

# Swine Disease Reporting System

## Report # 104 (October 06, 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, Purdue ADDL and Illinois VDL.

### Collaborators:

*Swine Disease Reporting System office:* Principal investigators: [Daniel Linhares](#) & [Giovani Trevisan](#); Project coordinator: [Quyen Le](#); Software Developer: Kinath Rupasinghe; Data Analyst: Sajan 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 VDL 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.

*Illinois VDL:* Wes Baumgartner, James Lowe.

**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.

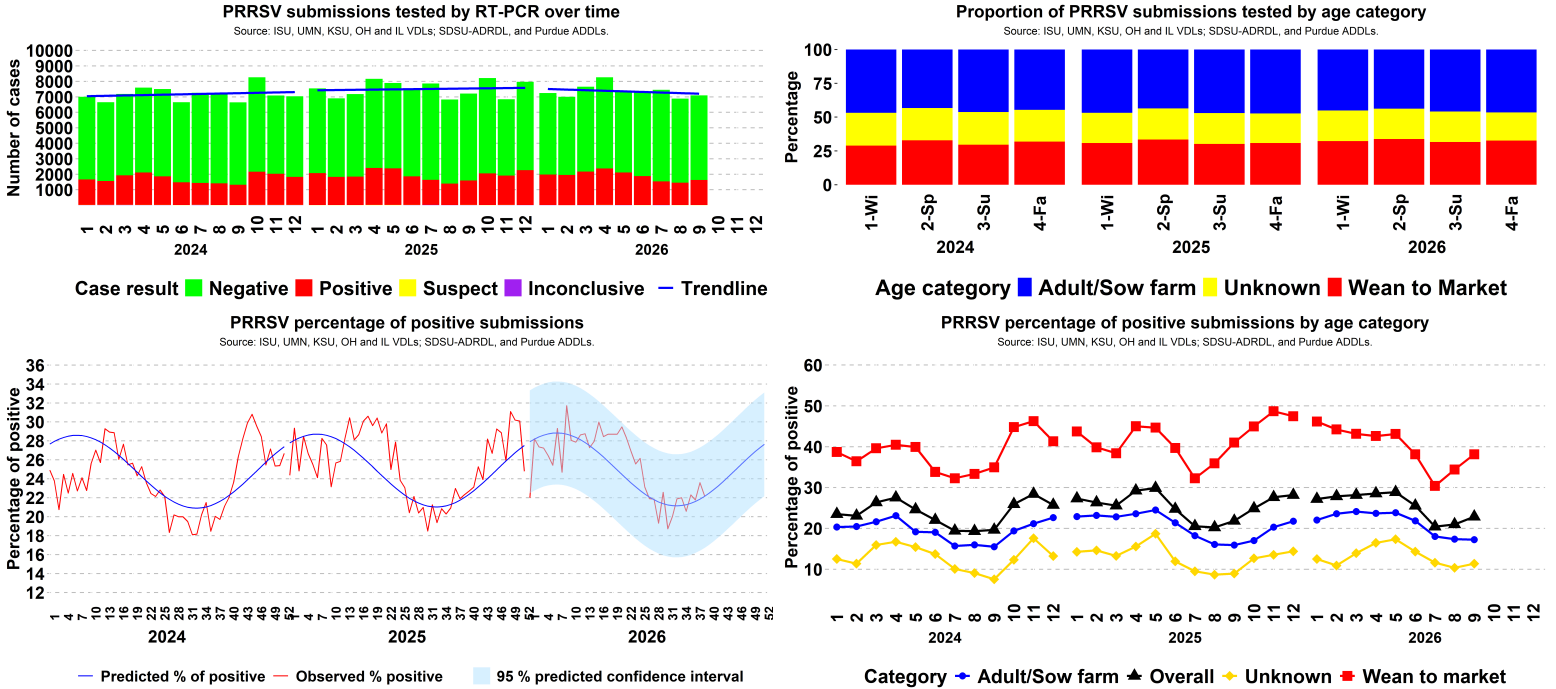
**PRRS virus Genotyping report and BLAST tool:** Benchmark PRRSV ORF5 sequences and compare your PRRSV sequence with what have been detected in the U.S.

**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 September 30, 2026.

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

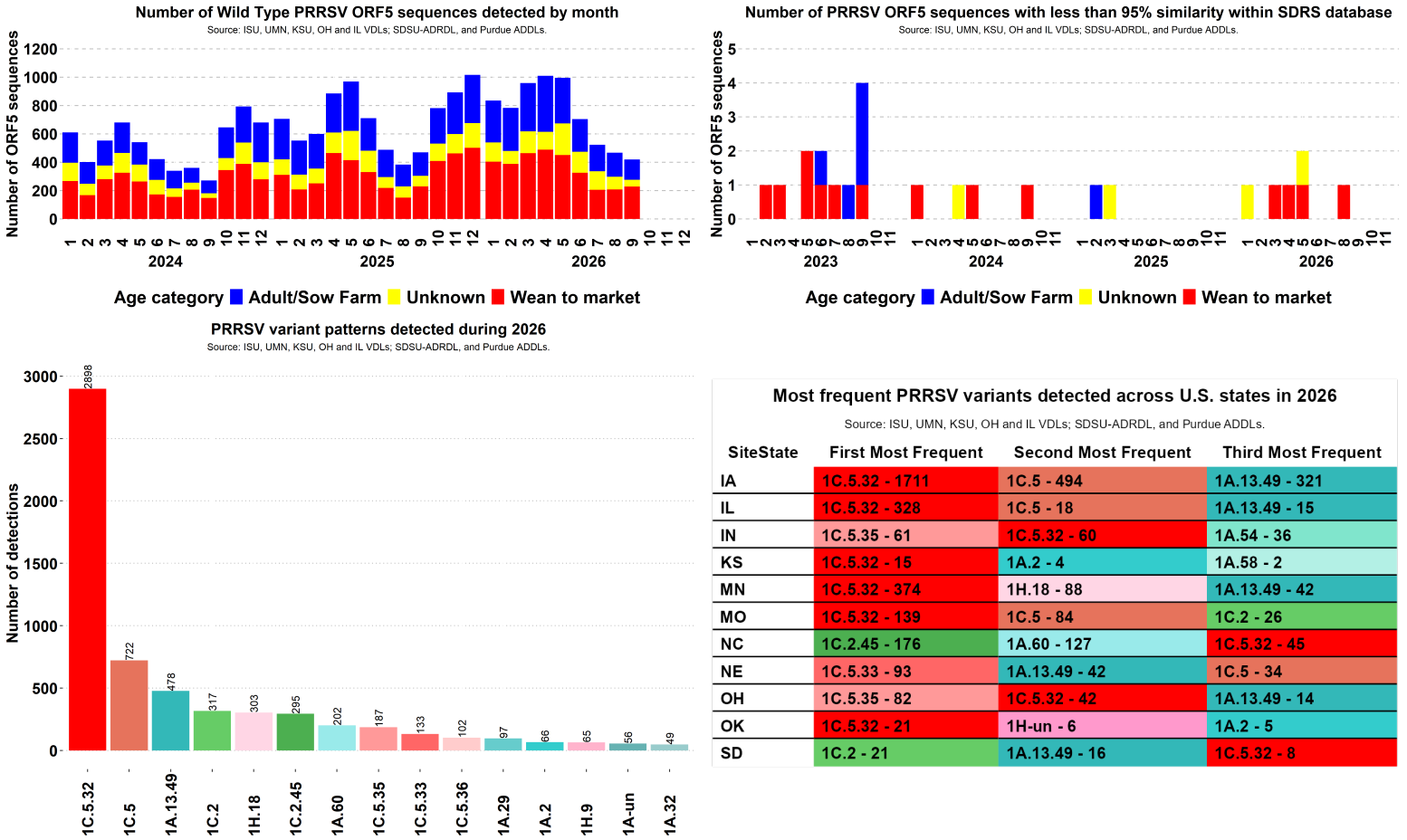


**Figure 1.** Top: Left: Results of PRRSV RT-PCR cases over time; Right: Proportion of accession ID cases tested for PRRSV by age group per year and season. Bottom: Left Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on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

- Overall, 22.88% of 7,095 cases tested PRRSV-positive in September, similar to 21.01% of 6,893 in August.
- Positivity in the adult/sow category in September was 17.28% (571 of 3,304), similar to 17.38% (549 of 3,158) in August.
- Positivity in the wean-to-market category in September was 38.15% (884 of 2,317), a moderate increase from 34.41% (732 of 2,127) in August.
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in MO, SD 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.

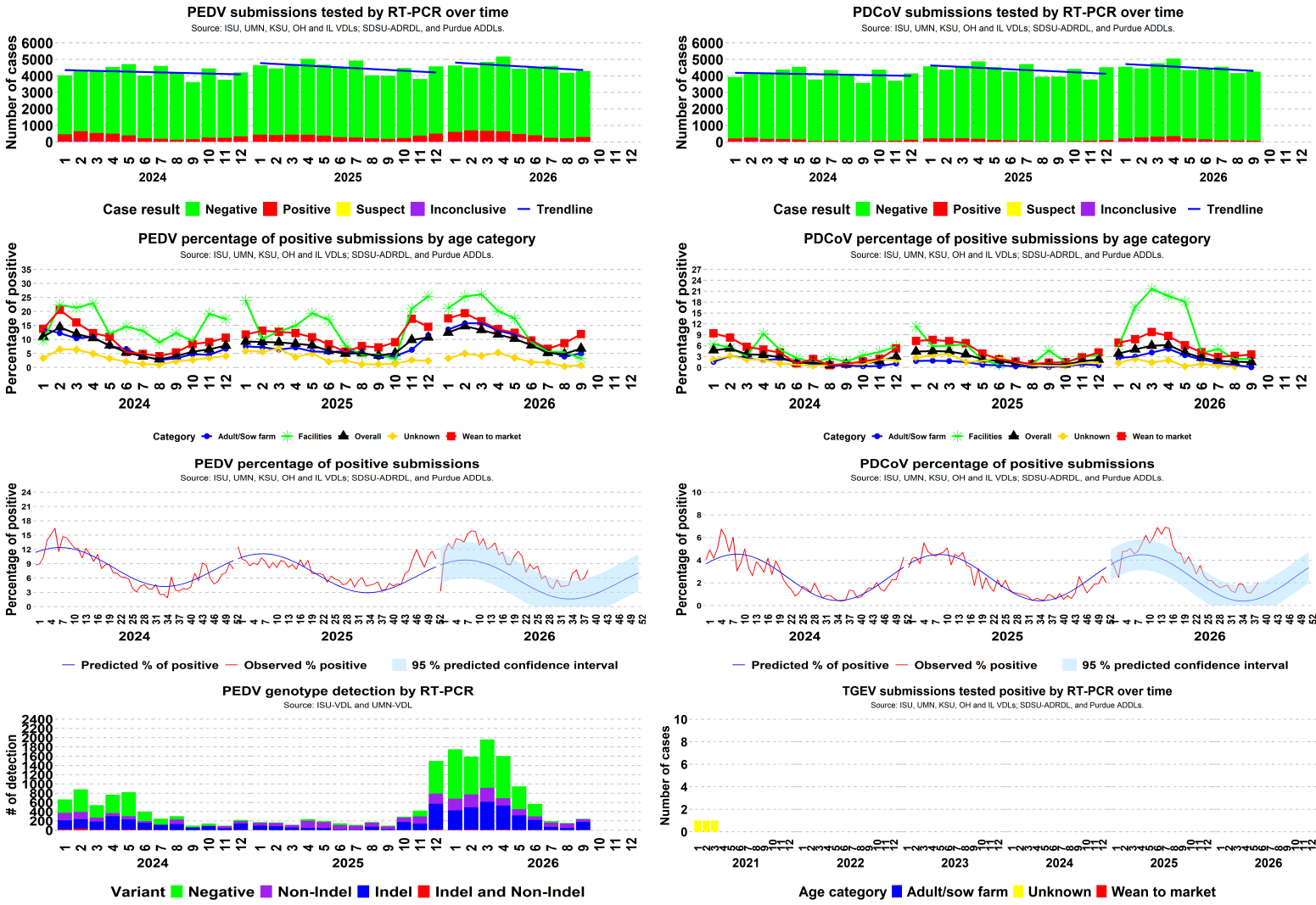
## Where Does Your PRRSV Sequence Fit?

- 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 September, the states with higher number of PRRSV 1C.5.32 detections were detected IA, MO, IL, MN, KS, NC, OH, IN, OK (respective number of sequences: 104, 18, 17, 16, 6, 3, 3, 2, 1);
- In September 1C.5.32 (170) was the PRRSV variant most detected in the U.S., followed by 1C.5 (69), and 1A.13.49 (49);
- SDRS database identified first-time detection of PRRSV variants according to provided site state:
  - September 2026: 1C.2.44 (IL)

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

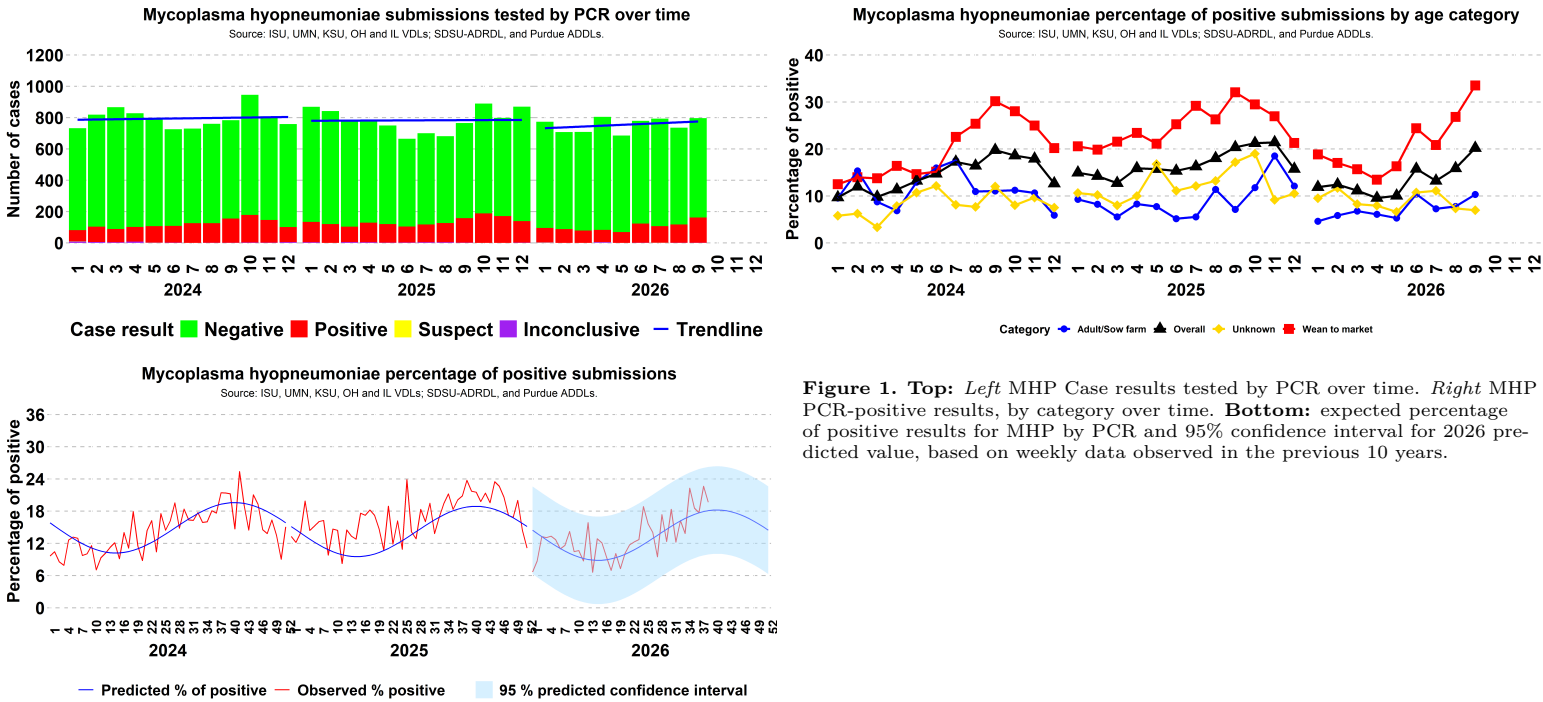


**Figure 1.** Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time. Second from top: Left PEDV; Right PDCoV percentage of positive RT-PCR results by age category. Third from top: Left PEDV; Right PDCoV expected percentage of positives with 95% CI for 2026 prediction. Bottom: Left PEDV genotype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

## SDRS Advisory Group highlights:

- Overall, 6.76% of 4,291 cases tested PEDV-positive in September, similar to 4.87% of 4,191 in August.
  - Positivity in the adult/sow category in September was 5.04% (77 of 1,529), similar to 3.91% (57 of 1,459) in August.
  - Positivity in the wean-to-market category in September was 11.92% (201 of 1,686), a moderate increase from 8.68% (136 of 1,567) in August.
  - Positivity in the facilities category in September was 3.2% (4 of 125), a moderate decrease from 5.47% (7 of 128) in August.
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in MO.
  - Overall, 1.12% of 268 samples had mixed PEDV genotype detection in September, similar to 0% of 155 in August.
- Overall, 1.5% of 4,263 cases tested PDCoV-positive in September, similar to 1.58% of 4,167 in August.
  - Positivity in the adult/sow category in September was 0.07% (1 of 1,515), similar to 0.69% (10 of 1,441) in August.
  - Positivity in the wean-to-market category in September was 3.58% (60 of 1,678), similar to 3.19% (50 of 1,565) in August.
  - Positivity in the facilities category in September was 2.4% (3 of 125), similar to 2.34% (3 of 128) in August.
  - 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 September, 2026 over a total of 4,126 cases tested. It has been 67 months (with a total of 258,804 cases tested) since the last TGEV PCR-positive result.
- Some SDRS Advisor Members noted that seasonal factors may be contributing to the recent increase in PEDV activity, while others reported no major changes in PEDV activity in the field. Additional field observations included sow herd instability in certain regions. Advisor Members reminded the constant need to remind farm personnel to follow and execute biosecurity practices.

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

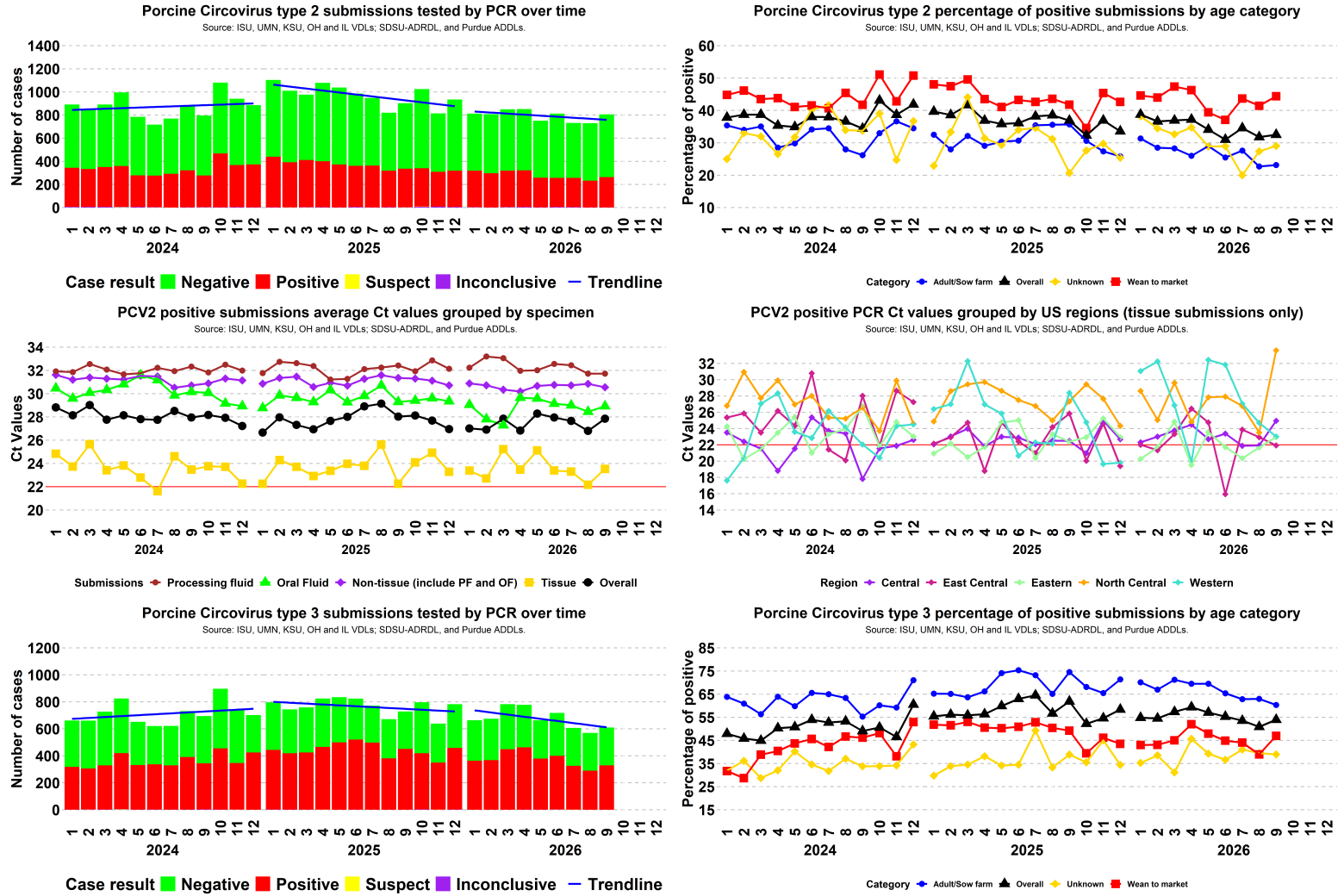


**Figure 1. Top:** *Left* MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 10 years.

#### SDRS Advisory Group highlights:

- Overall, 20.2% of 797 cases tested *M. hyopneumoniae*-positive in September, a moderate increase from 15.9% of 736 in August.
  - Positivity in the adult/sow category in September was 10.32% (32 of 310), a moderate increase from 7.77% (22 of 283) in August.
  - Positivity in the wean-to-market category in September was 33.52% (120 of 358), a substantial increase from 26.81% (85 of 317) in August.
- 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.

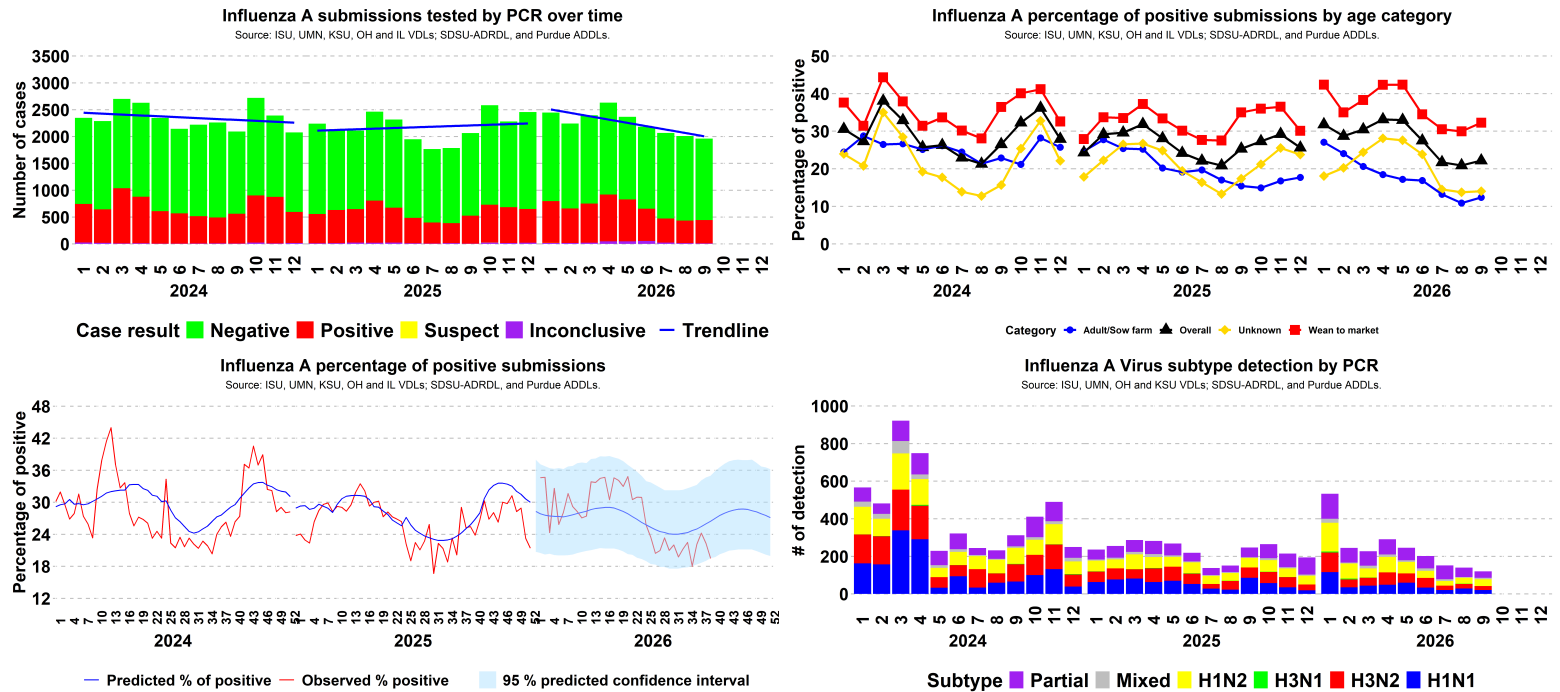


**Figure 1. Top:** Left: Results of PCV2 PCR cases over time; Right: PCV2 PCR-positive results, by category over time. **Middle:** Left: Average Ct values of PCV2 submissions by specimen; Right: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and WI), 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, 32.51% of 806 cases tested PCV2-positive in September, similar to 31.78% of 730 in August.
  - Positivity in the adult/sow category in September was 23.15% (94 of 406), similar to 22.68% (71 of 313) in August.
  - Positivity in the wean-to-market category in September was 44.38% (150 of 338), a moderate increase from 41.44% (138 of 333) in August.
  - In the month of September, the regions with the lowest PCV2 average Ct values in tissue submissions were East Central (21 submissions; average Ct 21.9), Eastern (16 submissions; average Ct 23), Western (17 submissions; average Ct 23), Central (35 submissions; average Ct 25), and North Central (4 submissions; average Ct 33.6).
- Overall, 53.93% of 610 cases tested PCV3-positive in September, a moderate increase from 50.88% of 570 in August.
  - Positivity in the adult/sow category in September was 60.34% (213 of 353), a moderate decrease from 62.99% (177 of 281) in August.
  - Positivity in the wean-to-market category in September was 46.97% (93 of 198), a substantial increase from 38.97% (83 of 213) in August.
- Some Advisors noted that replacement gilt stability may be an important consideration when interpreting increased PCV2 activity in wean-to-market pigs. Additionally, a reminder to routinely check and revisit vaccine compliance was given.

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

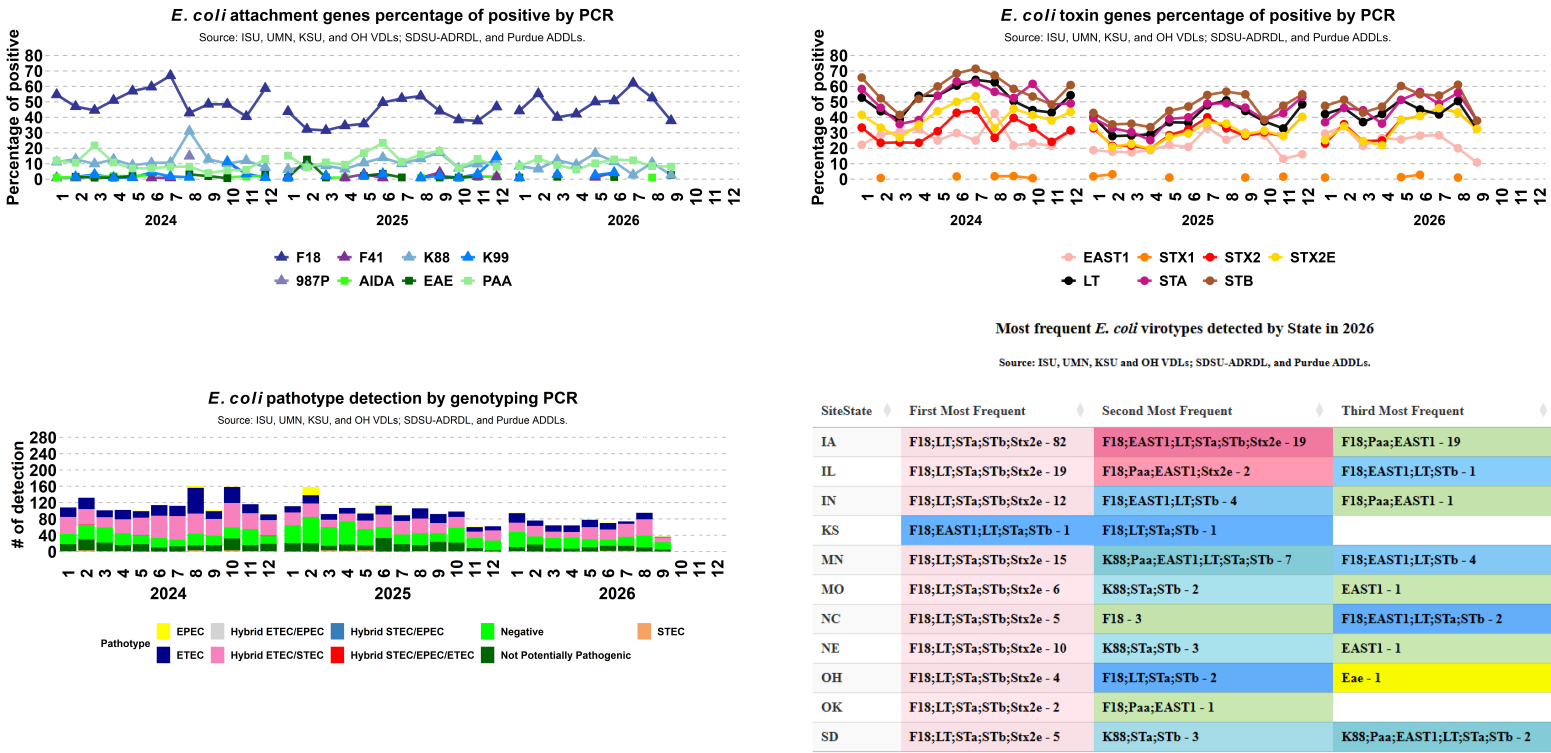


**Figure 1. Top:** *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2026 predicted value, based on weekly data observed in the previous 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, 22.18% of 1,961 cases tested IAV-positive in September, similar to 20.9% of 2,010 in August.
  - Positivity in the adult/sow category in September was 12.39% (57 of 460), similar to 10.87% (50 of 460) in August.
  - Positivity in the wean-to-market category in September was 32.28% (296 of 917), a moderate increase from 29.96% (290 of 968) in August.
  - Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA and OH.
- Overall, 6.67% of 120 samples had mixed subtype detection in September, a moderate increase from 2.86% of 140 in August.
- Some Advisors reported increased IAV activity in growing pigs, while others noted that IAV alone has had limited impact but may become more challenging when occurring alongside PRRSV.

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



**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:

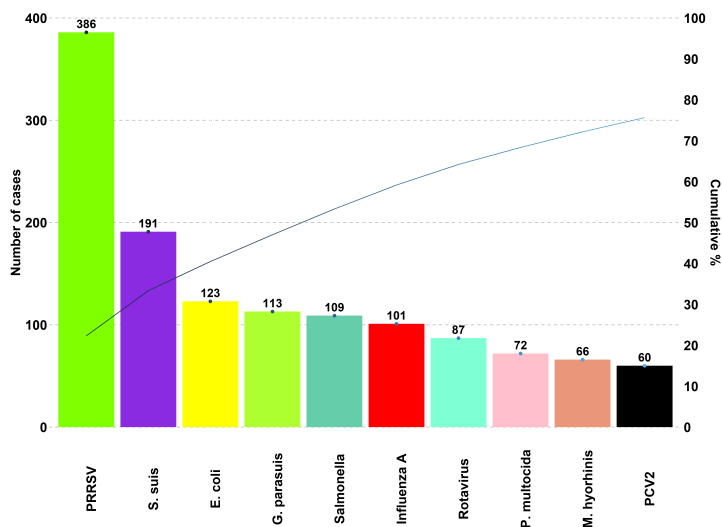
- Click on the links here to access the [E. coli PCR Genotyping Interpretation Tool](#)
- Attachment genes:** Fimbriae – F18, K88(F4), K99(F5), 987P(F6), F41; Adhesins – EAE (Intimin), PAA, AIDA
- Toxin genes:** Heat-labile – LT; Heat-stable – STa and STb; Shiga toxins – Stx1, Stx2 and Stx2e; and EAST1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

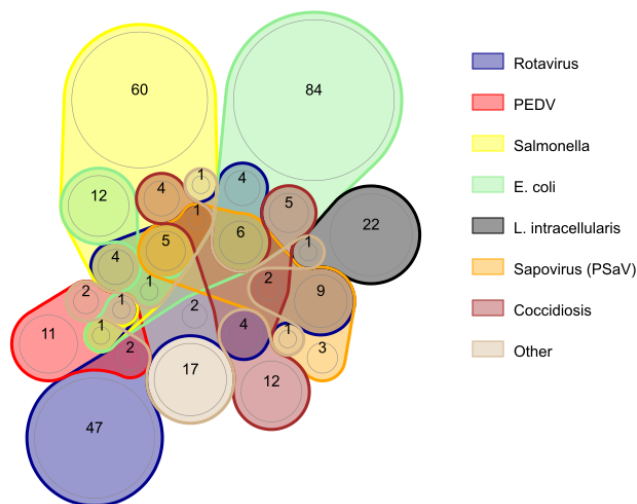
- Overall, 37 samples were tested for *E. coli* PCR in September.
  - In September, the *E. coli* pathotypes with higher number of sample detections were Hybrid ETEC/STEC (12 detections), Not Potentially Pathogenic (5 detections), and EPEC (1 detections).
  - In September, the *E. coli* attachment genes with higher detection rate were F18 (37.84%), PAA (8.11%), and EAE (2.70%).
  - In September, the *E. coli* toxin genes with higher detection rate were STA (37.84%), STB (37.84%), and LT (32.43%).

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

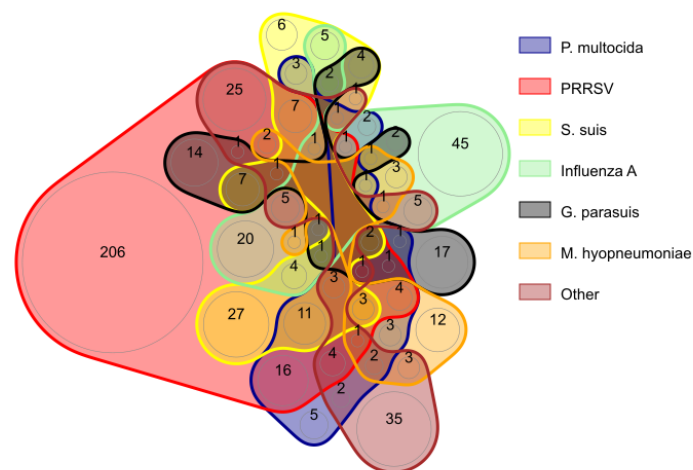
### Overall diagnosis



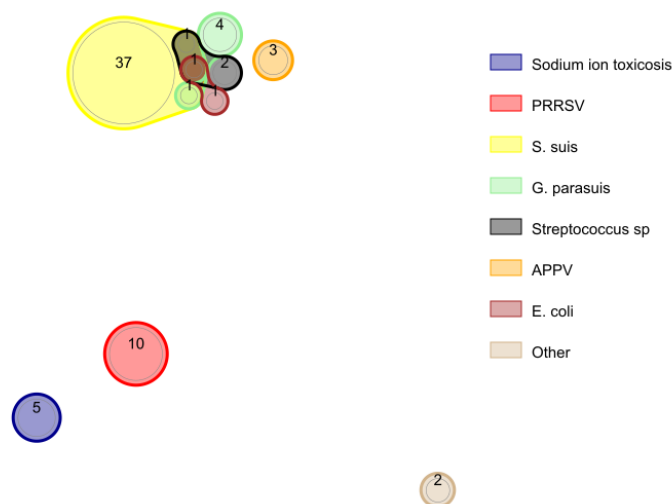
### Digestive



### 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 Aug 01, 2026 to Sep 29, 2026

### SDRS Advisory Group highlights:

- PRRSV (386) led cases with confirmed etiology, followed by *S. suis* (191), and *E. coli* (123). PRRSV (370 of 825) led the number of confirmed respiratory diagnoses, *E. coli* (114 of 412) lead the number of confirmed digestive diagnoses, and *S. suis* (40 of 71) led the number of confirmed neurological diagnoses.
- Some Advisors suggested that increased *Salmonella* activity may be associated with specific production flows and may occur alongside PEDV and *E. coli* outbreaks. Increased testing activity was also noted as a possible contributor to the observed trend.

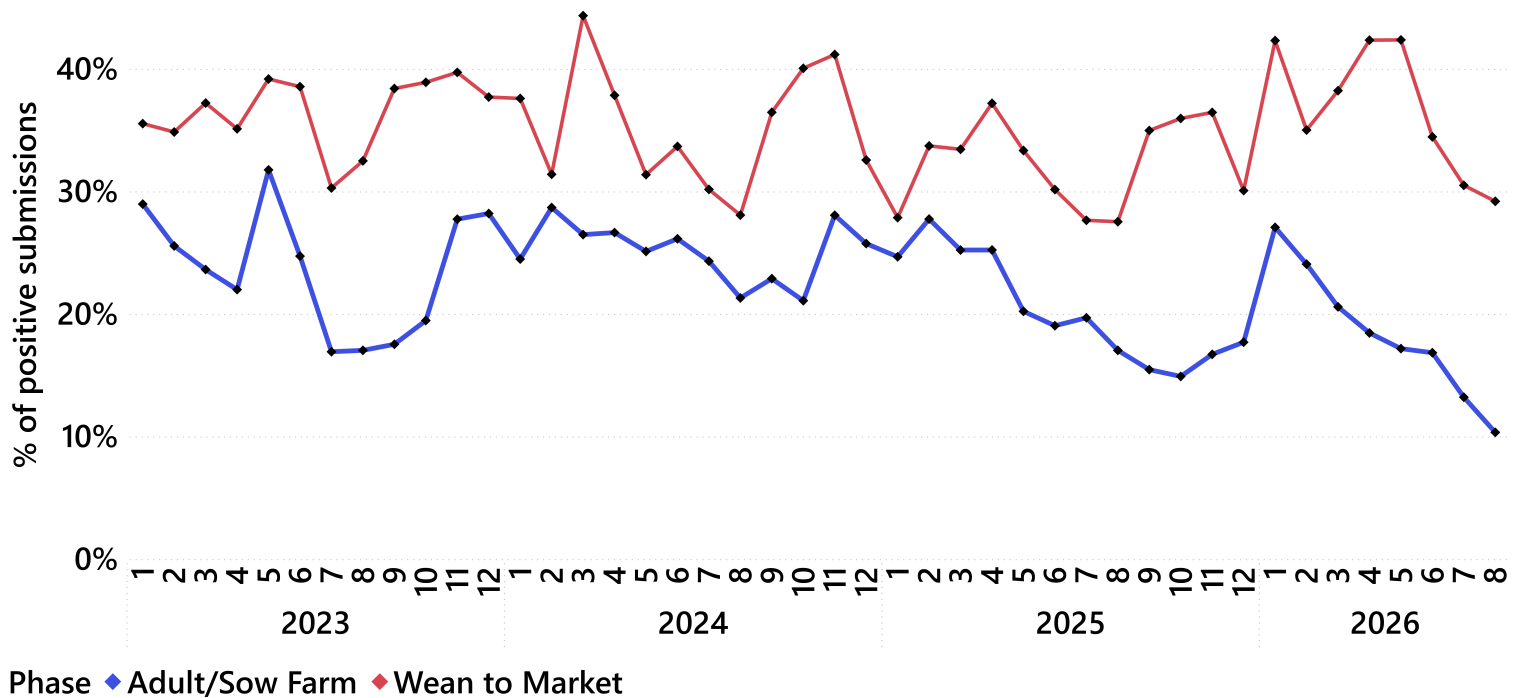
**Note:** The SDRS is a collaborative project among multiple VDLs in the US swine industry. The VDL collaborators and industry partners are all invited to submit content to share on this bonus page related to disease prevention, control, and management. Stay tuned for more content in future editions.

# Current insights on Influenza A Virus in Swine and Humans

Michael Zeller<sup>1</sup>, Hu Ke<sup>1</sup>, Phillip Gauger<sup>1</sup>, Quyen Le<sup>1</sup>, Daniel Linhares<sup>1</sup>, Giovanni Trevisan<sup>1</sup>  
<sup>1</sup>Iowa State University

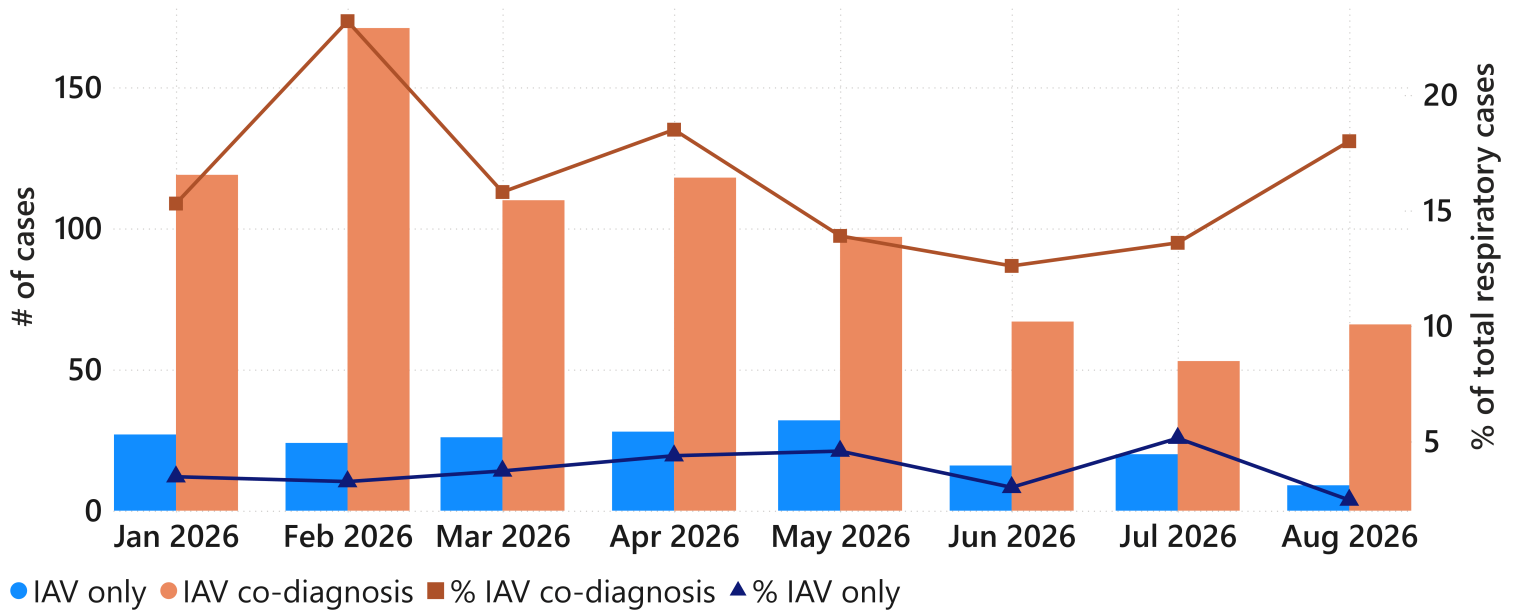
## 1. A snapshot of Swine Influenza A Virus activity in 2026

SDRS influenza A virus (IAV) RT-rtPCR surveillance detection data through August 2026 showed contrasting patterns between production phases. IAV positivity in adult/sow farm submissions declined throughout 2026, reaching approximately 10% in August (Figure 1), the lowest level observed since 2014. In contrast, positivity in wean-to-market submissions remained elevated, generally ranging from 30% to 45% during the year, indicating continued IAV circulation among growing pig populations.



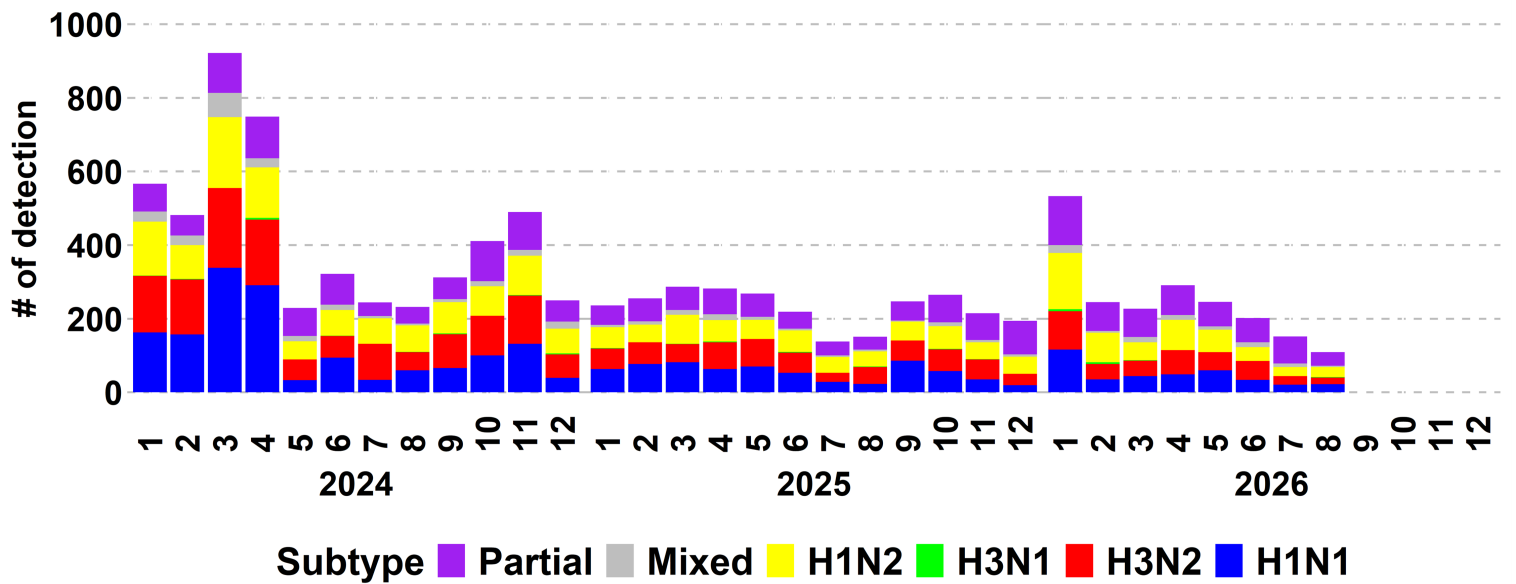
**Figure 1.** IAV positivity trends by production phase (Adult/Sow Farm vs Wean-to-Market)

To better understand the contribution of IAV to respiratory cases during this period, confirmed tissue diagnoses were further evaluated (Figure 2). Cases involving IAV and at least one additional respiratory pathogen (co-diagnosis) accounted for approximately **13% to 23% of all respiratory tissue diagnoses** from January through August 2026, whereas IAV-only cases represented approximately **2% to 5%**. The highest number of co-diagnosis cases was observed in February (171 cases; 22% of respiratory diagnoses). Among IAV co-diagnosis cases, the most frequently identified pathogens were PRRSV (37.1%), *Streptococcus suis* (20.2%), *Glaesserella parasuis* (14%), and *Pasteurella multocida* (10.6%), collectively accounting for more than 80% of all co-diagnosis events. In comparison, IAV-only diagnoses remained relatively infrequent throughout the period, ranging from 7 to 31 cases per month and contributing less than 5% of respiratory tissue diagnoses in any month evaluated.



**Figure 2.** Monthly number and proportion of confirmed respiratory tissue diagnoses in which IAV was identified alone or in combination with at least one additional respiratory pathogen, January-August 2026.

Further insight into circulating IAV strains was obtained through subtype detections by participating laboratories (**Figure 3**). Among 2,005 subtype detections by RT-rtPCR reported from January to August 2026, partially characterized viruses accounted for 613 detections (30.6%), followed by H1N2 with 516 detections (25.7%), H3N2 with 395 detections (19.7%), and H1N1 with 381 detections (19%). Mixed subtype detections represented 87 cases (4.3%), whereas H3N1 was detected infrequently, with 13 detections (0.6%). Overall, H1N1, H1N2, and H3N2 accounted for approximately **64% of all subtype detections reported during 2026**.



**Figure 3.** Monthly IAV subtype detection by PCR

These findings provide a current snapshot of IAV activity, disease association, and subtype diversity within U.S. swine populations. The following section highlights recent observations and perspectives related to IAV beyond swine surveillance.

## 2. Changes in H3 diversity in Swine Influenza

H3N2 has been a predominant subtype in North American swine influenza ecology since the late 1990s, accounting for 20%-33% of the annual influenza detections between 2007 to 2026. During this time, the composition of the genetic clades has shifted substantially. In the decade prior to 2026, approximately 40% of the H3N2 cases belonged to clade 3.1990.4a (formerly Cluster IVA), while another 40% to clade 3.2010.1 (formerly 2010.1). Most of the remaining detections were other 3.1990.4 clades, primarily 3.1990.4b (formerly cluster IVB). By 2025, clade 3.2010.1 accounted for approximately 70% of all H3 detections and increased further to over 85% in August, 2026. In contrast, detections of 3.1990.4a declined to just 4% in 2025. There has been a notable increase of detections of 3.1990.4i, which rose to nearly 6% in 2025. Another notable trend since 2023 has been the growing number of H3 viruses introduced into swine through human-to-swine transmission, referred to as spillover events.

Between November 2022 and August 2026, 77 introductions of human-origin H3 viruses were detected in the U.S. swine population. In many cases, these viruses are genetically similar to H3 strains that were circulating in humans at the time of the spillover event. The human-derived clades detected in swine include G.1.1, G.2, G.2.2, J.2, J.2.5, and K. These spillover viruses can be readily monitored because they do not share a recent common ancestor with contemporary swine H3 viruses. To track these human-derived H3 in pigs, a phylogenetic based investigation using both swine and contemporary human H3 to understand how these viruses evolve after entering the swine population. This approach has shown that while many detections appear to represent recent spillover events, some G.1.1 viruses continue to circulate within swine populations and now form a distinct evolutionary group, suggesting ongoing swine-to-swine transmission and the establishment of a new H3 genetic clade.

Previous spillover H3 viruses, such as 3.2010.1 and 3.2010.2, underwent reassortment before becoming widely established in swine. Although reassortment may not be required for a spillover virus to become endemic, it appears to improve the likelihood of successful adaptation and spread among pigs. The G.1.1 viruses detected recently in swine have also undergone reassortment. Detections from 2025 onwards contain a human-origin G.1.1 H3 paired with a swine-origin N2.2002B neuraminidase. The remaining internal genes consist of a triple-reassortant polymerase complex and non-structural segment, along with pandemic-origin matrix and nucleoprotein segments. Viruses with this genetic configuration have been detected in Illinois, Iowa, and Minnesota. Whether this lineage will continue to spread and become established across North American swine populations remains unknown. However, its emergence highlights the ongoing role of human-to-swine transmission in generating new genetic diversity within the H3 influenza population.