

Swine Disease Reporting System

Report # 102 (August 04, 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-Ferreira, 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, Ryan Yanez

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 July 31, 2026.

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

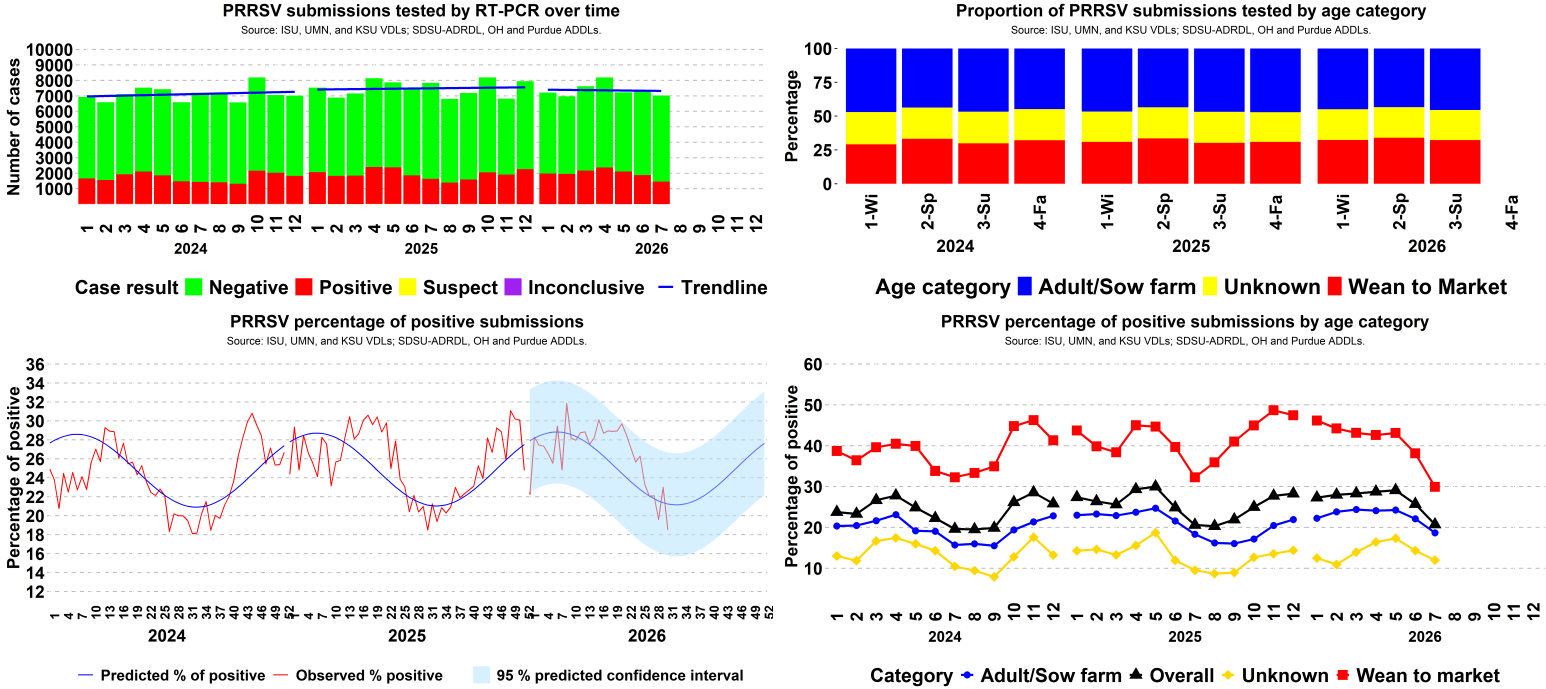


Figure 1. Top: *Left:* Results of PRRSV RT-PCR cases over time; *Right:* Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom:** *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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, 20.73% of 7,025 cases tested PRRSV-positive in July, a moderate decrease from 25.72% of 7,275 in June.
 - Positivity in the adult/sow category in July was 18.7% (597 of 3,193), a moderate decrease from 22.14% (732 of 3,306) in June.
 - Positivity in the wean-to-market category in July was 29.93% (666 of 2,225), a substantial decrease from 38.14% (913 of 2,394) in June.
 - Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, MO and IL.

Topic 1.2 – PRRSV ORF5 sequences detection over time

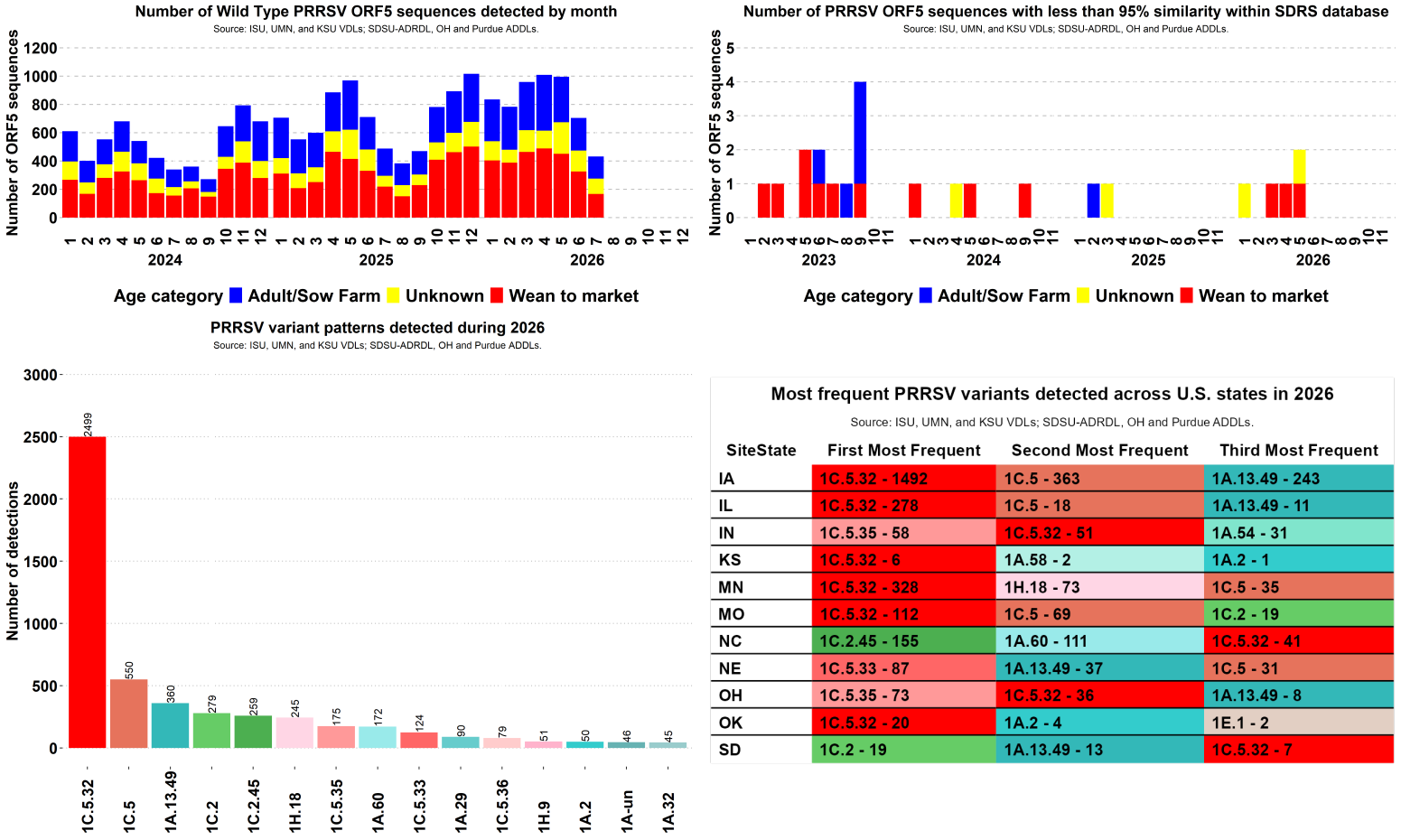


Figure 1. Top: Left: Number of PRRSV ORF5 sequences detected by age category; **Right:** Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher 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 July, the states with higher number of PRRSV 1C.5.32 detections were detected IA, IL, MN, MO, IN, NC, OH, KS, OK, SD (respective number of sequences: 78, 23, 15, 8, 7, 3, 2, 1, 1, 1);
- In July 1C.5.32 (139) was the PRRSV variant most detected in the U.S., followed by 1C.5 (37), and 1A.13.49 (35);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
 - June 2026: 1K.4 (IN), 1A.29 (MO), 1H.48 (PA)
 - July 2026: 1A.29 (LA), 1C.2 (TN)

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

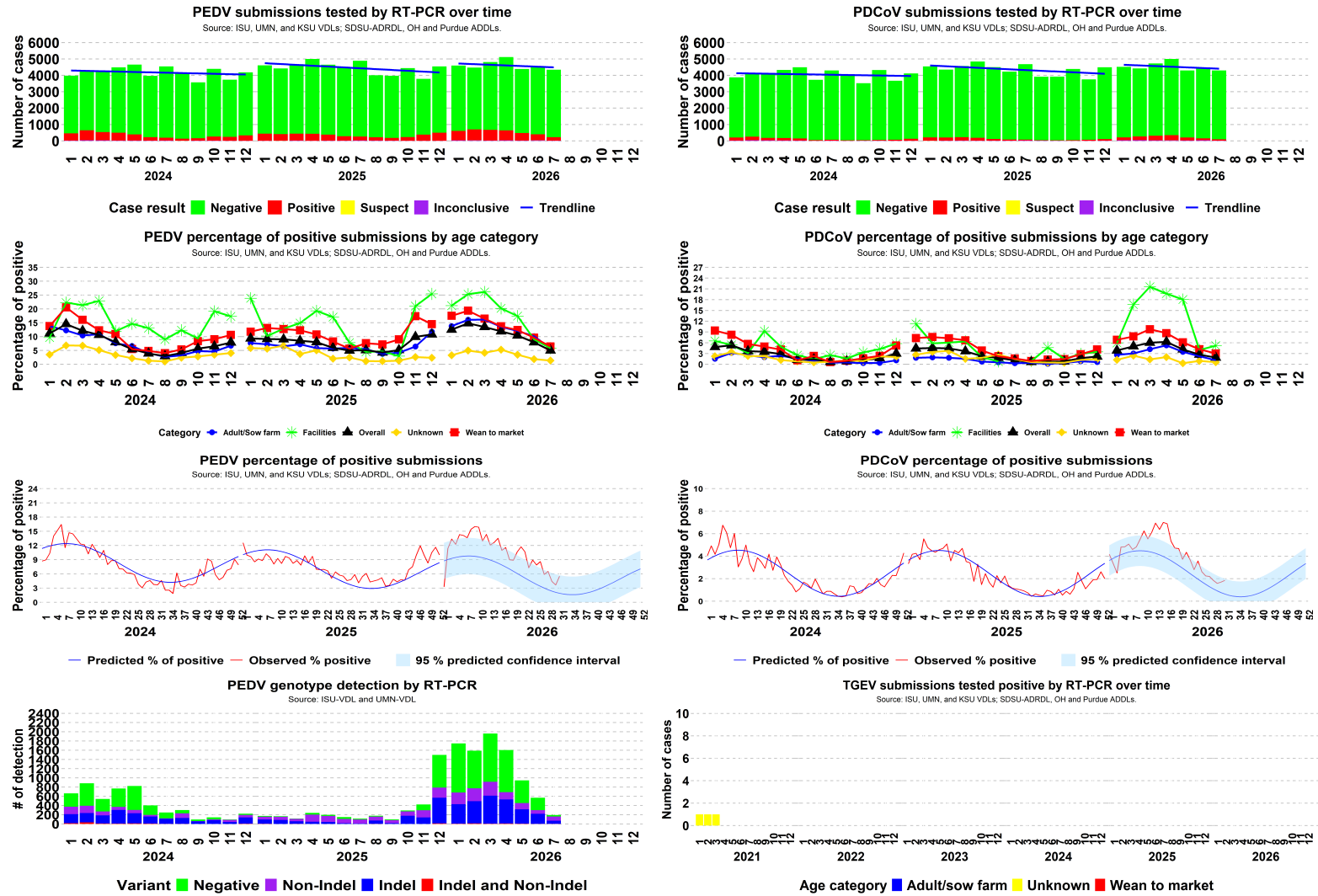


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype detection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

SDRS Advisory Group highlights:

- Overall, 5% of 4,342 cases tested PEDV-positive in July, a moderate decrease from 7.96% of 4,523 in June.
 - Positivity in the adult/sow category in July was 5.8% (89 of 1,534), a moderate decrease from 10.13% (170 of 1,678) in June.
 - Positivity in the wean-to-market category in July was 6.43% (105 of 1,634), a moderate decrease from 9.61% (152 of 1,582) in June.
 - Positivity in the facilities category in July was 5.84% (9 of 154), a moderate decrease from 9.05% (18 of 199) in June.
 - Overall PEDV-percentage of positive cases was within state-specific baselines in all 11 monitored states.
 - Overall, 0.52% of 193 samples had mixed PEDV genotype detection in July, similar to 0.35% of 569 in June.
- Overall, 1.86% of 4,296 cases tested PDCoV-positive in July, similar to 2.69% of 4,420 in June.
 - Positivity in the adult/sow category in July was 1.13% (17 of 1,510), similar to 2.26% (37 of 1,636) in June.
 - Positivity in the wean-to-market category in July was 3.02% (49 of 1,623), similar to 4.19% (64 of 1,529) in June.
 - Positivity in the facilities category in July was 5.19% (8 of 154), similar to 4.02% (8 of 199) in June.
 - Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in OK.
- There was 0 positive case for TGEV RNA-PCR in July, 2026 over a total of 4,177 cases tested. It has been 65 months (with a total of 247,225 cases tested) since the last TGEV PCR-positive result.

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

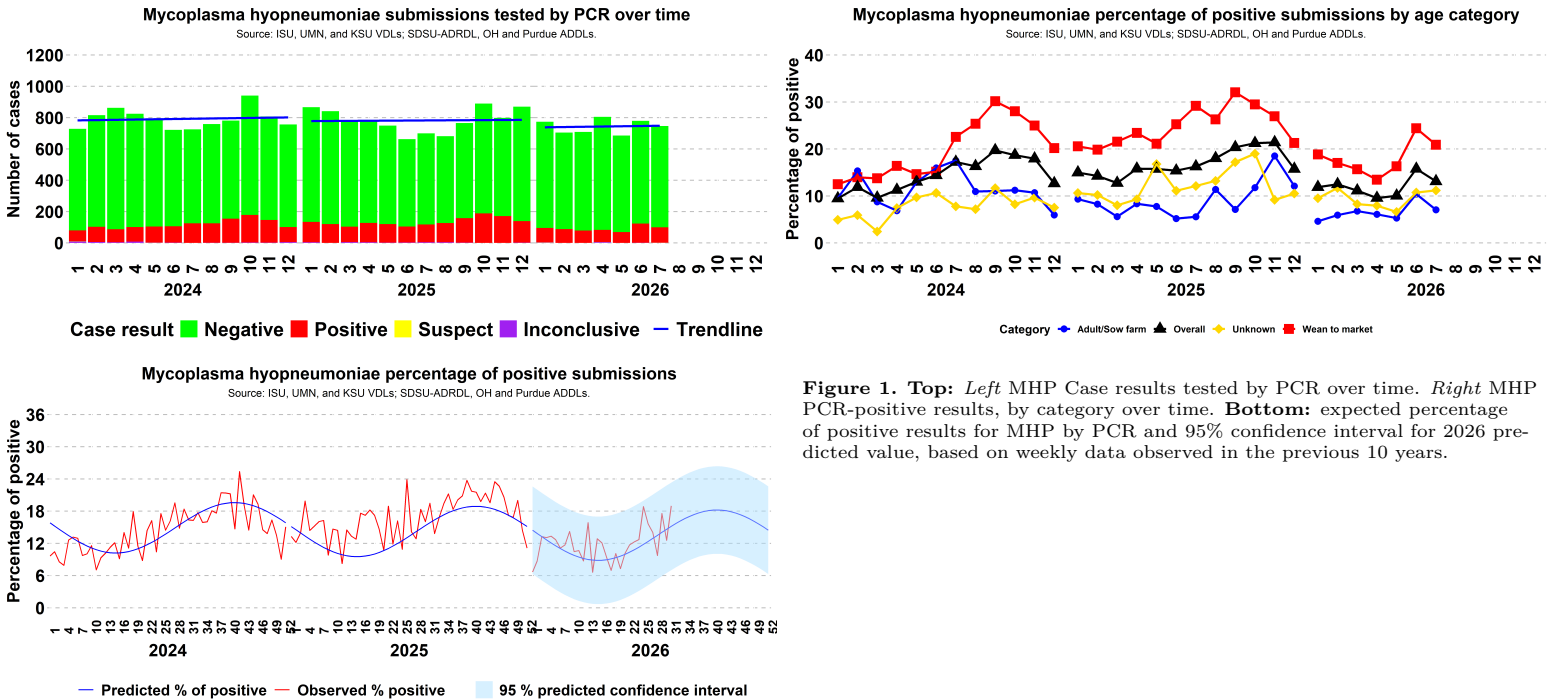


Figure 1. Top: *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

SDRS Advisory Group highlights:

- Overall, 13.12% of 747 cases tested *M. hyopneumoniae*-positive in July, a moderate decrease from 15.77% of 780 in June.
- Positivity in the adult/sow category in July was 7.06% (23 of 326), a moderate decrease from 10.42% (35 of 336) in June.
- Positivity in the wean-to-market category in July was 20.91% (60 of 287), a moderate decrease from 24.41% (72 of 295) in June.
- 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.

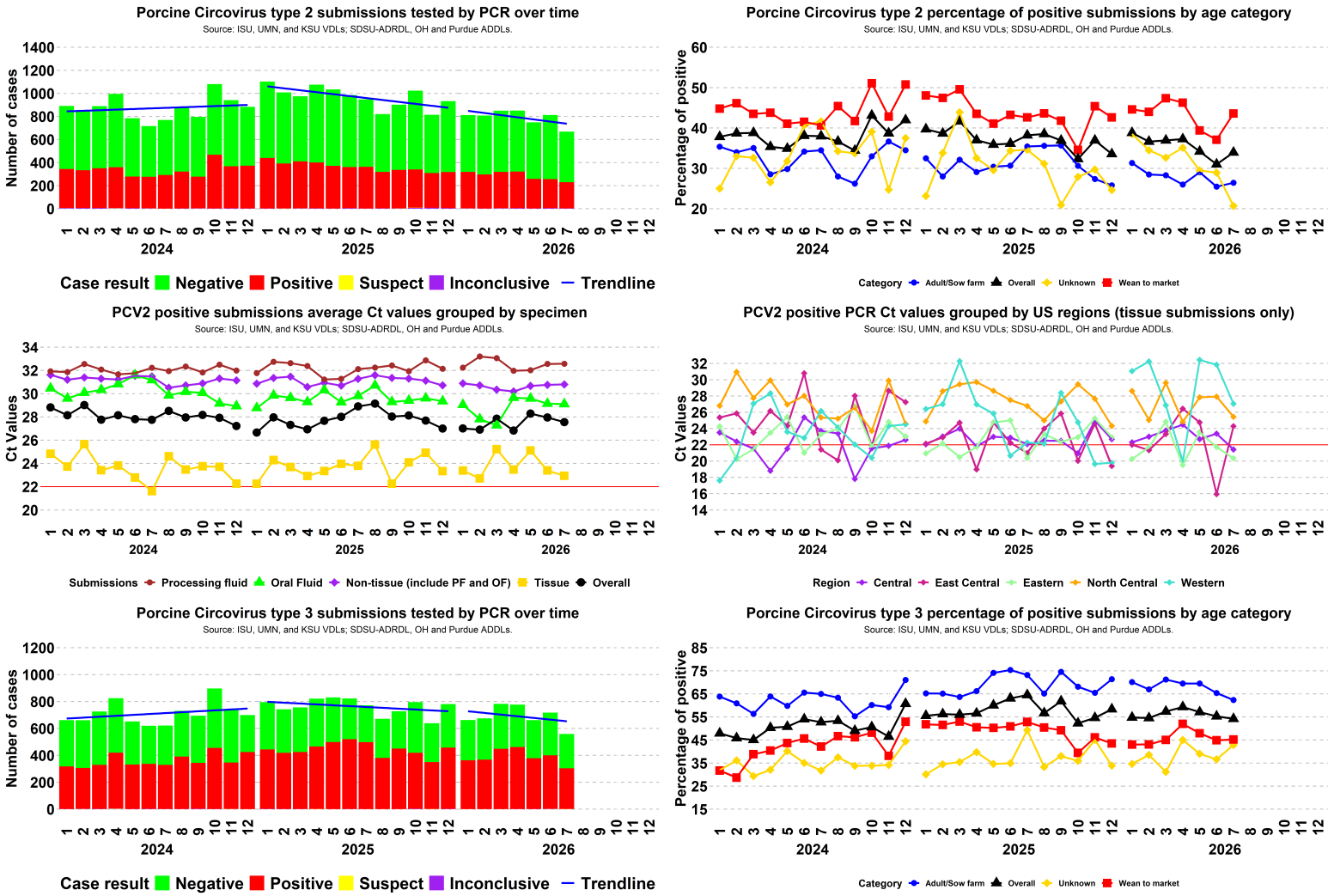


Figure 1. Top: Left: Results of PCV2 PCR cases over time; **Right:** PCV2 PCR-positive results, by category over time. **Middle: Left:** Average Ct values of PCV2 submissions by specimen; **Right:** Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 33.93% of 669 cases tested PCV2-positive in July, a moderate increase from 31% of 813 in June.
 - Positivity in the adult/sow category in July was 26.42% (79 of 299), similar to 25.47% (95 of 373) in June.
 - Positivity in the wean-to-market category in July was 43.59% (136 of 312), a substantial increase from 37.09% (135 of 364) in June.
- In the month of July, the regions with the lowest PCV2 average Ct values in tissue submissions were Eastern (17 submissions; average Ct 20.3), Central (38 submissions; average Ct 21.4), East Central (16 submissions; average Ct 24.3), North Central (7 submissions; average Ct 25.4), and Western (10 submissions; average Ct 27).
- Overall, 54.2% of 559 cases tested PCV3-positive in July, similar to 55.29% of 718 in June.
 - Positivity in the adult/sow category in July was 62.33% (187 of 300), a moderate decrease from 65.39% (257 of 393) in June.
 - Positivity in the wean-to-market category in July was 45.24% (95 of 210), similar to 44.88% (114 of 254) in June.
- Some of the Advisors suggested that interactions with other pathogens and vaccine effectiveness may be important factors to consider when interpreting PCV2 trends.

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

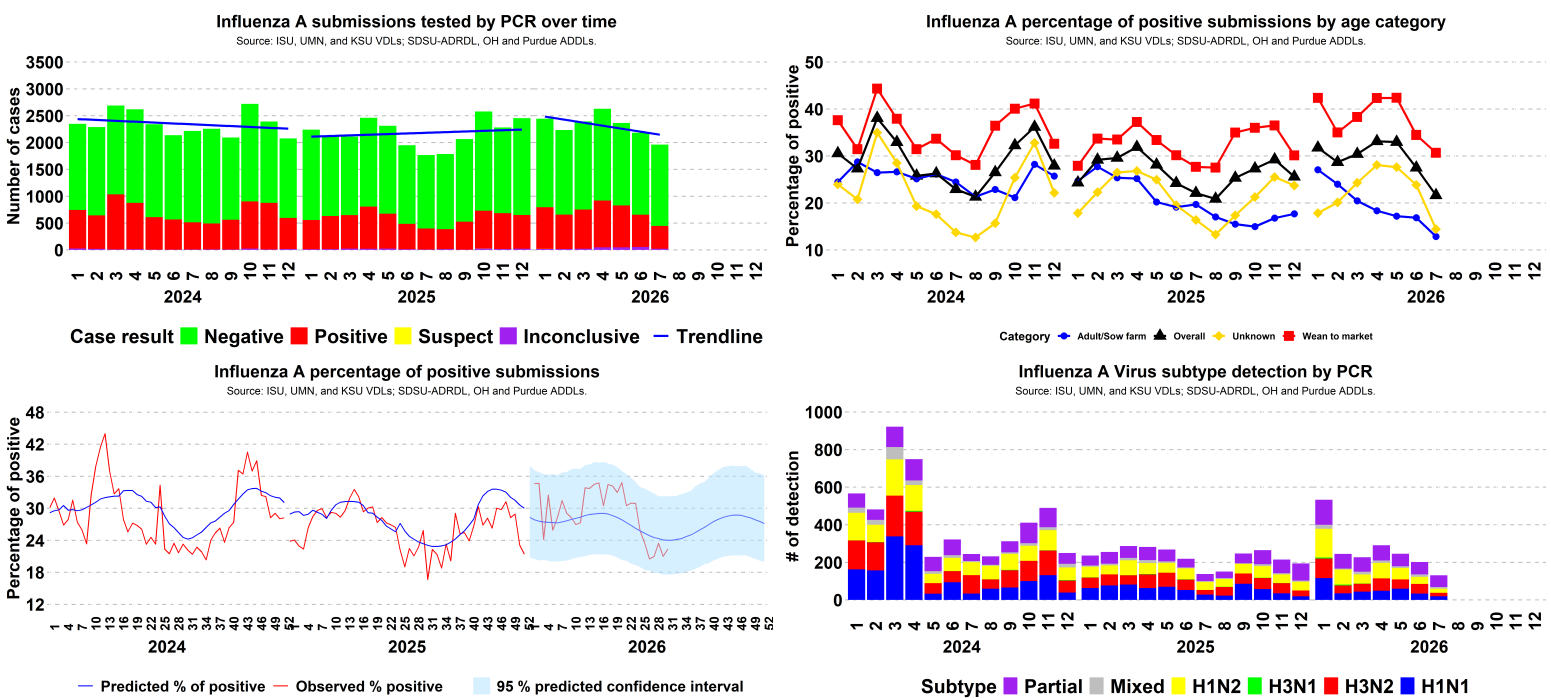
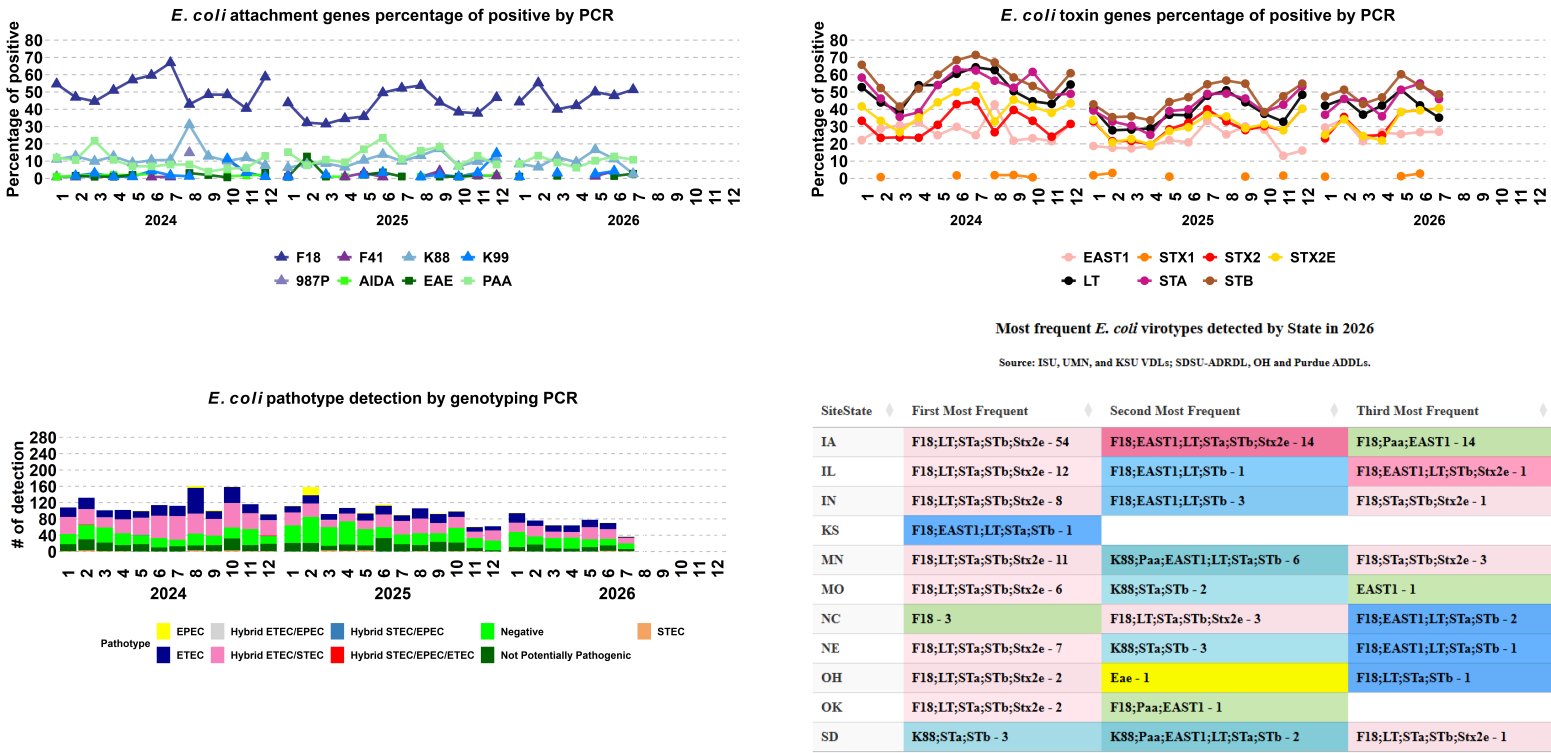


Figure 1. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 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, 21.65% of 1,963 cases tested IAV-positive in July, a substantial decrease from 27.5% of 2,182 in June.
 - Positivity in the adult/sow category in July was 12.86% (63 of 490), a moderate decrease from 16.87% (84 of 498) in June.
 - Positivity in the wean-to-market category in July was 30.69% (282 of 919), a moderate decrease from 34.48% (371 of 1,076) in June.
 - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA, OK and OH.
- Overall, 6.87% of 131 samples had mixed subtype detection in July, similar to 6.44% of 202 in June.

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



Education Material:

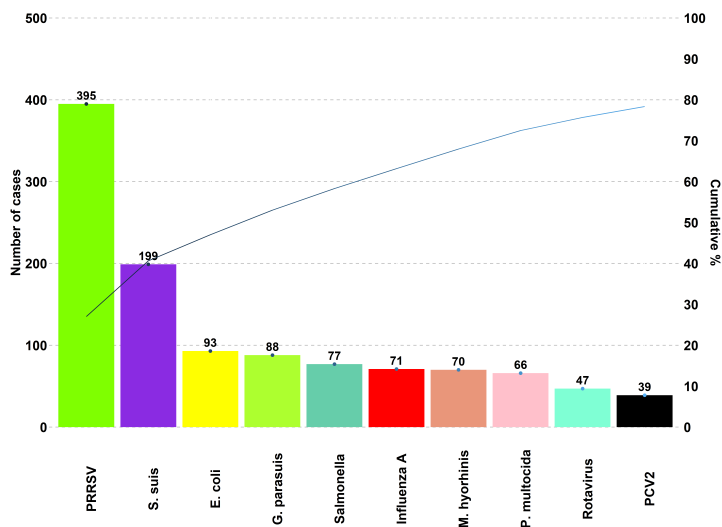
- Click on the links here to access the [E. coli PCR Genotyping Interpretation Tool](#)
- Attachment genes:** Fimbriae – F18, K88(F4), K99(F5), 987P(F6), F41; Adhesins – EAE (Intimin), PAA, AIDA
- Toxin genes:** Heat-labile – LT; Heat-stable – STa and STb; Shiga toxins – Stx1, Stx2 and Stx2e; and EAST1
- 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:

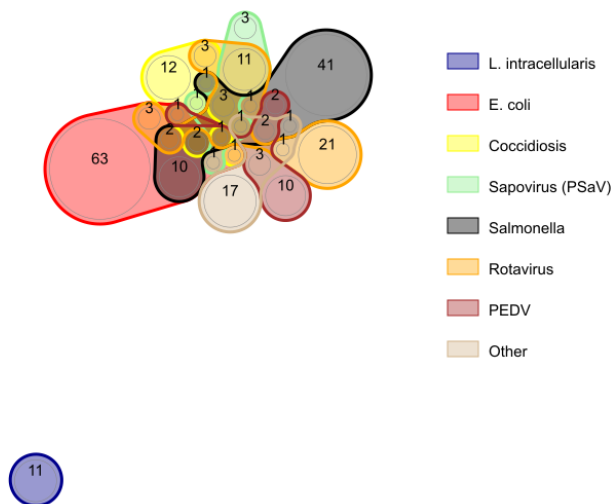
- Overall, 37 samples were tested for *E. coli* PCR in July.
 - In July, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (14 detections), Not Potentially Pathogenic (5 detections), and ETEC (2 detections).
 - In July, the *E. coli* attachment genes with higher detection rate were F18 (51.35%), PAA (10.81%), and EAE (2.70%).
 - In July, the *E. coli* toxin genes with higher detection rate were STB (48.65%), STA (45.95%), and STX2 (40.54%).

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

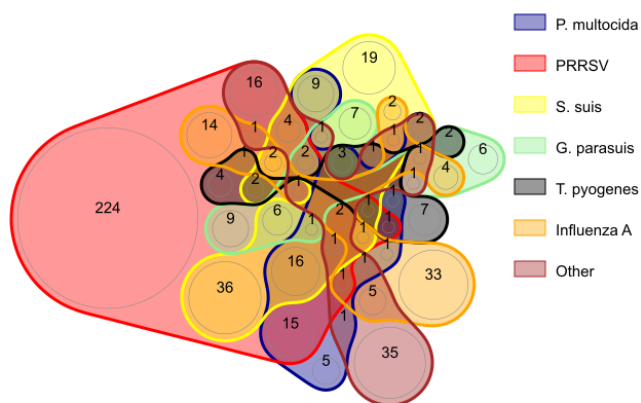
Overall diagnosis



Digestive



Respiratory



Nervous

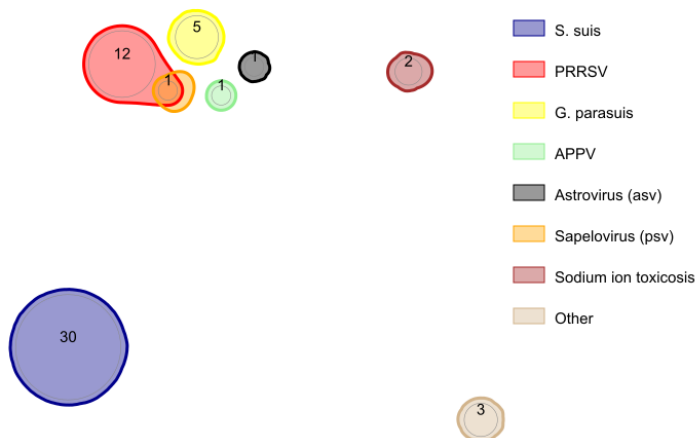


Figure 4. ISU-VDL and OH-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. 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 June 01, 2026 to July 29, 2026

SDRS Advisory Group highlights:

- PRRSV (395) led cases with confirmed etiology, followed by *S. suis* (199), and *E. coli* (93). PRRSV (361 of 760) led the number of confirmed respiratory diagnoses, *E. coli* (84 of 295) lead the number of confirmed digestive diagnoses, and *S. suis* (30 of 56) 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.

MSHMP and SDRS complementary programs for a similar purpose

MSHMP and SDRS Teams

Cesar A. Corzo¹, Quyen Le², Daniel Linhares², Giovanni Trevisan²

¹University of Minnesota; ²Iowa State University

The U.S. swine industry benefits from two nationally recognized disease/pathogen-monitoring initiatives: the **Morrison Swine Health Monitoring Project (MSHMP)** and the **Swine Disease Reporting System (SDRS)**. While both programs support swine health decision-making, they collect different types of information and answer different epidemiological questions. Together, both programs offer valuable insights on infectious disease activity in the US swine population. The objective of this science page is to provide a comparative summary of both initiatives (*Figure 1*).

Established — **MSHMP:** 2011 **SDRS:** 2018

Lead Institution — **MSHMP:** University of Minnesota

SDRS: Consortium including 7 VDLs located in IA, IL, IN, KS, MN, OH, and SD

Primary Objective — **MSHMP:** Monitor disease occurrence/elimination in breeding herds, build capacity for foreign animal disease preparedness, and characterize pathogen evolution. **SDRS:** Describe pathogen detection patterns, confirmed disease diagnosis, and PRRSV ORF5, from veterinary diagnostic laboratories.

Population Monitored — **MSHMP:** Breeding herds accounting for 3.9 million sows; growing pig herds accounting for 12 million growing pigs. **SDRS:** Breeding herds, growing pigs, boar studs, gilt development units, environmental samples, truck wash facilities.

Coverage — **MSHMP:** Approximately 65% and 18% of the U.S. breeding and growing pig herd, respectively. **SDRS:** Diagnostic submissions representing most U.S. swine production systems.

Participation — **MSHMP:** Weekly voluntary herd status reporting and pathogen sequence sharing. **SDRS:** Near real-time aggregated and anonymized diagnostic laboratory data.

Geographic Resolution — **MSHMP:** Individual herd locations (latitude/longitude) and Premise ID. **SDRS:** State-level reporting.

Unit of Analysis — **MSHMP:** Herd. **SDRS:** Diagnostic case (accession).

Key Disease Metrics — **MSHMP:** Incidence and prevalence. **SDRS:** PCR positivity rates and disease diagnoses based on tissue cases; individual PRRSV ORF5 sequences.

Additional Farm Information — **MSHMP:** Herd size, filtration status, mortality management, herd depopulation, sequences. **SDRS:** Site state, farm type, age group, specimen type.

Pathogens Included — **MSHMP:** PRRSV-1, PRRSV-2, PEDV non-INDEL, PEDV INDEL, PDCoV, SVA, with *Mycoplasma hyopneumoniae* and Influenza A in the works. **SDRS:** PRRSV-1 and PRRSV-2 PCR, PRRSV genotyping, PEDV, PEDV genotyping, PDCoV, TGEV, PCV2, PCV3, IAV PCR, IAV genotype, MHP, *E. coli* genotyping, and tissue-based diagnostic codes.

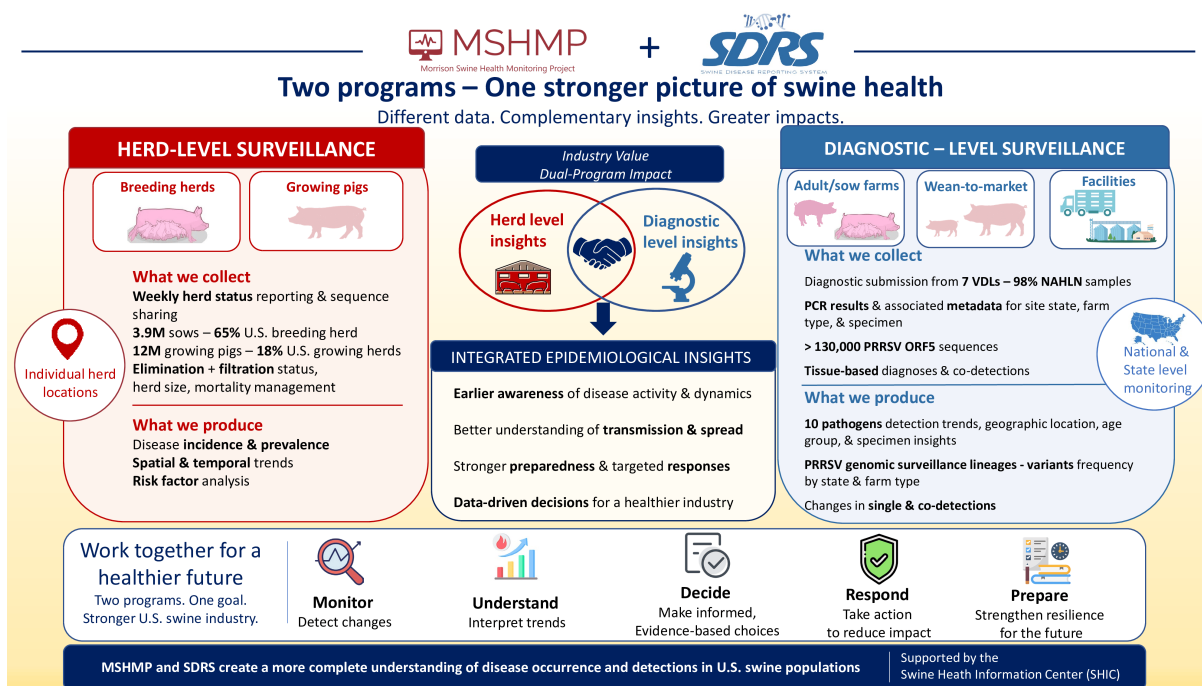


Figure 1. Overview of MSHMP and SDRS programs for monitoring U.S. swine health

What questions does each program help answer?

MSHMP:

What is the incidence and prevalence of disease over time together with pathogen dissemination dynamics?

Where are outbreaks occurring and what herd-level factors influence disease risk and transmission?

How fast are pathogens evolving and whether they are being disseminated throughout the country?

SDRS:

What pathogens are being detected and are PCR positivity rates increasing or decreasing?

Which age groups and specimen types are testing positive?

How does diagnosis of single or co-infections change over time, age group, or farm type?

Where are PRRSV variants detected, what is their frequency of detection by state, and where are new PRRSV variants being introduced across states?

Both programs monitor swine diseases, each using different data: MSHMP delivers herd-level epidemiological insights that support disease control and preparedness efforts, while SDRS provides near-real-time diagnostic intelligence from VDLs. Together, the programs create a complete understanding of disease occurrence, transmission, and detection in U.S. swine populations. Their complementary approaches strengthen industry preparedness, support informed decision-making, and enhance the ability to respond to emerging and endemic disease threats.

Current funding support for both initiatives is provided by the Swine Health Information Center (SHIC).