

Swine Disease Reporting System

Report # 37 (March 2, 2021)

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 (USA), and reports the major findings to the swine industry. Our goal is to share information on 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 the input of our advisory group, which consists of veterinarians and producers across the USA 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 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, and Kansas State University VDL.

Collaborators:

Iowa State University: Giovani Trevisan, Edison Magalhães, Leticia Linhares, Bret Crim, Poonam Dubey, Kent Schwartz, Eric Burrough, Phillip Gauger, Pablo Pineyro, Christopher Siepker; Rodger Main, Daniel Linhares.

Project coordinator [Giovani Trevisan](#). Principal investigator [Daniel Linhares](#).

University of Minnesota: Mary Thurn, Paulo Lages, Cesar Corzo, Jerry Torrison.

Kansas State University: Rob McGaughey, Eric Herrman, Roman Pogranichniy, Rachel Palinski, Jamie Henningson.

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

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.

FLUture: Aggregates influenza A virus (IAV) diagnostic data from the ISU-VDL and reports results, metadata, and sequences.

PRRS virus RFLP report: Benchmarks patterns of PRRSV RFLP pattern detected at the ISU-VDL over time, USA state, specimen, and age group.

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 [SwineCast](#), [YouTube](#), [LinkedIn](#), and the [SDRS webpage](#).

Advisory Group: Reviews and discusses the data, providing their comments and perspectives on a monthly: Clayton Johnson, Mark Schwartz, Paul Sundberg, Paul Yeske, Rebecca Robbins, Tara Donovan, Deborah Murray, Scott Dee, Melissa Hensch, Brigitte Mason, Randy Jones, Peter Schneider.

In addition to this report, interactive dashboards with aggregated test results are available at www.fieldepi.org/SDRS.

Note: This report contains data up to February 28, 2021.

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

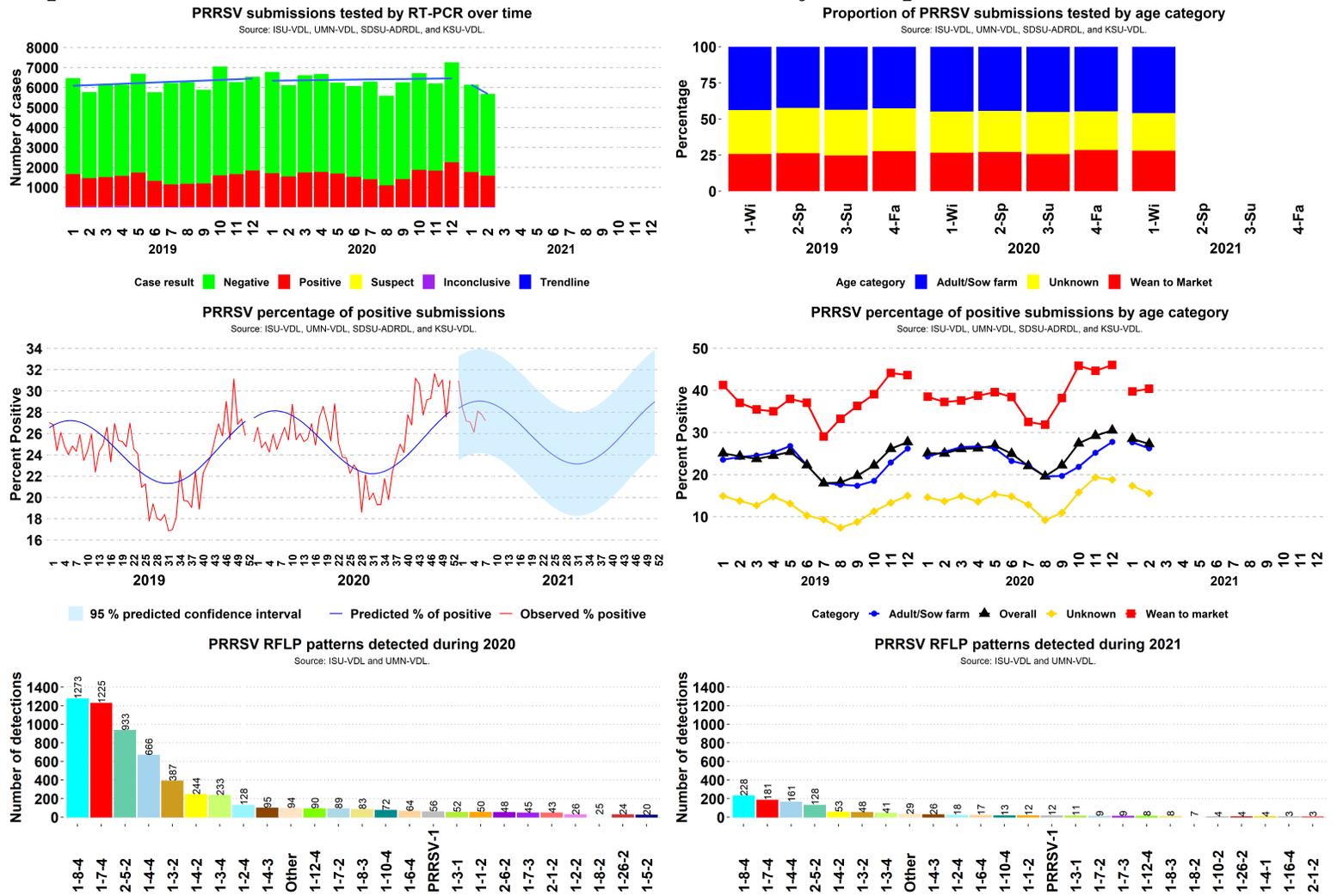


Figure 1. Top: *left:* Results of PRRSV RT-PCR cases over time. *Right:* Proportion of accession ID cases tested for PRRSV by age group per year and season. Middle: *Left* expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based on 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 the 25 most frequently detected RFLP patterns *left* year of 2020; *right* year of 2021.

SDRS Advisory Group highlights:

- Overall, 27.29% of 5,684 cases tested PRRSV-positive in February, similar to 28.5% of 6,140 in January;
 - The overall PRRSV detection was within the forecasted levels during February;
 - Positivity in adult/sow category in February was 26.23% (687 of 2,619), similar to 27.69% (777 of 2,806) in January;
 - Positivity in wean-to-market category in February was 40.38% (630 of 1,560), similar to 39.74% (701 of 1,764) in January;
 - Overall PRRSV-percentage of positive cases was 3 standard deviations from state-specific baselines in NE, IN, and OH;
- Grow-finish continues to be the age group with the highest positivity of PRRSV PCR. The advisory group pointed out that this month PRRSV detection in wean-to-market pigs was partly due to the placement of positive pigs from sow farms that went through PRRSV outbreaks during last fall and the beginning of winter. The placement of PRRSV-positive pigs led to increased pressure of infection and contributed to lateral breaks. Different regions faced different issues with specific emerging or re-merging PRRSV strains that encountered an opportunity to spread in those particular areas causing a considerable impact in infected herds. A significant number of outbreaks were observed in farms located in traditionally very low PRRSV prevalence regions. There was the perception that PRRSV RFLP 1-4-4 Lineage 1C variant infection continues to be associated with severe clinical signs and mortality in grow-finish pigs (Since October 2020).

Topic 2 – Detection of RNA of enteric coronavirus by RT-qPCR

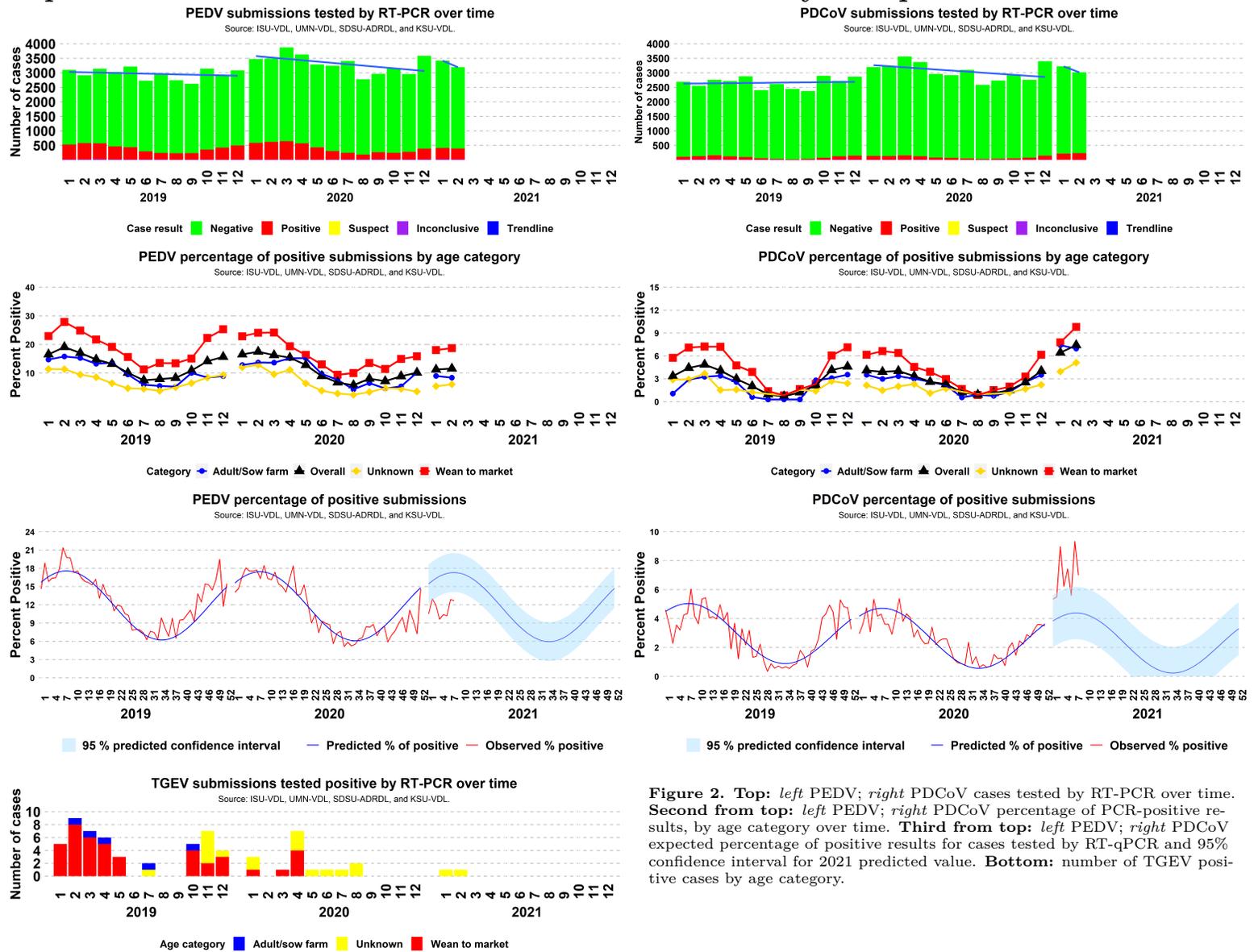


Figure 2. Top: left PEDV; **right** PDCoV cases tested by RT-PCR over time. **Second from top: left** PEDV; **right** PDCoV percentage of PCR-positive results, by age category over time. **Third from top: left** PEDV; **right** PDCoV expected percentage of positive results for cases tested by RT-qPCR and 95% confidence interval for 2021 predicted value. **Bottom:** number of TGEV positive cases by age category.

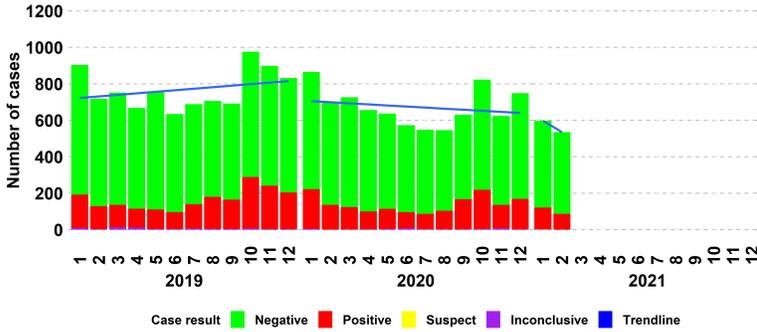
SDRS Advisory Group highlights:

- Overall, 11.58% of 3,195 cases tested PEDV-positive in February, similar to 11.24% of 3,416 in January;
 - Positivity in adult/sow category in February was 8.38% (82 of 978), similar to 9% (96 of 1,067) in January;
 - Positivity in wean-to-market category in February was 18.73% (227 of 1,212), similar to 18.04% (230 of 1,275) in January;
 - Overall PEDV-percentage of positive cases was within 3 standard deviations from state-specific baselines in all 11 monitored states;
- Overall, 7.42% of 3,020 cases tested PDCoV-positive in February, similar to 6.43% of 3,221 in January;
 - The overall PDCoV detection was outside of the upper boundaries of the forecasted levels between January 18 to February 28;
 - Positivity in adult/sow category in February was 6.96% (64 of 920), similar to 7.4% (73 of 986) in January;
 - Positivity in wean-to-market category in February was 9.8% (110 of 1,123), a moderate increase from 7.78% (93 of 1,196) in January;
 - Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in OK, KS, and NC;
- There was 1 positive case for TGEV RNA in February, 2021 over a total of 2,918 cases tested;
- The advisory group pointed out that the swine industry continued to invest in preparedness during the last year. Measures such as depopulation of PEDV-positive sow farms, intense cleaning and disinfection practices, improved truck washing and baking procedures, use of validated feed mitigants, and a less intense finishing barns turnaround allowed reducing the pressure of infection by implementing more adequate facility sanitation practices and reducing the potential of PEDV transmission originated from packing plants to finishing sites. Increased detection of PDCoV has been identified as a local issue. The participant VDLs specialists have identified no evidence of recent PDCoV significant genetic changes.

Topic 3 – Detection of *Mycoplasma hyopneumoniae* (MHP) DNA by PCR.

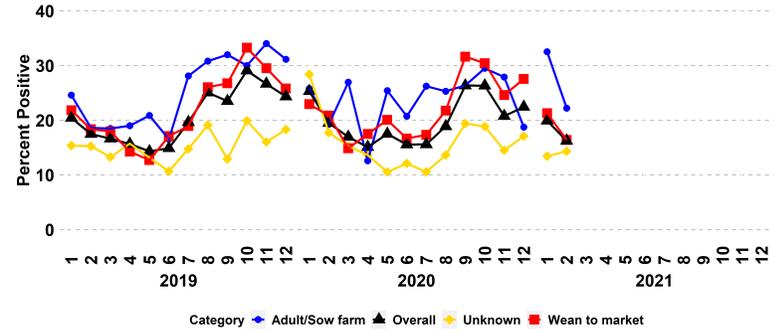
Mycoplasma hyopneumoniae submissions tested by RT-PCR over time

Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.



Mycoplasma hyopneumoniae percentage of positive submissions by age category

Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.



Mycoplasma hyopneumoniae percentage of positive submissions

Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.

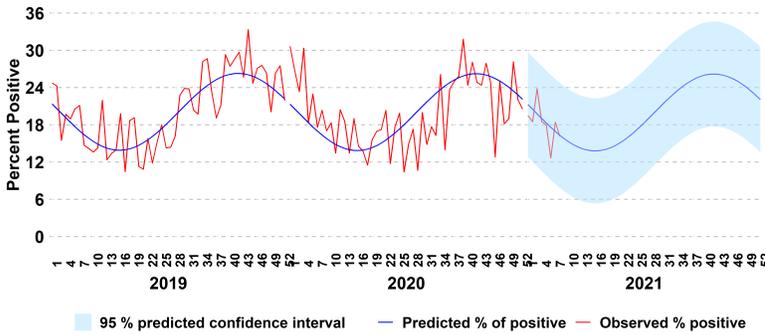


Figure 3. Left top: results of MHP PCR cases over time. Right top: percentage of MHP PCR-positive results, by category over time. Bottom: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2020 predicted value, based on weekly data observed in the previous 3 years.

SDRS Advisory Group highlights:

- Overall, 16.26% of 535 cases tested *M. hyopneumoniae*-positive cases in February, a moderate decrease from 19.93% of 597 in January;
- As expected the observed overall detection of *M. hyopneumoniae*-positive cases is following the forecasted expected decrease in the levels of detection for this time of the year.

Topic 4 – Disease diagnosis at the ISU-VDL.

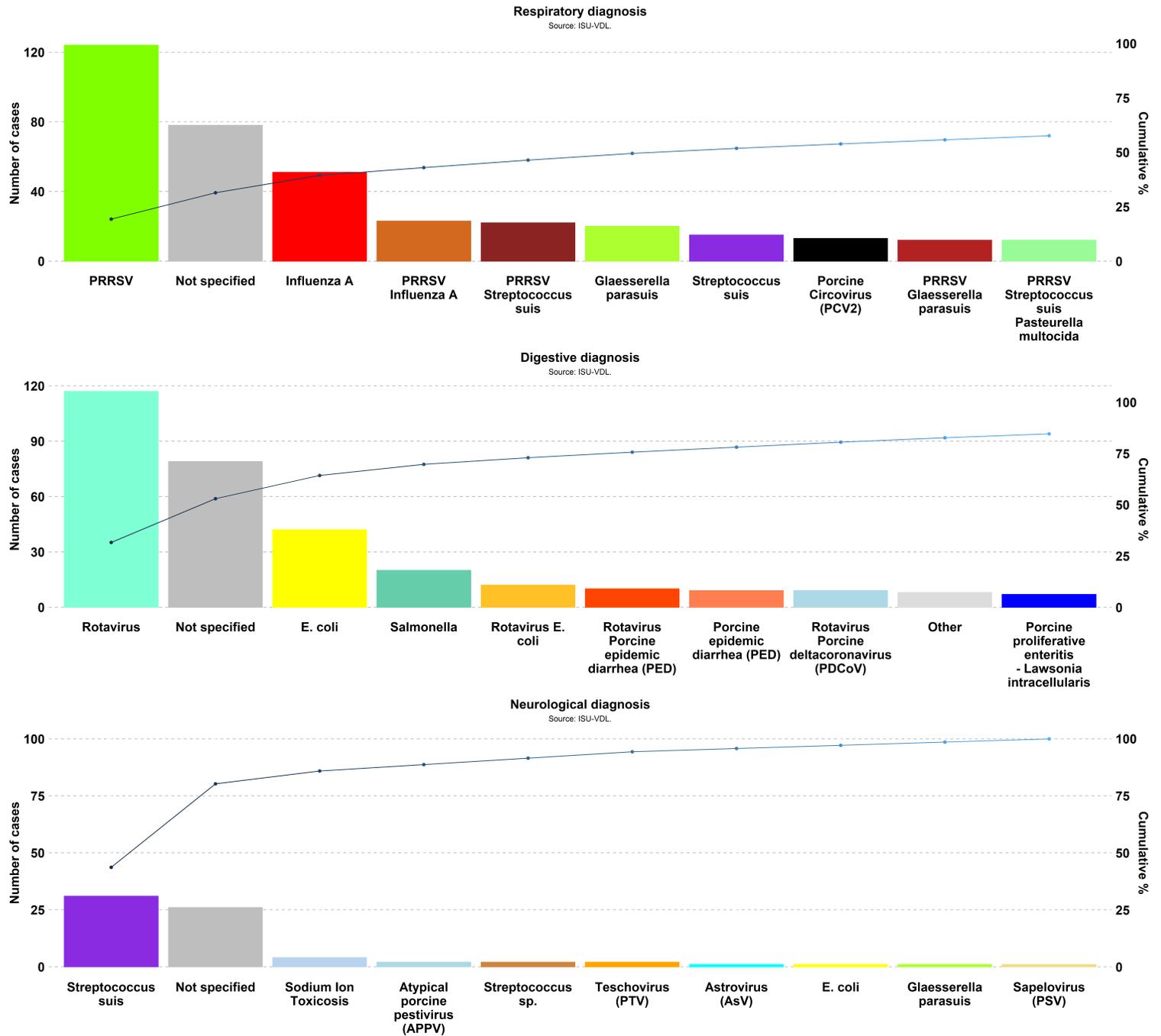


Figure 4. Most frequent disease diagnosis by physiologic system at ISU-VDL . Presented system is described in the title of the chart. Colors represent one agent and/or the combination of 2 or more agents. Only the physiologic systems with historic number of cases per season above 100 are presented in the report.

Note: Disease diagnosis takes one to two weeks to be performed. The graphs and analysis contain data from January 1, 2021 to February 14, 2021.

SDRS Advisory Group highlights:

- PRRSV (124 of 642) continues to lead the number of respiratory diagnoses. Rotavirus (117 of 370) continues to lead the number of digestive diagnoses. *Streptococcus suis* (31 of 71) continues to lead the number of neurological diagnosis;
- During January 2021, there was a significant increase (signal) in the diagnosis of *B. bronchiseptica*.

Overview of PRRSV RFLP and genetic sequencing at the ISU VDL from Fall to Winter of 2020

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Between October 1, 2020 to January 31, 2021, more than 2,000 cases have been processed by the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) requesting PRRSV open read frame-5 (ORF5) sequencing. The 5 most common RFLPs detected at the ISU VDL in this timeframe have been 1-8-4, 1-7-4, 2-5-2, 1-4-4, and 1-3-2. Combined, these five RFLPs accounted for approximately 70% of the total observed RFLP patterns detected during this time.

A PRRSV genetic lineage system was proposed by Paploski *et al.* 2019, from the University of Minnesota (UMN) that divides PRRSV-2 circulating in North America into lineages 1-9, and then further divides lineage 1 PRRSV into subgroups A-E. RFLP patterns tend to correlate with genetic lineage; however, using the Paploski lineage system, PRRSV with a 1-8-4 RFLP are primarily detected within Lineage 1D, although there is a genetic cluster that also exists in Lineage 1A. The ORF5 with a 1-7-4 RFLP exist primarily in Lineage 1A and the 2-5-2 RFLPs are found in Lineage 5. The 1-3-2 RFLPs are detected most often in Lineage 1C, 1E, and Lineage 8. Although the lineage system encapsulates the RFLPs fairly well, less observed RFLP patterns are regularly observed within each lineage. Interestingly, strains with the 1-4-4 RFLP are an exception within the top 5 RFLP patterns as it has been observed in multiple, genetically distinct lineages. Given that the 1-4-4 RFLP are detected in multiple lineages, it is difficult to compare two PRRSV 1-4-4s without understanding their phylogenetic relationship.

Recent reports of high mortality within farms from a 1-4-4 RFLP have been described primarily in Iowa (IA) and southern Minnesota (MN) swine farms. Analysis conducted at both the ISU VDL and UMN VDL have found that the PRRSV associated with this variant 1-4-4 are closely related genetically, demonstrating >98% nucleotide homology within their phylogenetic group. When these strains are compared to Paploski's lineage system, they form a tight but distinct cluster within the Lineage 1C. Not all Lineage 1C PRRSV exhibit increased clinical signs and pathogenicity compared to the designated PRRSV 1-4-4 variant. To mark this difference, the ISU VDL reports genetically similar PRRSV ORF5 sequences as 'PRRSV 1-4-4 L1C variant'. From October 2020 to January 2021, the ISU VDL has detected 230 of 2,000 (11.4%) sequences with 1-4-4 RFLP, 76 of 230 (33%) are closely related PRRSV 1-4-4 L1C, 104 of 230 (45.2%) are L1A, 39 of 230 (17%) L1D, 2 of 230 (0.9%) L7, 4 of 230 (1.7%) L8, and 5 of 230 (2.2%) are unknown. 37 of 76 (48.7%) are classified as 'PRRSV 1-4-4 L1C variants' with the first detection occurring in June (figure 1).



Figure 1. Number of detections of PRRSV that are genetically similar to the PRRSV 1-4-4 L1C variant per state of detection, from the first detection in June, 2020 till January of 2021

The detections have occurred primarily in MN and IA with 19 and 16 detections respectively, with one detection in Indiana (IN) and Michigan (MI) each. Although these PRRSV are primarily 1-4-4 RFLP, one detection has demonstrated a 1-4-3 RFLP, underscoring the importance of using the genetic lineage to determine if PRRSV are genetically related.

The ISU VDL will continue to work with collaborators and clients to track the spread of the 'PRRSV 1-4-4 L1C variant'. Given the shortcomings of the RFLP system, the ISU VDL provides the lineage of the PRRSV ORF5 sequence based on Paploski's lineage system on client's diagnostic reports in addition to specifying those PRRSV ORF5 sequences that are similar to the 1-4-4 L1C variant.

Highlights:

- More than 2,000 PRRSV cases have been processed between October 1, 2020 to January 31, 2021. RFLPs 1-8-4, 1-7-4, 2-5-2, 1-4-4, and 1-3-2, the 5 most common, accounted for 70% of those PRRSV sequences;
- While RFLP is determined based on the predicted digestion pattern of 3 enzymes, the Genetic Lineage system accounts for the entire ORF5 sequence;
- A distinct group of 76 of 230 (33%) 1-4-4 RFLP PRRSV that falls within Lineage 1C, and 37 of 76 (48.7%) are known as the PRRSV 1-4-4 L1C variant, have been reportedly causing severe clinical cases of respiratory disease, abortion and mortality;
- The PRRSV 1-4-4 L1C variants form a phylogenetic clade >98% similar based on nucleotide homology;
- Currently, 37 cases of the PRRSV 1-4-4 L1C variant have been detected at the ISU VDL: 19 in MN, 16 in IA, 1 in IN, and 1 in MI;

Note: Contact the SDRS project if you would like to share your work on the bonus page.

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.