Swine Disease Reporting System
Report # 83 (January 7, 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 University: Edison Magalhães, Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Srijita Chandra, Eric Burrough, Phillip Gauger, Joseph Thomas, Darin Madson, Michael Zeller, Rodger Main.

University of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, Stephanie Rossow, Matt Sturos, Hemant Naikare.

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

South Dakota State University 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 University 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 December 31, 2024.

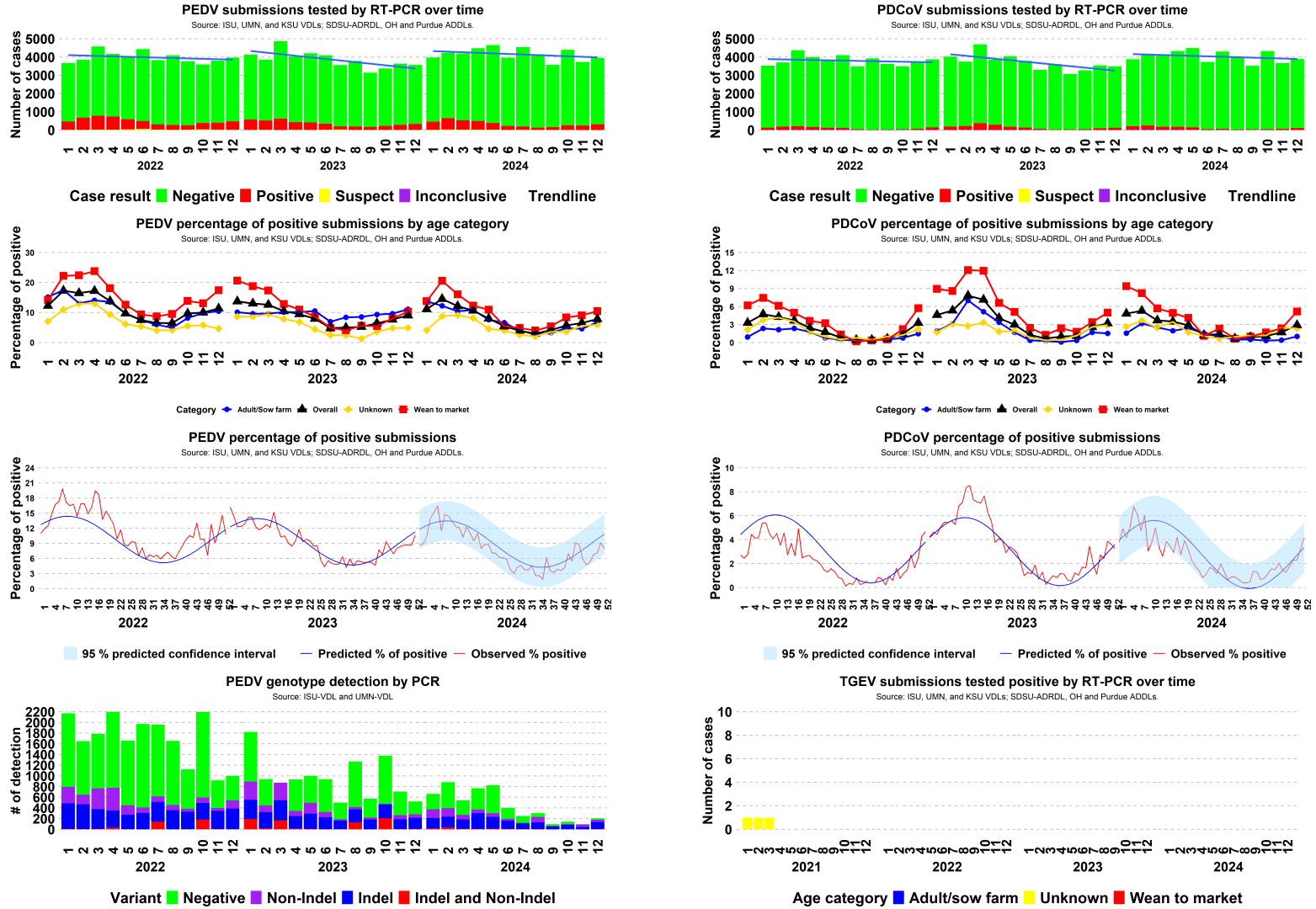# Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.
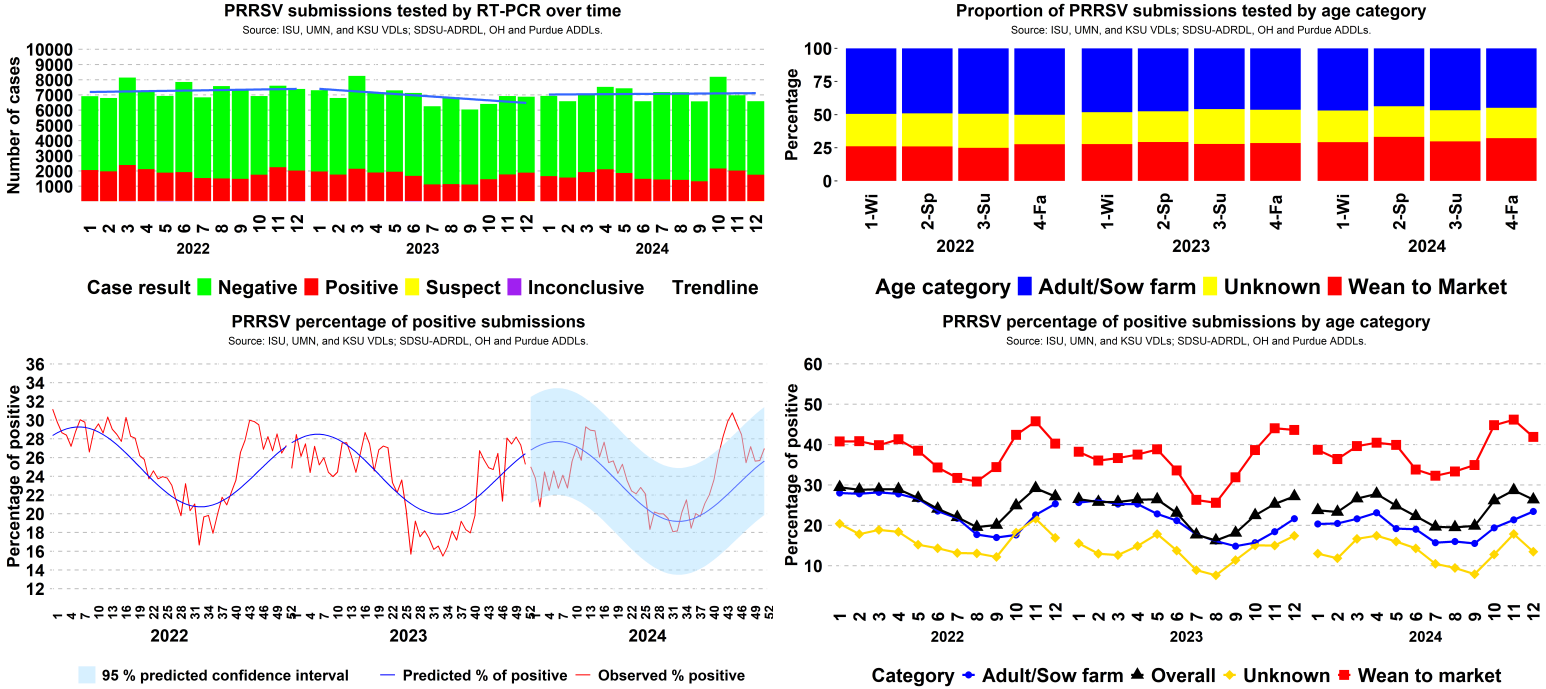
Figure 1. **Top**: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 3 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, 26.4% of 6,584 cases tested PRRSV-positive in December, a moderate decrease from 28.7% of 6,980 in November;
- Positivity in the adult/sow category in December was 23.47% (726 of 3,093), a moderate increase from 21.38% (665 of 3,110) in November;
- Positivity in the wean-to-market category in December was 41.89% (798 of 1,905), a moderate decrease from 46.17% (1,055 of 2,285) in November;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baselines in IA, IN, OK, and SD;

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.

Age category ■ Adult/Sow Farm ■ Unknown ■ Wean to market

PRRSV Lineage/RFLP patterns detected during 2024
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	L1C.2 1-2-4	L1A 1-7-4	L1C.5 1-4-4
IN	L1A 1-7-4	L1A 1-7-2	L1H 1-8-4
KS	L1H 1-8-4	L1A 1-7-4	L1H 1-4-4
MN	L1C.5 1-4-4	L1A 1-7-4	L1C.2 1-2-4
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	PRRSV-1
NE	L1C.5 1-4-4	L1H 1-8-4	L1C.5 1-2-3
OH	L1A 1-4-4	L1C.5 1-4-3	L1A 1-7-2
OK	L1A 1-7-4	L5A 2-2-2	L1H 1-4-4
SD	L1C.5 1-4-4	L1C.3 1-4-1	L1A 1-7-4

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 December 2024, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MN, MO, IL, NE, SD, IN, OH, WI (respective number of sequences: 213, 39, 28, 10, 8, 7, 2, 2, 1).
• In December L1C.5 1-4-4 (249) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (49), and L1A 1-7-4 (45);
• 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.
• The advisory group highlighted that the L1C.5 strain continues to occur in the field at significant numbers, but there are reports of mild clinical presentation compared with the original 2020 L1C.5 strain. They noted that environmental conditions, including sanitation and daily care, play a crucial role in softening the severity of outbreaks. Sequencing is typically reserved for more severe cases to trace origins during outbreaks, and mortality rates vary widely, often influenced by co-infections. They noted that higher viral loads recovered from L1C.5 positive samples could facilitate its transmission due to higher viral pressure of infection. Positive sow farms can perpetuate the virus in an area, increasing the incidence of secondary infections like *Mycoplasma hyopneumoniae* and Influenza A virus. Also, another factor that contributed to the perpetuation of the L1C.5 was that the herds affected by this strain are taken longer to eliminate the virus.

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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 PCR positive results, by age category over time. **Third from top**: *Left PEDV*; *Right PDCoV* expected percentage of positive results for cases tested by RT-PCR and 95% confidence interval for 2024 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, 7.83% of 3,947 cases tested PEDV-positive in December, similar to 6.51% of 3,734 in November;
  - Positivity in the adult/sow category in December was 6.74% (95 of 1,410), a moderate increase from 4.6% (60 of 1,304) in November;
  - Positivity in the wean-to-market category in December was 10.45% (148 of 1,416), similar to 9.06% (124 of 1,369) in November;
  - Overall PEDV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
  - Overall, 2.43% of 206 samples had mixed PEDV genotype detection in December, a moderate increase from 0% of 96 in November;
- Overall, 2.9% of 3,892 cases tested PDCoV-positive in December, similar to 1.72% of 3,670 in November;
  - Positivity in the adult/sow category in December was 1.02% (14 of 1,371), similar to 0.4% (5 of 1,262) in November;
  - Positivity in the wean-to-market category in December was 5.17% (73 of 1,412), a moderate increase from 2.35% (32 of 1,361) in November;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in MN;
- There was 0 positive case for TGEV RNA-PCR in December, 2024 over a total of 3,754 cases tested. It has been 45 months (with a total of 165,267 cases tested) since the last TGEV PCR-positive result;
- The advisory group highlighted that PEDV had generally decreased since 2014, thanks to enhanced biocontainment and biosecurity practices to contain the spread of diseases like PEDV. These biosecurity measures aided in clearing virus circulation and allowed a quicker recovery. Increased focus sow farm biosecurity, including transport and supply management, has been crucial for PEDV control. In grow-finish operations, stricter testing and inspections have helped manage outbreaks, although occasional upticks, such as during pumping season, still occur. Some advisory members noted reduced testing in grow-finish, which might lead to missed cases. Also, the advisory recommended being vigilant during winter, when PEDV activity increases, reinforcing biosecurity practices, mainly in transportation.
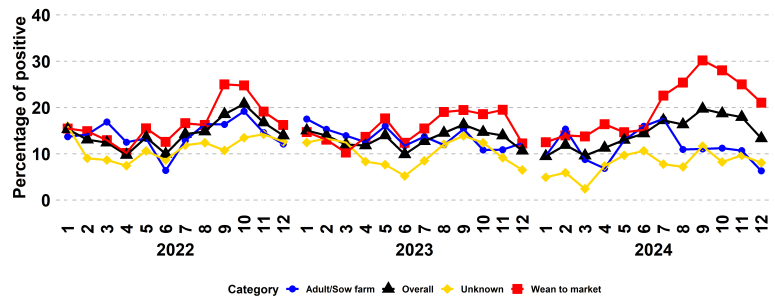
Topic 3 – Detection of *M. hyopneumoniae* DNA by PCR.

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

Case result: ■ Negative ■ Positive ■ Suspect ■ Inconclusive — Trendline
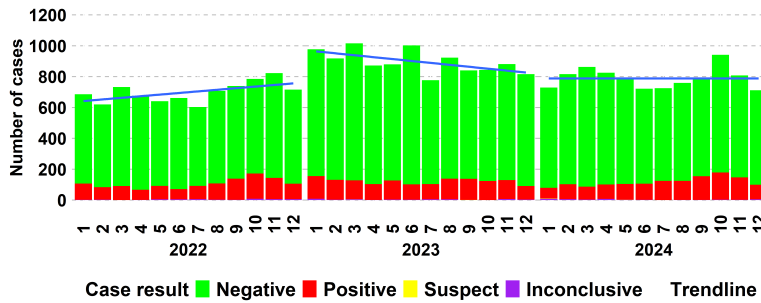
Mycoplasma hyopneumoniae percentage of positive submissions by age category
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Category: ◆ Adult/Sow farm ▲ Overall ◆ Unknown ■ Wean to market

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

■ 95 % predicted confidence interval — Predicted % of positive — Observed % positive
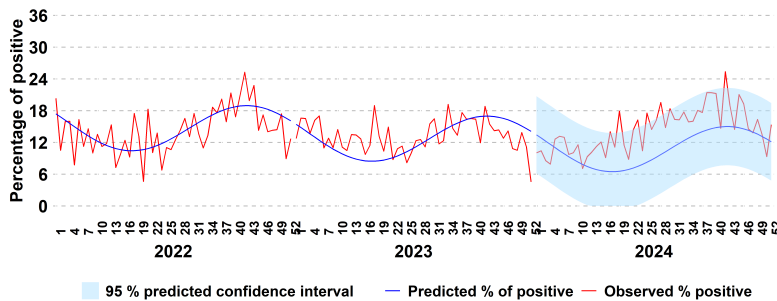
Figure 3. Top: *Left* MHP; MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 13.34% of 712 cases tested *M. hyopneumoniae*-positive cases in December, a moderate decrease from 17.95% of 808 in November;
  - Positivity in the adult/sow category in December was 6.32% (16 of 253), a moderate decrease from 10.7% (26 of 243) in November;
  - Positivity in the wean-to-market category in December was 21.05% (68 of 323), a moderate decrease from 25% (105 of 420) in November;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baselines SD, IL, IN and OK;
- The advisory group highlighted that *Mycoplasma hyopneumoniae* issues have been relatively stable, with occasional flare-ups in finishing sites linked to vaccination protocol deviations or comorbidity with other pathogens such as PRRSV and IAV. The advisory highlighted that the trend for *Mycoplasma hyopneumoniae* elimination in sow farms has been successful, and sow inventory negative for this pathogen should continue to increase in 2025.

# Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.
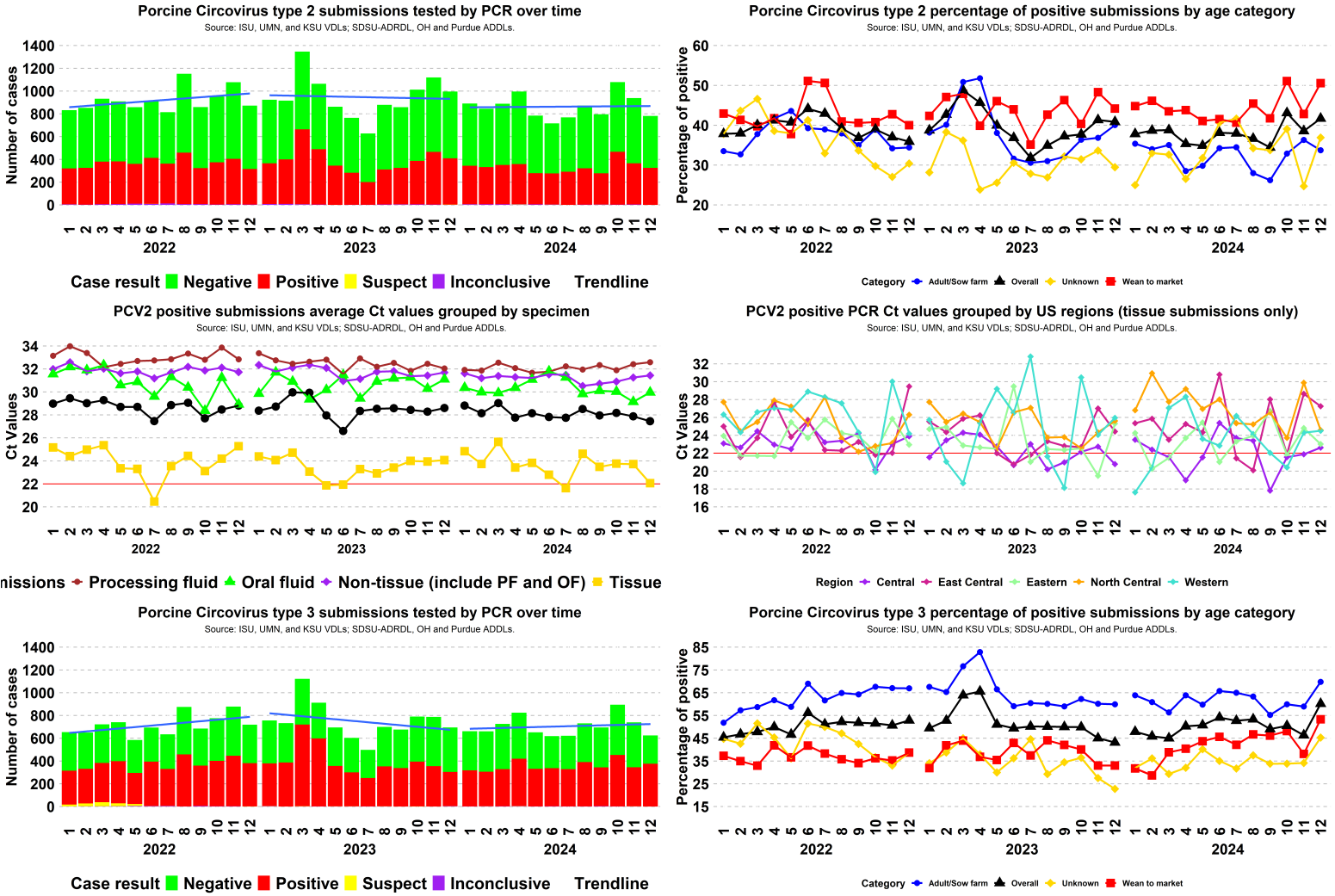
Figure 1. Top: *Left*: Results of PCV2 PCR cases over time; *Right*: PCV2 PCR-positive results, by category over time. **Middle**: *Left*: Average Ct values of PCV2 submissions by specimen; *Right*: Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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). **Bottom** *Left*: Results of PCV3 PCR cases over time; *Right*: PCV3 PCR-positive results, by category over time.

SDRS Advisory Group highlights:

- Overall, 41.69% of 782 cases tested PCV2-positive in December, a moderate increase from 38.55% of 939 in November;
  - Positivity in the adult/sow category in December was 33.72% (116 of 344), a moderate decrease from 36.31% (134 of 369) in November;
  - Positivity in the wean-to-market category in December was 50.56% (179 of 354), a substantial increase from 42.83% (206 of 481) in November;
  - In the month of December, the regions with the lowest PCV2 average Ct values in tissue submissions was Central (64 submissions; average Ct 22.6), Eastern (28 submissions; average Ct 23), Western (11 submissions; average Ct 24.5), North Central (16 submissions; average Ct 24.6), and East Central (8 submissions; average Ct 27.3);
- Overall, 60.16% of 625 cases tested PCV3-positive in December, a marked increase from 46.35% of 740 in November;
  - Positivity in the adult/sow category in December was 69.76% (203 of 291), a marked increase from 58.96% (181 of 307) in November;
  - Positivity in the wean-to-market category in December was 53.33% (144 of 270), a marked increase from 38.14% (135 of 354) in November.

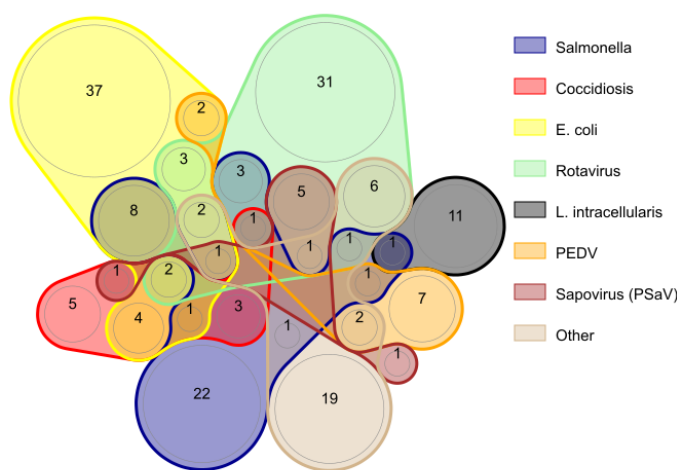# Topic 5 – Detection of Influenza A Virus (IAV) RNA by RT-PCR.
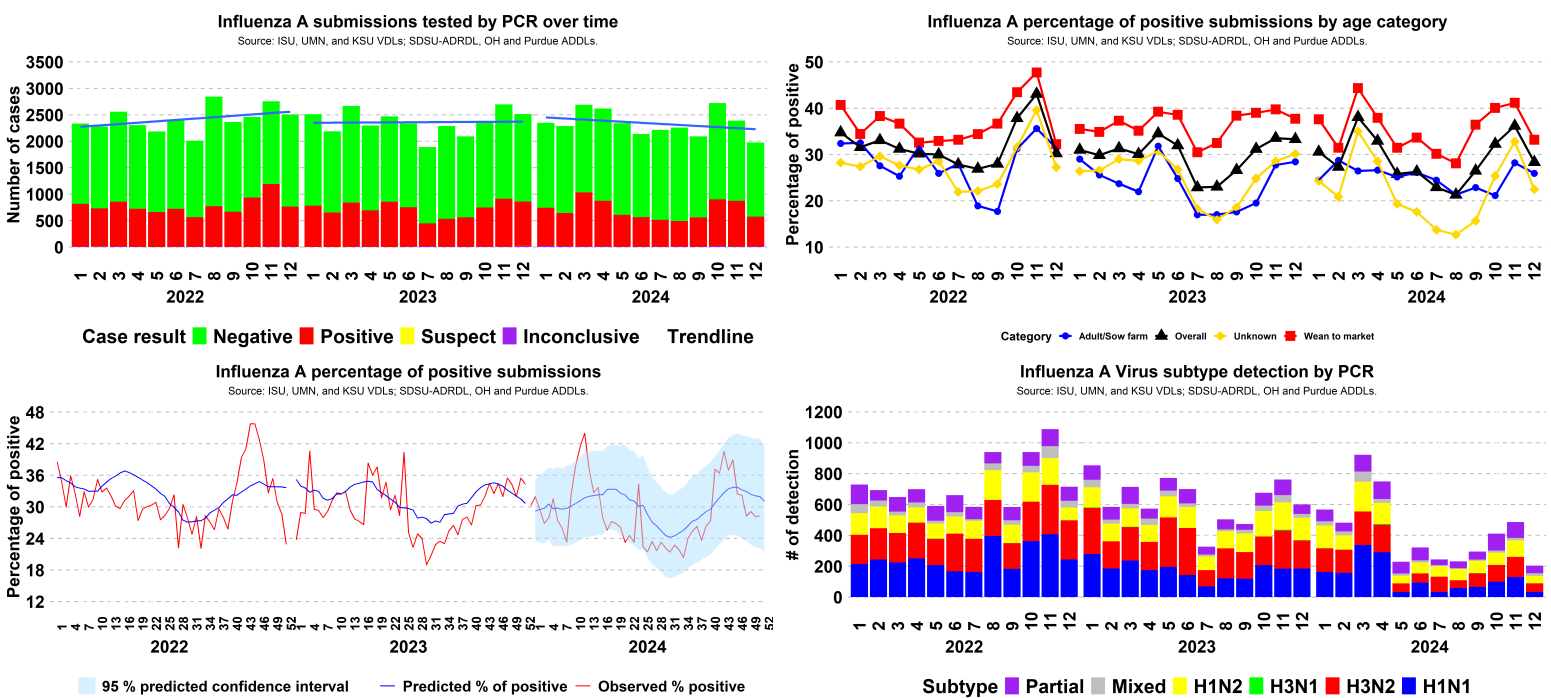
Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 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").
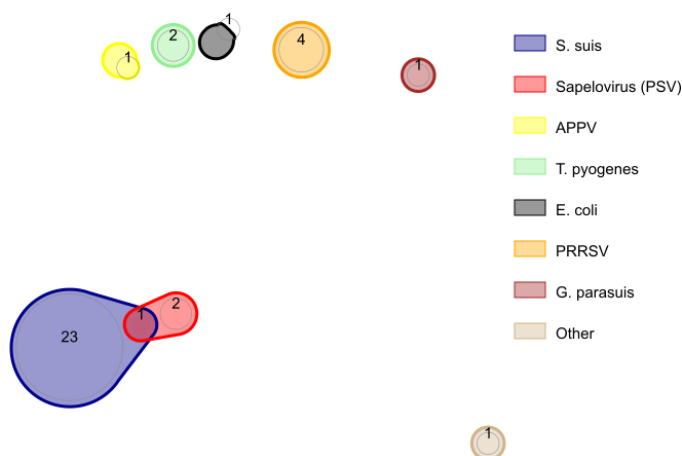
SDRS Advisory Group highlights:

- Overall, 28.35% of 1,975 cases tested IAV-positive cases in December, a substantial decrease from 36.18% of 2,391 in November;
  - Positivity in the adult/sow category in December was 25.94% (117 of 451), a moderate decrease from 28.21% (147 of 521) in November;
  - Positivity in the wean-to-market category in December was 33.19% (311 of 937), a substantial decrease from 41.17% (515 of 1,251) in November.
- Overall IAV-percentage of positive cases was 3 standard deviations above state-specific baselines in MO;
- Overall, 8.82% of 204 samples had mixed subtype detection in December, a substantial increase from 3.29% of 486 in November.
- The advisory group highlighted that endemic Influenza A virus remained prevalent and widespread. Notably, PRRSV outbreaks have also been associated with Influenza flaring up in the farms since early fall.

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, Mainenti, Piñeyro, Siepker, Madson, Thomas 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 November. 1 to December. 20, 2024.

SDRS Advisory Group highlights:

• PRRSV (414) led cases with confirmed etiology, followed by *S. suis* (240), and P. multocida (133). PRRSV (386 of 1039) led the number of confirmed respiratory diagnoses, *E. coli* (60 of 243) lead the number of confirmed digestive diagnoses, and *S. suis* (24 of 37) led the number of confirmed neurological diagnoses.

A 2024 *Swine Disease Reporting System-SDRS* retrospective

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

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

The SDRS's goal is to share information on the activity of endemic and emerging pathogens affecting the swine population in the U.S., assisting veterinarians and producers in making informed decisions on disease prevention, detection, and management. Currently, SDRS is the only publicly available source of swine health information from U.S. veterinary diagnostic laboratories (VDLs). With a database containing information for nine endemic porcine pathogens and more than 1.5 million cases, SDRS is one of the largest U.S. and international databases for veterinary diagnostic information. The SDRS has provided science-based spatiotemporal information on pathogen activity in all age categories, from boar studs to breeding herds to finishing with great representativeness of the U.S. swine industry. Thank you to the six VDL partners, SDRS Advisory Board, and collaborators for all of the accomplishments during 2024.

2024 SDRS retrospective includes but is not limited to:

- Addition of weekly monitoring of Influenza A virus (IAV) PCR detection;
- Incorporation of new SDRS dashboards with revamped information, making them easier to navigate and providing new tools such as the Influenza A virus state-level monitoring;
- Addition of PEDV genotype data: the new information provides PEDV variants data that can be classified based on specific genetic characteristics on the spike protein as INDEL and Non-INDEL variants;
- Addition of a new PRRSV ORF 5 sequence page in the PDF report, which includes charts with information about the total number of PRRSV ORF5 sequences performed in the VDLs, the total number of sequences with less than 95% similarity with the SDRS database, number for most frequent sequences detected in the U.S. by Lineage + RFLP, and most frequent sequences detected across U.S. states;
- Implementation of PRRSV ORF5 variant classification system and display in the SDRS Blast tool;
- Addition of SDRS Blast tool for PRRSV. The web-based tool allows veterinarians, producers, and other users to compare their ORF5 sequences with those in the SDRS database, identify sequences present in the database by level of nucleotide identity, when and where similar sequences occurred before, and their genetic nomenclatures: lineage, RFLP, and variant;
- SDRS has and will continuously actively support the AASV PEDV Elimination Task Force, providing data to aid the U.S. swine industry to keep track of PEDV activity in the field;
- Addition of an ongoing SDRS survey where the audience can make suggestions of new pathogens and improvements on the SDRS project. If you have suggestions for us, click here.

SDRS Extension and Education:

- SDRS project website pages (*www.fieldepi.org/SDRS*), including the dashboards and Blast tool, had 2,215 unique IP visitors in 2024;
- 12 editions of PDF, audio, and video reports have been shared through e-mail for 474 receivers registered from 195 organizations from 15 different countries and posted on the SDRS webpage;
- On the FieldEpi LinkedIn page, the SDRS videos achieved more than 51,395 visualizations;
- Generated two published peer reviews manuscripts: Monitoring emerging pathogens using negative nucleic acid test results and Macroepidemiological aspects of porcine circoviruses 2 and 3 in the United States from 2002-2023;
- SDRS hosted talks during the last 12 editions with 11 special guests:
    -> The SDRS YouTube channel achieved 5,162 views on the video reports and education material.
    -> Audio reports have been shared through podcast platforms, including *Spotify*, *Apple Podcast*, and *Amazon Music*, achieving 3,206 downloads from 23 different countries;

Pathogen activity highlights:

- During the fall of 2024 (September to November), PRRSV had the historically highest percentage of PCR-positive submissions in the wean-to-market category (42.3% of positive cases) since Fall 2020. The wean-to-market category represented 56% of the L1C.5 detections. The majority of this activity was related to the record of PRRSV lineage 1C.5 detection that had the historical highest detection within a month (501 in November 2024);
- The most frequent wild-type PRRSV-2 strains detected were: L1C.5 (L1C variant) 1-4-4, L1A 1-7-4, and L1C.2 1-2-4. Out of all the wild-type strains detected in 2024, over 50% (3,144) were L1C.5, breaking the record of detection within a year since its emergence in 2020. The majority of the sequences were detected in Iowa (1,873), followed by Minnesota (524), Missouri (309), Nebraska (160), and Ohio (40);
- During the summer of 2024 (June to August), PEDV had the historically lowest percentage of positive submission detection in the Adult/sow farm category (4.42% of positive cases). Besides the summer lower detection, PEDV followed the historical levels of detection throughout the year. PDCoV also followed the historical trend except for the weeks of March 4th and 25th where the positivity was below the expected;
- March 22nd of 2021 marked the last field sample received at the SDRS laboratory network with an RT-PCR positive result for TGEV. Up to December 2024, more than 165,000 submissions, including more than 400,000 samples, have been tested for TGEV, and no TGEV-positive result has been detected;
- *M. hyopneumoniae* percentage of PCR-positive submissions from breeding herds have decreased substantially from 2021 (21.75%) to 2022 (13.5%) and has kept a lower level since then until 2024 (12%). However, in the wean-to-market category *M. hyopneumoniae* positivity reached the highest levels (27%) since the fall of 2020. In addition, using Iowa State University VDL data, the number of cases with a confirmed tissue diagnosis for *M. hyopneumoniae* (cases where diagnosticians gather available data including as clinical history, tests performed, and microscopic and macroscopic lesions) decreased over time, reaching a record low number in 2024 (203 cases);
- PCV3 kept its trend of detection being the only pathogen monitored by the SDRS having positivity in the age category Adult/sow farm above the positivity in the wean-to-market category in all the months. PCV2 average yearly positivity in the Adult/sow farm category decreased from 39% in 2023 to 33% in 2024. Also, PCV2-confirmed tissue diagnosis decreased in 2024 (399 cases) compared with 2023 (540);
- Influenza A virus bi-seasonality pattern of PCR detection cases continued to occur in the spring and fall of 2024 as expected. However, the peaks of overall positivity were slightly higher in 2024 compared with 2023. In 2023, the peaks of overall IAV positivity occurred in May (34% positivity) and November (33% positivity). In 2024, the peaks of positivity occurred in March (38%) and November (35%);
- In 2024, there were decreases in the number of Influenza A virus subtyping and PEDV genotype tests. The majority of this decrease was attributed to testing strategies by some participant VDLs that started to offer the screening PCR separately from the subtype/genotype PCRs that previously were offered together. Also, some production systems started to test PEDV genotype in-house;

Highlights for disease diagnosis from *Iowa State University Veterinary Diagnostic Laboratory*:

- PRRSV had the highest number of porcine-confirmed diagnoses (2,566) followed by *Streptococcus suis* (1,735) and Influenza A virus (935) in 2024;
- Different agents including PRRSV, Influenza A virus, *P. multocida*, *Actibacillus suis*, *Streptococcus suis*, and *Salmonella* have given signals for increased diagnosis during October and November of 2024.

Happy 2025!!! and keep tuned for new SDRS developments in 2025.

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