Swine Disease Reporting System
Report # 42 (August 3, 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, 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 and Lineage report: Benchmarks patterns of PRRSV RFLP pattern and Lineages detected at the ISU-VDL, UMN-VDL, and KSU-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: Mark Schwartz, Paul Sundberg, Paul Yeske, Tara Donovan, Deborah Murray, Scott Dee, Melissa Hensch, Brigitte Mason, Peter Schneider, Sam Copeland, and Luc Dufresne.

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 July 31, 2021.

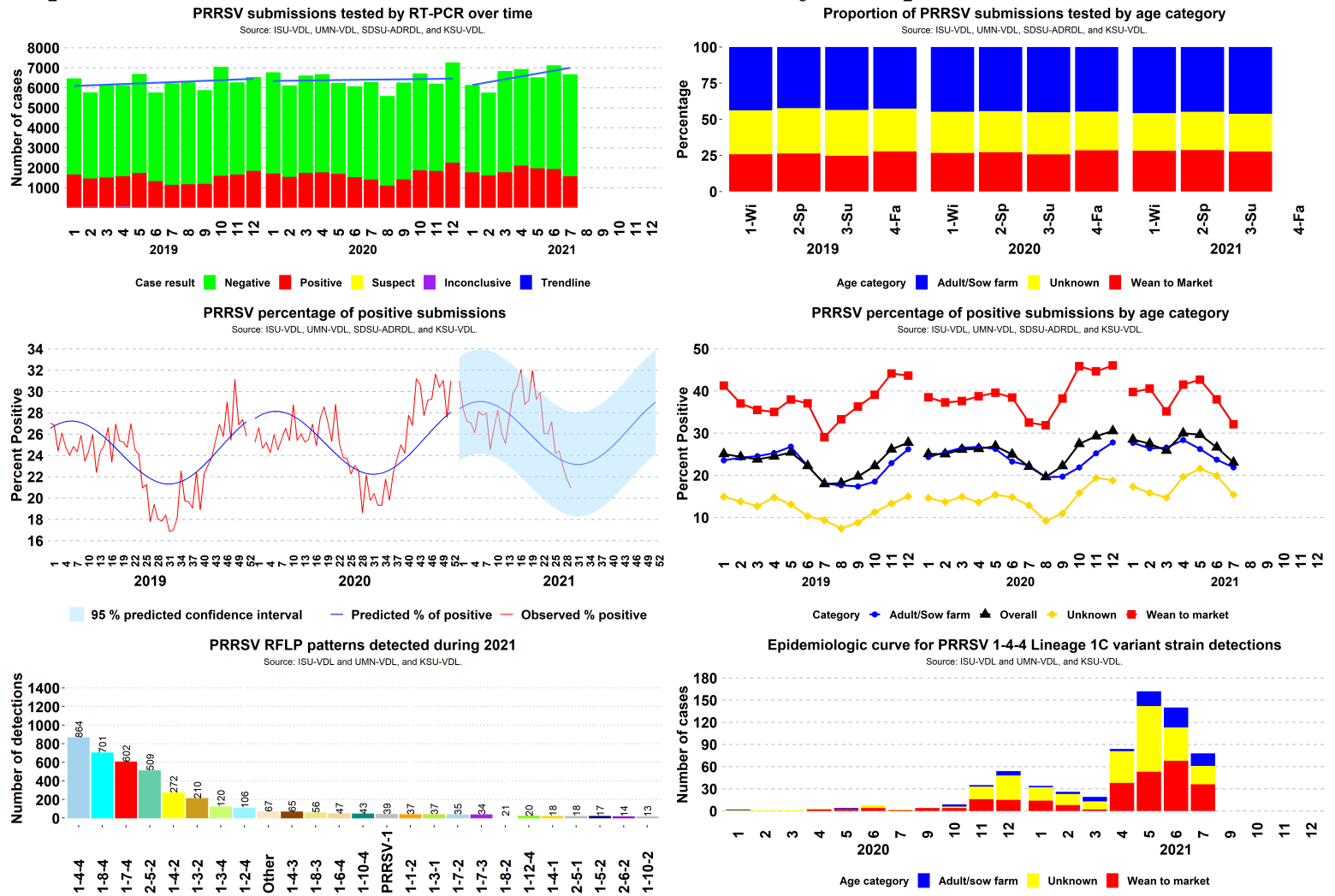# Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.

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** *left* the 25 most frequently detected RFLP patterns druing 2021; *right* Epidemiological curve of detection for PRRSV 1-4-4 Lineage 1C variant strain.

SDRS Advisory Group highlights:

- Overall, 23.04% of 6,676 cases tested PRRSV-positive in July, a moderate decrease from 26.61% of 7,125 in June;
  - Positivity in adult/sow category in July was 21.86% (683 of 3,124), similar to 23.69% (771 of 3,255) in June;
  - Positivity in wean-to-market category in July was 32.1% (592 of 1,844), a substantial decrease from 37.98% (746 of 1,964) in June;
  - Overall PRRSV-percentage of positive cases was 3 standard deviations from state-specific baselines in OH;
- The advisory group pointed that a lowering in the levels of PRRSV detection is following an expected trend for this time of the year. Some regions with high PRRSV activity levels during the winter months already saw a decline in PRRS activit;
- The decline in detection of PRRSV 1-4-4 Lineage 1C variant strains during July doesn't necessarily mean that the epidemic is over. The advisory group strongly encourages keeping looking for best practices to contain the spread of this strain and sharing such information with the industry to prevent the spread further;
- During the 2021 April-June PRRSV 1-4-4 Lineage 1C variant detection wave, some strains had ORF-5 similarity as low as 97-98% relative to the October 2020 outbreak referent strains.

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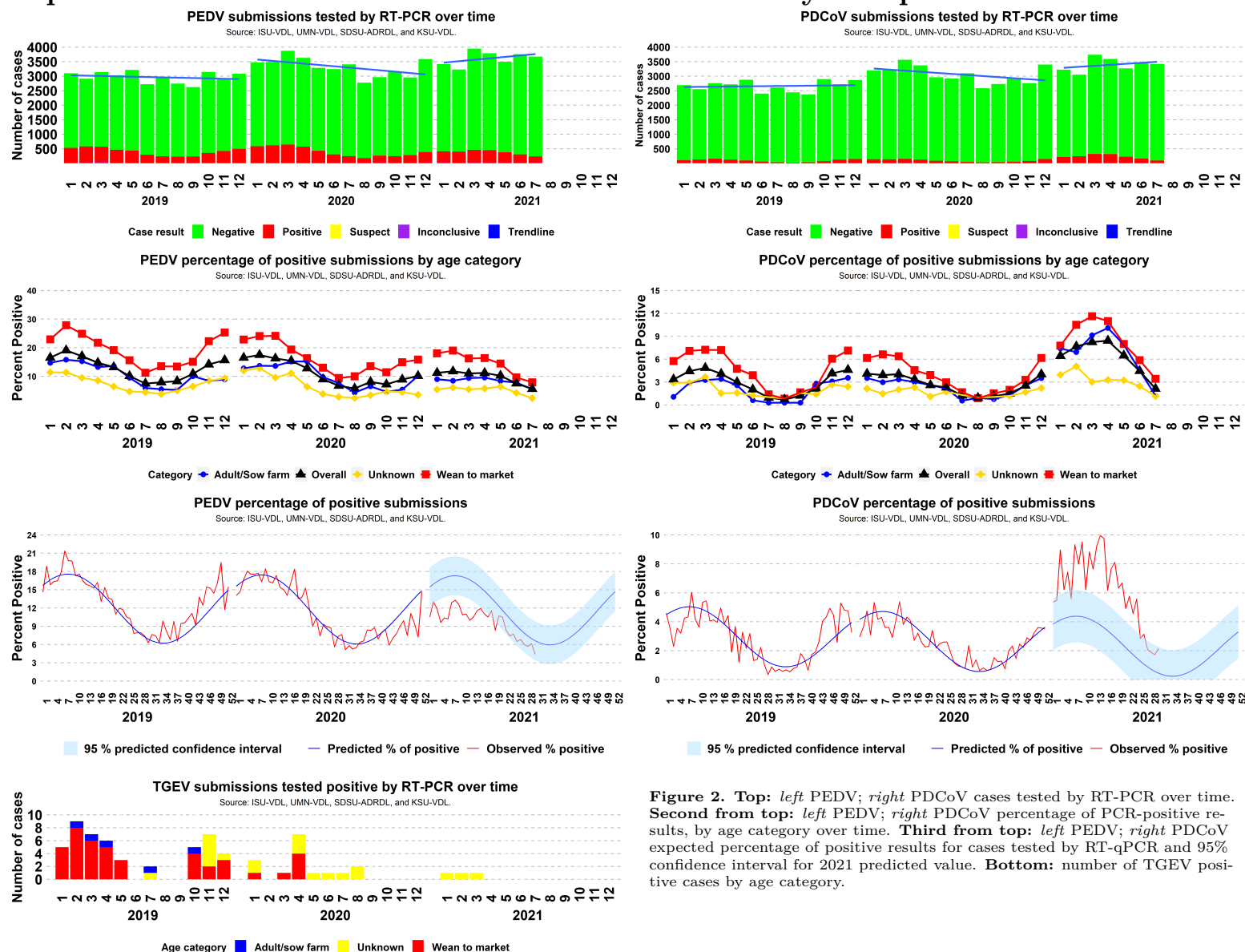
Figure 2. Top: *left* PEDV; *right* PDCoV cases tested by RT-PCR over time. **Second from top:** *left* PEDV; *right* PDCoV percentage of PCR-positive results, by age category over time. **Third from top:** *left* PEDV; *right* PDCoV expected percentage of positive results for cases tested by RT-qPCR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

SDRS Advisory Group highlights:

- Overall, 5.61% of 3,674 cases tested PEDV-positive in July, similar to 7.54% of 3,755 in June;
  - Positivity in adult/sow category in July was 5.49% (55 of 1,001), a moderate decrease from 7.82% (90 of 1,151) in June;
  - Positivity in wean-to-market category in July was 7.91% (125 of 1,581), similar to 9.63% (147 of 1,527) in June;
  - The overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in IL;
- Overall, 2.13% of 3,421 cases tested PDCoV-positive in July, a moderate decrease from 4.45% of 3,461 in June;
  - The overall PDCoV detection was outside of the upper boundaries of the forecasted levels since January;
  - Positivity in adult/sow category in July was 1.2% (11 of 917), a moderate decrease from 4.53% (49 of 1,082) in June;
  - Positivity in wean-to-market category in July was 3.42% (50 of 1,463), a moderate decrease from 5.87% (80 of 1,362) in June;
  - Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in OK, KS, and MO;
- There was 0 positive case for TGEV RNA in July 2021 over a total of 3,309 cases tested.

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

Mycoplama hyopneumoniae submissions tested by RT-PCR over time
Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.

Case result: Negative, Positive, Suspect, Inconclusive, Trendline
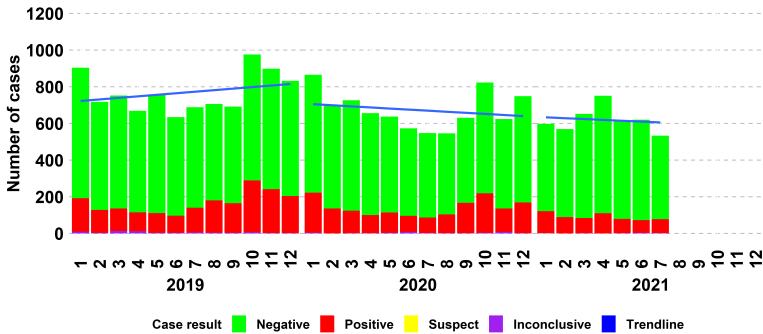
Mycoplasma hyopneumoniae percentage of positive submissions by age category
Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.

Category: Adult/Sow farm, Overall, Unknown, Wean to market
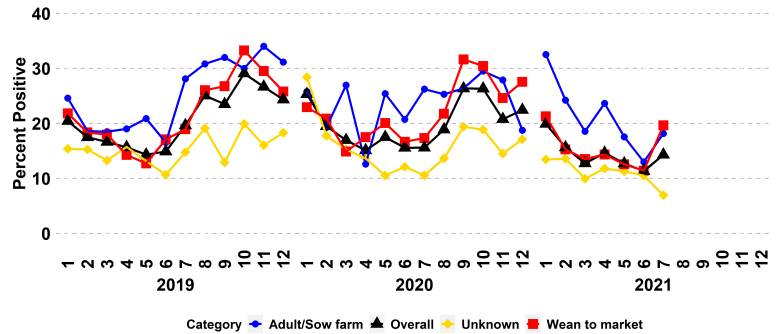
Mycoplasma hyopneumoniae percentage of positive submissions
Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.

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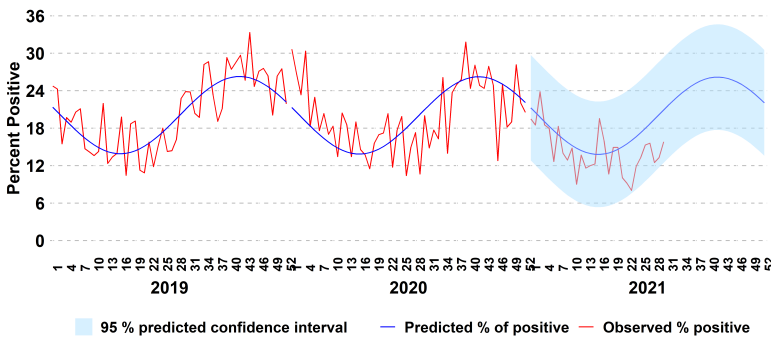
Figure 3. *Left top*: results of MHP PCR cases over time. *Right top*: percentage of MHP PCR-positive results, by category over time. *Bottom*: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2020 predicted value, based on weekly data observed in the previous 3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

SDRS Advisory Group highlights:

- Overall, 14.31% of 531 cases tested *M. hyopneumoniae*-positive in July, a moderate increase from 11.35% of 617 in June;
  - Positivity in adult/sow category in July was 18.18% (14 of 77), a substantial increase from 13% (13 of 100) in June;
  - Positivity in wean-to-market category in July was 19.67% (47 of 239), a substantial increase from 11.42% (33 of 289) in June;
  - Overall MHP-percentage of positive was within state-specific baselines in all 11 monitored states.

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Topic 4 – Disease diagnosis at the ISU-VDL.

Respiratory diagnosis
Source: ISU-VDL.

Digestive diagnosis
Source: ISU-VDL.

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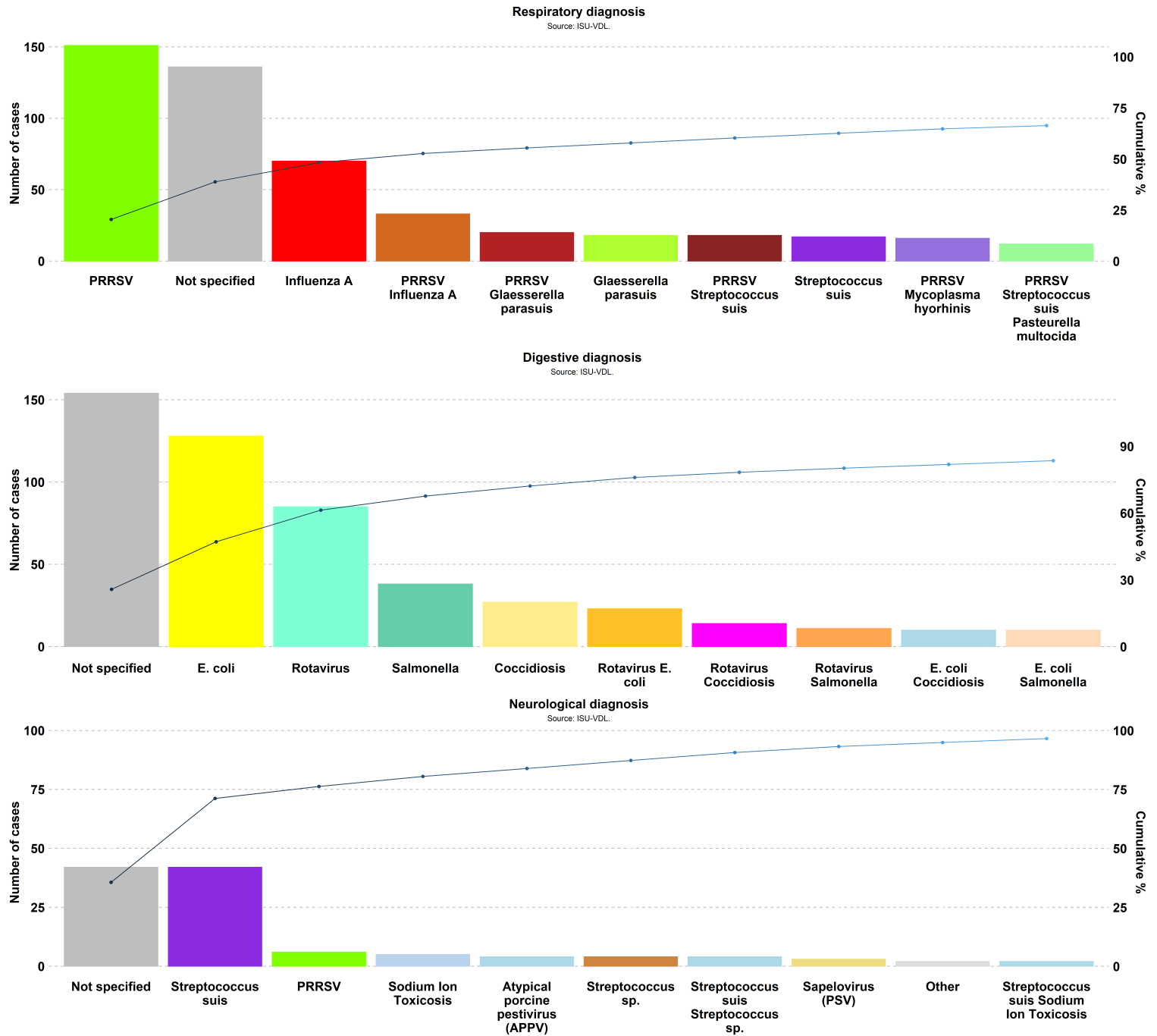
Figure 4. Most frequent disease diagnosis by physiologic system at ISU-VDL . Presented system is described in the title of the chart. Colors represent one agent and/or the combination of 2 or more agents. Only the physiologic systems with historic number of cases per season above 100 are presented in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

Note: Disease diagnosis takes one to two weeks to be performed. The graphs and analysis contain data from June 1, 2021 to July 3,2021.

SDRS Advisory Group highlights:

- PRRSV (151 of 739) continues to lead the number of respiratory diagnoses. After not specified (154 of 599), *E.Coli* (128 of 598) continues to lead the number of digestive diagnoses. After not specified (42 of 118) *S. suis* (52 of 118) continues to lead the number of neurological diagnosis;
- From June 14 to July 3, there was a significant increase (signal) in the diagnosis of *E. coli* and Salmonellas;
- From July 4 to 18, there was a significant increase (signal) in the diagnosis of *M. hyopneumoniae.*

PRRSView, an analytical assessment website for PRRSV

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Porcine Reproductive and Respiratory Syndrome virus (PPRSV) is a leading cause of production and economic losses in swine. Annually, the Iowa State University Veterinary Diagnostic Lab (ISU VDL) generates over 4,500 PRRSV open reading frame 5 (ORF5) sequences. Currently, very limited resources exist for clients and veterinarians to examine the specific strain of PRRSV that has been detected in outbreaks or through routine surveillance on their farm. Clients are further limited by the continued use of the RFLP nomenclature, which is not directly related to the genetic lineage of the virus and lacks relevance to the genetic similarity between different viruses. To help clients and veterinarians easily acquire additional PRRSV strain information, ISU PRRSView has been created to allow clients to analyze the sequence genetic data from their case reports.

Currently, three analytical tools are available on the PRRSView website. The first tool is the ORF5 BLAST tool, which is designed to compare input sequences provided in FASTA format to other PRRSV cases sequenced and retained in the ISU VDL database. For any ORF5 sequence input, up to 10 hits identified by BLAST with greater than 96% nucleotide homology will be returned containing case metadata. Each entry returned will include the date the sample was collected in the first column, the state and country that the sequence was collected if available, the matching genetic lineages based on Paploski et. al 2021, sequence RFLP pattern, and sequence identity compared to the query strain input by the user. The state locations of the top 10 hits will also be presented graphically in a pie chart. The summary of these results can be downloaded through the "Download Results" button.

The PRRSV ORF5 vaccine identity tool is designed to report the sequence identity of submitted sequences to the modified live virus (MLV) PRRSV vaccine ORF5 currently available. This tool will additionally calculate the RFLP and estimate the genetic lineage of the ORF5 sequence using neighbor joining phylogenetics. Under each returned result is the option to view a phylogenetic analysis (Under the "Lineage" column) that will

Figure 1. Phylogenetic tree generated in the ISU PRRSView ORF5 vaccine identity tool

show the placement of a query sequence on a tree relative to reference ORF5 sequences. A summary of these results can be downloaded for additional use.

The ORF5 Restriction fragment length polymorphism tool, or RFLP tool, is designed to quickly identify the RFLP of ORF5 sequences submitted by the user. After running the analysis, hovering over the RFLP result allows the user to view the location of each of the 3 cut sites that designate the RFLP pattern.

PRRSView and additional resources such as a description of the current genetic lineage designations, user tutorials (under the general information tab) can be accessed through the web URL https://prrsv.vdl.iastate.edu.

Highlights:
- ISU PRRSView will help analyze the genetic sequence data;
- There are three analytical tools available for the analysis;
  - Blast tool - To compare input sequence with other ISU VDL PRRSV sequences;
  - ORF5 Vaccine identity tool - To compare sequence identity of input sequence to modified live virus (MLV) PRRSV vaccine ORF5;
  - ORF5 RFLP tool - To Classify the input sequence according to RFLP pattern and PRRSV Lineage classification;

References:
Paploski et al. Phylogenetic Structure and Sequential Dominance of Sub-Lineages of PRRSV Type-2 Lineage 1 in the United States. Vaccines (Basel). 2021; 9(6) doi:10.3390/vaccines9060608;
Wesley et al. Differentiation of a porcine reproductive and respiratory syndrome virus vaccine strain from North American field strains by restriction fragment length polymorphism analysis of ORF 5. J Vet Diagn Invest. 1998;10(2):140-4. doi:10.1177/104063879801000204.