Swine Disease Reporting System
Report # 101 (July 7, 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-ADDL.

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

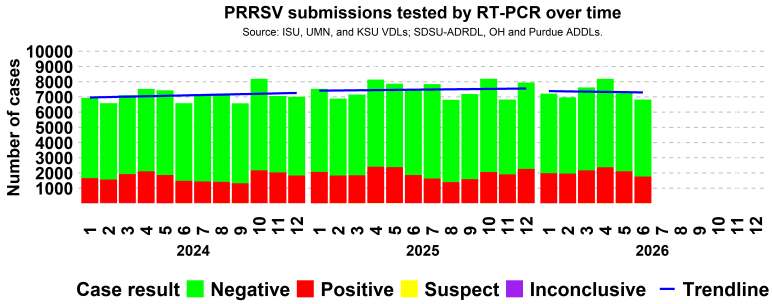
PRRS virus Genotyping report and BLAST tool: Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

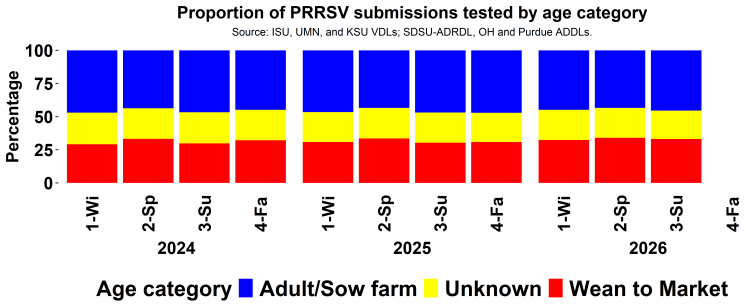
Audio and video reports: Key findings from SDRS projects are summarized monthly in a conversation between investigators and is available in the Spotify, Apple Podcast, YouTube, LinkedIn, and the SDRS webpage. In addition to this report, interactive dashboards and educational material are publicly available.

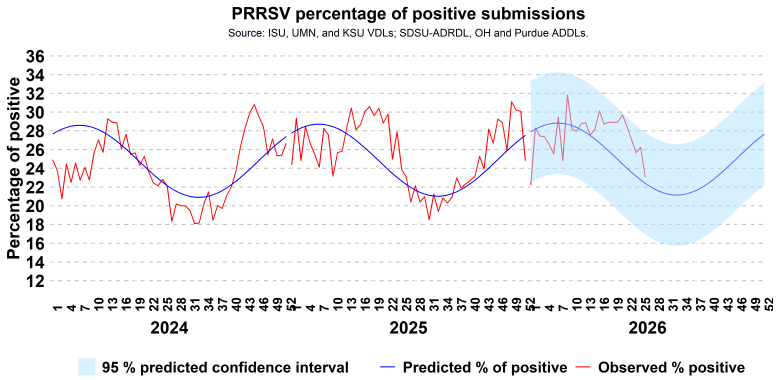
Advisory Group: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Davenport, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, Lauren Glowzenski, Brooke Kitting and Dustin Oedekoven.

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

Topic 1.1 – Detection of PRRSV RNA over time by RT-qPCR.







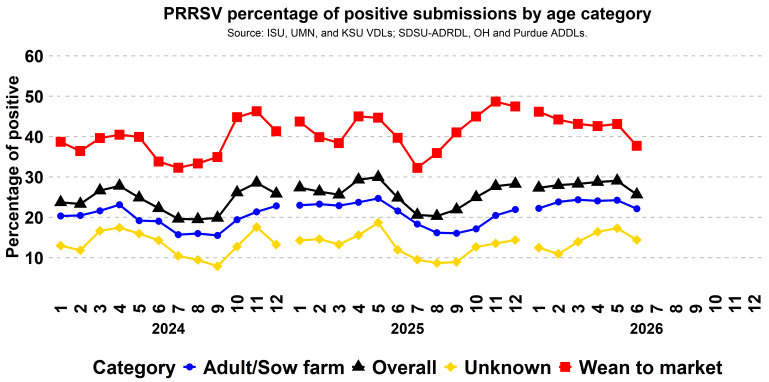
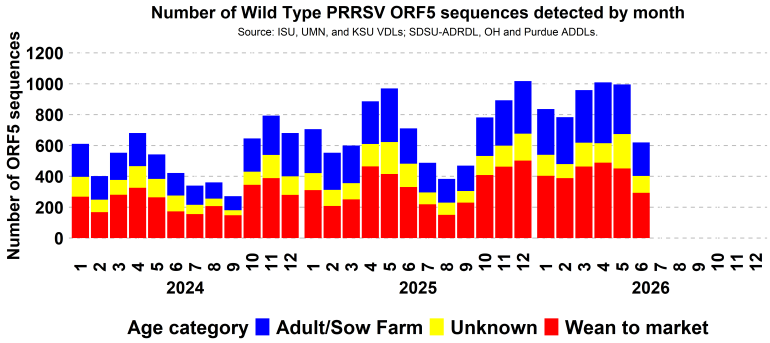


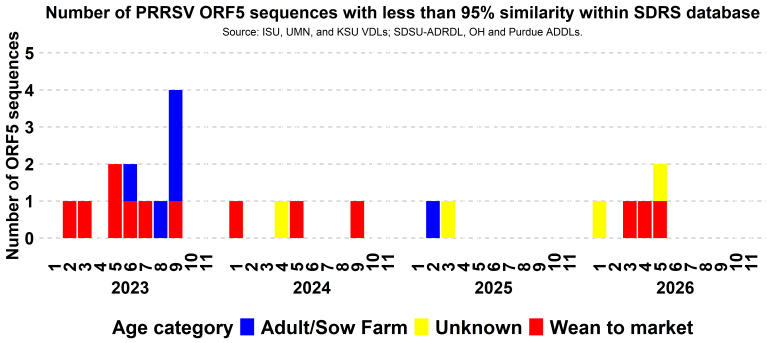
Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based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

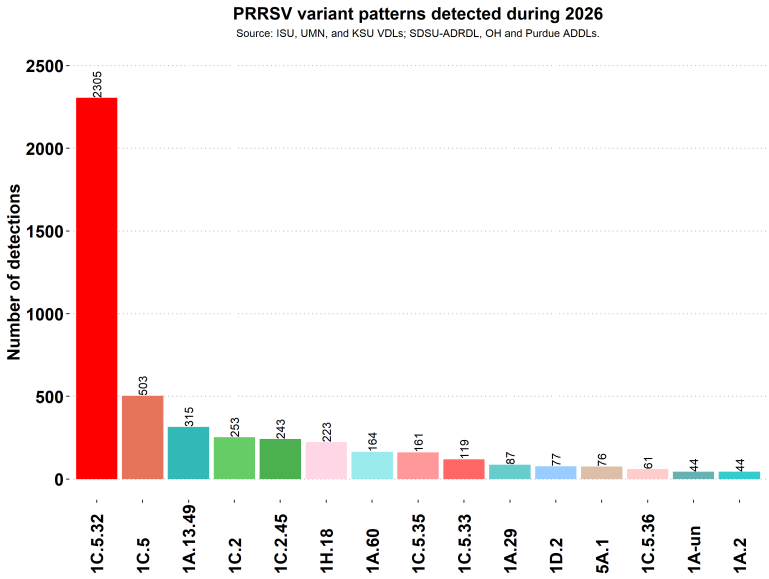
SDRS Advisory Group highlights:

- Overall, 25.65% of 6,826 cases tested PRRSV-positive in June, a moderate decrease from 29.08% of 7,231 in May.
  - Positivity in the adult/sow category in June was 22.15% (687 of 3,102), a moderate decrease from 24.25% (771 of 3,180) in May.
  - Positivity in the wean-to-market category in June was 37.71% (853 of 2,262), a substantial decrease from 43.12% (1,053 of 2,442) in May.
  - Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MO and MN.

Topic 1.2 – PRRSV ORF5 sequences detection over time







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 - 1394	1C.5 - 323	1A.13.49 - 215
IL	1C.5.32 - 253	1C.5 - 15	1C.5.35 - 11
IN	1C.5.35 - 51	1C.5.32 - 44	1A.54 - 30
KS	1C.5.32 - 5	1A.58 - 2	1A.2 - 1
MN	1C.5.32 - 307	1H.18 - 70	1C.5 - 34
MO	1C.5.32 - 104	1C.5 - 67	1C.2 - 17
NC	1C.2.45 - 145	1A.60 - 106	1A.32 - 36
NE	1C.5.33 - 86	1A.13.49 - 32	1C.5 - 31
OH	1C.5.35 - 70	1C.5.32 - 33	1A.13.49 - 8
OK	1C.5.32 - 18	1A.2 - 4	1E.1 - 2
SD	1C.2 - 19	1A.13.49 - 9	1C.5.32 - 6

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**.

Where Does Your PRRSV Sequence Fit?

- Compare your PRRSV ORF5 sequence with the SDRS database using the **SDRS BLAST tool**. For additional insights, explore the **PRRSV genotype dashboard**, which summarizes PRRSV genotype trends reported through SDRS;
- SDRS applies prospective variant classification while continuously updating historical records, ensuring that trend analyses reflect the most current data.

SDRS Advisory Group highlights:

- During June, the states with higher number of PRRSV 1C.5.32 detections were detected IA, MN, IL, MO, IN, NC, NE, KS, OH, OK (respective number of sequences: 183, 39, 17, 12, 8, 6, 3, 1, 1, 1);
- In June 1C.5.32 (276) was the PRRSV variant most detected in the U.S., followed by 1A.13.49 (70), and 1C.5 (59);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
  - May 2026: 1C.5.35 (OK), 1E.12.13 (OH), 1H.18 (CA), 1C.5.32 (KY), 1H.47 (OH)
  - June 2026: 1K.4 (IN), 1A.29 (MO), 1H.48 (PA)

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

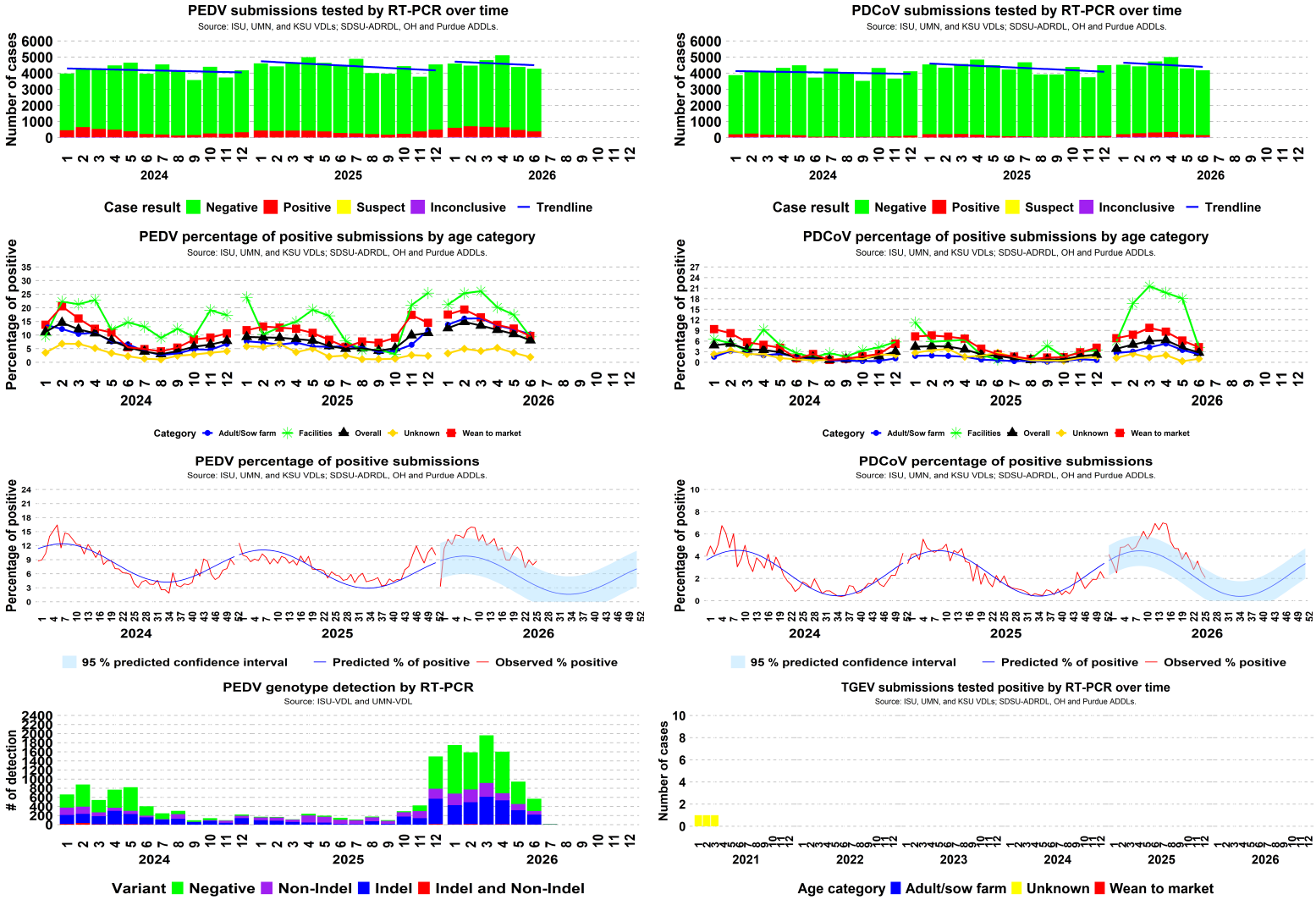


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection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

SDRS Advisory Group highlights:

- Overall, 8.09% of 4,279 cases tested PEDV-positive in June, a moderate decrease from 10.39% of 4,388 in May.
  - Positivity in the adult/sow category in June was 10.31% (164 of 1,591), similar to 12.06% (211 of 1,749) in May.
  - Positivity in the wean-to-market category in June was 9.66% (145 of 1,501), a moderate decrease from 12.37% (183 of 1,479) in May.
  - Positivity in the facilities category in June was 9.38% (18 of 192), a substantial decrease from 17.42% (27 of 155) in May.
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN.
  - Overall, 0% of 16 samples had mixed PEDV genotype detection in July, similar to 0.35% of 569 in June.
- Overall, 2.75% of 4,179 cases tested PDCoV-positive in June, similar to 4.16% of 4,301 in May.
  - Positivity in the adult/sow category in June was 2.26% (35 of 1,551), similar to 3.49% (60 of 1,721) in May.
  - Positivity in the wean-to-market category in June was 4.28% (62 of 1,449), similar to 6.14% (88 of 1,434) in May.
  - Positivity in the facilities category in June was 4.17% (8 of 192), a marked decrease from 18.06% (28 of 155) in May.
  - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in MO, IN, OH and NC.
- There was 0 positive case for TGEV RNA-PCR in June, 2026 over a total of 4,032 cases tested. It has been 64 months (with a total of 243,088 cases tested) since the last TGEV PCR-positive result.

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

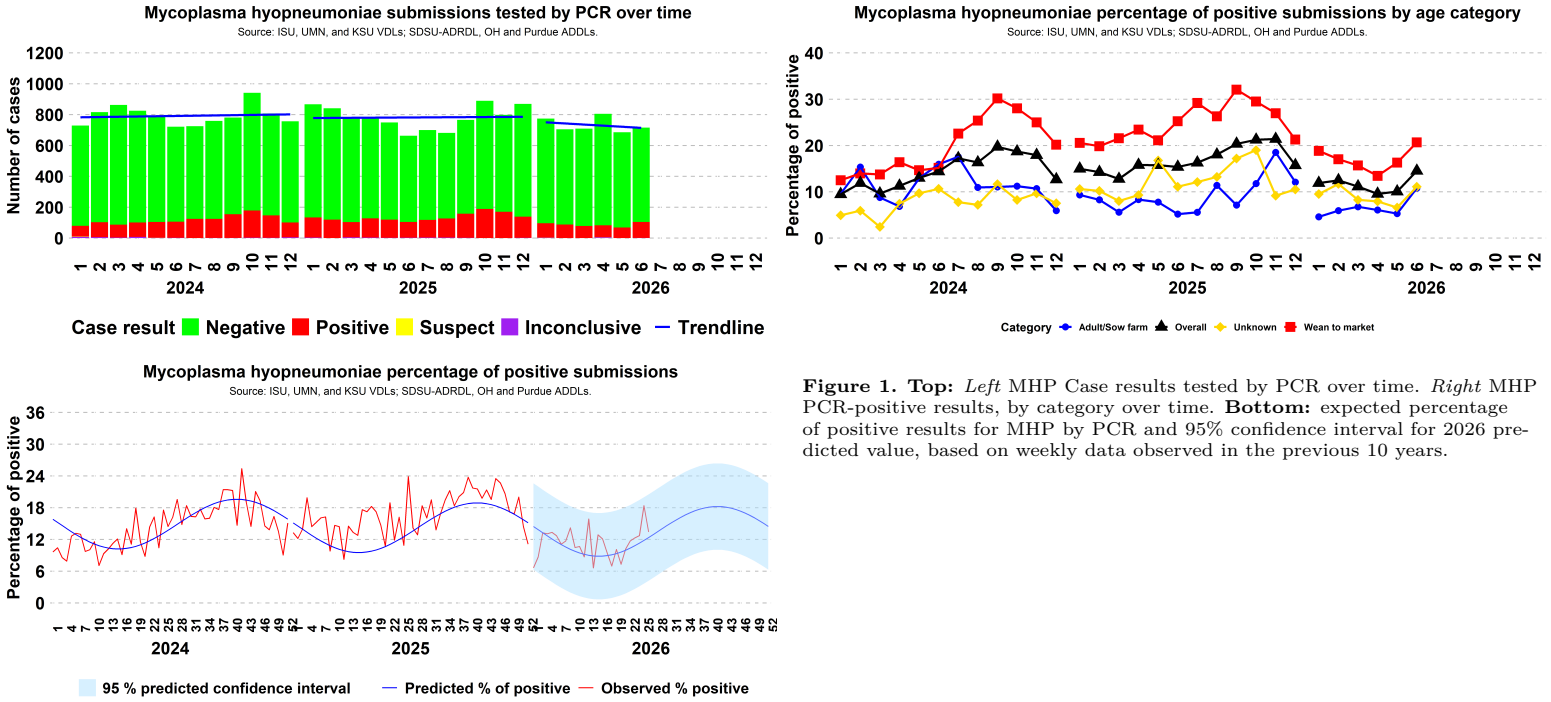
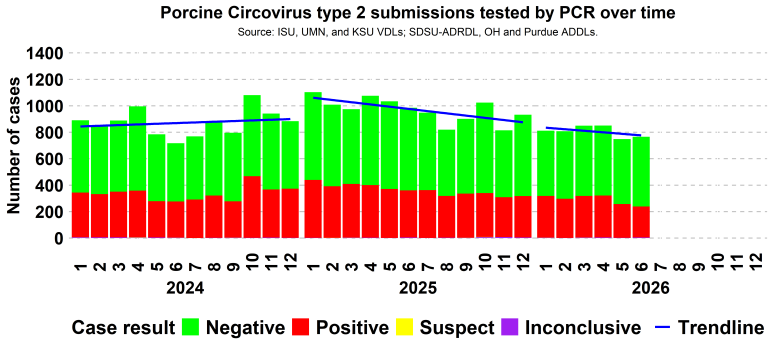


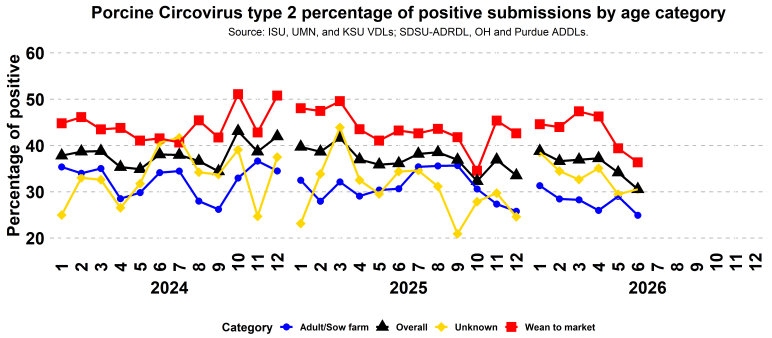
Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

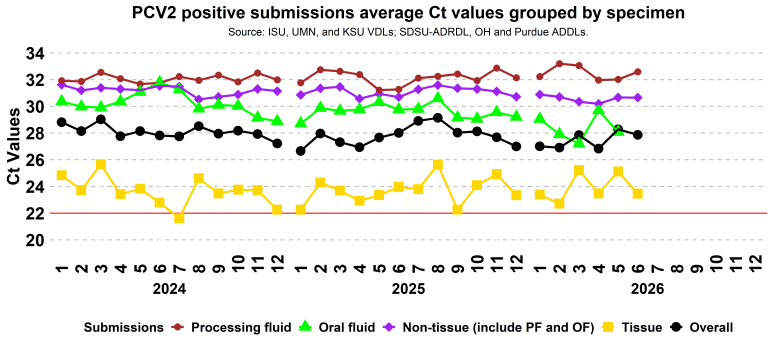
SDRS Advisory Group highlights:

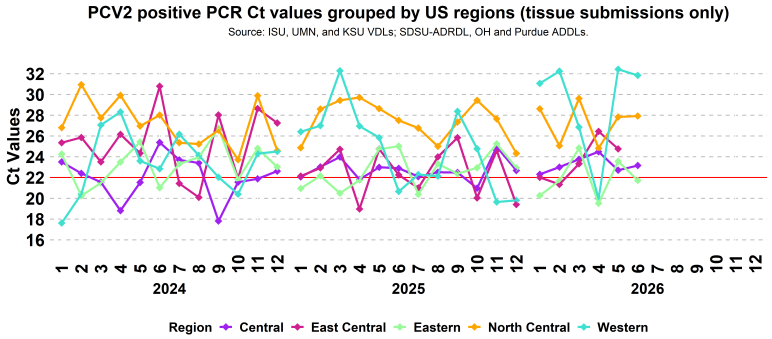
- Overall, 14.53% of 716 cases tested *M. hyopneumoniae*-positive in June, a moderate increase from 10.06% of 686 in May.
  - Positivity in the adult/sow category in June was 10.79% (34 of 315), a substantial increase from 5.3% (15 of 283) in May.
  - Positivity in the wean-to-market category in June was 20.68% (55 of 266), a moderate increase from 16.31% (46 of 282) in May.
  - Overall MHP-percentage of positive cases was was 3 standard deviations above state-specific baseline in MN.
  - Some of the Advisors suggested the uptick in MhP may reflect factors such as isolated situations or increased testing activity related to elimination efforts.

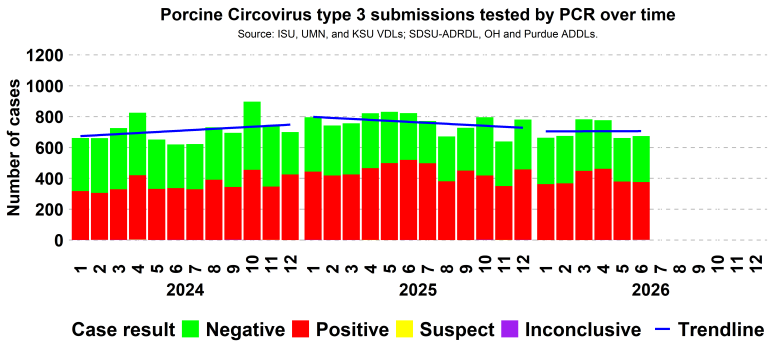
Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.











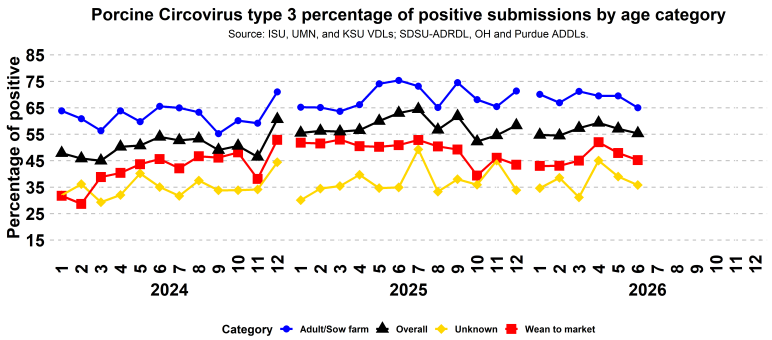


Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 30.55% of 766 cases tested PCV2-positive in June, a moderate decrease from 34.18% of 749 in May.
  - Positivity in the adult/sow category in June was 24.93% (88 of 353), a moderate decrease from 29.02% (83 of 286) in May.
  - Positivity in the wean-to-market category in June was 36.36% (124 of 341), a moderate decrease from 39.4% (145 of 368) in May.
  - In the month of June, the regions with the lowest PCV2 average Ct values in tissue submissions were East Central (8 submissions; average Ct 15.1), Eastern (15 submissions; average Ct 21.7), Central (33 submissions; average Ct 23.2), North Central (15 submissions; average Ct 27.9), and Western (7 submissions; average Ct 31.8).
- Overall, 55.34% of 674 cases tested PCV3-positive in June, similar to 57.1% of 662 in May.
  - Positivity in the adult/sow category in June was 65.07% (244 of 375), a moderate decrease from 69.52% (219 of 315) in May.
  - Positivity in the wean-to-market category in June was 45.26% (105 of 232), a moderate decrease from 47.92% (127 of 265) in May.

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

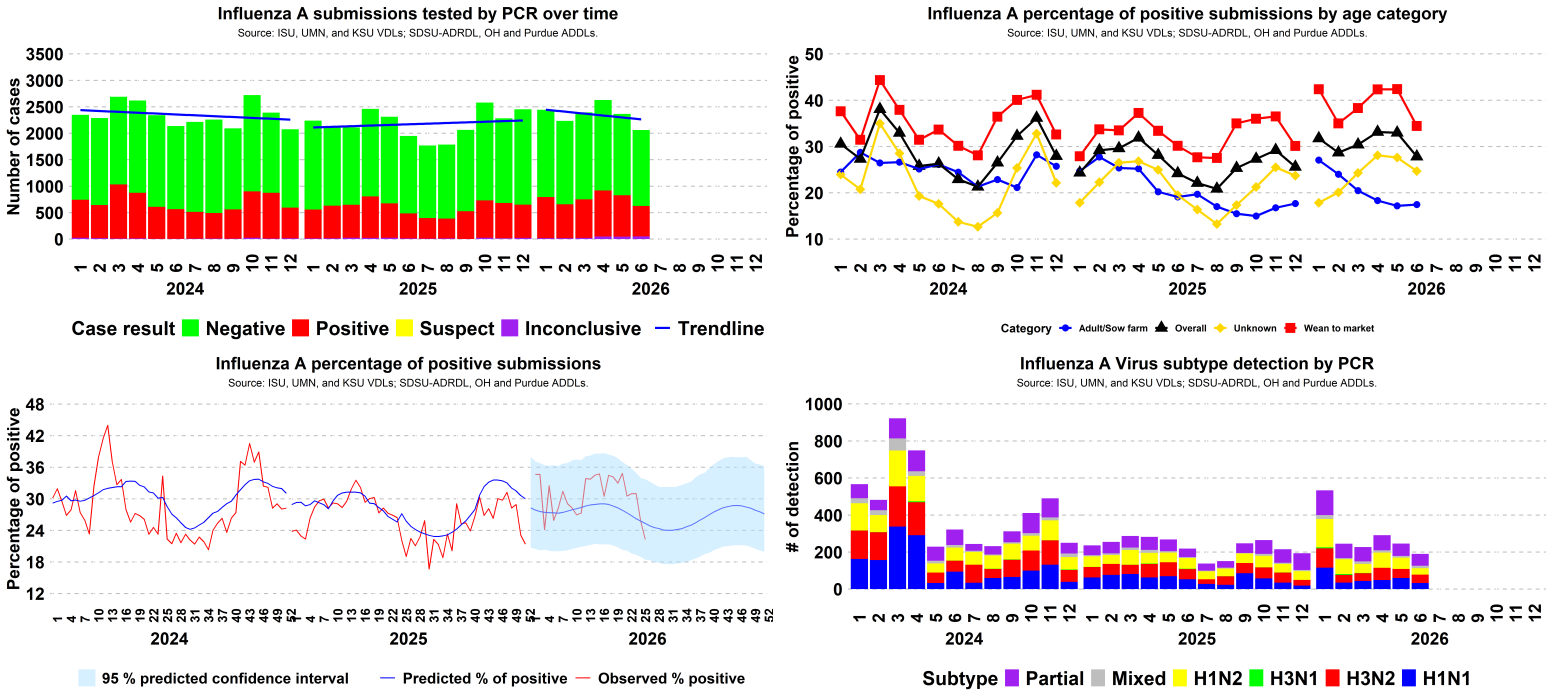
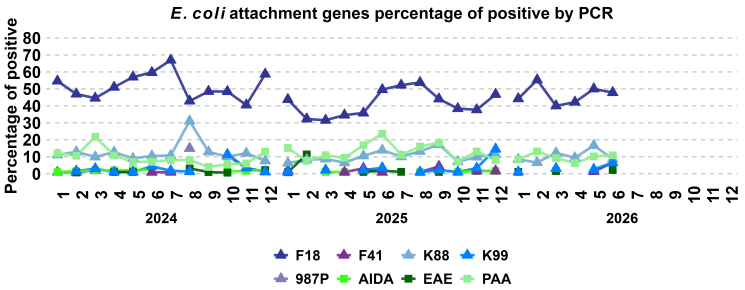


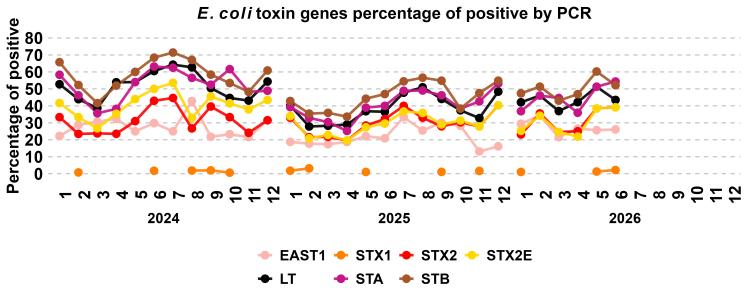
Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 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").

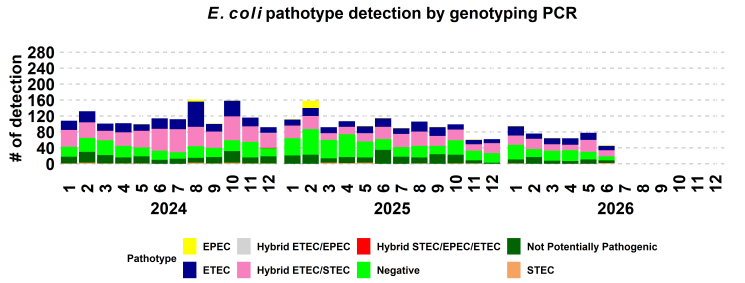
SDRS Advisory Group highlights:

- Overall, 27.84% of 2,062 cases tested IAV-positive in June, a substantial decrease from 32.97% of 2,366 in May.
  - Positivity in the adult/sow category in June was 17.47% (83 of 475), similar to 17.2% (91 of 529) in May.
  - Positivity in the wean-to-market category in June was 34.45% (350 of 1,016), a substantial decrease from 42.39% (521 of 1,229) in May.
  - Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states.
- Overall, 6.84% of 190 samples had mixed subtype detection in June, a moderate increase from 3.66% of 246 in May.

Topic 6 – Detection of *E. coli* DNA 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 - 51	EAST1 - 12	F18;EAST1;LT;STa;STb;Stx2e - 12
IL	F18;LT;STa;STb;Stx2e - 6	F18;EAST1;LT;STb - 1	F18;EAST1;LT;STb;Stx2e - 1
IN	F18;LT;STa;STb;Stx2e - 8	F18;EAST1;LT;STb - 3	F18;STa;STb;Stx2e - 1
KS	F18;EAST1;LT;STa;STb - 1		
MN	F18;LT;STa;STb;Stx2e - 9	K88;Paa;EAST1;LT;STa;STb - 4	K88;EAST1;LT;STb - 3
MO	F18;LT;STa;STb;Stx2e - 5	K88;STa;STb - 2	EAST1 - 1
NC	F18 - 3	F18;LT;STa;STb;Stx2e - 3	F18;EAST1;LT;STa;STb - 2
NE	F18;LT;STa;STb;Stx2e - 6	K88;STa;STb - 2	F18;EAST1;LT;STa;STb - 1
OH	F18;LT;STa;STb - 1	F18;LT;STa;STb;Stx2e - 1	F18;Paa;EAST1 - 1
OK	F18;LT;STa;STb;Stx2e - 1		
SD	K88;Paa;EAST1;LT;STa;STb - 2	K88;STa;STb - 2	F18;LT;STa;STb;Stx2e - 1

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 along with their respective detection counts 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, 46 samples were tested for *E. coli* PCR in June.
  - In June, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (15 detections), ETEC (11 detections), and Not Potentially Pathogenic (7 detections).
  - In June, the *E. coli* attachment genes with higher detection rate were F18 (47.83%), PAA (10.87%), and K88 (8.70%).
  - In June, the *E. coli* toxin genes with higher detection rate were STA (54.35%), STB (52.17%), and LT (43.48%).

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

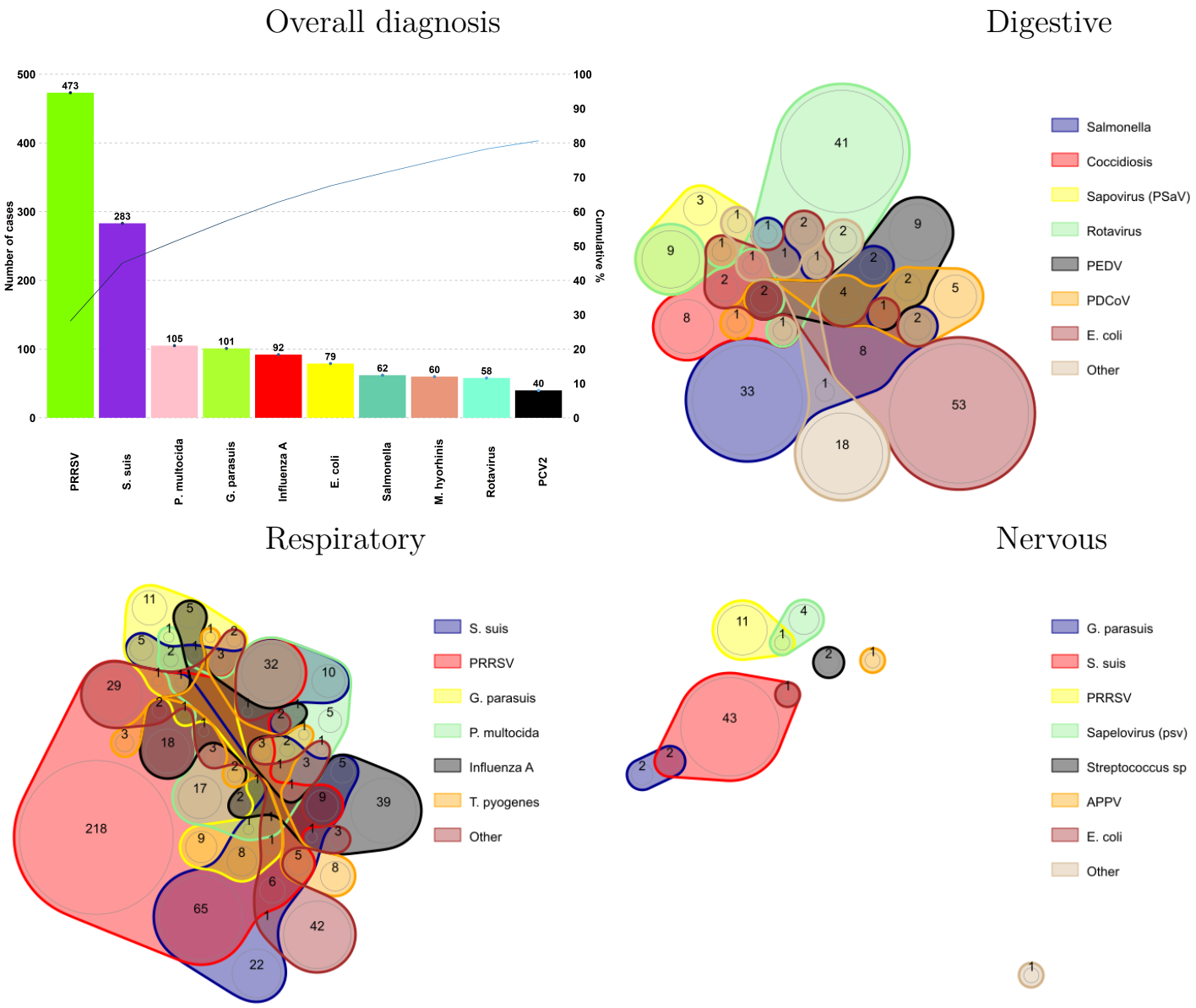


Figure 4. ISU-VDL and OH-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. 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 May 01, 2026 to June 26, 2026

SDRS Advisory Group highlights:

• PRRSV (473) led cases with confirmed etiology, followed by *S. suis* (283), and *P. multocida* (105). PRRSV (441 of 1012) led the number of confirmed respiratory diagnoses, *E. coli* (72 of 272) lead the number of confirmed digestive diagnoses, and *S. suis* (46 of 71) led the number of confirmed neurological diagnoses.

Note: *The SDRS is a collaborative project among multiple VDLs in the US swine industry. The VDL collaborators and industry partners are all invited to submit content to share on this bonus page related to disease prevention, control, and management. Stay tuned for more content in future editions.*

Ongoing evolution of Variant 1C.2 and Creation of Variant 1C.2.45

Kim VanderWaal[1], Mariana Kikuti[1], Cesar A, Corzo[1], Quyen Le[2], Daniel Linhares[2], Giovani Trevisan[2]
[1]University of Minnesota; [2]Iowa State University;

What are genetic variants?

Genetic variants are groups of closely related sequences (on average, <2.5% different on ORF5) that provide a finer-scale level of classification within PRRSV-2 sub-lineages. These provide a label that can facilitate communication and monitoring of different PRRSV-2 viruses circulating in a farm, system, or region. Compared to RFLPs, variant classifications are more reliable for determining relatedness (i.e., whether virus A is the same or different than virus B), and are useful for epidemiological investigations, such as determining possible sources of introduction and tracking between-farm spread. The UMN, SDSU, and ISU Veterinary Diagnostic Labs, MSHMP, and SDRS have capabilities to classify sequences by variant. The PRRS-Loom webtool (https://stemma.shinyapps.io/PRRSLoom-variants/) is also available for end-users to classify their own sequences and to report general epidemiological trends.

Because PRRSV-2 evolves so rapidly, it is essential to continually update the variant nomenclature to keep up with evolution. Thus, new sequence data is examined every three months to check for new variants, evaluate whether existing variants need to be split, and update reference sequences.

Variant 1C.2 is amongst the most prevalent and diverse variants in the U.S.

Variant 1C.2 has been amongst the most prevalent and diverse genetic variants in the U.S. for the past several years. Monitoring of 1C.2 occurrence through time has revealed six sub-groups within the 1C.2 variant that have significantly diverged from the parental 1C.2 group, though it is unknown at this time if any of these groups of viruses have different clinical impacts than 1C.2.
Because of the genetic distinctiveness of these sub-groups and continued epidemiological significance of 1C.2, six new variant IDs have been recently created to label these sub-groups to facilitate communication, monitoring, and investigations of these variants. Standard criteria for splitting variants include that the new variant must be a minimum of >3% and a median of >5% different (ORF5) from the parent variant1. Most of the 1C.2 offshoots have had limited circulation so far, except for 1C.2.45.

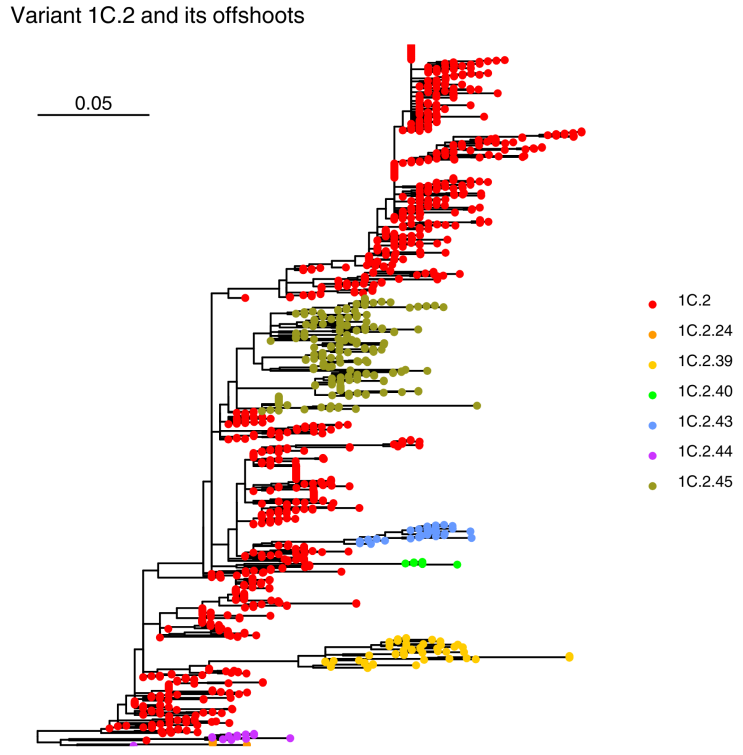


Figure 1. Phylogenetic tree of variant 1C.2 and its offshoots

This updated classification framework is applied within SDRS to support consistent tracking of these variants across both historical and prospective sequences. Building on this approach, SDRS detection data further illustrate the broader activity of variant 1C.2 and its offshoots ever since its emergence in 2014. As of June 2026, SDRS has recorded 3,051 detections of variant 1C.2 and its offshoots. Annual counts show that detections have been reported consistently over time, with noticeable increases in several years, including higher totals observed in the periods around 2021-2022 and again in 2024-2025. Overall, these data show sustained detection of 1C.2 and its related groups over time within the SDRS dataset (*Figure 2*).

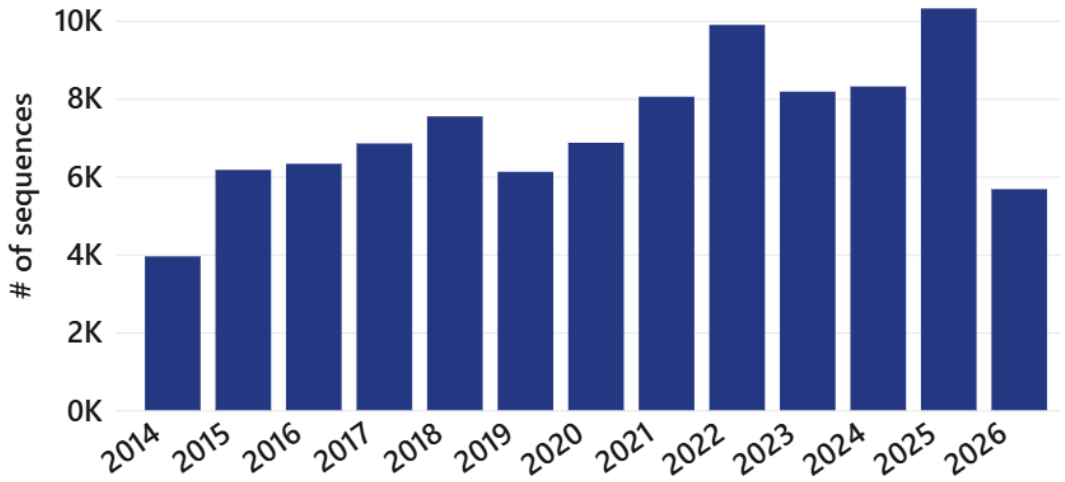


Figure 2. Detection of variant 1C.2 and its offshoots over time

Variant 1C.2.45 is already widespread.

The newly created **1C.2.45** variant includes >250 sequences across 13 systems and 5 states, based on data from MSHMP . Thus, the creation of a new variant ID to track this genetically distinct group means that some previous 1C.2 sequences (from 2022 onwards) will have the ".45" designation added to their variant ID (1C.2 → 1C.2.45) to indicate their membership in this group.

As of June 2026, 1C.2.45 has been detected in Iowa, Illinois, Minnesota, Missouri, and North Carolina, affecting 39 sites in the past six months. More information on the circulation of 1C.2.45 can be found in the Variants Under Monitoring report (https://mshmp.umn.edu/prrsv-variant-monitoring)

In addition to recent activity, SDRS records show a clear order of appearance across states. The earliest detection occurred in Iowa (wean-to-market) on December 22nd, 2021. This was followed by Missouri in May 2022 and Illinois in January 2023. Additional detections were later recorded in wean-to-market sites in states such as Minnesota and Indiana, followed by detections in adult/sow systems in North Carolina. More recent detections extend into 2026, including Nevada and Virginia .

Following this sequence of detections, the number of 1C.2.45 detections varies across states, with a larger proportion reported from a few states. Iowa accounts for the highest number of detections (501), followed by North Carolina (163) and Illinois (46), while lower counts are reported from Missouri (25), Indiana (14), and Minnesota (6). More recent detections in Nevada and Virginia remain limited, with one detection each, aligning with their later appearance in the SDRS records (*Figure 3*).

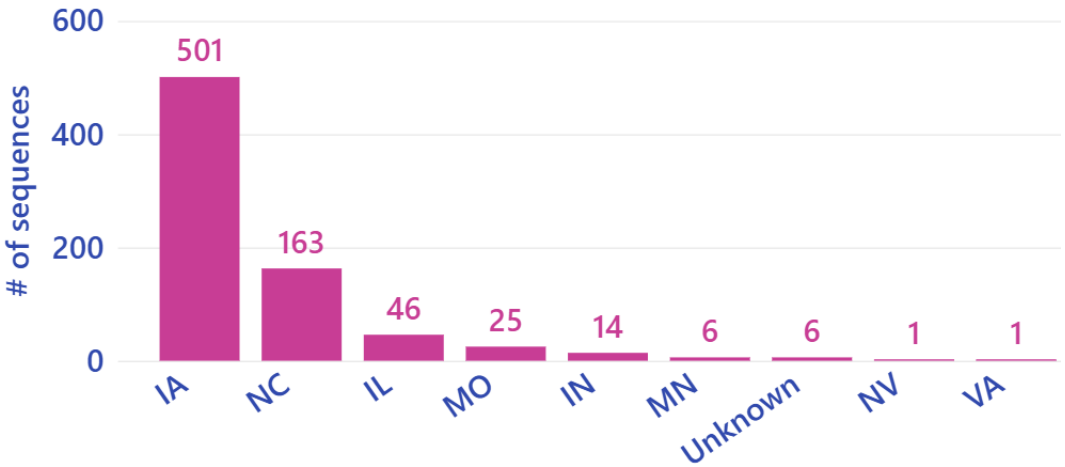


Figure 3. Detections of variant 1C.2.45 at state level

Do my sequences belong to 1C.2.45 or any other of the new variants?

The PRRS-Loom webtool (https://stemma.shinyapps.io/PRRSLoom-variants/) allows any user to upload their sequences (no data is retained by the webtool) for variant classification. In the webtool, sequences can be uploaded as a FASTA file or copy-pasted into the window. Sequences that cannot be assigned to any variant with >0.25 probability listed as "unclassified."

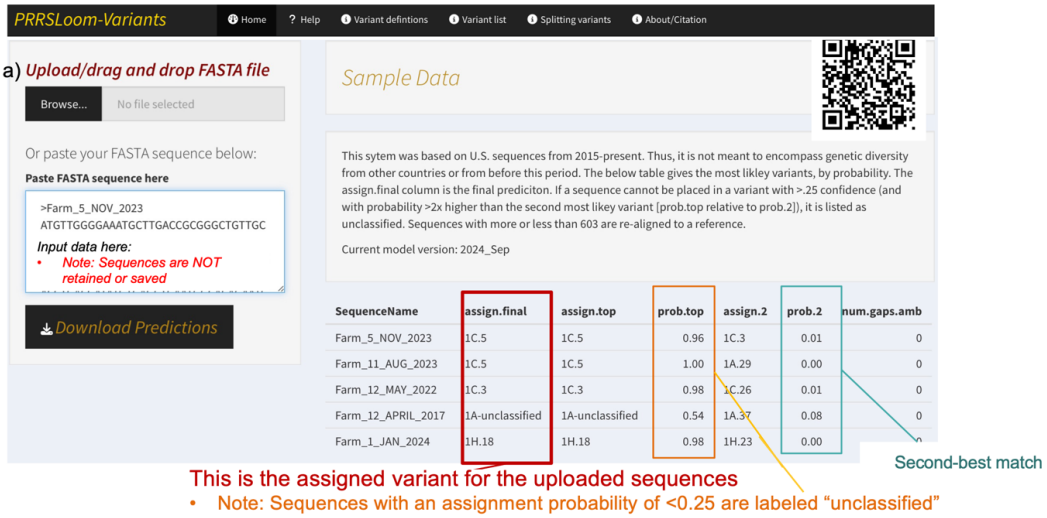


Figure 4. PRRSLoom-Variants webtool (https://stemma.shinyapps.io/PRRSLoom-variants/)

Have sequences similar to mine been detected in the past?

To gain a more detailed view of where and when closely related sequences have been detected, compare your PRRSV ORF5 sequence with the SDRS database using the SDRS BLAST tool (*Figure 5*).

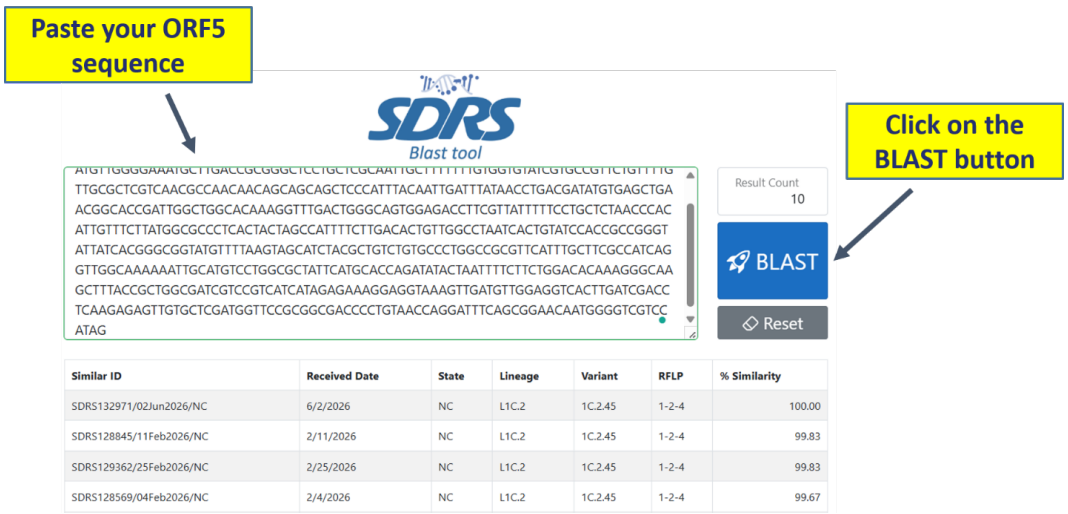


Figure 5. SDRS Blast tool (https://fieldepi.org/sdrs/blast-tool/)

Stay informed

Variant nomenclature changes are announced in the PRRS-Loom webtool and nomenclature briefs are distributed to a listserv. Overall variant occurrences and trends are tracked across multiple sources. The SDRS PRRSV genotype dashboard summarizes current sequence-level trends based on submissions from six diagnostic laboratories, offering a comprehensive overview of geographic distribution of variants. The PRRSV Variants Under Monitoring report summarizes trends in new sites affected in the previous 6 months, providing current site-level estimates of disease burden with categorization of variants according to their recent number of new site detections.

[1]See the paper: VanderWaal *et al.* 2025. PRRSV-2 variant classification: a dynamic nomenclature for enhanced monitoring and surveillance. mSphere 10:e00709-24. https://doi.org/10.1128/msphere.00709-24