

Swine Disease Reporting System

Report # 78 (August 06, 2024)

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](#), Extension and Outreach: [Edison Magalhães](#).

Iowa State University: Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Srijita Chandra, Eric Burrough, Phillip Gauger, Christopher Siepker, Marta Mainenti, 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, Ashley Johnson, 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 Glowzinski.

Note: This report contains data up to July 31, 2024.

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

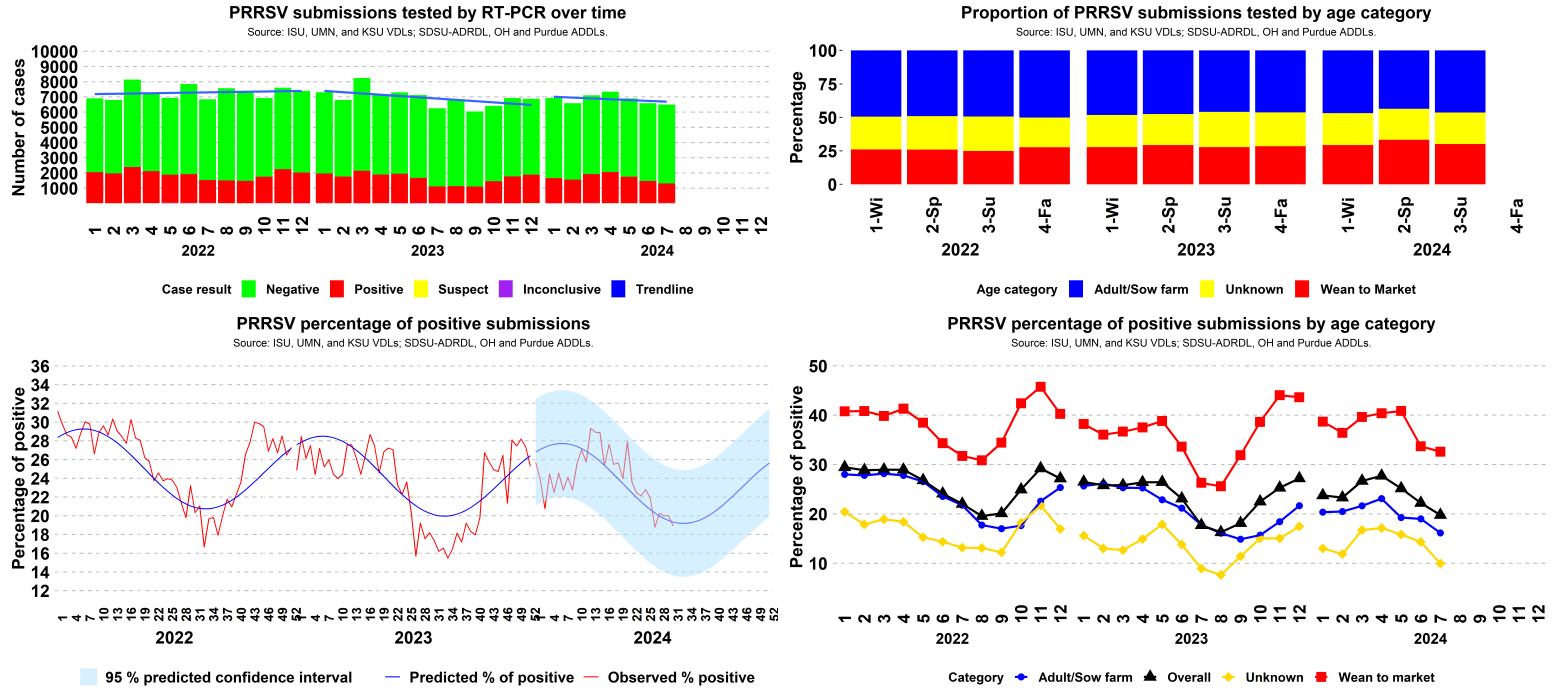
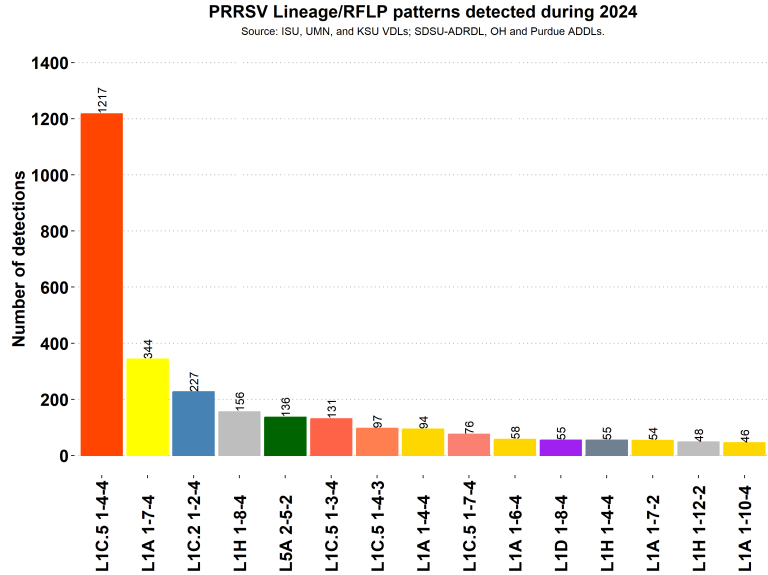
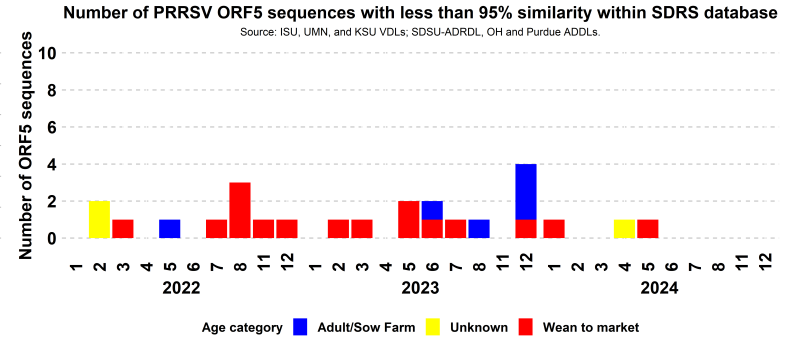
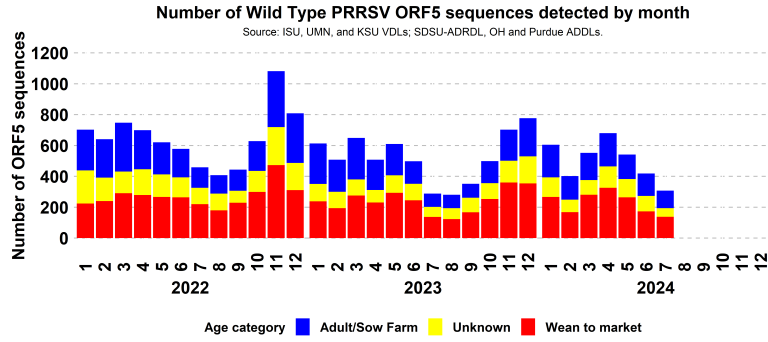


Figure 1. Top: *Left:* Results of PRRSV RT-PCR cases over time; *Right:* Proportion of accession ID cases tested for PRRSV by age group per year and season. **Bottom:** *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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, 19.78% of 6,502 cases tested PRRSV-positive in July, a moderate decrease from 22.23% of 6,587 in June;
 - Positivity in the adult/sow category in July was 16.17% (476 of 2,944), a moderate decrease from 19.01% (593 of 3,120) in June;
 - Positivity in the wean-to-market category in July was 32.6% (656 of 2,012), similar to 33.7% (651 of 1,932) in June;
- Overall PRRSV-percentage of positive cases was 3 standard deviations above state-specific baselines IN, OK, and SD;
- The advisory group highlighted that the percentage of positive submissions above the expected in Indiana state might be due to surveillance strategies in some production systems. However, regarding Kansas state, the advisory highlighted that it appears to have new PRRSV introductions, causing increased PRRSV activity.

Topic 2 – PRRSV ORF5 sequences detection over time



Most frequent PRRSV strains detected across U.S. states
Source: ISU, UMN, and KSU VDLs; SDSU-ADRDL, OH and Purdue ADDLs.

Site/State	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	L1A 1-3-4
IN	L1A 1-7-4	L1A 1-7-2	L1A 1-4-3
KS	L1H 1-8-4	L1A 1-10-3	L1A 1-7-4
MN	L1C.5 1-4-4	L1A 1-7-4	L1C.5 1-4-3
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	L1C.5 1-2-3	L1H 1-8-4
OH	L1C.5 1-4-3	L1A 1-7-4	L1A 1-4-4
OK	L5A 2-2-2	L1H 1-4-4	L5A 2-5-2
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 July 2024, The states with higher number of PRRSV L1C.5 (variant) detections were detected IA, MO, MN, NE, IL, IN, SD (respective number of sequences: 83, 22, 17, 4, 2, 2, 2).
- In July L1C.5 1-4-4 (89) was the PRRSV sequence most detected in the U.S., followed by L1A 1-7-4 (39), and L1C.2 1-2-4 (19);
- 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 the clinical importance of the PRRSV L1C.2 RFLP 1-2-4 (Illinois’s predominant lineage and the second most detected in Iowa). For some advisory members, this strain has caused similar clinical signs as the L1C.5 RFLP 1-4-4 in the farms. However, other advisory members highlighted this strain has caused an increased number of abortions in the field. In addition, the advisory highlighted that after the farm breaks with PRRSV L1C.2, the flows downstream performs similarly to the breaks with L1C.5, causing severe nursery losses without showing significant clinical differences based on the RFLP patterns within these two lineages.

Topic 2 – Enteric coronavirus RNA detection by RT-qPCR

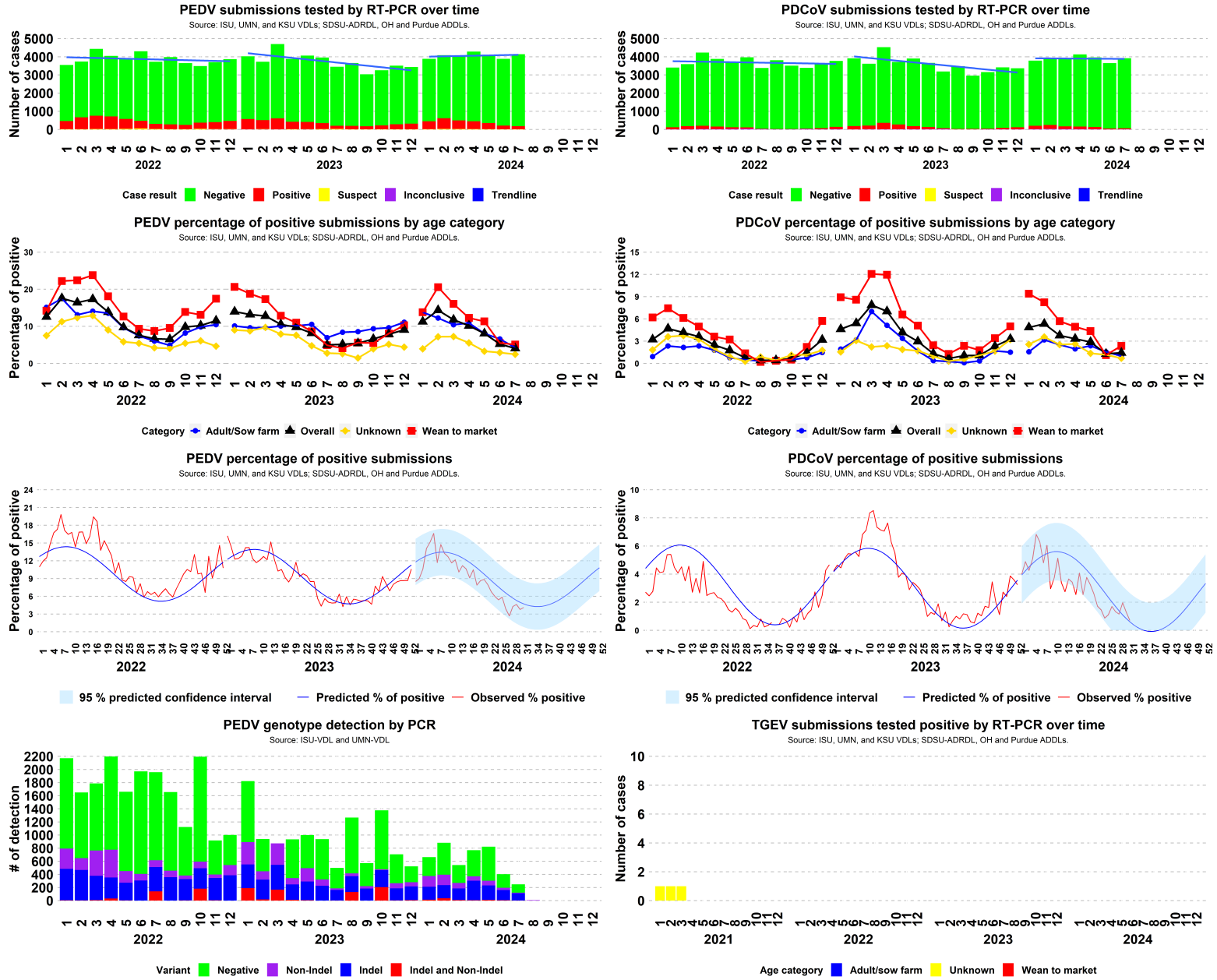


Figure 1. Top: Left PEDV; Right PDCoV cases tested by RT-PCR over time; **Second from top:** Left PEDV; Right PDCoV percentage of positive PCR positive results, by age category over time. **Third from top:** Left PEDV; Right PDCoV expected percentage of positive results for cases tested by RT-PCR and 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, 4.05% of 4,144 cases tested PEDV-positive in July, similar to 5.22% of 3,887 in June;
 - Positivity in the adult/sow category in July was 4.26% (59 of 1,384), a moderate decrease from 6.6% (94 of 1,424) in June;
 - Positivity in the wean-to-market category in July was 5.08% (80 of 1,575), similar to 5.51% (79 of 1,434) in June;
 - Overall PEDV-percentage of positive cases was within state-specific baselines in all 11 monitored states;
 - Overall, NA% of 8 samples had mixed PEDV genotype detection in August, NA 0.8% of 249 in July;
- Overall, 1.43% of 3,921 cases tested PDCoV-positive in July, similar to 1.29% of 3,651 in June;
 - Positivity in the adult/sow category in July was 0.99% (13 of 1,308), similar to 1.55% (21 of 1,358) in June;
 - Positivity in the wean-to-market category in July was 2.37% (35 of 1,477), similar to 1.12% (15 of 1,342) in June;
 - Overall PDCoV-percentage of positive was within state-specific baselines in all 11 monitored states;
- There was 0 positive case for TGEV RNA-PCR in July, 2024 over a total of 3,792 cases tested. It has been 41 months (with a total of 141,006 cases tested) since the last TGEV PCR-positive result;

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

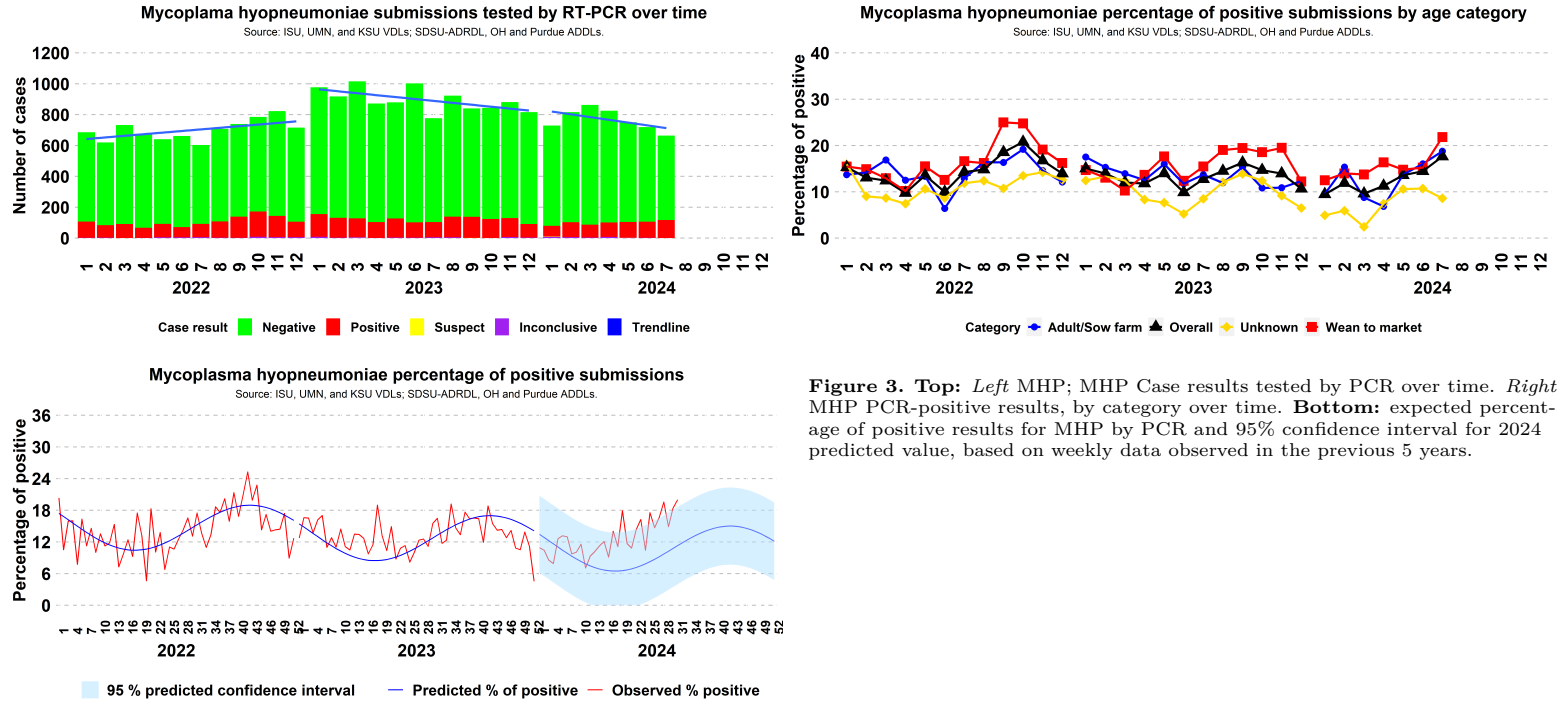


Figure 3. Top: *Left* MHP; MHP Case results tested by PCR over time. *Right* MHP PCR-positive results, by category over time. **Bottom:** expected percentage of positive results for MHP by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 5 years.

SDRS Advisory Group highlights:

- Overall, 17.62% of 664 cases tested *M. hyopneumoniae*-positive cases in July, a moderate increase from 14.46% of 719 in June;
 - Positivity in the adult/sow category in July was 18.77% (49 of 261), a moderate increase from 16.03% (42 of 262) in June;
 - Positivity in the wean-to-market category in July was 21.83% (55 of 252), a substantial increase from 15.22% (44 of 289) in June;
- Overall MHP-percentage of positive cases was 3 standard deviations above state-specific baselines IA;
- The advisory group highlighted that the increase in positive results for *Mycoplasma hyopneumoniae* are result of sow farms that broke in the winter, and now, the weaned pigs are in the finishing sites, being tested positive in the farms' PCR testing. However, some advisory members report clinical cases of *Mycoplasma hyopneumoniae* in finishing sites this summer.

Topic 4 – Detection of Porcine Circoviruses type 2 and 3 DNA by PCR.

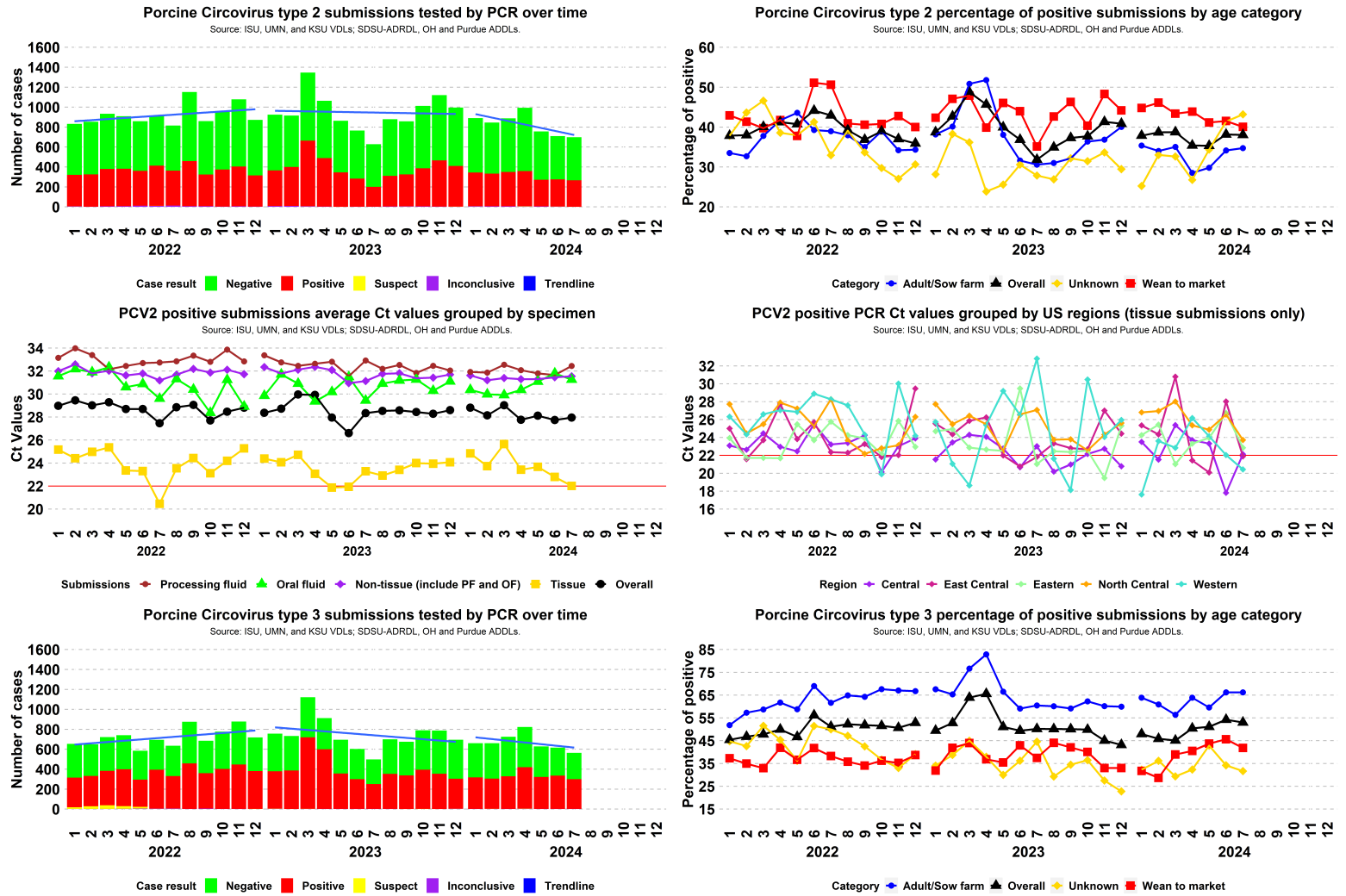


Figure 1. Top: *Left:* Results of PCV2 PCR cases over time; *Right:* PCV2 PCR-positive results, by category over time. **Middle:** *Left:* Average Ct values of PCV2 submissions by specimen; *Right:* Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 38.05% of 699 cases tested PCV2-positive in July, similar to 38.17% of 710 in June;
 - Positivity in the adult/sow category in July was 34.73% (108 of 311), similar to 34.16% (110 of 322) in June;
 - Positivity in the wean-to-market category in July was 40.07% (123 of 307), similar to 41.53% (125 of 301) in June;
 - In the month of July, the regions with the lowest PCV2 average Ct values in tissue submissions was Western (20 submissions; average Ct 20.4), East Central (6 submissions; average Ct 21.9), Central (37 submissions; average Ct 22.1), Eastern (10 submissions; average Ct 22.9), and North Central (13 submissions; average Ct 23.7);
- Overall, 53.01% of 564 cases tested PCV3-positive in July, similar to 54.22% of 616 in June;
 - Positivity in the adult/sow category in July was 66.2% (188 of 284), similar to 66.22% (198 of 299) in June;
 - Positivity in the wean-to-market category in July was 41.82% (92 of 220), a moderate decrease from 45.64% (110 of 241) in June.

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

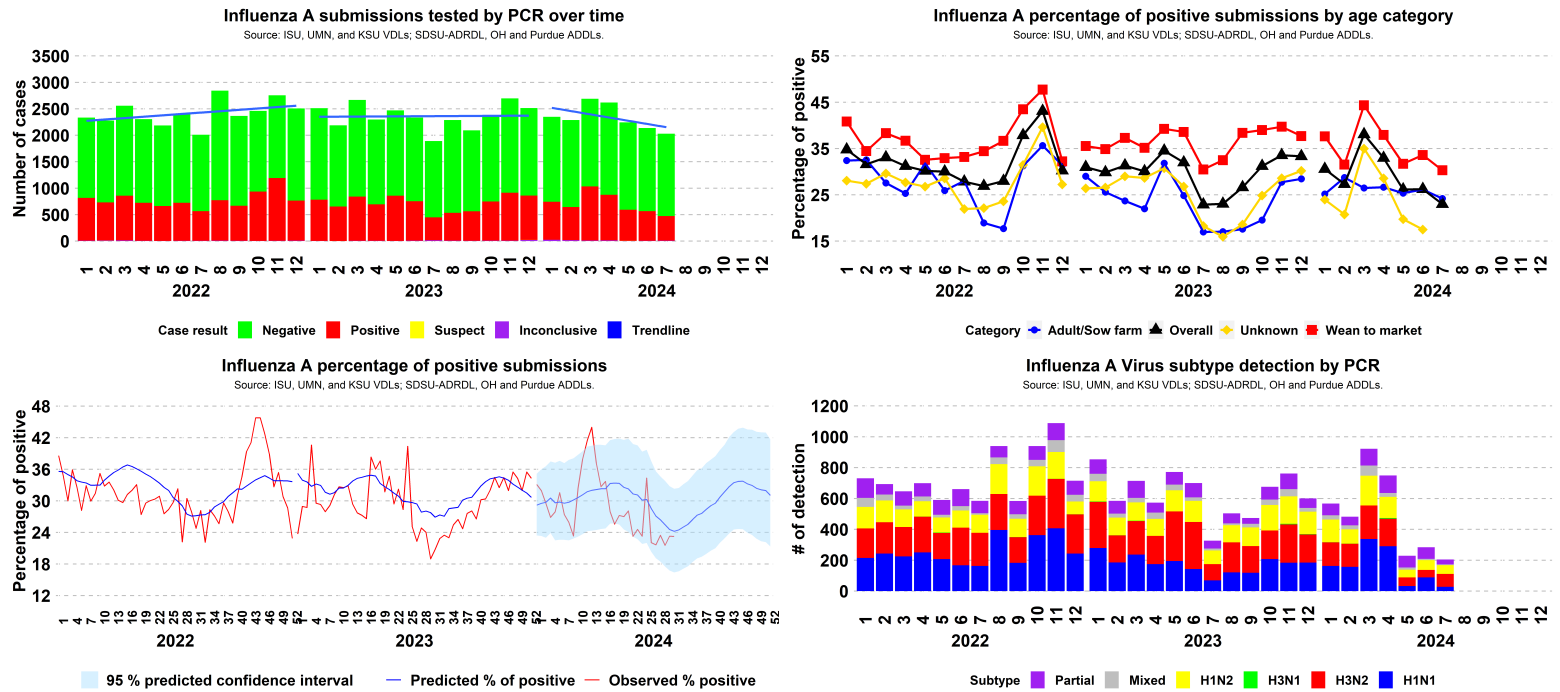


Figure 3. *Top: Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. *Bottom: Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 5 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, 23% of 2,030 cases tested IAV-positive cases in July, a moderate decrease from 26.22% of 2,136 in June;
 - Positivity in the adult/sow category in July was 24.19% (104 of 430), similar to 26.13% (127 of 486) in June;
 - Positivity in the wean-to-market category in July was 30.3% (260 of 858), a moderate decrease from 33.59% (301 of 896) in June.
- Overall IAV-percentage of positive was within state-specific baselines in all 11 monitored states;
- Overall, 2.44% of 205 samples had mixed subtype detection in July, similar to 2.82% of 284 in June.

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

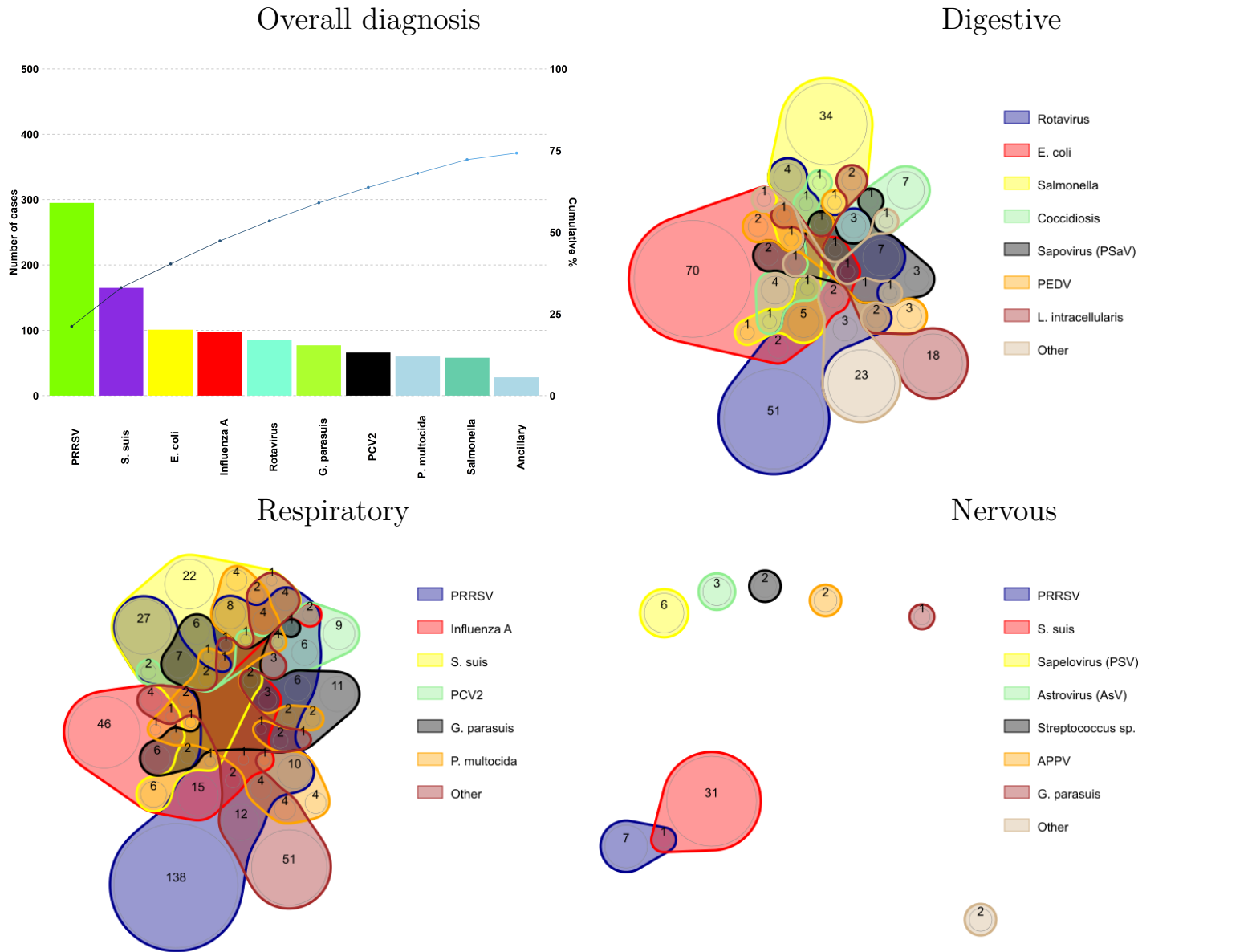


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less 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, Michael, 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 June. 1 to July. 22, 2024.

SDRS Advisory Group highlights:

- PRRSV (295) led cases with confirmed etiology, followed by *S. suis* (165), and *E. coli* (101). PRRSV (269 of 725) led the number of confirmed respiratory diagnoses, *E. coli* (96 of 339) lead the number of confirmed digestive diagnoses, and *S. suis* (35 of 50) 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.

Trends of PRRSV variant 1H.18 detection over time in the US

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Porcine reproductive and respiratory syndrome virus (PRRSV) is an eminent endemic animal health threat to the United States swine population. PRRSV was initially classified in the late 90s using restriction length polymorphism patterns (RFLP) to differentiate the 2-5-2 modified live vaccine RFLP from other wild-type PRRSV strains (Wesley et al., 1998). RFLP was based on enzyme cut patterns on a gel-based PCR technique. Later on, it was identified that RFLP was not very good at differentiating wild-type strains from one another. Lineage classification (Shi et al., 2010) was proposed using the PRRSV open reading frame-5 (ORF5) gene to classify PRRSV sequences using lineage numbers, e.g., L1, L4, L8; later on, a sub-lineage classification (Paploski et al., 2021) was proposed by adding an additional letter to the lineage, e.g., L1A, L1B, L1C. Further refinement for global lineage classification was done in 2023 (Yim-im et al., 2023). but these groupings are still quite genetically diverse. More recently, a variant classification has been proposed and added numbers to the sub-lineages, e.g., 1A.1, 1A.2, 1H.18 (VanderWaal et al., 2024). Since variant classification began being communicated (Kikuti et al., 2024), the SDRS has been receiving repeated requests about the dynamics of detection for PRRSV variant 1H.18. This work presents the summary of information generated for 1H.18 using the SDRS database.

SDRS PRRSV 2 ORF5 sequences having six or fewer ambiguities and sequence lengths lower than 606 base pairs were classified according to variants. The first 1H.18 appeared in the SDRS database in November 2018 and was identified as recovered from a sow farm in MN. Detection of 1H.18 has been intermittent since 2018, with a more consistent number of sequences recovered at the end of 2023 and during the first quarter of 2024 (Figure 1). The PRRSV 1H.18 strain has been detected in more than six states: Iowa (n=68), Illinois (n=3), Indiana (n=6), Michigan (n=1), Minnesota (n=84), Missouri (n=1), and South Dakota (n=2).

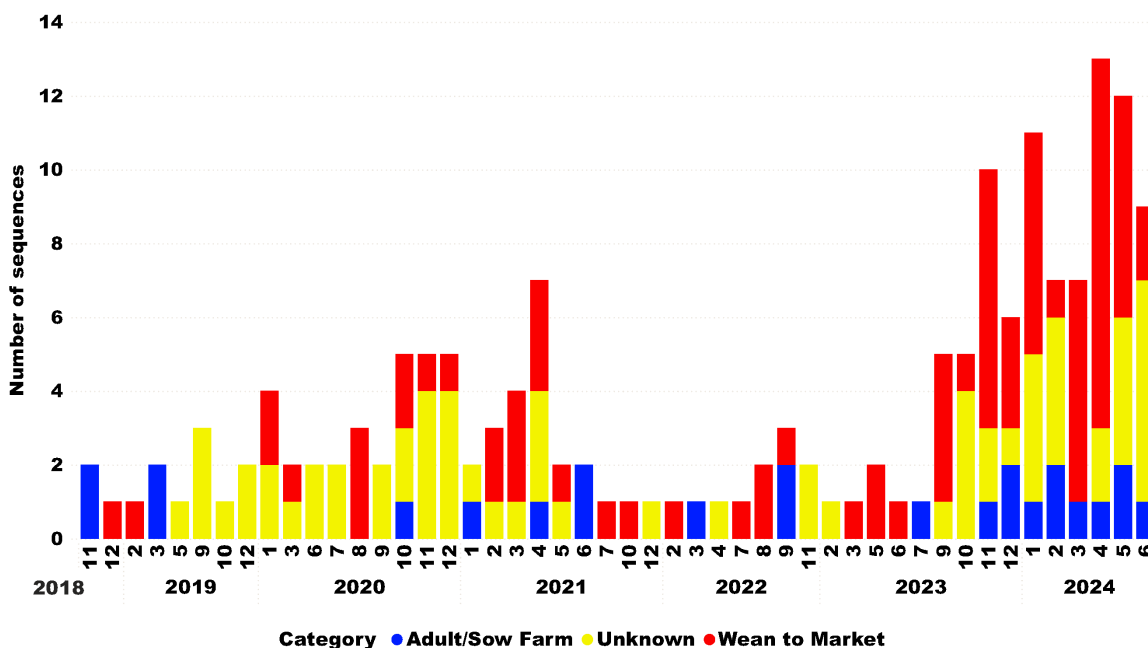


Figure 1: Number of L1H.18 detected by year and month.

The 1H.18 variants have been grouped under eight RFLPs: 1-12-1 (n=5), 1-12-2 (n=79), 1-12-4 (n=5), 1-30-2 (n=1), 1-3-2 (n=1), 1-8-2 (n=8), 1-8-3 (n=2), and 1-8-4 (n=67). The 1H.18 strain has predominantly exhibited two RFLP patterns: a) the 1-8-4 RFLP was more detected in the beginning and peaked around the end of 2020. While a few cases of the 1-8-4 RFLP (n=6) were detected in the third quarter of 2022, and have not been observed since then; and b) the RFLP 1-12-2 was first detected in this group in July 2022 and was recovered from a grow-to-finish farm type located in Minnesota. The 1H.18 has continued to surge, with RFLP 1-12-2 being the most common RFLP type. In 2024, a total of 59 1H.18 sequences were identified across five states, categorized into 5 distinct RFLP with the majority being RFLP 1-12-2 (n=44) However, more than one third of 1H.18 sequences since April, 2024 have other RFLP types, highlighting limitations in RFLP-typing for identifying related sequences. The majority of 1H.18 sequences were observed in the wean-to-market category (figure 2).

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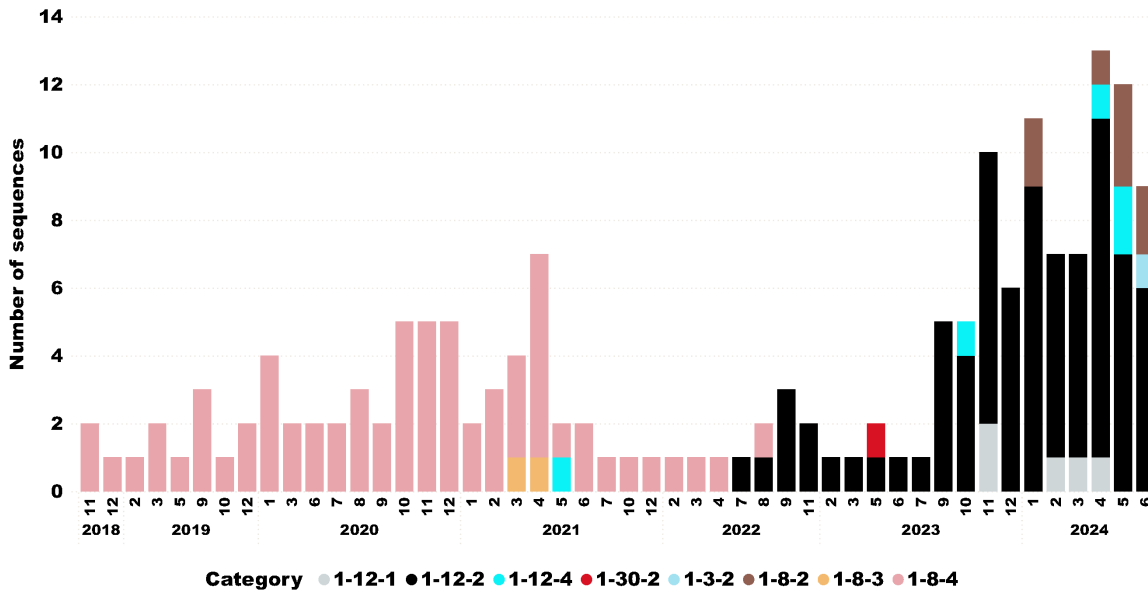


Figure 2: Number of L1H.18 detected per year and the corresponding RFLP pattern.

A phylogenetic tree for the 1H.18 variants color coded by year is presented in figure 3. Two distinct groups of sequences can be identified one before 2023 and another for 2023 and 2024.

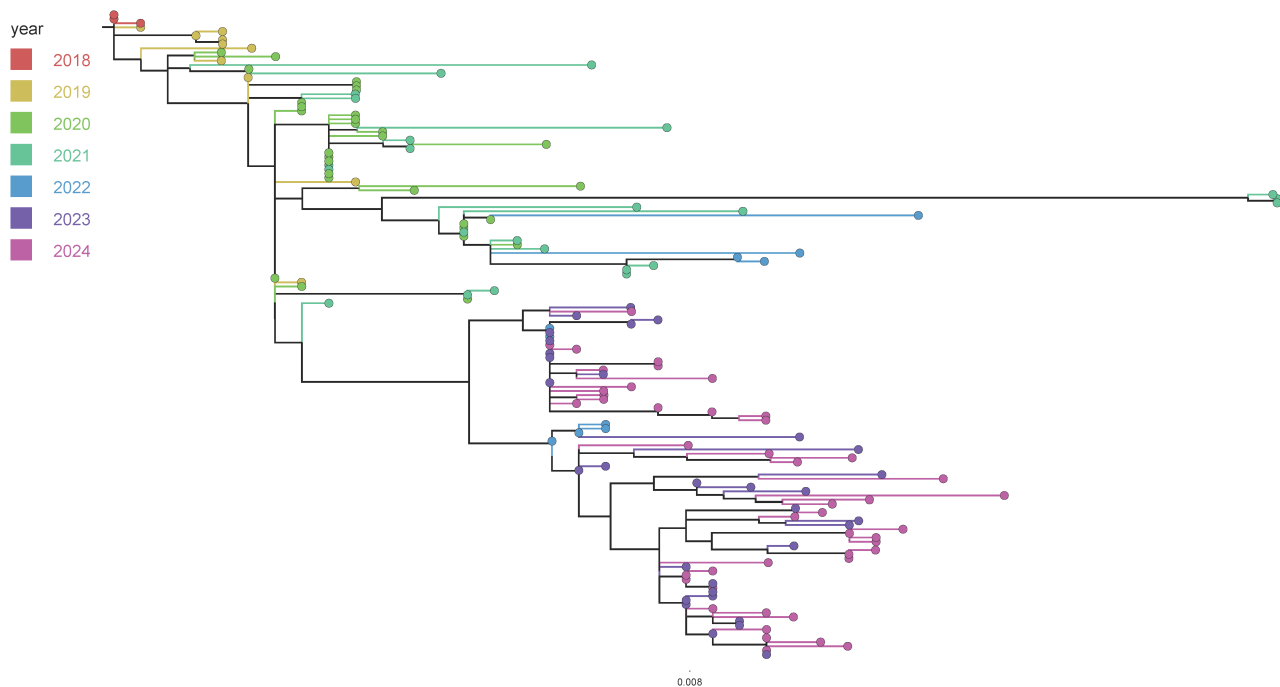


Figure 3: Phylogenetic tree representation of 168 PRRSV 1H.18 variants.

Highlights:

1. So far, no clinical relevance information has been shared with the SDRS about the 1H.18 variant;
2. Sequences belonging to variant 1H.18 prior to 2022 were predominantly RFLP 1-8-4, while RFLP 1-12-2 accounts for approximately one third of 1H.18 sequences in 2023 and 2024.
3. The 1H.18 1-12-2 variant was detected predominantly in grow-to-finish (n=26) and nursery (n=17) pigs.
4. The number of 1H.18 sequences has increased at the end of 2023 and beginning of 2024, but still represent a low number of sequences;