# Swine Disease Reporting System
# Report # 88 (June 03, 2025)

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

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

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

**Collaborators:**

*Swine Disease Reporting System office*: Principal investigators: Daniel Linhares & Giovani Trevisan; Project coordinator: Guilherme Cezar

*Iowa State Uni.*: Edison Magalhães, Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Srijita Chandra, Eric Burrough, Phillip Gauger, Christopher Rademacher, Darin Madson, Michael Zeller, Rodger Main.

*Uni. of Minnesota*: Mary Thurn, Paulo Lages, Cesar Corzo, Stephanie Rossow, 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, Beth Thompson.

*Ohio Animal Disease and Diag. Lab.* and *The Ohio State University*: Melanie Prarat, Dennis Summers, Andréia Arruda.

*Purdue Uni* and *Indiana State BOAH*: Craig Bowen, Kenitra Hendrix, Joseph Boyle, James Lyons, Kelli Werling.

**Disease Diagnosis System**: Consisting of reporting disease diagnosis (not just pathogen detection by PCR), based on diagnostic codes assigned by veterinary diagnosticians from ISU-VDL.

PRRSView and FLUture: Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL.

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

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

**Advisory Group:** Providing their comments and perspectives monthly: Mark Schwartz, Megan Niederwerder, Paul Yeske, Deborah Murray, Brigitte Mason, Peter Schneider, Sam Copeland, Luc Dufresne, Daniel Boykin, Corrine Fruge, William Hollis, Rebecca Robbins, Thomas Petznick, Kurt Kuecker, and Lauren Glowzenski.

**Note:** This report contains data up to May 31, 2025.

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

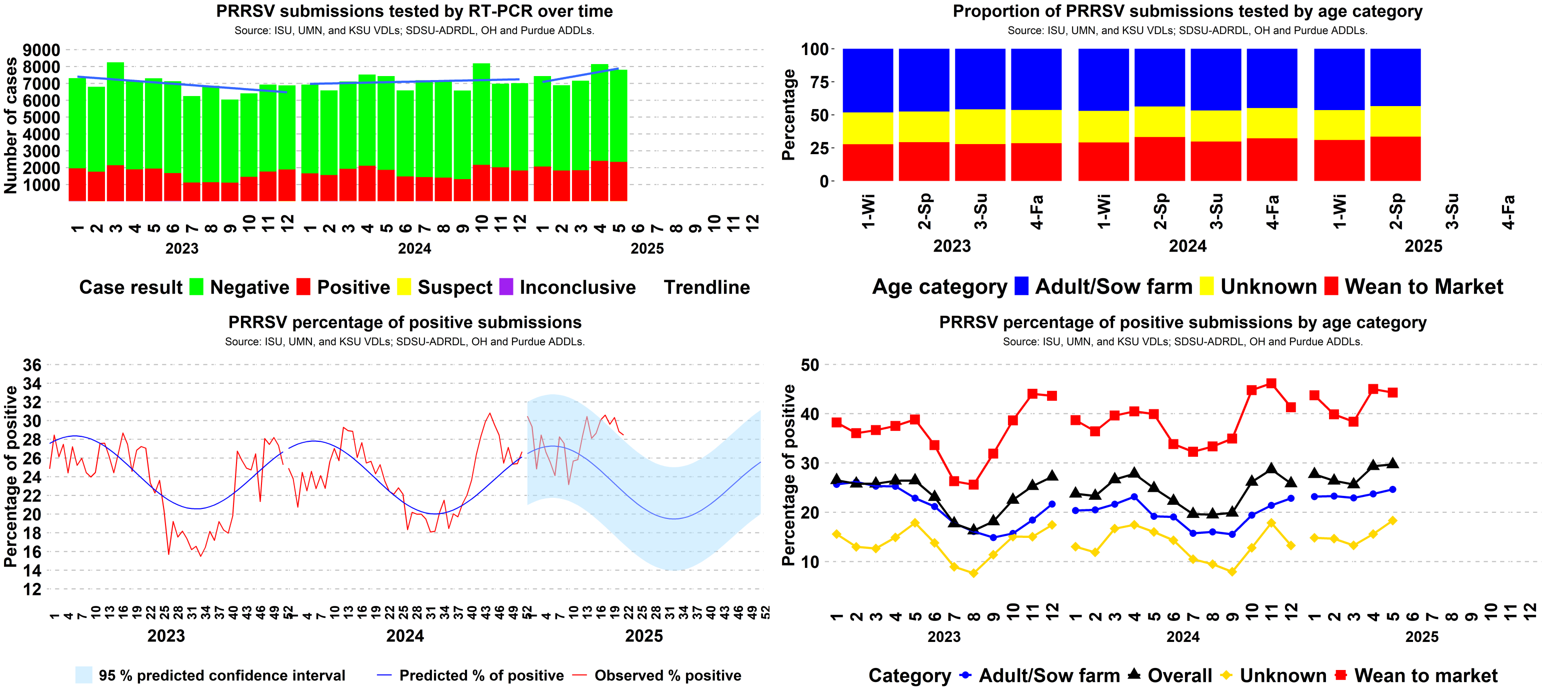
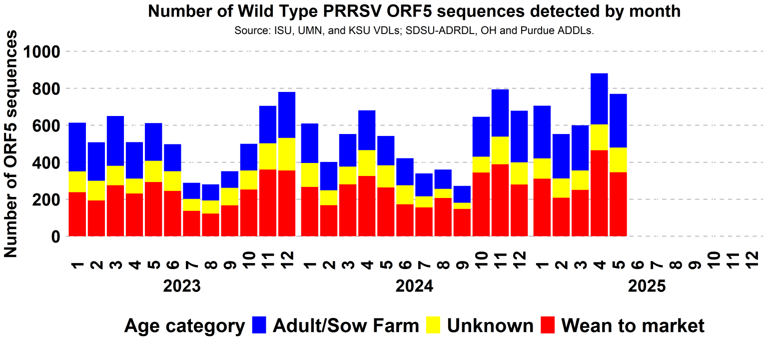

PRRSV submissions tested by RT-PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.
Proportion of PRRSV submissions tested by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.
PRRSV percentage of positive submissions
Source: ISU, UMN, and KSU VDLs;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

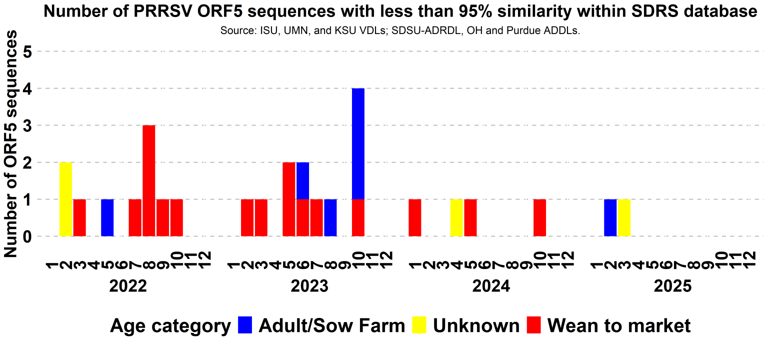
## SDRS Advisory Group highlights:

- Overall, 29.73% of 7,808 cases tested PRRSV-positive in May, similar to 29.34% of 8,143 in April;
  - Positivity in the adult/sow category in May was 24.64% (831 of 3,373), similar to 23.74% (818 of 3,445) in April;
  - Positivity in the wean-to-market category in May was 44.29% (1,155 of 2,608), similar to 45% (1,283 of 2,851) in April;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA and MN;
- There was a significant increase in PRRSV L1C.5 detections (Page 3) from early April to mid-May, particularly in Nebraska, Oklahoma, Missouri, and Illinois. Also, L1C.5 detections doubled in South Dakota, Minnesota, Indiana, and Iowa leading for positivity above the expected. The advisory group highlighted the re-emergence of strains not seen since 2023, suggesting that manure hauling might have contributed to the spread. Additionally, advisory members reported several outbreaks with severe clinical signs affecting both sow farms and growing sites across different regions aligning with the trend of rising positivity rates. Also, other advisory members have not encountered new positive cases of L1C.5. Still, they noted the return of dry conditions and strong, sustained winds in the Midwest, which could influence virus transmission of other variants they were dealing with.

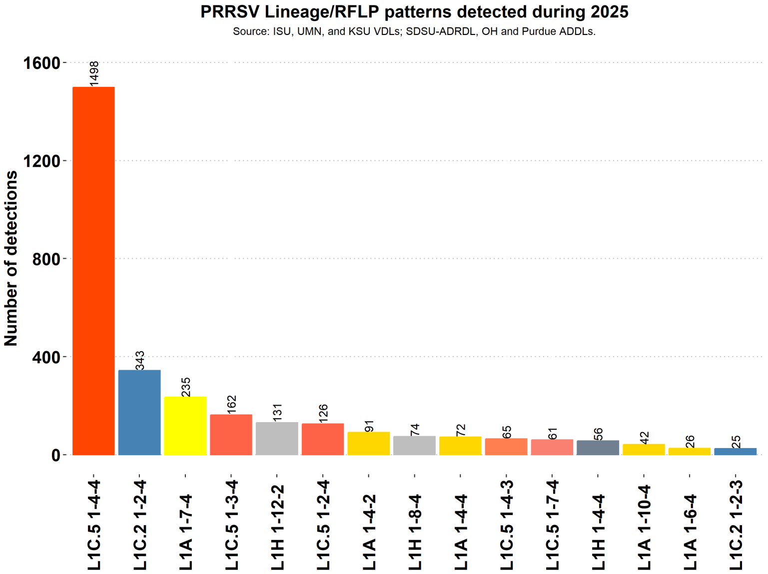
# Topic 2 – PRRSV ORF5 sequences detection over time


Number of Wild Type PRRSV ORF5 sequences detected by month

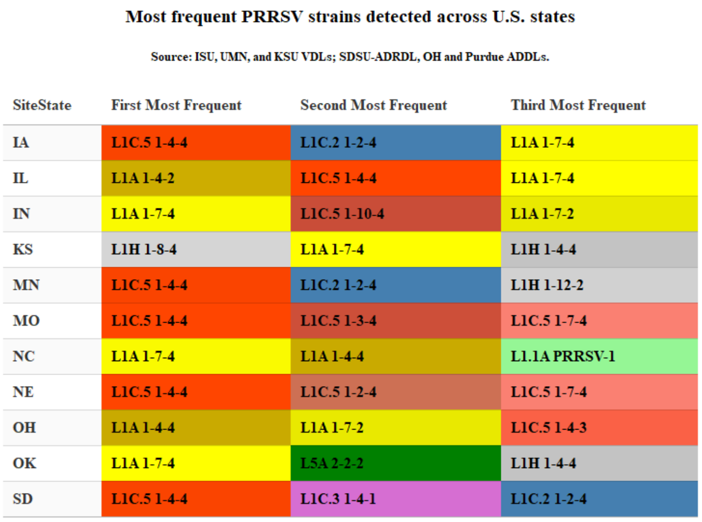
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.


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 Lineage/RFLP patterns detected during 2025

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


Most frequent PRRSV strains detected across U.S. states

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

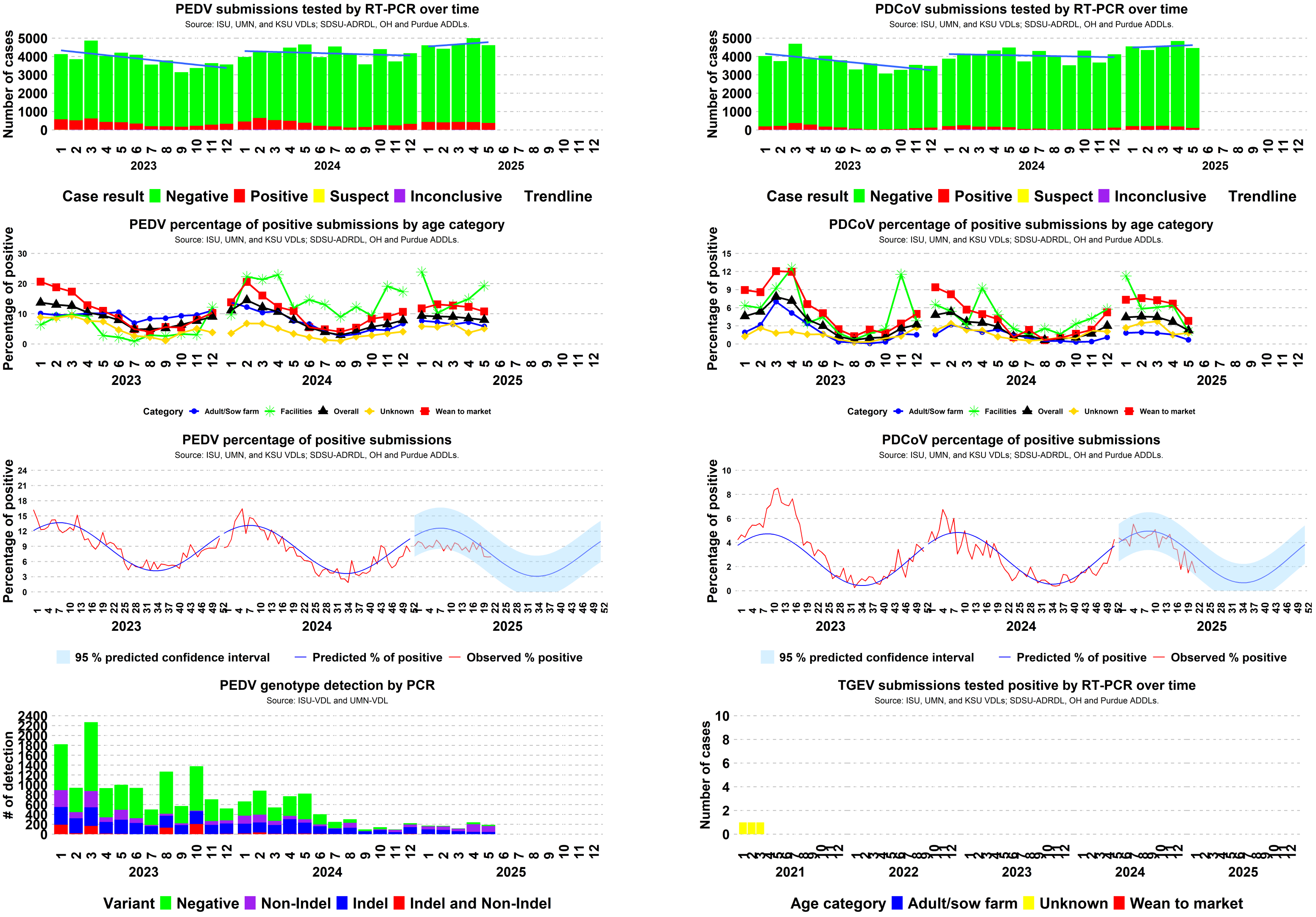
| SiteState | First Most Frequent | Second Most Frequent | Third Most Frequent |
|---|---|---|---|
| IA | L1C.5 1-4-4 | L1C.2 1-2-4 | L1A 1-7-4 |
| IL | L1A 1-4-2 | L1C.5 1-4-4 | L1A 1-7-4 |
| IN | L1A 1-7-4 | L1C.5 1-10-4 | L1A 1-7-2 |
| KS | L1H 1-8-4 | L1A 1-7-4 | L1H 1-4-4 |
| MN | L1C.5 1-4-4 | L1C.2 1-2-4 | L1H 1-12-2 |
| MO | L1C.5 1-4-4 | L1C.5 1-3-4 | L1C.5 1-7-4 |
| NC | L1A 1-7-4 | L1A 1-4-4 | L1.1A PRRSV-1 |
| NE | L1C.5 1-4-4 | L1C.5 1-2-4 | L1C.5 1-7-4 |
| OH | L1A 1-4-4 | L1A 1-7-2 | L1C.5 1-4-3 |
| OK | L1A 1-7-4 | L5A 2-2-2 | L1H 1-4-4 |
| SD | L1C.5 1-4-4 | L1C.3 1-4-1 | L1C.2 1-2-4 |

**Figure 1. Top**: **Left**: Number of PRRSV ORF5 sequences detected by age category; **Right**: Number of PRRSV ORF5 sequences with less than 95% similarity after BLAST analysis with the sequences in the SDRS database (Sequences with more than 6 ambiguities, sequences with less than 597 nucleotides or higher than 606 nucleotides are not included in this analysis); **Bottom** *Left*: 15 PRRSV ORF5 sequences most frequent detected by Lineage and RFLP; *Right*: Most frequent detected PRRSV ORF5 sequences by lineage and RFLP at U.S. state level.

## SDRS Advisory Group highlights:

- During May 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MN, MO, NE, IL, IN, OK, SD, OH, PA (respective number of sequences: 282, 110, 22, 14, 11, 11, 10, 5, 2, 2).
- In May L1C.5 1-4-4 (357) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (88), and L1A 1-7-4 (41);
- Click on the links here to access the PRRSV genotype dashboard and the SDRS Blast tool to compare your PRRSV ORF5 sequence with the SDRS database.
- PRRSV L1C.2 has shown a notable spike in activity during April 2025 and remains highly active into May, with its first detections reported in South Dakota and West Virginia this year. The advisory group highlighted the continued L1C.2 activity, particularly in Iowa finishers and a few sow farms. They noted the circulation of what appears to be two distinct variants of the virus—one more severe than the other—suggesting a complex and evolving epidemiological landscape.

# 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 PCR

Source: ISU-VDL and UMN-VDL

TGEV submissions tested positive by RT-PCR over time

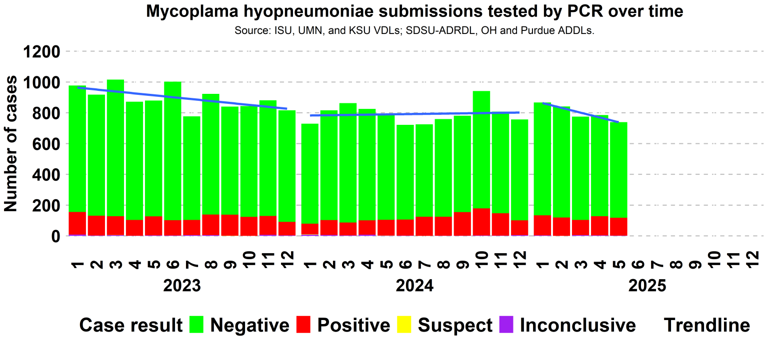
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

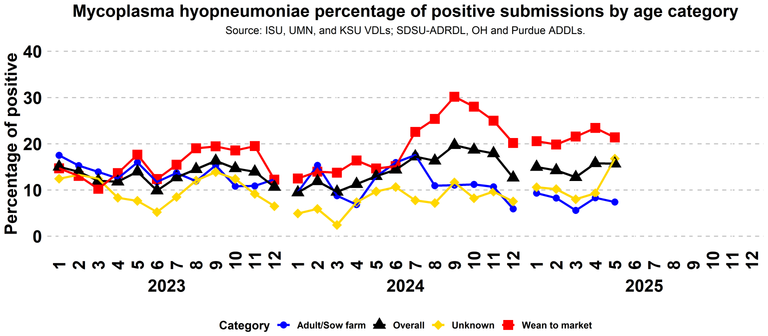
**Figure 1. Top**: *Left PEDV*; *Right PDCoV* cases tested by RT-PCR over time; **Second from top**: *Left PEDV*; *Right PDCoV* percentage of positive PCR positive results, by age category over time. Facilities are cases submissions from packing plants, truck washes, and vehicles. **Third from top**: *Left PEDV*; *Right PDCoV* expected percentage of positive results for cases tested by RT-PCR and 95% confidence interval for 2025 predicted value. **Bottom** *Left*: Number of PEDV genotype detection over time; *Right*: Number of TGEV positive cases by age category.

## SDRS Advisory Group highlights:

- Overall, 8% of 4,615 cases tested PEDV-positive in May, similar to 8.54% of 4,998 in April;
  - Positivity in the adult/sow category in May was 5.85% (88 of 1,503), similar to 7.23% (125 of 1,729) in April;
  - Positivity in the wean-to-market category in May was 10.77% (193 of 1,792), similar to 12.29% (236 of 1,921) in April;
- Positivity in the facilities category in May was 19.31% (28 of 145), a moderate increase from 14.89% (21 of 141) in April;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN;
  - Overall, 0% of 189 samples had mixed PEDV genotype detection in May, similar to 0% of 241 in April;
- Overall, 2.24% of 4,464 cases tested PDCoV-positive in May, similar to 3.66% of 4,842 in April;
  - Positivity in the adult/sow category in May was 0.69% (10 of 1,454), similar to 1.56% (26 of 1,671) in April;
  - Positivity in the wean-to-market category in May was 3.82% (66 of 1,728), a moderate decrease from 6.69% (124 of 1,854) in April;
- Positivity in the facilities category in May was 2.07% (3 of 145), a moderate decrease from 6.38% (9 of 141) in April;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN, OH, and MO;
- There was 0 positive case for TGEV RNA-PCR in May, 2025 over a total of 4,369 cases tested. It has been 50 months (with a total of 187,594 cases tested) since the last TGEV PCR-positive result;
- There had been a regional uptick in PEDV-positive cases across the U.S., particularly in Iowa, Kansas, Indiana, and North Carolina. The advisory group highlighted significant outbreaks in sow units and grow-finish sites throughout the U.S. Some advisory members expressed concerns that the virus may have been introduced through contaminated vehicles, emphasizing the importance of biosecurity and hauling sanitation.

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


Mycoplama hyopneumoniae submissions tested by PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.


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

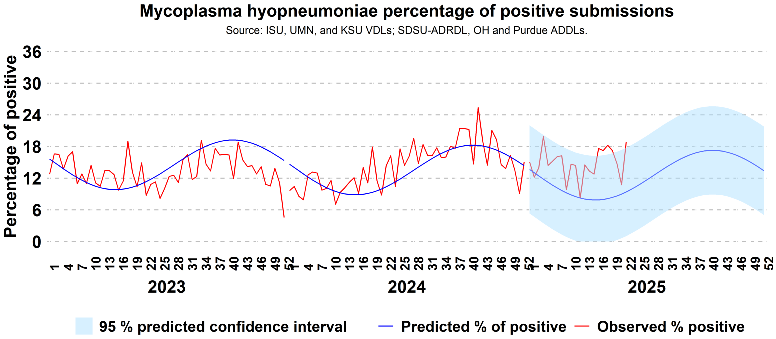
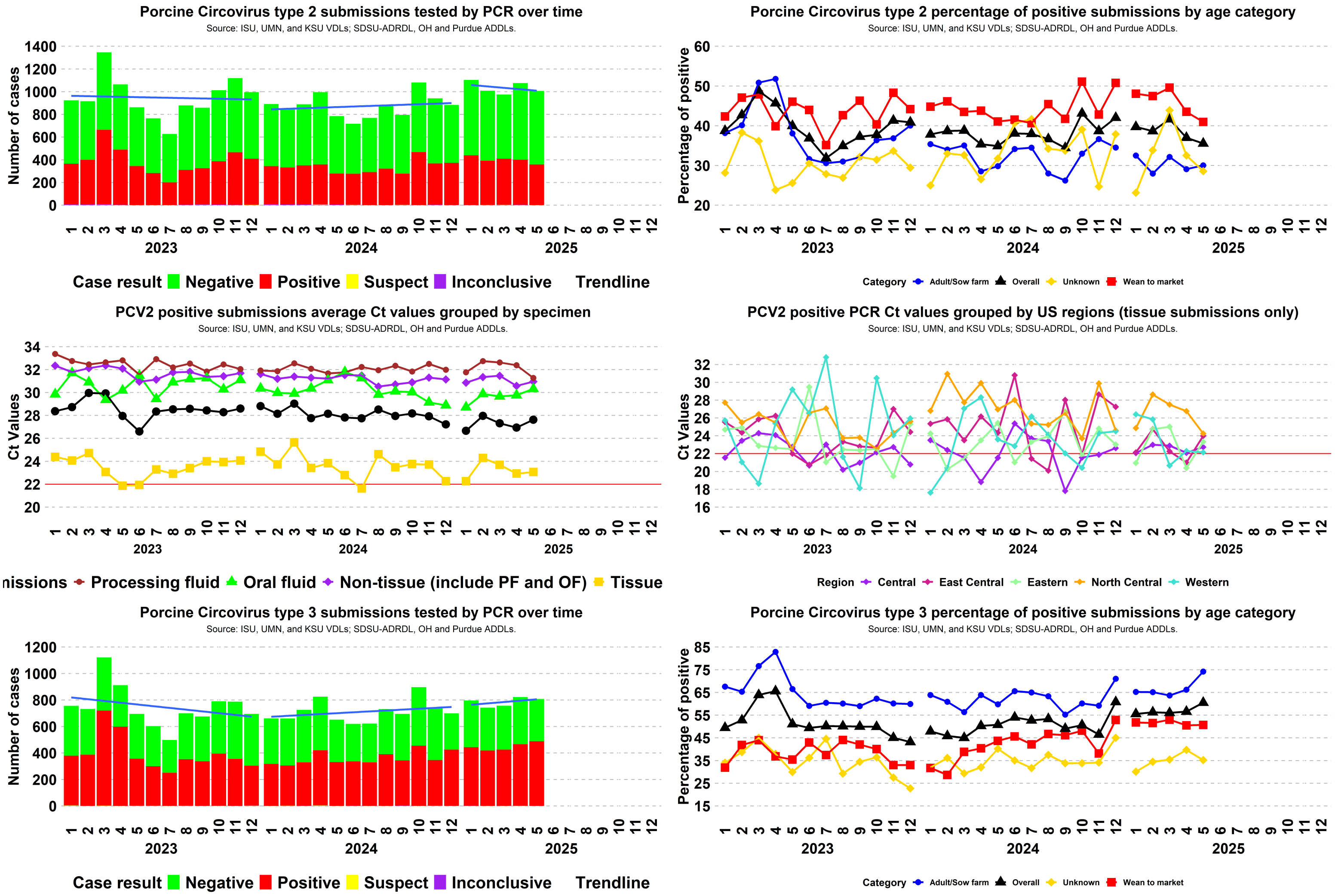

Mycoplasma hyopneumoniae percentage of positive submissions
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

**Figure 3. Top:** *Left* MHP; MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years.

## SDRS Advisory Group highlights:

- Overall, 15.7% of 739 cases tested *M. hyopneumoniae*-positive cases in May, similar to 15.8% of 785 in April;
  - Positivity in the adult/sow category in May was 7.42% (19 of 256), similar to 8.33% (23 of 276) in April;
  - Positivity in the wean-to-market category in May was 21.39% (74 of 346), a moderate decrease from 23.42% (89 of 380) in April;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN and IL;
- Despite a decline in *Mycoplasma hyopneumoniae* positive cases from Adult/sow farms in 2025, the positivity rate remains elevated in the wean-to-market category. Also, several lung-positive submissions came from Iowa, Indiana, Illinois, and North Carolina. The advisory group highlighted that most regions had no recent issues in their sow herds. Still, the highly dense areas suffer from seasonal patterns—more clinical signs in pigs born during winter due to reduced ventilation—could explain the increased activity, which typically subsides by fall. Also, it was hypothesized that the concurrent rise in PRRSV cases might be affecting the previous stable MHP infections due to the co-infection.

# 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

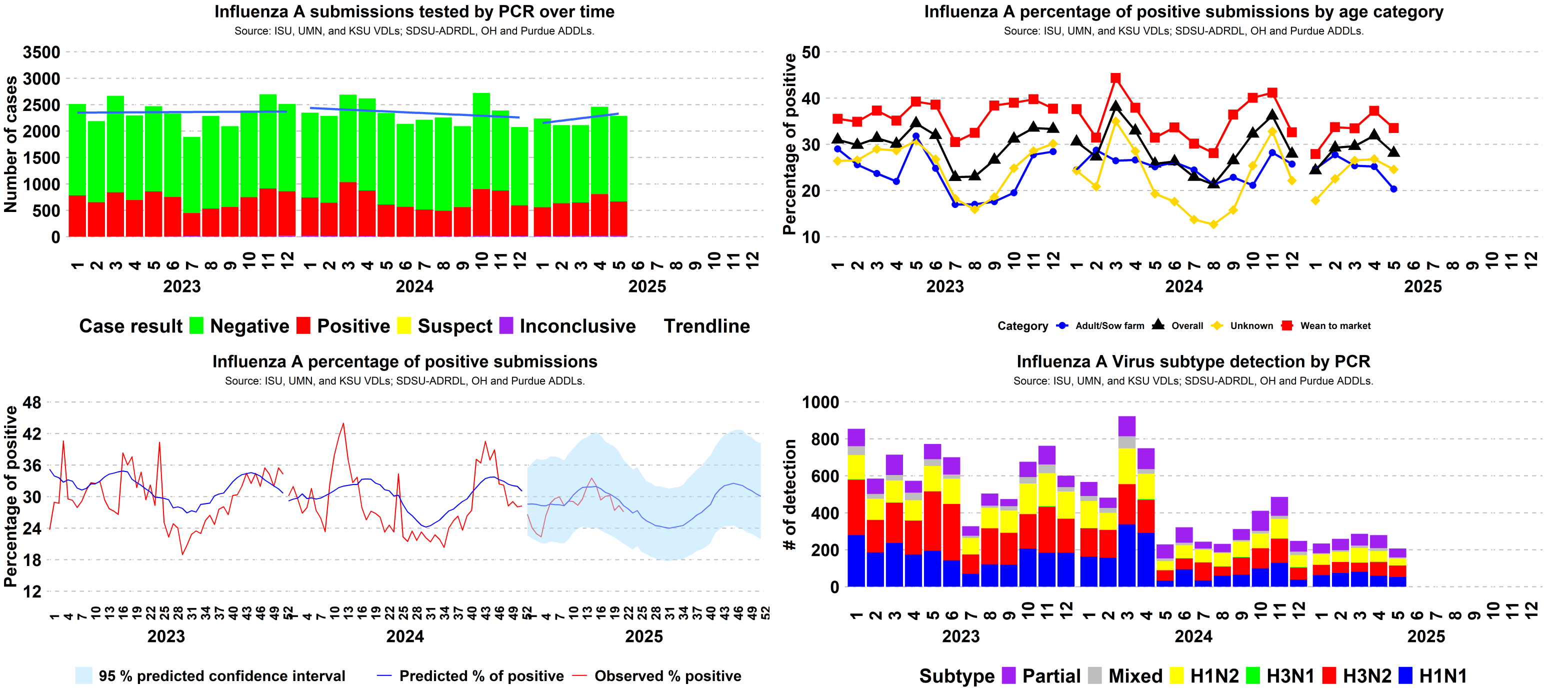
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

**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, 35.55% of 1,007 cases tested PCV2-positive in May, similar to 36.99% of 1,076 in April;
  - Positivity in the adult/sow category in May was 30.02% (121 of 403), similar to 29.08% (123 of 423) in April;
  - Positivity in the wean-to-market category in May was 40.96% (213 of 520), a moderate decrease from 43.51% (248 of 570) in April;
  - In the month of May, the regions with the lowest PCV2 average Ct values in tissue submissions was Western (15 submissions; average Ct 22.1), Central (54 submissions; average Ct 22.7), Eastern (18 submissions; average Ct 23.3), East Central (11 submissions; average Ct 24), and North Central (30 submissions; average Ct 24.3);
- Overall, 60.52% of 808 cases tested PCV3-positive in May, a moderate increase from 56.57% of 822 in April;
  - Positivity in the adult/sow category in May was 74.22% (285 of 384), a substantial increase from 66.21% (243 of 367) in April;
  - Positivity in the wean-to-market category in May was 50.71% (179 of 353), similar to 50.52% (193 of 382) in April.

# 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.

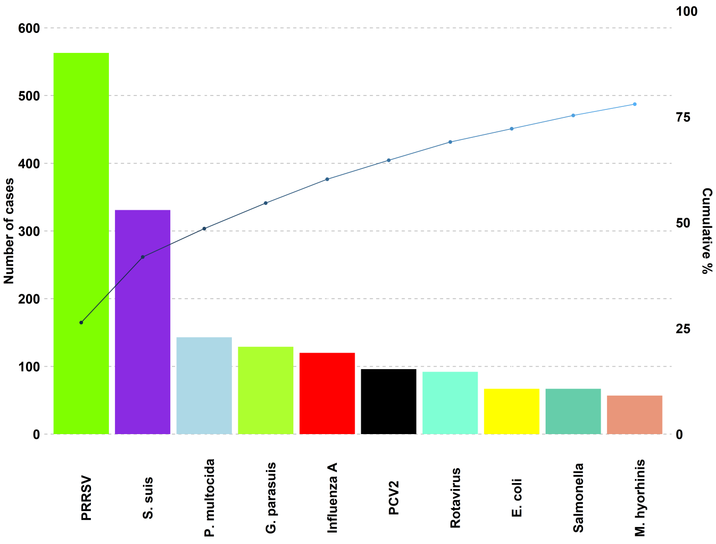
**Figure 3. Top:** *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 5 years. *Right* Number of IAV subtyping PCR detection over time; (Partial - only hemagglutinin or neuraminidase region detected; Mixed - 3 or more haemagglutinin and neuroamnidase regions detected. i.e., "H1 H3 N1").

## SDRS Advisory Group highlights:

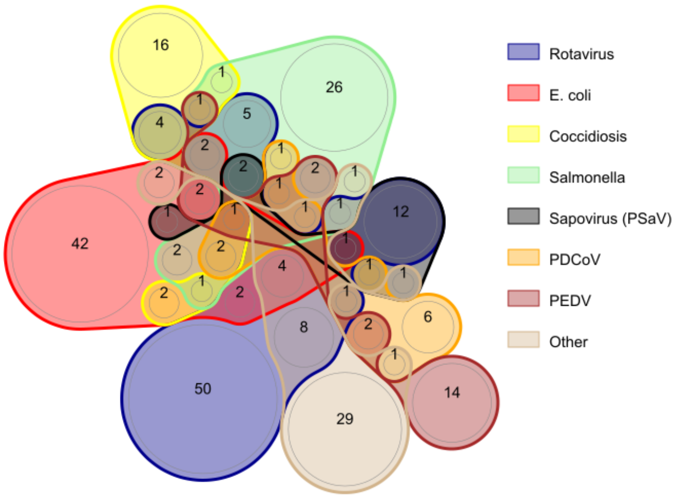
- Overall, 28.12% of 2,287 cases tested IAV-positive cases in May, a moderate decrease from 31.9% of 2,461 in April;
  - Positivity in the adult/sow category in May was 20.35% (93 of 457), a moderate decrease from 25.22% (116 of 460) in April;
  - Positivity in the wean-to-market category in May was 33.51% (376 of 1,122), a moderate decrease from 37.24% (473 of 1,270) in April.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 2.9% of 207 samples had mixed subtype detection in May, a moderate decrease from 5.73% of 279 in April.

# Topic 6 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.

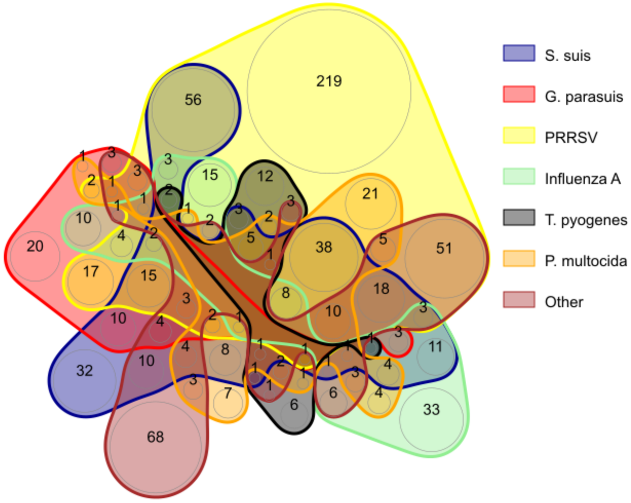
Overall diagnosis



Digestive



Respiratory



Nervous

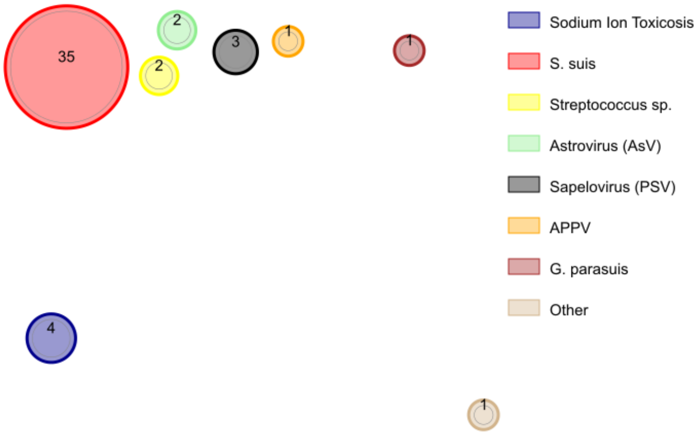


**Figure 4.** ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented.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

Note: Disease diagnosis takes 1 to 2 weeks to be performed. The graphs and analysis contain data from April. 1 to May. 24, 2025.

**SDRS Advisory Group highlights:**

- PRRSV (563) led cases with confirmed etiology, followed by *S. suis* (331), and P. multocida (143). PRRSV (530 of 1419) led the number of confirmed respiratory diagnoses, Rotavirus (92 of 339) lead the number of confirmed digestive diagnoses, and *S. suis* (35 of 49) 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.*

# PRRSV Blast Tool Educational material available online on YouTube

Guilherme Cezar[1], Kinath Rupasinghe[1], Daniel Linhares[1], Giovani Trevisan[1]

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

The SDRS has implemented a PRRSV BLAST Tool capability that allows veterinarians and producers to compare their PRRSV ORF5 sequences with the sequences stored at the SDRS database. By using this comparison tool, producers and veterinarians can input a given sequence to identify related sequences in the SDRS database based on nucleotide identity. The tool returns epidemiological information for similar sequences, including when and where they were detected (e.g., state) and their genetic signatures, such as lineage, variant, and RFLP type.. Therefore, the SDRS team created educational materials to help producers and veterinarians use this tool. You can have access to the video by clicking on this link and see the step-by-step of how to submit your sequence and interpret the results of the Blast tool.