Swine Disease Reporting System
Report # 87 (May 06, 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 April 31, 2025.

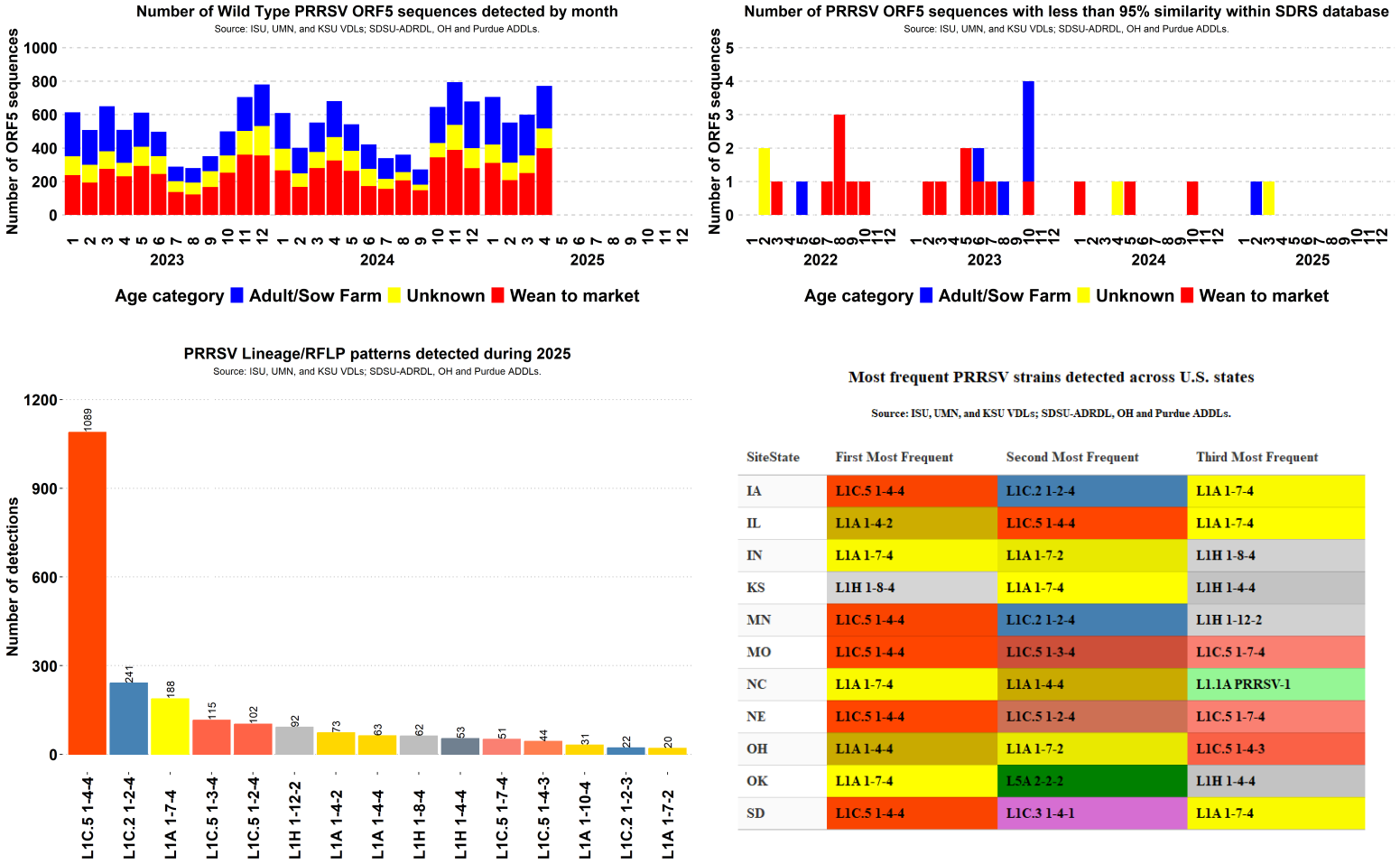# Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.
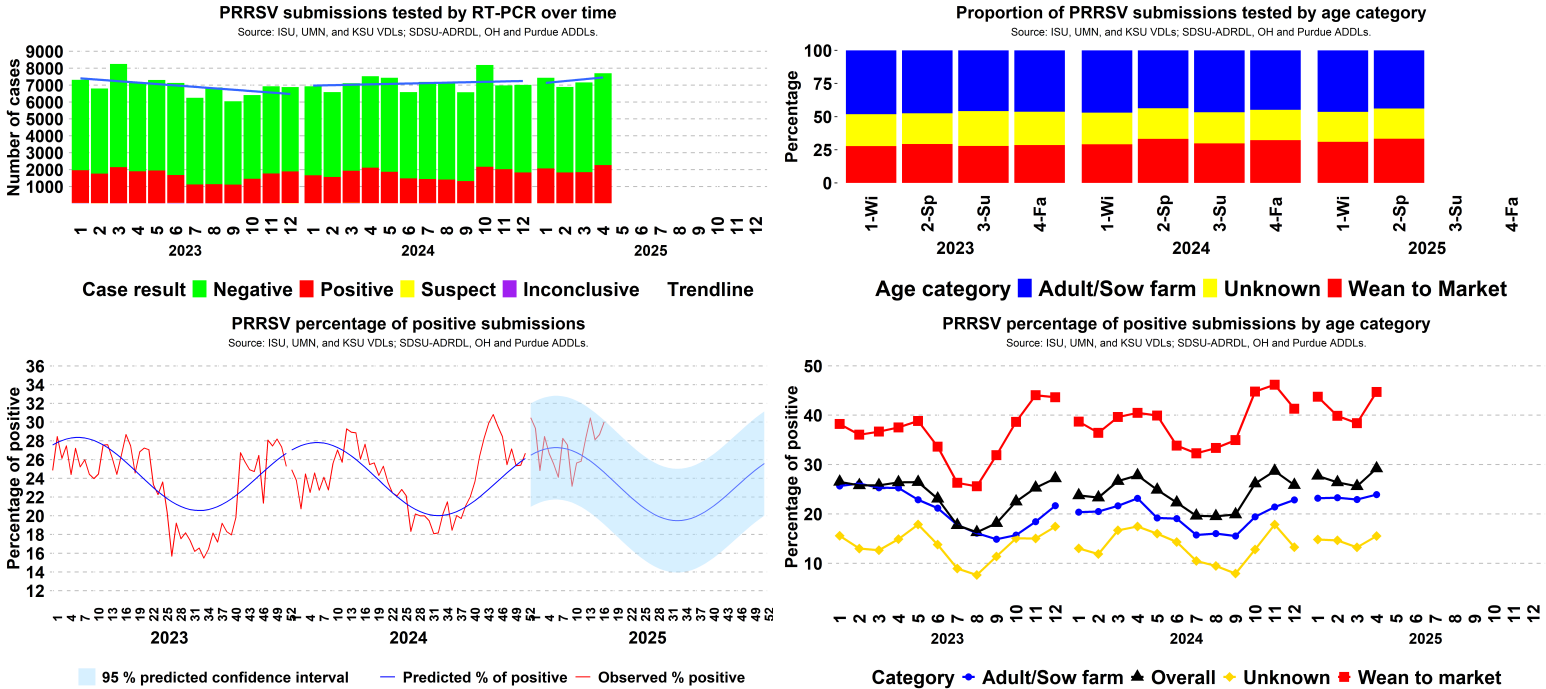
Figure 1. Top: *Left*: Results of PRRSV RT-PCR cases over time; *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom**: *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on weekly data observed in the previous 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, 29.21% of 7,700 cases tested PRRSV-positive in April, a moderate increase from 25.62% of 7,159 in March;
- Positivity in the adult/sow category in April was 23.91% (789 of 3,300), similar to 22.92% (738 of 3,220) in March;
- Positivity in the wean-to-market category in April was 44.7% (1,190 of 2,662), a substantial increase from 38.38% (877 of 2,285) in March;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baseline in IA and MN;
- The 44% of PRRSV positive submissions represent the highest April positivity since 2018. Iowa and Minnesota were the states contributing with the highest number of positive cases. In addition, the overall positivity increased for PRRSV was driven by positive cases coming from grow-finish sites, which emphasizes the need for biosecurity and biocontainment to mitigate further spread
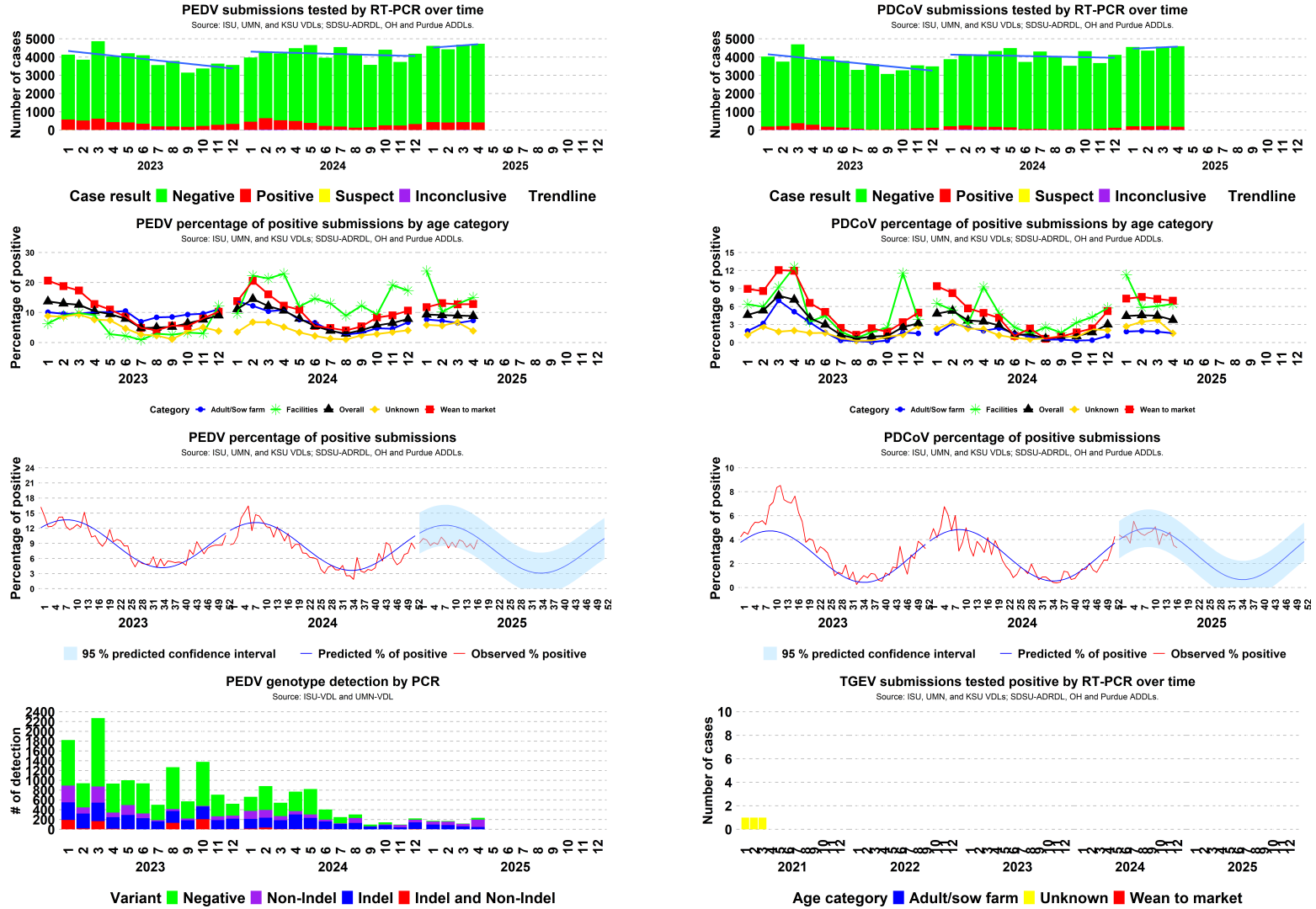
Topic 2 – PRRSV ORF5 sequences detection over time

Number of Wild Type PRRSV ORF5 sequences detected by month
Source: ISU, UMN, and KSU VDLs; SDS-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	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	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	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 April 2025, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MN, NE, MO, SD, IL, IN, OK, OH, PA (respective number of sequences: 252, 85, 32, 26, 10, 9, 7, 5, 4, 2).
- In April L1C.5 1-4-4 (342) was the PRRSV sequence most detected in the U.S., followed by L1C.2 1-2-4 (86), and L1C.5 1-2-4 (46);
- 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.
- In 2025, the PRRSV L1C.5.32 variant became the most predominant variant detected, with 25% of all the detections in 2025, followed by the original variant L1C.5 with 18% of all detections. Therefore, only these two variants represent 43% of all the U.S. PRRSV ORF5 sequences recovered in the SDRS participant laboratories in 2025. According to the advisory group, the variant L1C.5.32 are still clinically similar to the original L1C.5 so far, causing severe losses.

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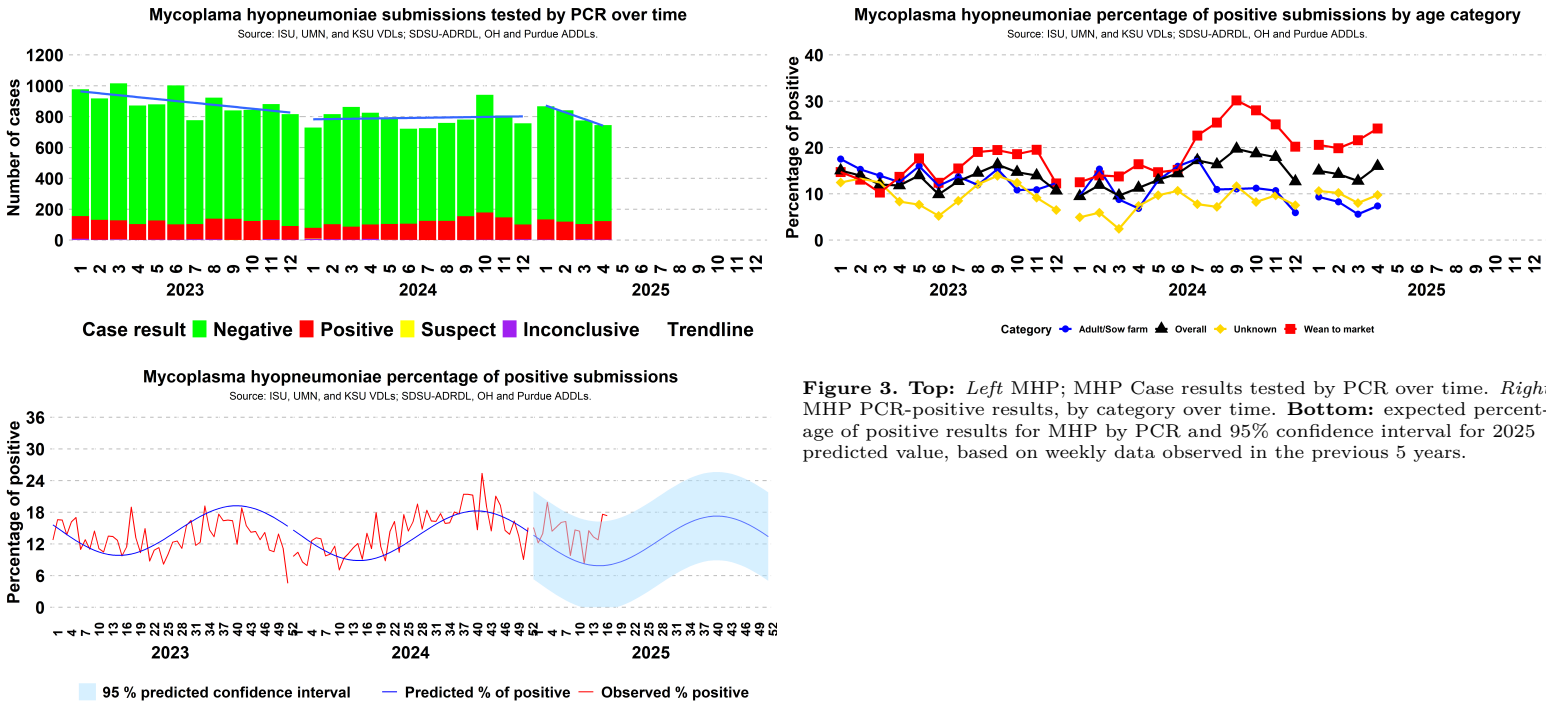# Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

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. 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, 8.84% of 4,728 cases tested PEDV-positive in April, similar to 9.02% of 4,680 in March;
  - Positivity in the adult/sow category in April was 7.37% (122 of 1,656), similar to 6.52% (106 of 1,627) in March;
  - Positivity in the wean-to-market category in April was 12.81% (231 of 1,803), similar to 12.73% (217 of 1,705) in March;
- Positivity in the facilities category in April was 15% (21 of 140), a moderate increase from 12.88% (17 of 132) in March;
  - Overall PEDV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN;
  - Overall, 0% of 236 samples had mixed PEDV genotype detection in April, similar to 0.85% of 117 in March;
- Overall, 3.76% of 4,597 cases tested PDCoV-positive in April, similar to 4.46% of 4,571 in March;
  - Positivity in the adult/sow category in April was 1.56% (25 of 1,604), similar to 1.81% (28 of 1,549) in March;
  - Positivity in the wean-to-market category in April was 6.97% (122 of 1,751), similar to 7.26% (123 of 1,695) in March;
- Positivity in the facilities category in April was 6.43% (9 of 140), similar to 6.06% (8 of 132) in March;
- Overall PDCoV-percentage of positive cases was 3 standard deviations above state-specific baseline in IN and MO;
- There was 0 positive case for TGEV RNA-PCR in April, 2025 over a total of 4,494 cases tested. It has been 50 months (with a total of 183,421 cases tested) since the last TGEV PCR-positive result;
- There were some regional positive cases of PEDV coming from sow farms in the first week of April (IN, IA, OK, KS). In the last week of April, more positive cases started to come from Minnesota. However, the number of positive cases coming from these states were still within the historical baseline for the month of April with the exception of IN (above the expected).
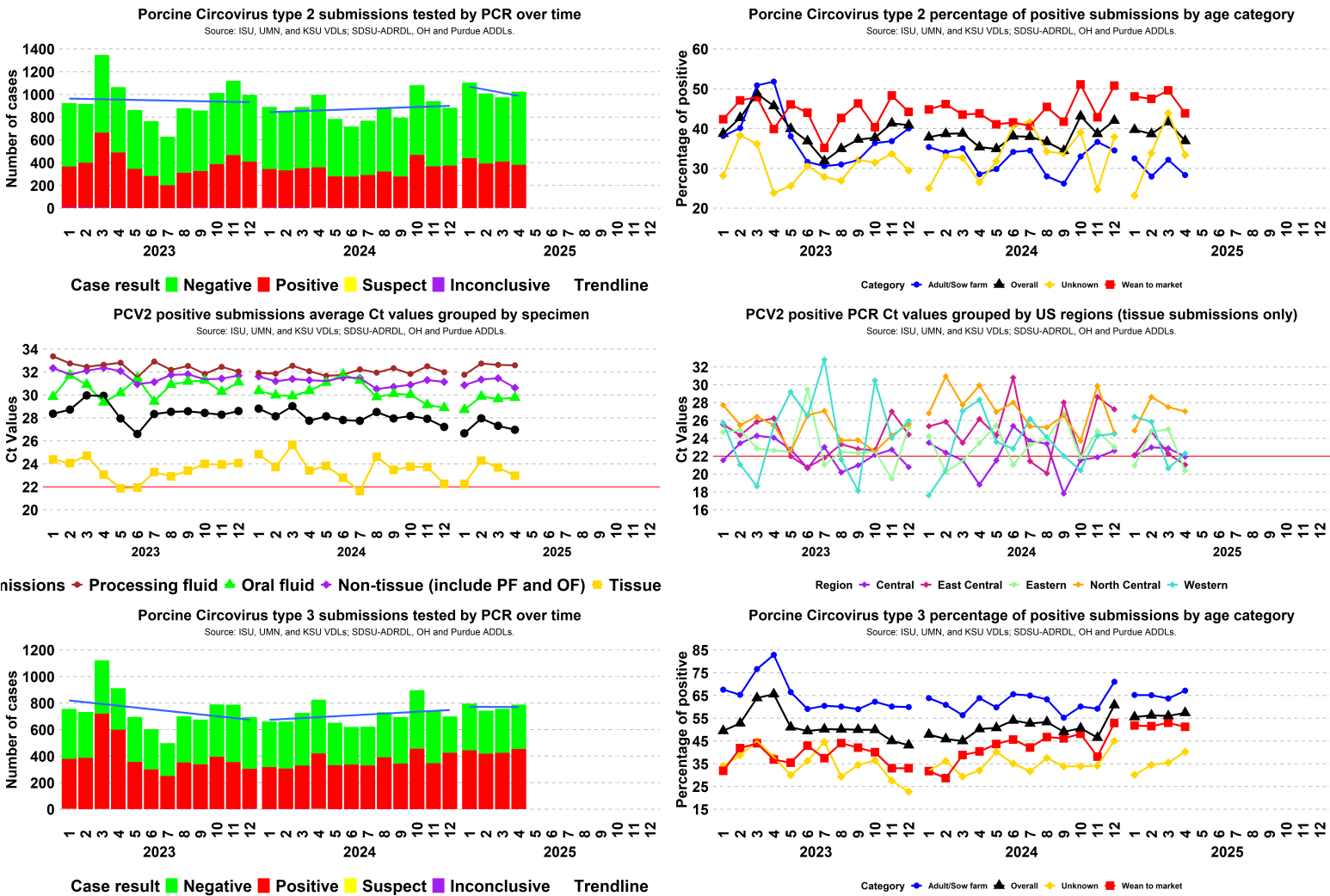
Mycoplama hyopneumoniae submissions tested by PCR over time
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

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 2025 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 15.97% of 745 cases tested *M. hyopneumoniae*-positive cases in April, a moderate increase from 12.77% of 775 in March;
  - Positivity in the adult/sow category in April was 7.39% (19 of 257), similar to 5.6% (15 of 268) in March;
  - Positivity in the wean-to-market category in April was 24.11% (88 of 365), a moderate increase from 21.56% (69 of 320) in March;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baseline in MN and IN;
- In 2025, *Mycoplasma hyopneumoniae* had the first quarter of the year with the lowest number of confirmed tissue diagnoses historically (31 cases) in the ISU-VDL.

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# 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, 36.91% of 1,024 cases tested PCV2-positive in April, a moderate decrease from 41.64% of 975 in March;
    - Positivity in the adult/sow category in April was 28.33% (115 of 406), a moderate decrease from 32.13% (134 of 417) in March;
    - Positivity in the wean-to-market category in April was 43.83% (238 of 543), a substantial decrease from 49.58% (236 of 476) in March;
    - In the month of April, the regions with the lowest PCV2 average Ct values in tissue submissions was Eastern (20 submissions; average Ct 20.4), East Central (22 submissions; average Ct 21), Central (73 submissions; average Ct 21.9), Western (14 submissions; average Ct 22.3), and North Central (31 submissions; average Ct 27);
- Overall, 57.41% of 789 cases tested PCV3-positive in April, similar to 56.01% of 757 in March;
    - Positivity in the adult/sow category in April was 67.14% (237 of 353), a moderate increase from 63.66% (219 of 344) in March;
    - Positivity in the wean-to-market category in April was 51.22% (189 of 369), similar to 52.99% (177 of 334) in March.
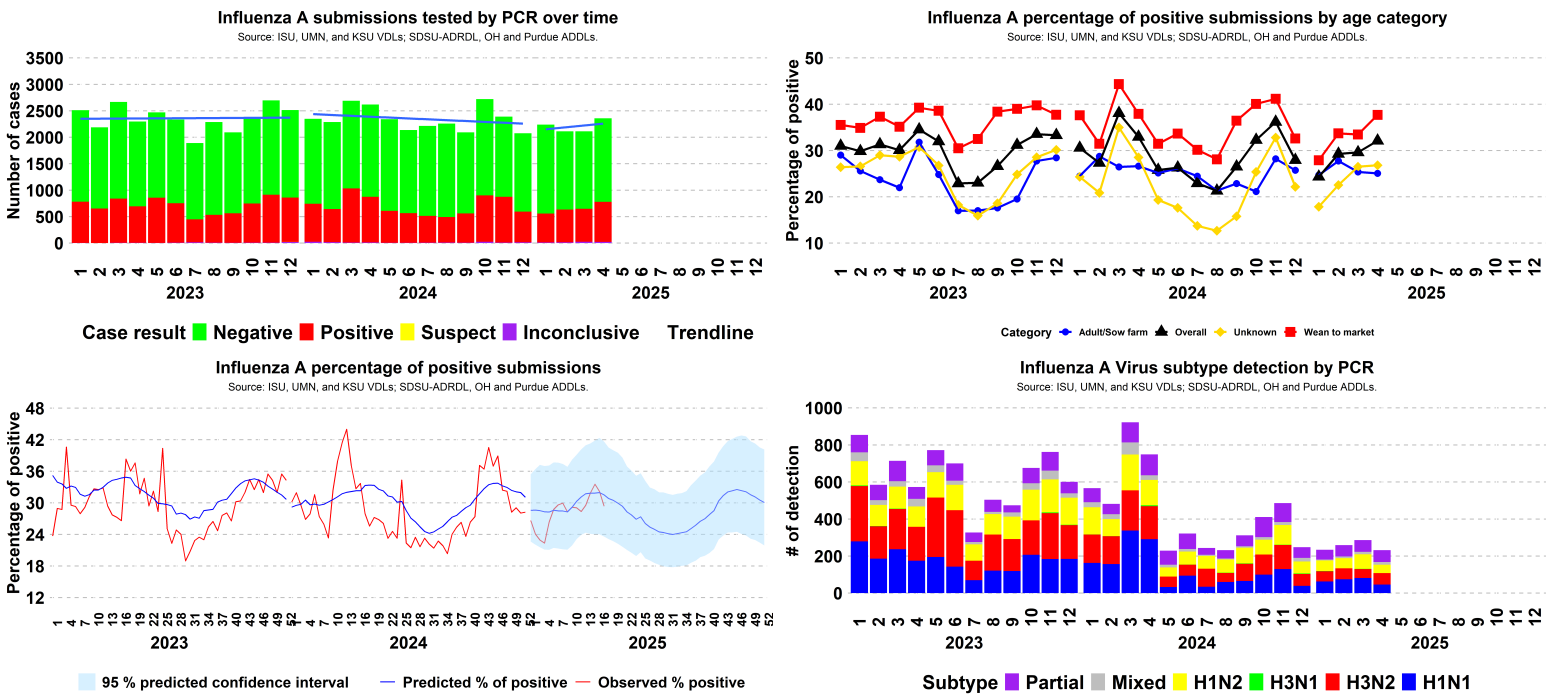
Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2025 predicted value, based on weekly data observed in the previous 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, 32.1% of 2,358 cases tested IAV-positive cases in April, a moderate increase from 29.59% of 2,112 in March;
  - Positivity in the adult/sow category in April was 25.06% (110 of 439), similar to 25.37% (119 of 469) in March;
  - Positivity in the wean-to-market category in April was 37.68% (459 of 1,218), a moderate increase from 33.46% (339 of 1,013) in March.
- Overall IAV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- Overall, 6.47% of 232 samples had mixed subtype detection in April, similar to 4.55% of 286 in March.

Topic 6 – Confirmed tissue cases etiologic/disease diagnosis at the ISU-VDL.
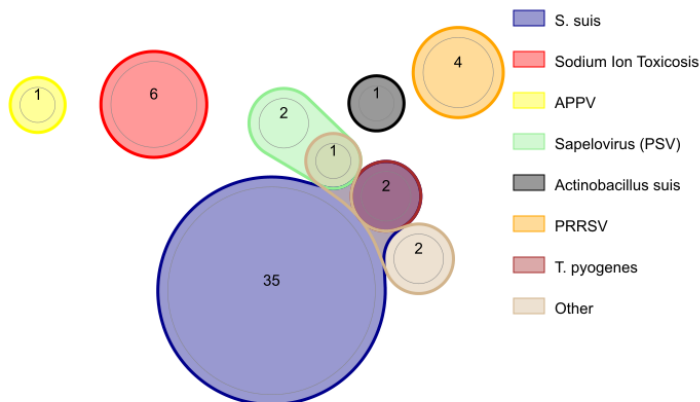
Overall diagnosis
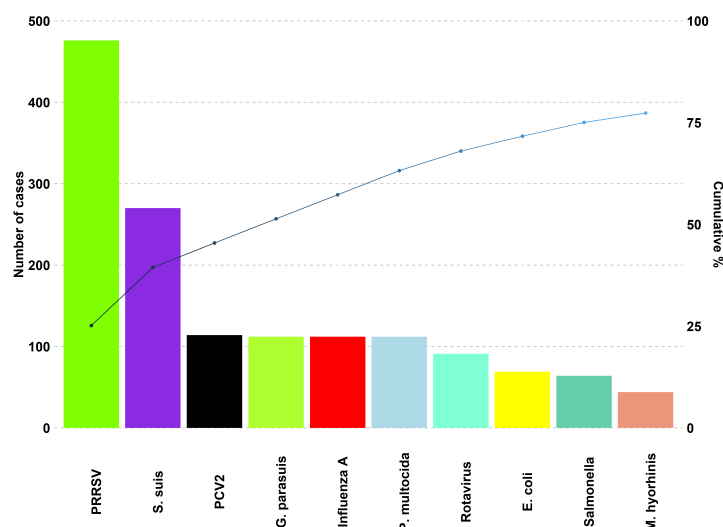
Digestive
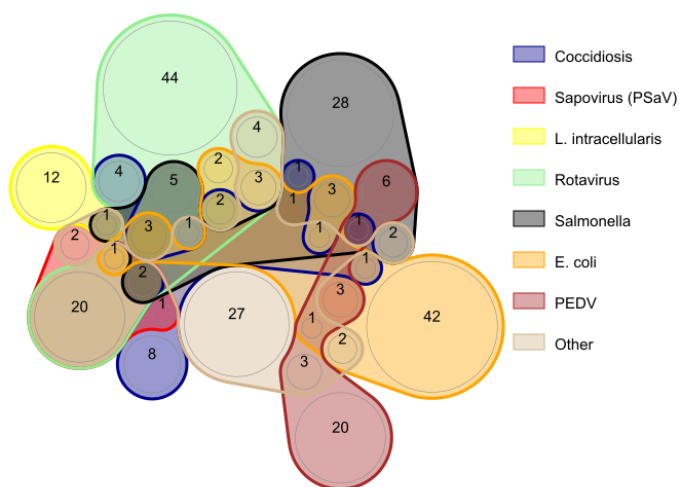
Respiratory
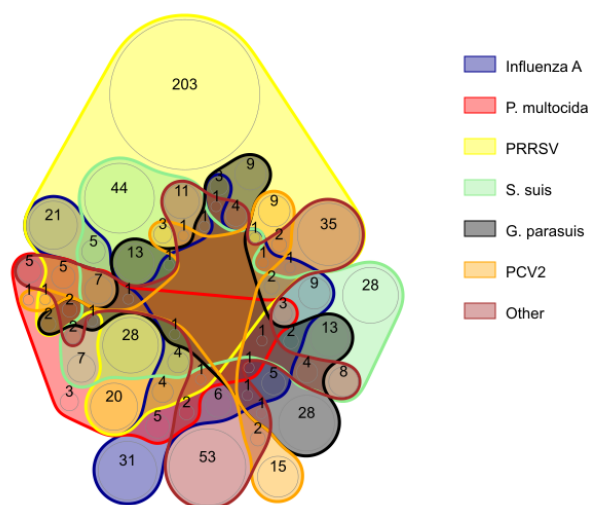
Nervous

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 March. 1 to April. 25, 2025.

SDRS Advisory Group highlights:

• PRRSV (476) led cases with confirmed etiology, followed by *S. suis* (270), and PCV2 (114). PRRSV (447 of 1169) led the number of confirmed respiratory diagnoses, Rotavirus (91 of 350) lead the number of confirmed digestive diagnoses, and *S. suis* (37 of 57) led the number of confirmed neurological diagnoses.

• There were consecutive signals on the week of March 31st and April 7th for overall increased cardiovascular confirmed tissue diagnosis. Also, on the same weeks there were signals for increased *Trueperella pyogenes* and PRRSV confirmed tissue diagnosis.

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Application of Lineage and Variant Classification in the SDRS PRRSV Sequence Analysis

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

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

The SDRS has implemented lineage and variant classification algorithms to systematically categorize incoming PRRSV ORF5 sequences in the SDRS PRRSV Sequencing Database. This classification enhances the ability for epidemiological tracking, identify emerging variants, and provide insights into the genetic relationships between sequences over time. Specifically, the implementation aimed to:

1. Assign lineages to PRRSV-1 and PRRSV-2 ORF5 sequences to determine their evolutionary origin.
2. Further classify PRRSV-2 sequences into genetic variants using a fine-scale machine learning-based classification model.

The implementation of lineage and variant classification provided insights into PRRSV evolution and distribution of specific strains over time, space, and age groups. Among the 117,950 sequences analyzed from January 2006 till March 31, 2025, Ingelvac MLV vaccine-like sequences represented 12.84% (n = 15,146) of submissions followed by 2.84% (n = 3,349) Ingelvac ATP and 2.67% (n= 3,136) Prevacent vaccine-like sequences. 77.81% (n = 91,775) of received sequences were wild type sequences. The most common variant, 5A.1, accounted for 17.32% (n = 20,051) of all sequences, with significant activity in recent years. This was closely followed by variant 1C-unclassified (n = 13,866). Temporal analysis revealed a rise in variant 1C.5 detections (n = 6,777), particularly between 2020 and 2024 (n = 6,764), indicating an increasing field presence.

In 2024, the SDRS PRRSV Sequencing Database processed 8,306 sequences spanning 14 distinct lineages (Figure 1) and 82 unique variants. Lineage 1C was the most detected, accounting for 46.69% (n = 3,878) of all sequences, followed by lineage 5A at 15.53% (n = 1,290) and lineage 1A at 14.64% (n = 1,216). The most frequently detected variants were 1C.5 (n = 1,309) and 5A.1 (n = 1,286). Variants 1C.5.32 (n = 1,137) and 1C.5.37 (n = 159) were also detected within 1C.5 (Figure 2). Among the sequences received in 2024, 12% (n = 996) were Ingelvac MLV vaccine-like sequences, followed closely by 11.16% (n = 927) Prevacent vaccine-like sequences, and 75.86% (n = 6,301) were categorized as wild type sequences.

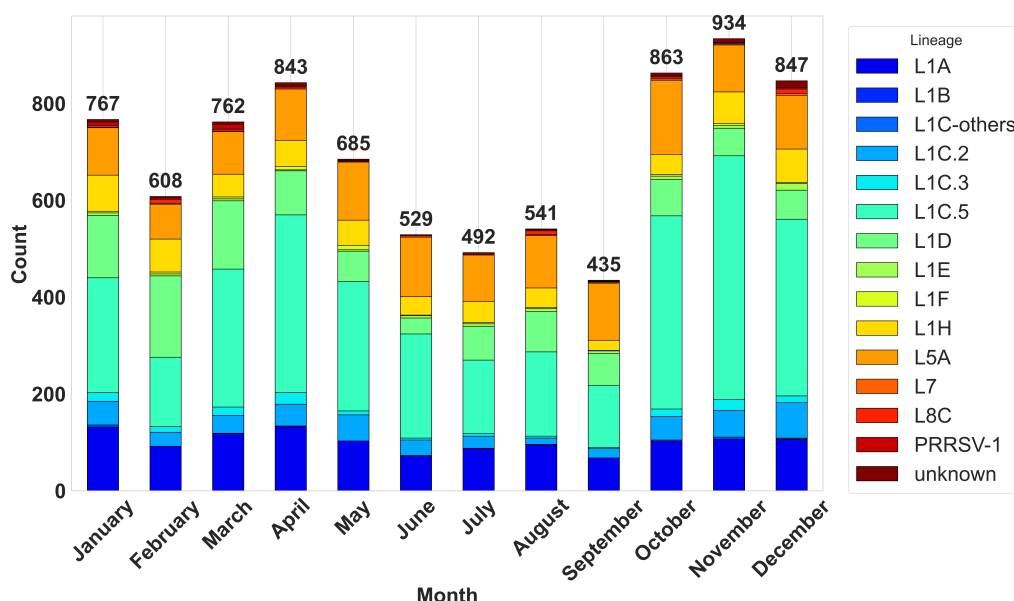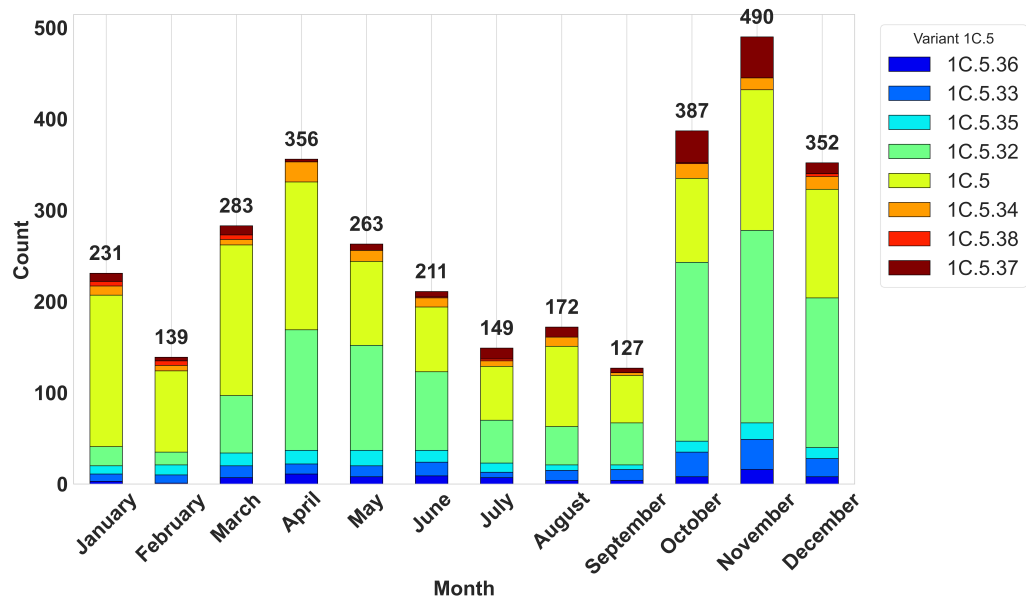**Figure 1.** Lineage distribution in sequences detected in 2024 on a monthly basis.

Figure 2. Temporal distribution of variants under the lineage 1C.5 in 2024.

Integrating a robust lineage and variant classification system into the SDRS PRRSV Sequencing Database has improved the tracking and analysis of PRRSV evolution. This classification framework enhances real-time disease surveillance, supports risk assessment, and informs vaccine strategies by identifying genetic shifts in the PRRSV population.

The SDRS PRRSV BLAST tool (Figure 3) serves as a powerful platform for users to compare their sequences against the SDRS PRRSV Sequencing Database, enabling the identification of similar sequences present in the database and corresponding received date, site state, RFLP, lineages, and variants. This tool ensures that users can access the most up-to-date reference data. It facilitates epidemiological tracking if similar sequences have been seen before, when, where, and their respective genetic nomenclatures, and supports real-time disease surveillance efforts. Click here to access full manuscript

Figure 3. SDRS PRRSV BLAST tool interface where the lineage, location, variant, RFLP and percentage similarity to the query sequence can be viewed. The number of results returned can be changed to view more results.

Similar ID	Received Date	State	Lineage	Variant	RFLP	% Similarity
SDRS31582/04Dec2012/MN	12/4/2012	MN	L5A	5A.1	2-5-2	100.00
SDRS31583/04Dec2012/MN	12/4/2012	MN	L5A	5A.1	2-5-2	99.83
SDRS37663/17Jan2014/CO	1/17/2014	CO	L5A	5A.1	2-5-2	99.83
SDRS60255/14Dec2017/UN	12/14/2017	UN	L5A	5A.1	2-5-2	99.83
SDRS62193/28Feb2018/UN	2/28/2018	UN	L5A	5A.1	2-5-2	99.83
SDRS66168/02Oct2018/MN	10/2/2018	MN	L5A	5A.1	2-5-2	99.83
SDRS81944/04Feb2021/MN	2/4/2021	MN	L5A	5A.1	2-5-2	99.83
SDRS85250/02Jul2021/Unknown	7/2/2021	Unknown	L5A	5A.1	2-5-2	99.83
SDRS117679/21Jan2025/IA	1/21/2025	IA	L5A	5A.1	2-5-2	99.67
SDRS117978/23Jan2025/Unknown	1/23/2025	Unknown	L5A	5A.1	2-5-2	99.67