

Swine Disease Reporting System

Report # 73 (March 5, 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. The SDRS projects are:

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 (web dashboards and monthly PDF report), 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 Animal Disease and Diagnostic Laboratory (ADDL), and Purdue ADDL.

Collaborators:

Swine Disease Reporting System office: Principal investigators: [Daniel Linhares](#) & [Giovani Trevisan](#); Project coordinator: [Guilherme Cezar](#), Communications: [Edison Magalhães](#), Data analyst: Srijita Chandra.

Iowa State University: Gustavo Silva, Marcelo Almeida, Bret Crim, Kinath Rupasinghe, Eric Burrough, Phillip Gauger, Christopher Siepker, Marta Mainenti, Michael Zeller, Rodger Main.

University of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, Albert Rovira, Hemant Naikare.

Kansas State University: Rob McGaughey, Franco Matias-Ferreira, Jamie Retallick, Jordan Gebhardt.

South Dakota State University: Jon Greseth, Darren Kersey, Travis Clement, Angela Pillatzki, Jane Christopher-Hennings.

Ohio Animal Disease and Diag. Lab.: Melanie Prarat, Ashley Johnson, Dennis Summers.

Purdue University: Craig Bowen, Kenitra Hendrix, Joseph Boyle.

The Ohio State University: Andreia Arruda.

Disease Diagnosis System: A pilot program with the ISU-VDL consisting of reporting disease detection (not just pathogen detection by PCR), based on diagnostic codes assigned by veterinary diagnosticians. [PRRSView](#) and [FLUture](#): Aggregates PRRSV and influenza A virus diagnostic data from the ISU-VDL and reports results, metadata, and sequences.

PRRS virus RFLP/Lineage report and BLAST tool: Benchmark PRRSV ORF5 sequence 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 available in the form of an “audio report” and “video report” through [Spotify](#), [Apple Podcast](#), [Google podcast](#), [SwineCast](#), [YouTube](#), [LinkedIn](#), and the [SDRS webpage](#).

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.

In addition to this report, [interactive dashboards](#) and [educational material](#) are publicly available.

Note: This report contains data up to February 29, 2024.

Communications and information contained in this report are for general informational and educational purposes only and are not to be construed as recommending or advocating a specific course of action.

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

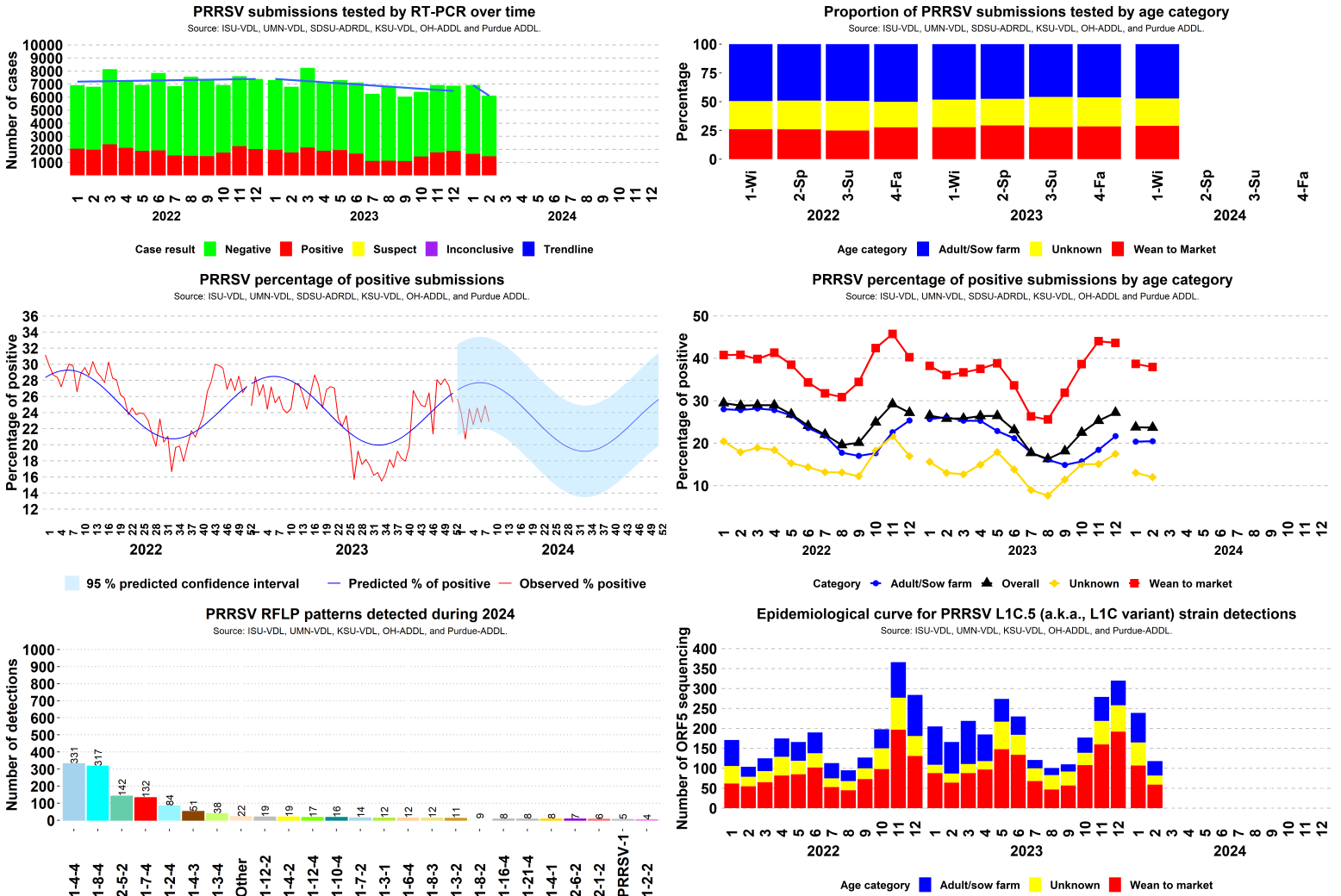
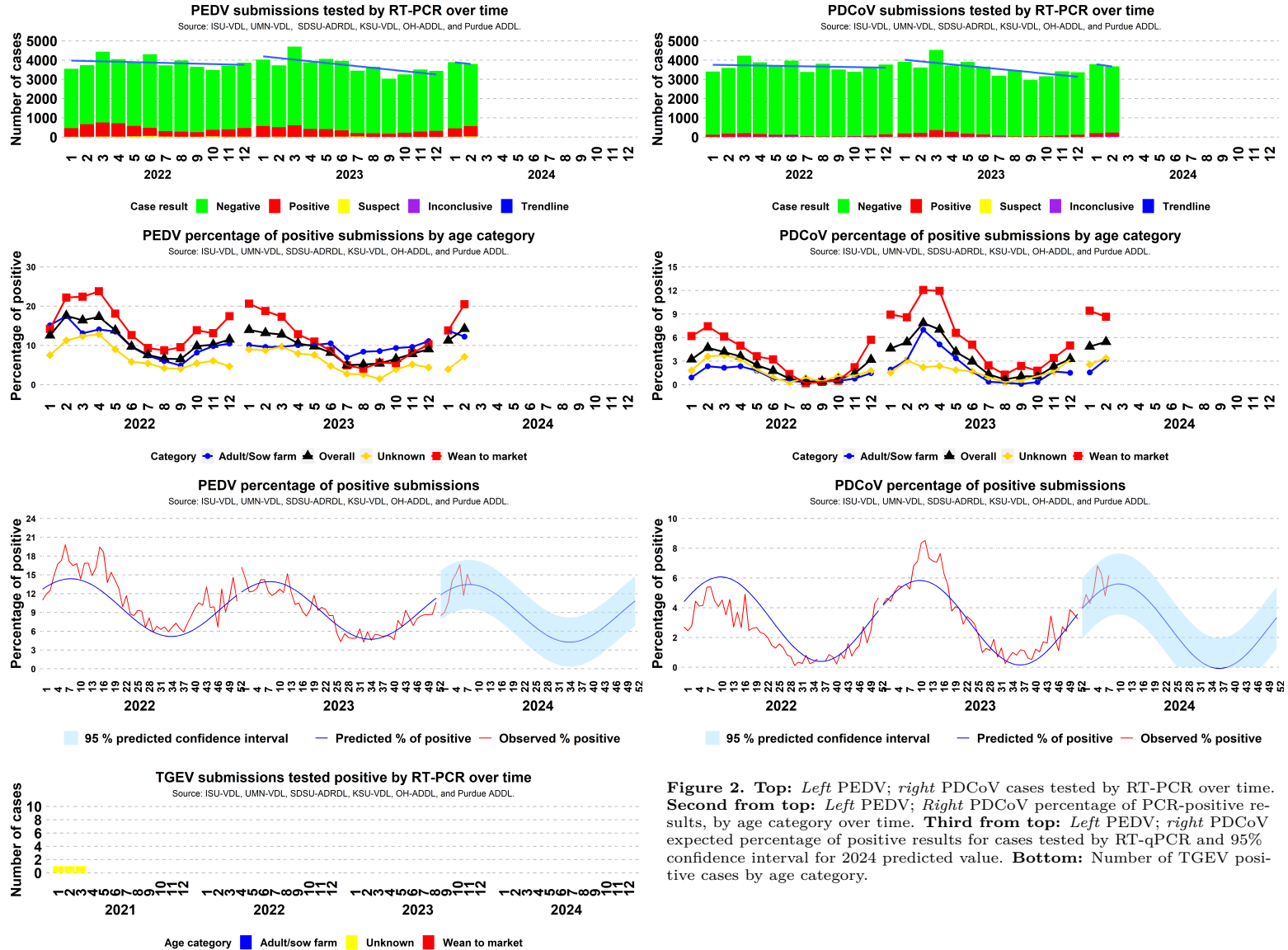


Figure 1. Top: *Left:* Results of PRRSV RT-PCR cases over time; *Right:* Proportion of accession ID cases tested for PRRSV by age group per year and season. **Middle:** *Left* Expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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. **Bottom Left:** The 25 most frequently detected RFLP patterns during 2024; *Right:* Epidemiological curve of detection for PRRSV Lineage 1C variant (L1C.5) strain.

SDRS Advisory Group highlights:

- Overall, 23.68% of 6,116 cases tested PRRSV-positive in February, similar to 23.75% of 6,926 in January;
 - Positivity in the adult/sow category in February was 20.46% (586 of 2,864), similar to 20.36% (670 of 3,291) in January;
 - Positivity in the wean-to-market category in February was 37.95% (690 of 1,818), similar to 38.69% (756 of 1,954) in January;
- Sow Farm PRRSV-percentage of positive cases was 3 standard deviations from state-specific baselines in OH;
- During February 2024, PRRSV L1C variant (L1C.5) strains were detected in IA (61), MO (24), MN (18), NE (6), IL (5), SD (2), OH (2), and SC (1).
- Analyzing the PRRSV ORF5 sequence data from the SDRS, we could identify the first PRRSV L1C.5 detection in South Carolina. The detection was in a sample identified as having been collected from a finishing site, with 100% nucleotide identity with another PRRSV ORF5 sequence recovered in another state and identified as L1C.5 RFLP 1-4-3. This finding raises an alert for the U.S. east region and breeding herd inventories.

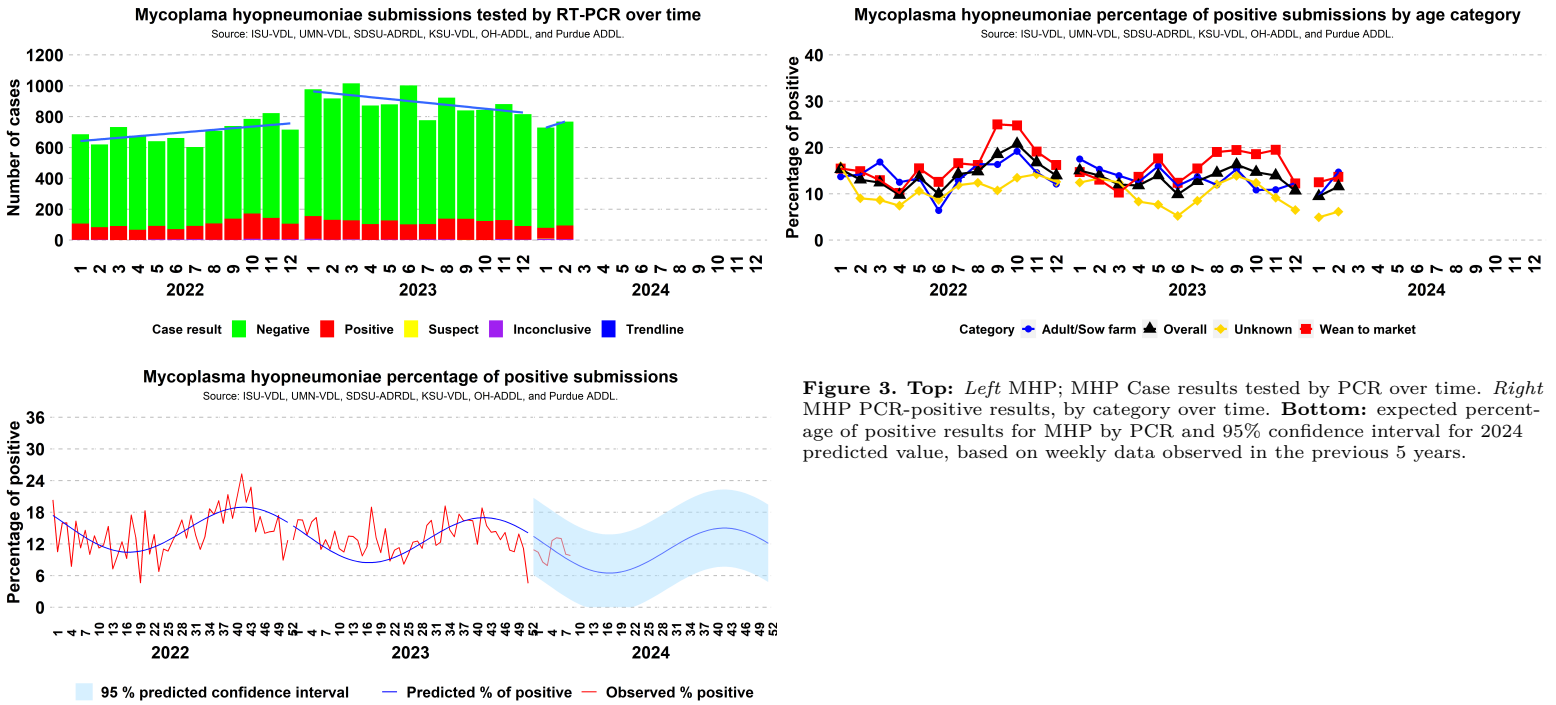
Topic 2 – Enteric coronavirus RNA detection by RT-qPCR



SDRS Advisory Group highlights:

- Overall, 14.24% of 3,798 cases tested PEDV-positive in February, a moderate increase from 11.27% of 3,886 in January;
 - Positivity in the adult/sow category in February was 12.24% (166 of 1,356), similar to 13.77% (193 of 1,402) in January;
 - Positivity in the wean-to-market category in February was 20.49% (308 of 1,503), a substantial increase from 13.83% (206 of 1,490) in January;
- Overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in KS;
- Overall, 5.45% of 3,669 cases tested PDCoV-positive in February, similar to 4.86% of 3,786 in January;
 - Positivity in the adult/sow category in February was 3.23% (41 of 1,271), similar to 1.56% (21 of 1,344) in January;
 - Positivity in the wean-to-market category in February was 8.65% (128 of 1,479), similar to 9.42% (138 of 1,465) in January;
- Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in MO;
- There was 0 positive case for TGEV RNA-PCR in February, 2024 over a total of 3,539 cases tested. It has been 36 months (with a total of 121,905 cases tested) since the last TGEV PCR-positive result;
- The advisory group highlighted that the increased PEDV positivity in the wean-to-market category was largely due to lateral introductions of the virus because biosecurity bridges, hauling transportation, employee movement, and farm equipment sharing in finishing sites. Also, the harsh weather, with blizzards and low temperatures in January/February, affected the sanitation of chutes, trucks, and shower practices.

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



SDRS Advisory Group highlights:

- Overall, 11.59% of 768 cases tested *M. hyopneumoniae*-positive cases in February, a moderate increase from 9.47% of 729 in January;
 - Positivity in the adult/sow category in February was 14.72% (34 of 231), a substantial increase from 9.57% (22 of 230) in January;
 - Positivity in the wean-to-market category in February was 13.65% (40 of 293), similar to 12.5% (37 of 296) in January;
- Overall MHP-percentage of positive cases was within state-specific baselines in all 11 monitored states;
- The advisory group highlighted that the substantial increase in *Mycoplasma hyopneumoniae* positivity is due to few sow farms, and does not represent abnormal activity in sow farms.

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

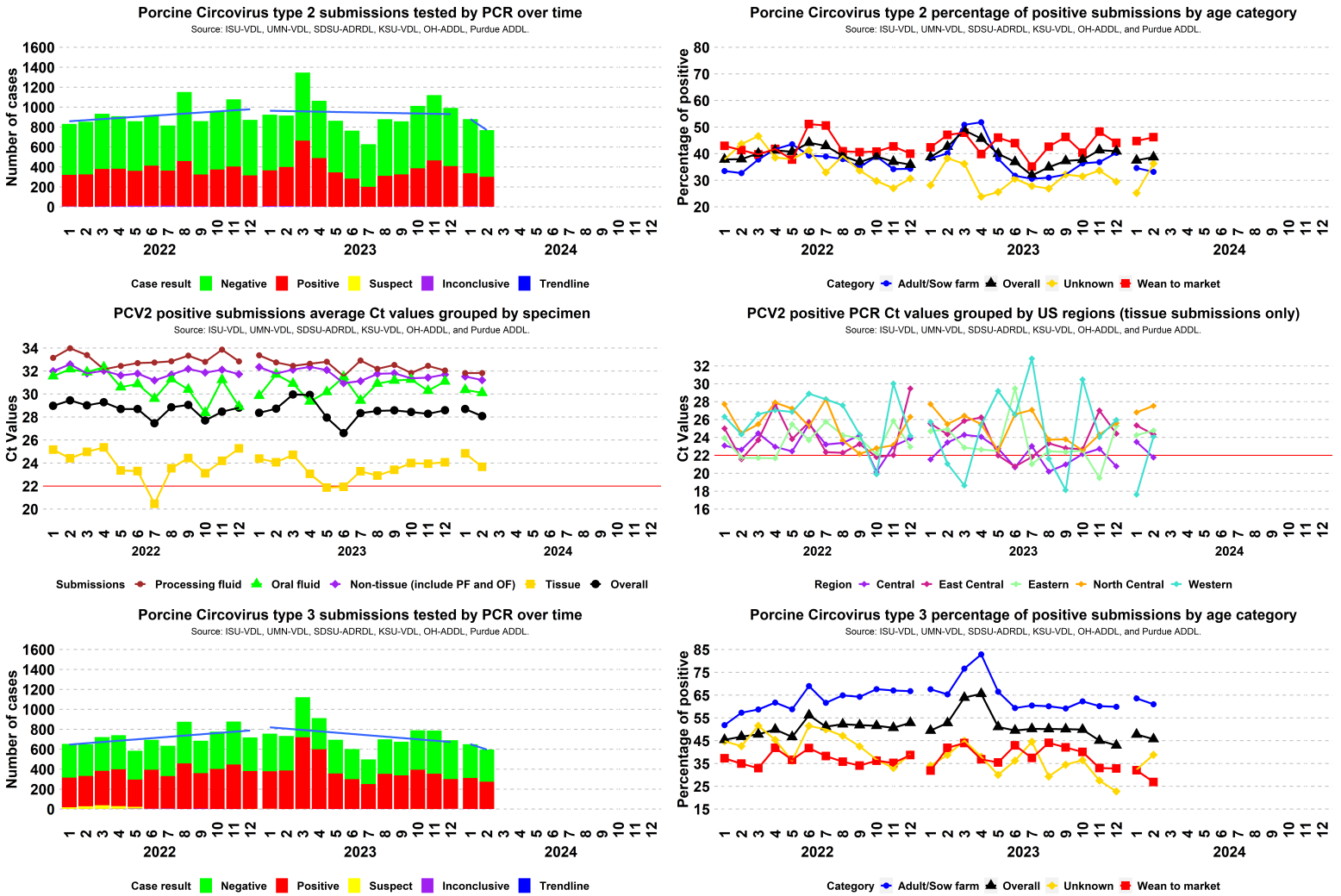


Figure 1. Top: *Left:* Results of PCV2 PCR cases over time; *Right:* PCV2 PCR-positive results, by category over time. **Middle:** *Left:* Average Ct values of PCV2 submissions by specimen; *Right:* Average Ct values of PCV2 tissue submissions by U.S. region; Central (IA), East Central (IL, IN, MO and 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, 38.7% of 770 cases tested PCV2-positive in February, similar to 37.5% of 880 in January;
 - Positivity in the adult/sow category in February was 33.15% (121 of 365), similar to 34.64% (150 of 433) in January;
 - Positivity in the wean-to-market category in February was 46.2% (140 of 303), similar to 44.77% (154 of 344) in January;
- In the month of February, the regions with the lowest PCV2 average Ct values in tissue submissions was Central (41 submissions; average Ct 21.8), Western (13 submissions; average Ct 24.1), East Central (17 submissions; average Ct 24.3), Eastern (33 submissions; average Ct 24.8), and North Central (20 submissions; average Ct 27.5);
- Overall, 45.73% of 597 cases tested PCV3-positive in February, a moderate decrease from 47.77% of 651 in January;
 - Positivity in the adult/sow category in February was 61% (183 of 300), a moderate decrease from 63.58% (206 of 324) in January;
 - Positivity in the wean-to-market category in February was 26.89% (57 of 212), a substantial decrease from 32.03% (74 of 231) in January.

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

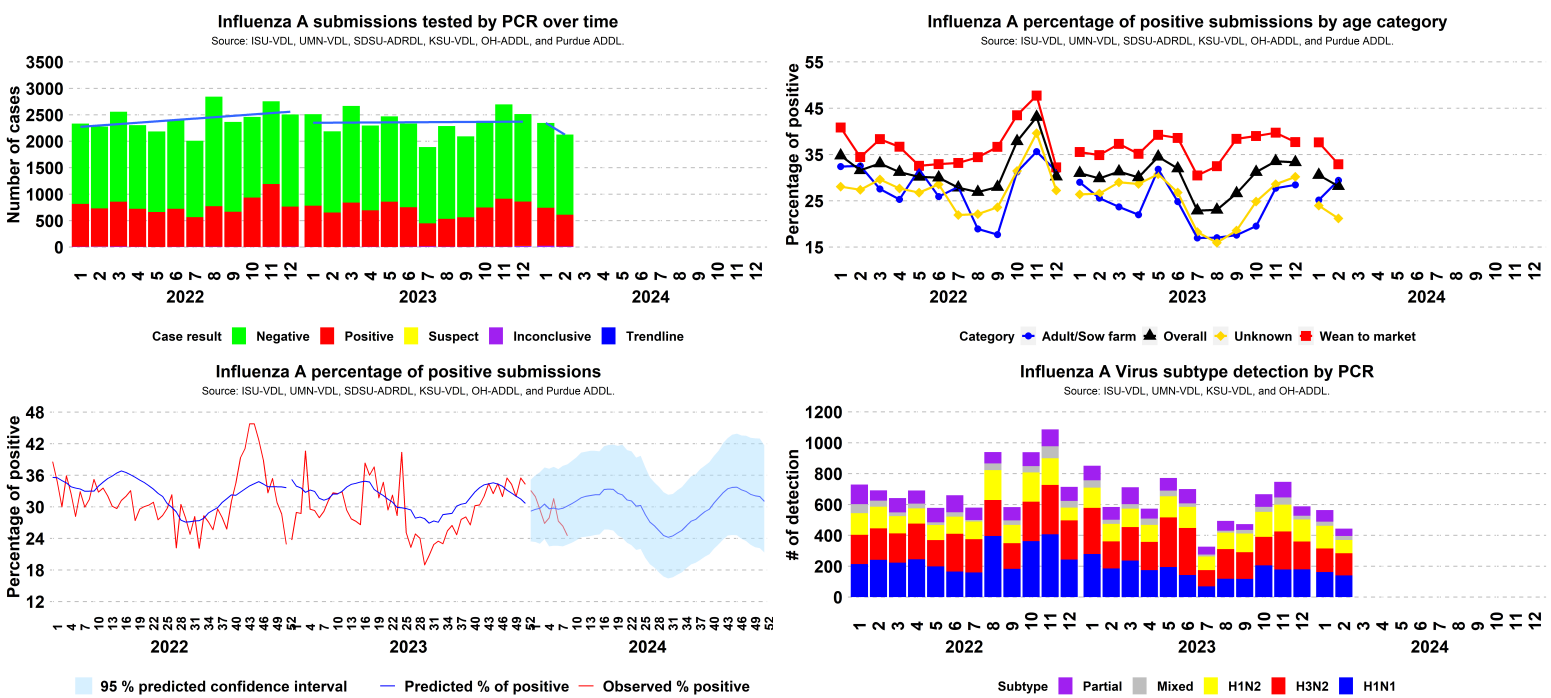


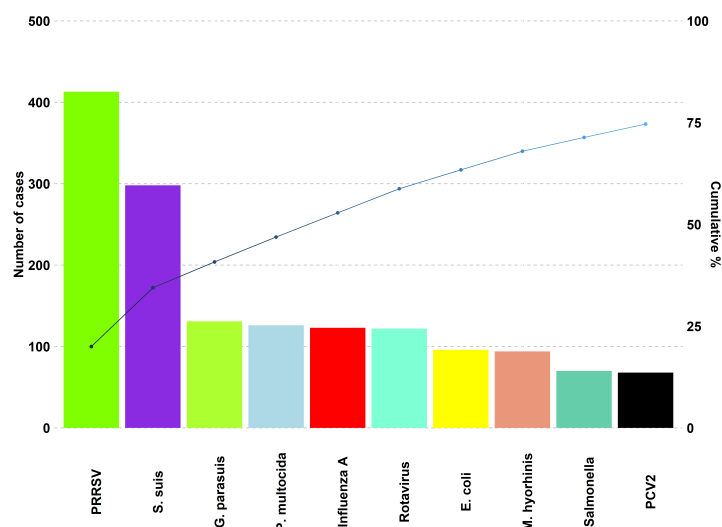
Figure 3. Top: *Left* Results of IAV PCR cases over time. *Right* Percentage of IAV PCR-positive results, by category over time. **Bottom:** *Left* expected percentage of positive results for IAV by PCR and 95% confidence interval for 2024 predicted value, based on weekly data observed in the previous 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:

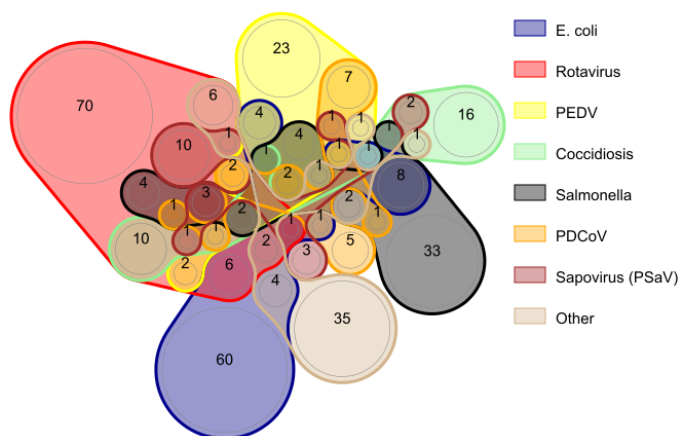
- Overall, 28.16% of 2,127 cases tested IAV-positive cases in February, a moderate decrease from 30.56% of 2,346 in January;
- Positivity in the adult/sow category in February was 29.42% (143 of 486), a moderate increase from 25.17% (109 of 433) in January;
- Positivity in the wean-to-market category in February was 32.9% (304 of 924), a moderate decrease from 37.63% (412 of 1,095) in January.
- Overall, 5.86% of 444 samples had mixed subtype detection in February, similar to 4.79% of 564 in January.

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

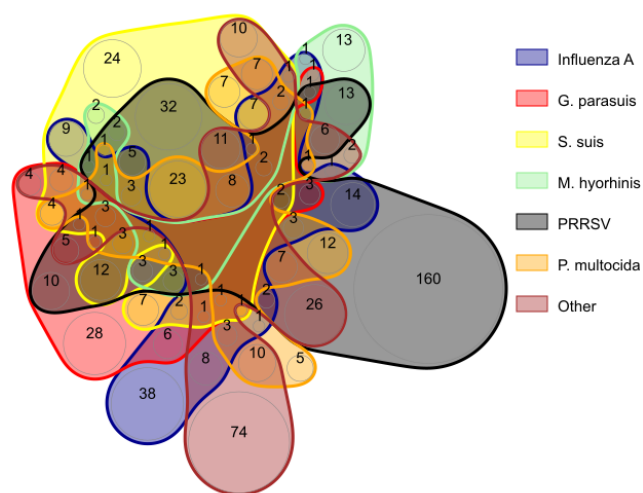
Overall diagnosis



Digestive



Respiratory



Nervous

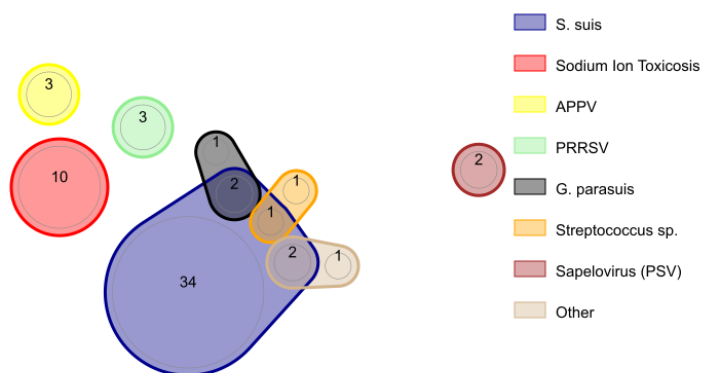


Figure 4. ISU-VDL most frequent overall confirmed tissue disease diagnosis. The presented system is described in the title of the chart. Colors represent one agent; line intersections present diagnosis of 2 or more agents within a submission. Only the most frequent etiology/disease are presented. Less 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, 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 January. 1 to February. 17, 2024.

SDRS Advisory Group highlights:

- PRRSV (413) led cases with confirmed etiology, followed by *S. suis* (298), and *G. parasuis* (131). PRRSV (384 of 1224) led the number of confirmed respiratory diagnoses, Rotavirus (122 of 458) lead the number of confirmed digestive diagnoses, and *S. suis* (39 of 65) led the number of confirmed neurological diagnoses.
- Even though it was a small number of cases, there were consecutive alarms for the number of PDCoV confirmed diagnosis in the last two weeks of January 2024.

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.

SDRS PRRSV BLAST Tool – An informative tool for swine veterinarians, producers and stakeholders

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The SDRS is introducing the SDRS PRRSV BLAST tool, a one-of-a-kind implementation of a Basic Local Alignment Search Tool (BLAST) specific to the PRRSV ORF5 sequences. The tool’s focus is to help answer spatiotemporal questions regarding query sequences and detect any new sequences entering the SDRS database. 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, and view where the resulting sequences occurred before, when they occurred, what is the percentage similarity of these sequences with the query sequence as well as the lineage and RFLP of the sequences. The web-based application (Figure 1) can be found on the [SDRS website](#). The SDRS team can be contacted if additional information or help interpreting the tool’s results is required.

Another essential function of the tool is identifying new sequences entering the database. Any sequence with more than 6 ambiguities, less than 597 base pairs, and nucleotide identity less than 95% with any pre-existing sequence in the database is flagged as a new sequence, and the SDRS team is notified of these sequences. The tool has identified 133 new sequences since 2010. Following its initial detection and considering a nucleotide identity of more than 98%, 88.7% (118 of 133) of the sequences had less than 10 detections, 8.3% (11 of 133) had between 10 and 19, and 3% (4 of 133) had 20 or more occurrences forming a clusters of detections. It can be inferred from the results that 3% of the sequences flagged as new have field relevance. Lineage 5A (15.0%), PRRSV-1 (9.8%) and lineage 1A (8.3%) are the most dominant lineages in these sequences, and the most dominant RFLP patterns are 1-4-4 (12.0%), PRRSV-1 (9.8%) and 1-2-4 (6%).

SDRS BLAST Tool

>MZ852092.1

ATGTTGGGGAAATGCTTGACCGCGGGCTGCTGCTCGCAATTGCCTTTTTTGTTGGTGTATCGTGCCGTTCT
GTTTTGTTGCGCTCGTCAACGCCAGCAACAACAGCAGCTCCCATTTACAGTTGATTATAACCTGACGAT
ATGTGAGCTGAATGGCACAGATTGGCTAAATAAAAGTTTGGATTGGGCGGTGGAAACCTTTGTATTTT
CCTGTGCTGACTCACATTGTTTCTATGGCGCCTCACTACCAGCCATTCTCTTGACACTGTGCGGCTGA
TCACTGTGTCCGCCCGCGGATATTACCAGGGCGGTATGCTTGAGTAGCATTTATGCCGCTGCGCCTT
GGCTGCGTTAACTTGCTTCGTCATCAGGCTAACAAAAAATTGTATGTCCTGGCGTTACTCATGCACCAGA
TACACTAACTTTCTTTGGACACCAAGGGCAAACCTATCGTTGGCGGTCTCCTGTCATCATAGAGAAAG

Result Count

20

BLAST

Reset

Similar ID	Received Date	State	Lineage	RFLP	% Similarity
SDRS40959/19Dec2014/UN	12/19/2014	UN	L1A	1-6-4	98.18
SDRS40161/01Nov2014/Unknown	11/1/2014	Unknown	L1A	1-6-4	98.18
SDRS40524/26Nov2014/UN	11/26/2014	UN	L1A	1-6-4	98.18
SDRS41153/06Jan2015/NC	1/6/2015	NC	L1A	1-7-4	98.01
SDRS41596/03Feb2015/NC	2/3/2015	NC	L1A	1-6-4	98.01
SDRS39791/01Oct2014/Unknown	10/1/2014	Unknown	L1A	1-7-4	98.01
SDRS45346/07Oct2015/NC	10/7/2015	NC	L1A	1-7-4	97.84
SDRS41880/18Feb2015/NC	2/18/2015	NC	L1A	1-7-4	97.84
SDRS42118/03Mar2015/NC	3/3/2015	NC	L1A	1-7-4	97.84
SDRS42518/24Mar2015/NC	3/24/2015	NC	L1A	1-7-4	97.84

Figure 1: Web interface of the SDRS PRRSV BLAST tool;

The tool has an interactive web interface where users can enter their query sequence in a FASTA format and modify the number of results displayed. The result returned has the ID, Received Date, State, Lineage, RFLP, and Percentage Similarity columns displayed, which can provide helpful insight into the query sequence's evolution pattern.

Highlights:

- The SDRS PRRSV BLAST tool is now available to producers, veterinarians, stakeholders, and any other users to compare their own sequences against the SDRS database and identify the states, lineage, and RFLP of similar sequences.
- The tool has also been designed to identify new sequences and notify the SDRS team. These sequences will then be reported in the monthly reports.

Funding:

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References:

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