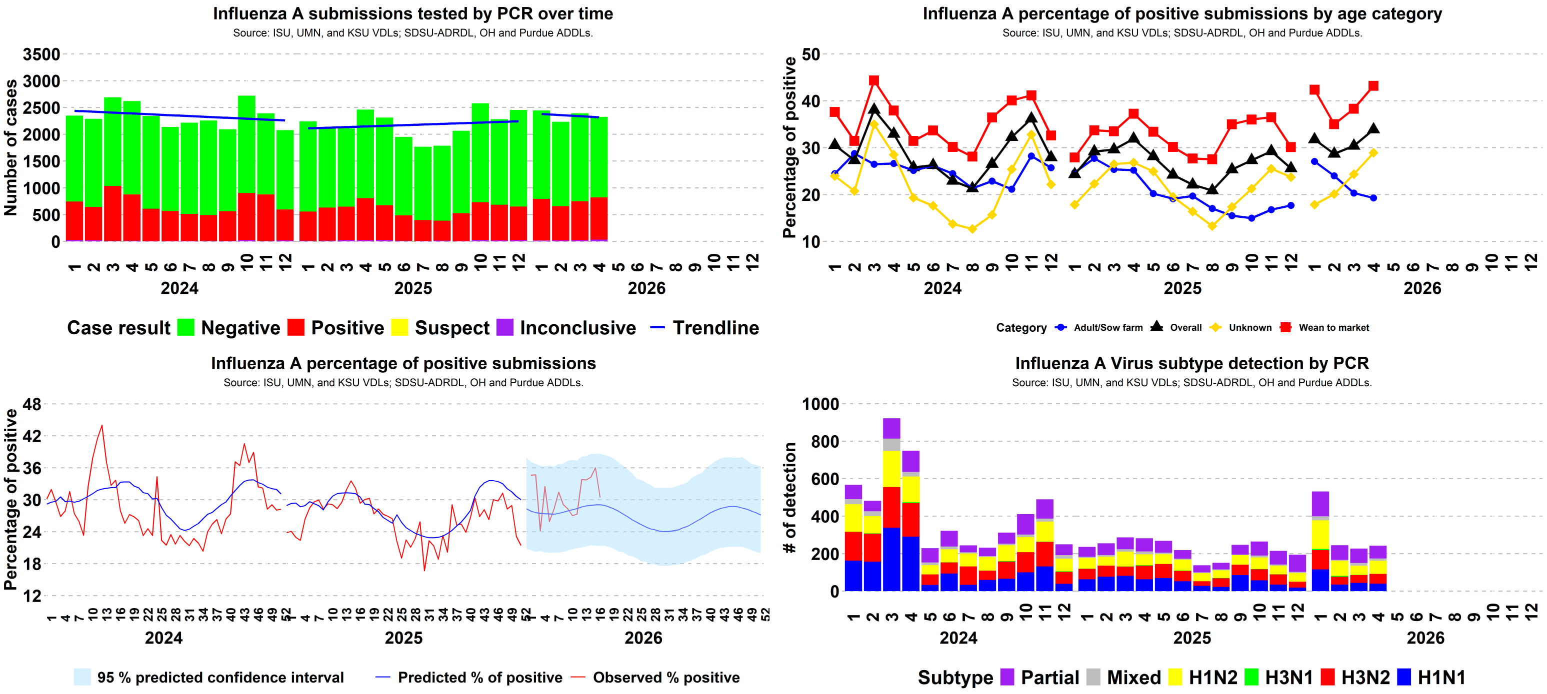
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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, 38.35% of 764 cases tested PCV2-positive in April, similar to 36.94% of 850 in March.
  - Positivity in the adult/sow category in April was 27.48% (83 of 302), similar to 28.28% (110 of 389) in March.
  - Positivity in the wean-to-market category in April was 47.15% (182 of 386), similar to 47.38% (172 of 363) in March.
  - In the month of April, the regions with the lowest PCV2 average Ct values in tissue submissions were Western (8 submissions; average Ct 20), Eastern (26 submissions; average Ct 20.1), Central (32 submissions; average Ct 24.3), North Central (36 submissions; average Ct 25.5), and East Central (22 submissions; average Ct 26).
- Overall, 59.91% of 691 cases tested PCV3-positive in April, a moderate increase from 57.34% of 783 in March.
  - Positivity in the adult/sow category in April was 70.43% (231 of 328), similar to 71.22% (297 of 417) in March.
  - Positivity in the wean-to-market category in April was 52.08% (150 of 288), a substantial increase from 45.05% (123 of 273) in March.

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.

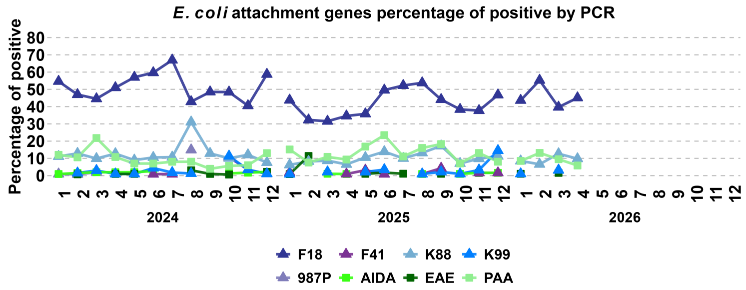
Influenza A Virus subtype detection by PCR
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

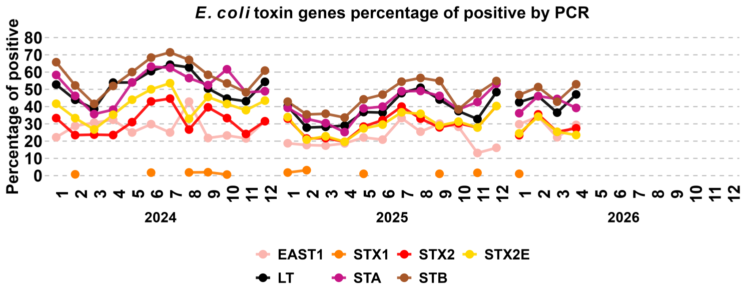
Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 4 years. *Right* Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroamnidase regions detected. i.e., "H1 H3 N1").

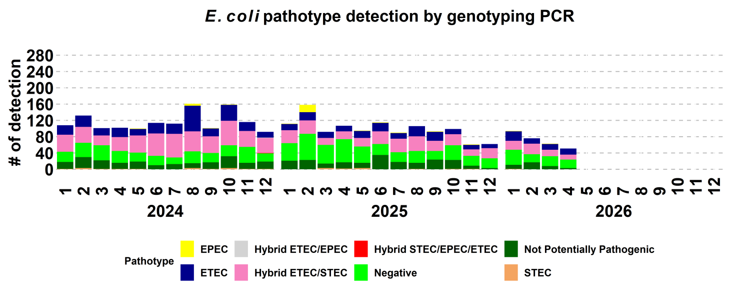
SDRS Advisory Group highlights:

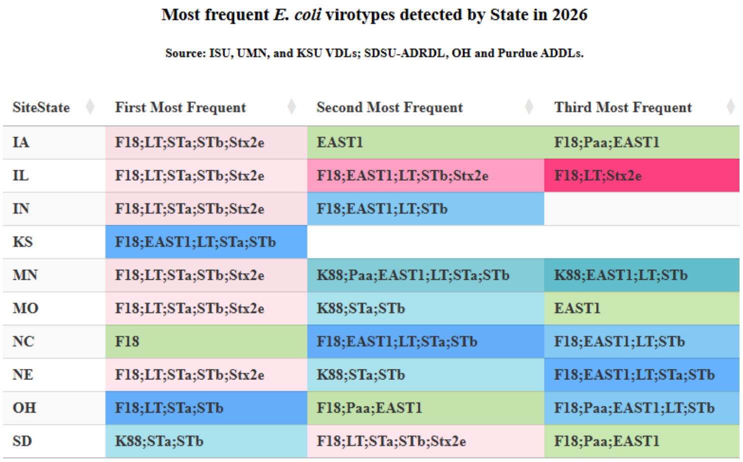
- Overall, 33.86% of 2,324 cases tested IAV-positive in April, a moderate increase from 30.39% of 2,392 in March.
  - Positivity in the adult/sow category in April was 19.27% (100 of 519), similar to 20.31% (105 of 517) in March.
  - Positivity in the wean-to-market category in April was 43.2% (499 of 1,155), a moderate increase from 38.31% (454 of 1,185) in March.
  - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, OH, and NC.
- Overall, 4.96% of 242 samples had mixed subtype detection in April, similar to 6.17% of 227 in March.
- Some of the Advisors noted that, while IAV has been identified, reported levels remain comparable to historical patterns. However, some Advisors also reported observing more severe and frequent outbreaks. They noted that changes in circulating IAV strains may be contributing to more pronounced clinical impacts, particularly when PRRSV is also present.

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


***E. coli* attachment genes percentage of positive by PCR**


***E. coli* toxin genes percentage of positive by PCR**


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


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

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	EAST1	F18;Paa;EAST1
IL	F18;LT;STa;STb;Stx2e	F18;EAST1;LT;STb;Stx2e	F18;LT;Stx2e
IN	F18;LT;STa;STb;Stx2e	F18;EAST1;LT;STb	
KS	F18;EAST1;LT;STa;STb		
MN	F18;LT;STa;STb;Stx2e	K88;Paa;EAST1;LT;STa;STb	K88;EAST1;LT;STb
MO	F18;LT;STa;STb;Stx2e	K88;STa;STb	EAST1
NC	F18	F18;EAST1;LT;STa;STb	F18;EAST1;LT;STb
NE	F18;LT;STa;STb;Stx2e	K88;STa;STb	F18;EAST1;LT;STa;STb
OH	F18;LT;STa;STb	F18;Paa;EAST1	F18;Paa;EAST1;LT;STb
SD	K88;STa;STb	F18;LT;STa;STb;Stx2e	F18;Paa;EAST1

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 2026 at U.S. state level (color code on table cells associated with the pathotype legend).

Education Material:

- Click on the links here to access the *E. coli* PCR Genotyping Interpretation Tool
- **Attachment genes: Fimbriae** – F18, K88(F4), K99(F5), 987P(F6), F41; **Adhesins** – EAE (Intimin), PAA, AIDA
- **Toxin genes: Heat-labile** – LT; **Heat-stable** – STa and STb; **Shiga toxins** – Stx1, Stx2 and Stx2e; and EAST1
- **Enterotoxigenic *E. coli* (ETEC):** Has fimbriae and toxin (not Stx2e) genes. Associated with neonatal and post-weaning diarrhea
- **Shiga toxin-producing *E. coli* (STEC):** Has fimbriae (F18) and toxin (must be Stx2e) gene. Associated with edema disease
- **Enteropathogenic *E. coli* (EPEC):** Presence of the EAE (Intimin) adhesin
- **Hybrids (ETEC/STEC, ETEC/EPEC, STEC/EPEC, ETEC/STEC/EPEC):** Combination of characteristics of more than one pathotype

SDRS Advisory Group highlights:

- Overall, 51 samples were tested for *E. coli* PCR in April.
  - In April, the *E. coli* pathotypes with higher number of sample detections were ETEC (15 detections), Hybrid ETEC/STEC (12 detections), and Not Potentially Pathogenic (3 detections).
  - In April, the *E. coli* attachment genes with higher detection rate were F18 (45.10%), K88 (9.80%), and PAA (5.88%).
  - In April, the *E. coli* toxin genes with higher detection rate were STB (52.94%), LT (47.06%), and STA (39.22%).

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

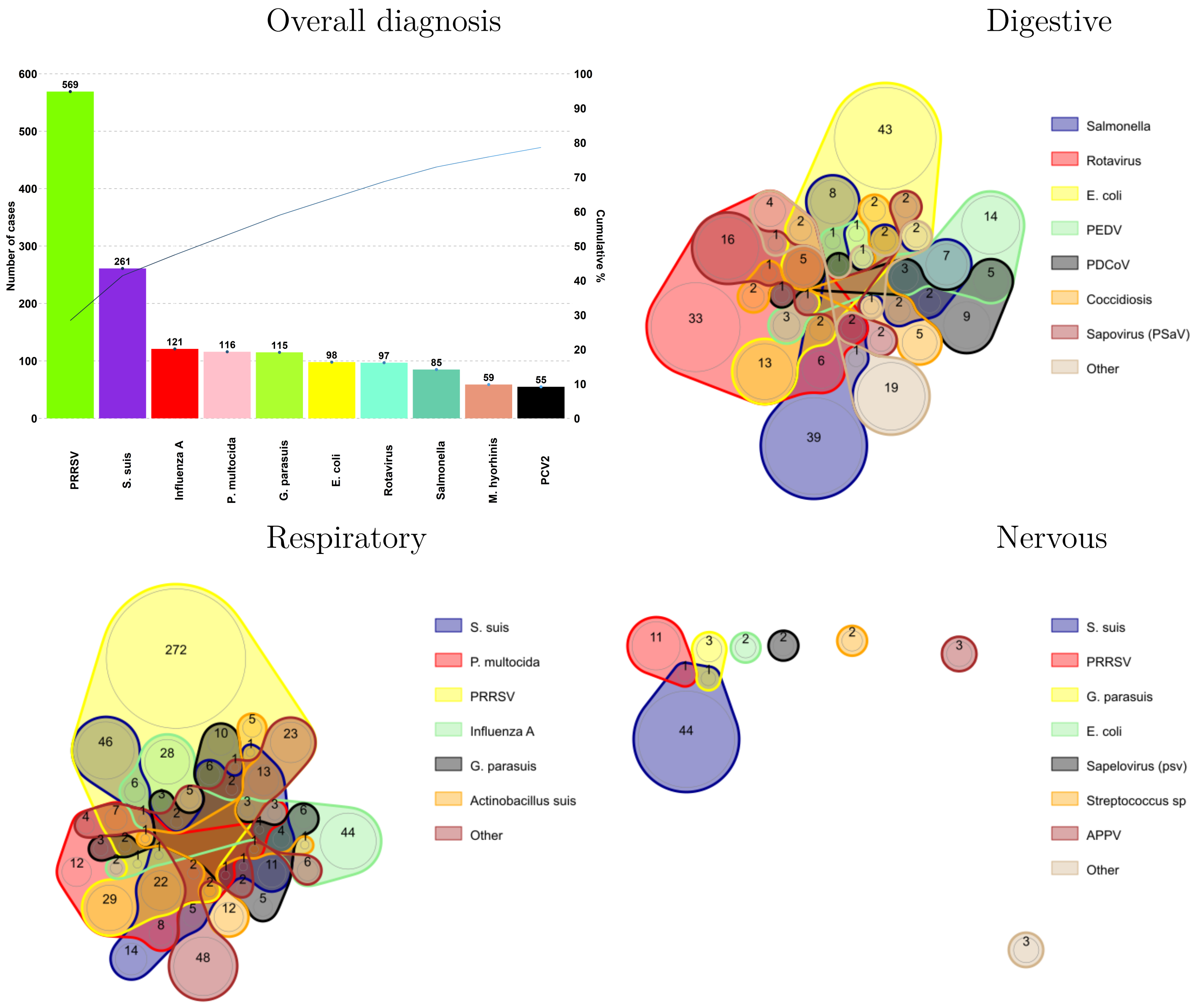


Figure 4. ISU-VDL and OH-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less frequent etiology/disease are grouped as "other". Non-confirmed diagnoses are not presented. This work is made possible due to the commitment and teamwork from the ISU-VDL diagnosticians who assign standardized diagnostic codes to each case submitted for histopathology: Drs. Almeida, Burrough, Derscheid, Gauger, Magstadt, Piñeyro, Siepker, Madson, Thomas, Gris, Yanez and previous VDL diagnosticians who have contributed to this process.

Note: Disease diagnosis takes 1 to 2 weeks to be performed. The graphs and analysis contain data from March 02, 2026 to April 28, 2026

SDRS Advisory Group highlights:

- PRRSV (569) led cases with confirmed etiology, followed by *S. suis* (261), and Influenza A (121). PRRSV (494 of 1086) led the number of confirmed respiratory diagnoses, Rotavirus (92 of 390) lead the number of confirmed digestive diagnoses, and *S. suis* (46 of 74) 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.*

Production impact update on PRRSV 1C.5.32 variant

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The PRRS Outbreak Management Program (POMP) initiative was established to improve understanding of the factors and management practices that influence recovery of PRRS outbreaks. The project systematically collects, standardizes, and analyzes PRRS outbreak management data across commercial breeding herds. Additionally, POMP offers producers diagnostic support, PRRSV sequencing, and benchmarking tools to quantify productivity and recovery performance (https://fieldepi.org/pomp/).

While SDRS provides national-scale surveillance of PRRSV detection, variant emergence, and geographic spread, complementary insights from POMP help contextualize the production impact of specific variants. By documenting patterns in production losses and recovery across participating herds, POMP offers practical insight into the field-level impact of PRRSV outbreaks and supports more informed decision-making for veterinarians and producers.

Production impact of 1C.5.32 variant outbreaks

The piglet losses per 1,000 sows is an outbreak recovery metric that reports the number of piglets not weaned during a PRRSV outbreak, standardized per 1,000 sows. Across POMP-enrolled outbreaks, piglet losses/thousand sows were **2.2x higher in outbreaks with the 1C.5.32 variant** compared with those attributed to the L1A lineage (median 4,144 versus 1,920, respectively). When compared to other L1C.5 variants (1C.5.34, 1C.5.35, 1C.5.36, 1C.5.38, 1C.5, and unclassified) and stratified by AASV status at the time of outbreak, this pattern remained consistent. Among herds classified as **IA or IB**, the median piglet losses for outbreaks associated with the 1C.5.32 variant were 3,545 piglets per thousand sows, **1.19 times higher** than that observed for other 1C.5 variants (median 2,990). Similarly, in herds with **II or II-VX** status, outbreaks attributed to 1C.5.32 had median losses of 5,701, **1.32 times higher** than those observed for other 1C.5 variants (median 4,323; Table 1 and Figure 1). Overall, these findings indicate that outbreaks with the 1C.5.32 are characterized by **higher piglet losses** than those with other PRRSV variants, **even compared to other L1C.5's**. Outbreaks classified as AASV III–IV were excluded from the analysis because, as of April 14, 2026, only one POMP outbreak associated with the 1C.5.32 variant had complete production data available. Including this could result in an unbalanced comparison and potentially bias the interpretation of the results.

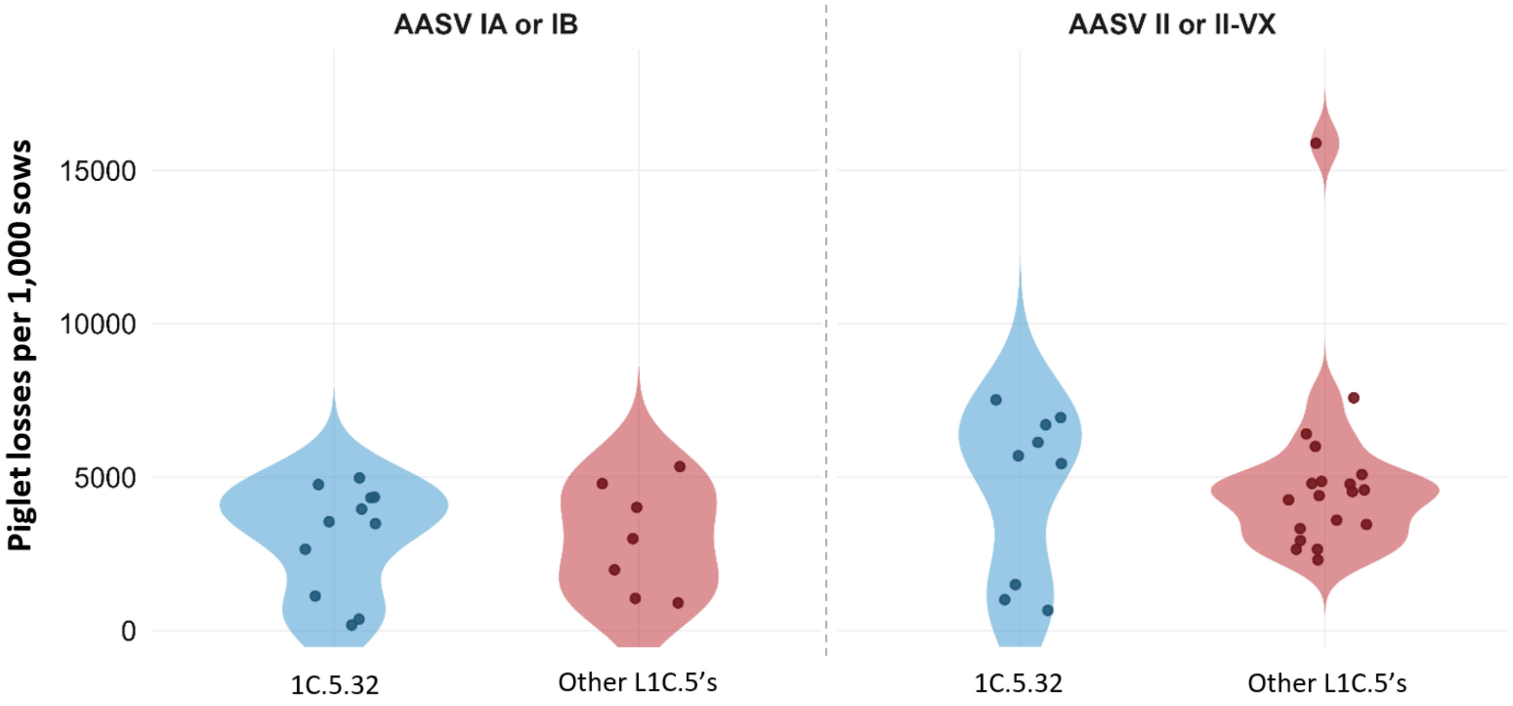

Figure 1. Distribution of piglet losses per 1,000 sows by PRRSV lineage/variant.

The violin plots from Figure 1 illustrate the distribution of piglet losses per thousand sows across variant 1C.5.32 and other 1C.5 variants. The width of each violin represents the density of the data, with wider sections indicating a higher concentration of outbreaks at those values. Each dot corresponds to a single outbreak, allowing visualization of both the overall distribution and the individual observations within each group.

Table 1. Piglet losses per 1,000 sows by PRRSV variant/lineage and AASV status at outbreak.

AASV status at outbreak	Variant/Lineage	Number of outbreaks	Median (range) piglet losses per 1,000 sows
IA or IB	1C.5.32	11	3,545 (182 – 4,970)
	Other L1C.5's	7	2,990 (894 – 5,345)
II or II-VX	1C.5.32	9	5,701 (660 – 7,521)
	Other L1C.5's	14	4,323 (2308 – 6,405)

Table 1 summarizes the number of outbreaks and the distribution of piglet losses per thousand sows by PRRSV variant/lineage, stratified by AASV status at the time of the outbreak. Among herds classified as IA or IB, outbreaks associated with the 1C.5.32 variant showed the highest median piglet losses (3,545) compared to other 1C.5 variants (2,990).