Swine Disease Reporting System
Report # 35 (January 5, 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:**
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> *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.
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> Project coordinator Giovani Trevisan. Principal investigator Daniel Linhares.
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> *University of Minnesota*: Mary Thurn, Paulo Lages, Cesar Corzo, Jerry Torrison.
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> *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, Scanlon Daniels, Brigitte Mason, Randy Jones.

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 December 31, 2020.*

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Swine Disease Reporting System:
Domestic Swine Disease Surveillance

IOWA STATE UNIVERSITY — Veterinary Diagnostic Laboratory | UNIVERSITY OF MINNESOTA VETERINARY DIAGNOSTIC LAB | SOUTH DAKOTA ADRDL — ANIMAL DISEASE RESEARCH & DIAGNOSTIC LABORATORY — BROOKINGS, SOUTH DAKOTA | Kansas State Veterinary DIAGNOSTIC LABORATORY | SHIC Swine Health Information Center

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

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

Case result: Negative | Positive | Suspect | Inconclusive | Trendline

Proportion of PRRSV submissions tested by age category
Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.

Age category: Adult/Sow farm | Unknown | Wean to Market

PRRSV percentage of positive submissions
Source: ISU-VDL, UMN-VDL, SDSU-ADRDL, and KSU-VDL.

95 % predicted confidence interval | Predicted % of positive | Observed % positive

PRRSV 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

PRRSV RFLP patterns detected during 2019
Source: ISU-VDL and UMN-VDL.

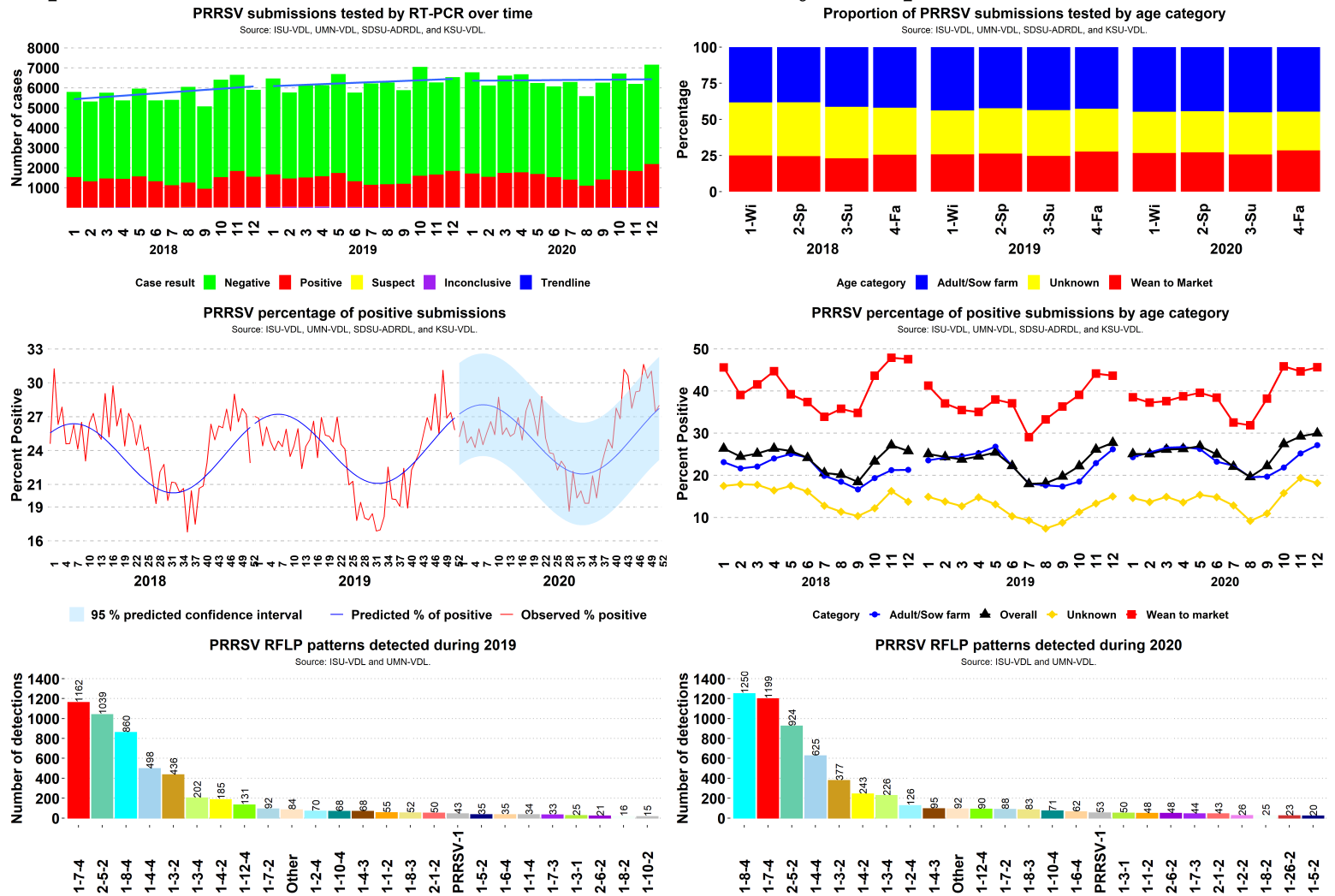**PRRSV RFLP patterns detected during 2020**
Source: ISU-VDL and UMN-VDL.

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 2019; *right* year of 2020.

SDRS Advisory Group highlights:

- Overall, 29.97% of 7,161 cases tested PRRSV-positive in December, similar to 29.25% of 6,201 in November;
  - The overall PRRSV detection was outside of the upper boundaries of the forecasted levels between November 30 - December 6;
  - Positivity in adult/sow category in December was 27.16% (888 of 3,269), similar to 25.2% (685 of 2,718) in November;
  - Positivity in wean-to-market category in December was 45.64% (915 of 2,005), similar to 44.65% (802 of 1,796) in November;
- Overall PRRSV-percentage of positive cases was above 3 standard deviations from state-specific baselines in MN, SD, IA, NE, MO, and IN;
- The advisory group pointed out that during the last decade, improvements were made for PRRS control and more susceptible animals are currently in the field. Recent PRRS-break in sow farms has contributed to PRRS-positive growing animal placement, and the association with colder weather favors PRRSV survival and spread, potentially increasing the infection pressure. Additionally, a PRRSV 1-4-4 has been associated with a large number of breaks in the midwest region.

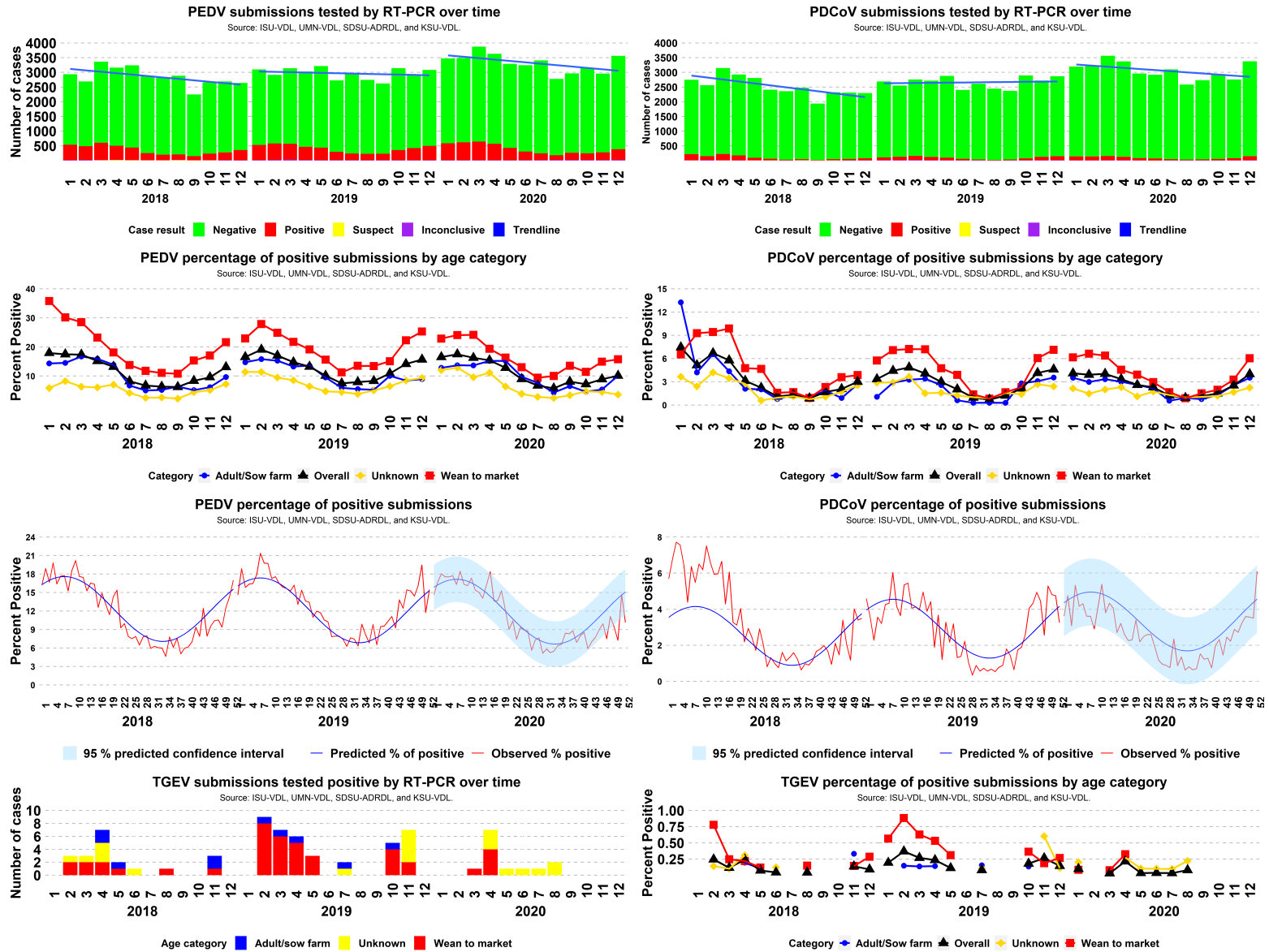# Topic 2 – Detection of RNA of enteric coronavirus by RT-qPCR

Figure 2. Top: *left* PEDV *right* PDCoV cases tested by RT-PCR over time. **Second from top**: B:*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 2020 predicted value. **Bottom**: *left* number of TGEV positive cases by age category *right* percentage of TGEV PCR-positive cases by age category. Each color represents one distinct age category.

SDRS Advisory Group highlights:

- Overall, 10.11% of 3,561 cases tested PEDV-positive in December, similar to 8.89% of 2,957 in November;
  - Positivity in adult/sow category in December was 10.14% (114 of 1,124), a moderate increase from 5.37% (43 of 801) in November;
  - Positivity in wean-to-market category in December was 15.75% (205 of 1,302), similar to 14.93% (176 of 1,179) in November;
  - Overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in IL;
  - Overall PEDV-percentage of positive cases was on the lower boundaries of the forecasted levels for this time of the year;
- Overall, 4% of 3,374 cases tested PDCoV-positive in December, similar to 2.54% of 2,759 in November;
  - Positivity in adult/sow category in December was 3.52% (37 of 1,051), similar to 2.56% (19 of 741) in November;
  - Positivity in wean-to-market category in December was 6.04% (73 of 1,209), a moderate increase from 3.29% (35 of 1,063) in November;
  - Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in OK and IL;
- There was 0 positive case for TGEV RNA in December 2020 over a total of 3,308 cases tested;
- The advisory group pointed out that efforts were made during warm months to reduce enteric coronavirus circulation. Intense efforts to better characterize health status of all herds within production system, improvements on biosecurity and biocontainment practices, sow farm depopulations, reduce number of sow farms on the unstable category, improvements on truck washing capabilities, and validated feed mitigants usage are potential contributors to lowering the PEDV detection.

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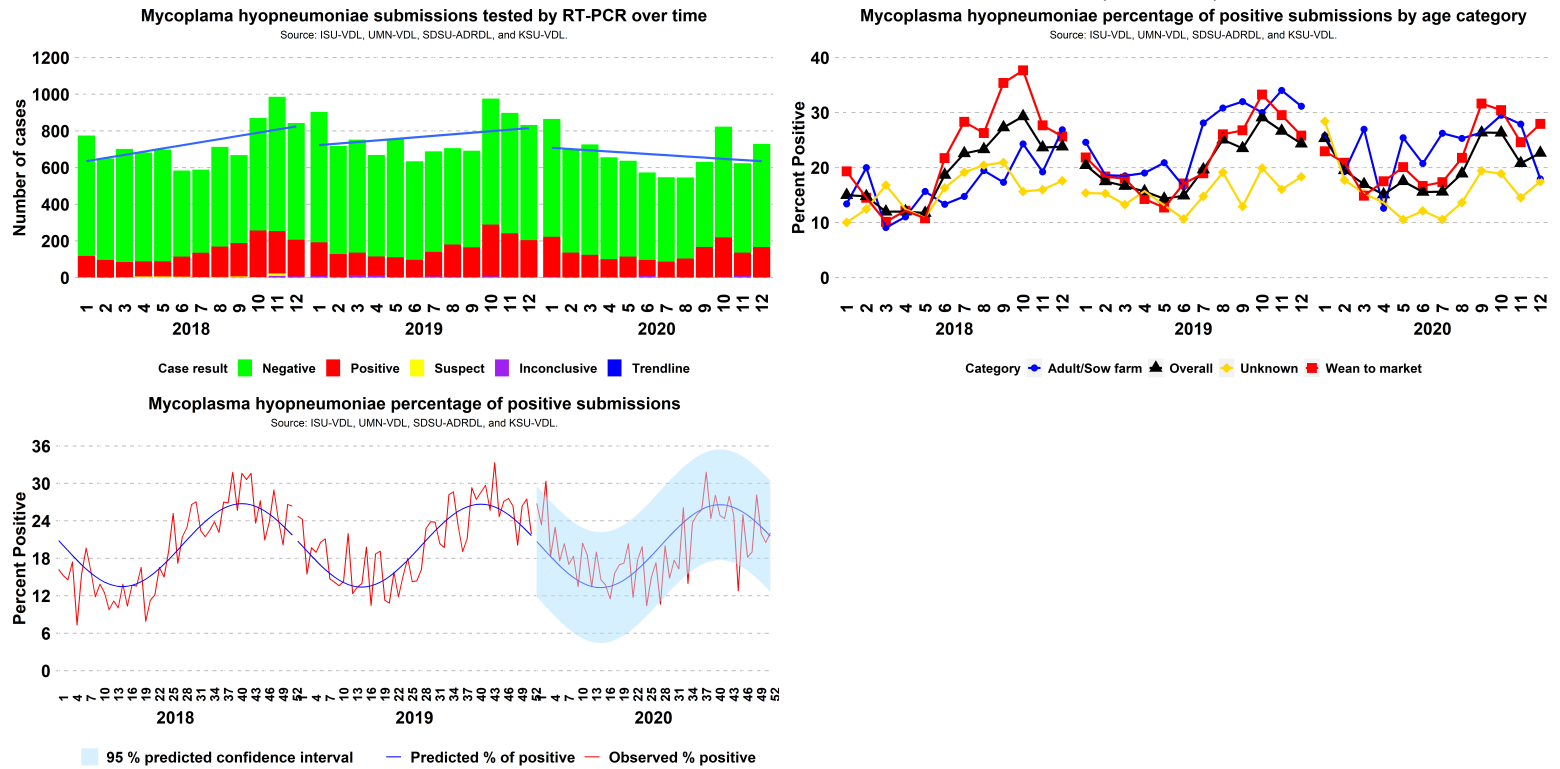

Figure 3. *Left top*: results of MHP PCR cases over time. *Right top*: percentage of MHP PCR-positive results, by category over time. *Bottom*: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2020 predicted value, based on weekly data observed in the previous 3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

SDRS Advisory Group highlights:

- Overall, 22.66% of 728 cases tested *M. hyopneumoniae*-positive cases in December, similar to 20.78% of 616 in November;
- The advisory group pointed out that during the last 3 months, there was more MHP activity in the field, leading to identification of clinical disease and unexpected destabilization of negative herds.

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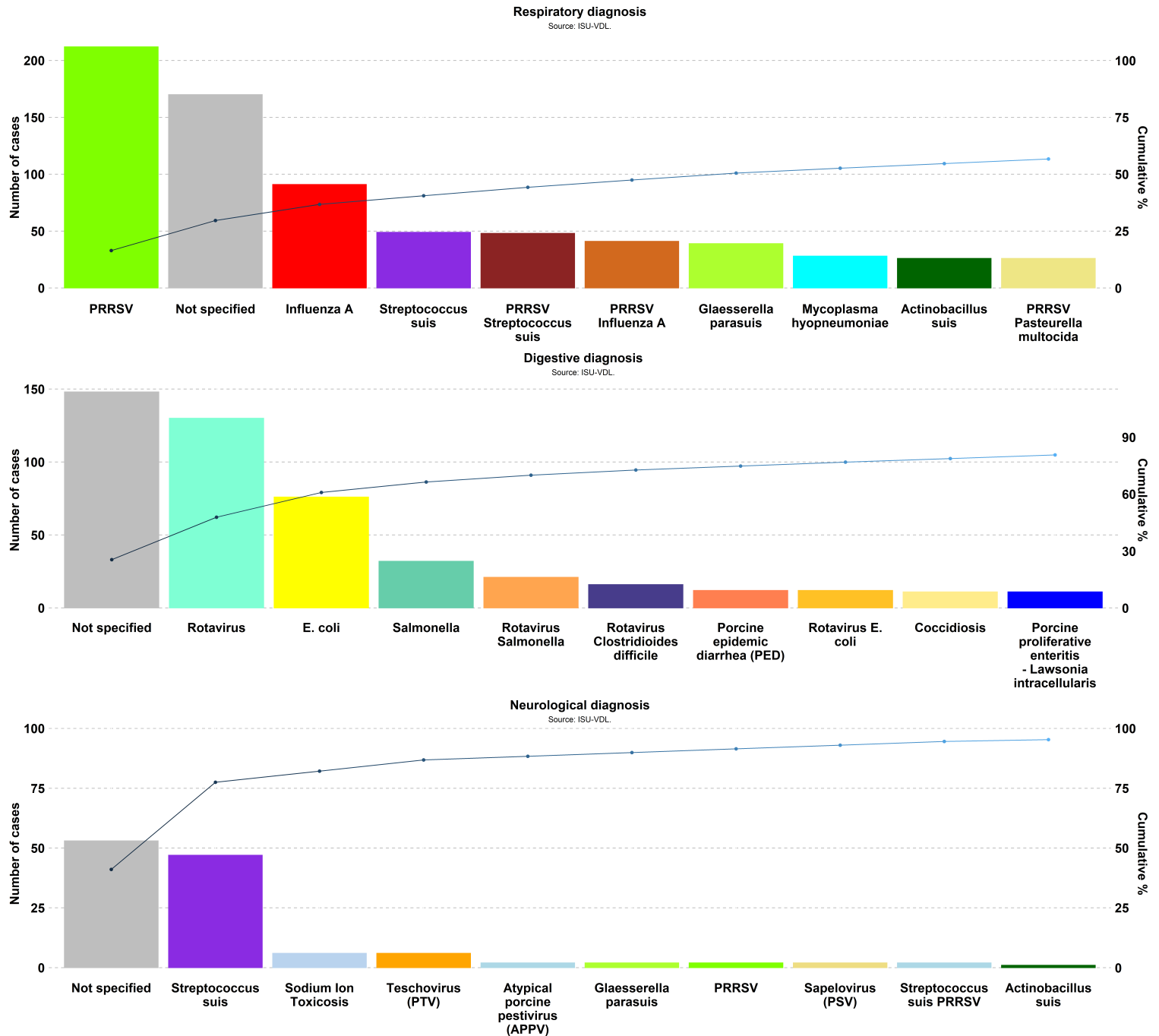
Topic 4 – Disease diagnosis at the ISU-VDL.

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 November 1 to December 6.

SDRS Advisory Group highlights:

- PRRSV (212 of 1287) continues to lead the number of respiratory diagnoses. After Not specified (148 of 581), Rotavirus (130 of 581) leads the digestive diagnoses. After *Not specified* (53 of 129), *S. suis* (47 of 129) leads the the neurological diagnosis;
- From November 30 to December 6, there was a significant increase (signal) for agents classified as cardiovascular-blood-endocrine-immune and from December 7-13 for agents classified as digestive and musculoskeletal.
- From November 30 to December 13, there was a significant increase (signal) for Salmonella and from December 7-20 for PEDV

Identifying porcine reproductive and respiratory syndrome virus (PRRSV) genetic variability within breeding herds

Giovani Trevisan[1], Ganwu Li[1], Daniel Linhares[1]

1 - Iowa State University.

Porcine reproductive and respiratory syndrome (PRRS) is one of the most economically important swine diseases in the United States. PRRS related clinical signs include reproductive failure in breeding herds and respiratory affliction in growing animals. PRRS has as etiology an RNA virus named PRRS virus (PRRSV). The whole-PRRSV genome is comprised of about 15,100 nucleotide base pairs (bp) and composed of at least 9 distinct regions identified open read frame (ORF) 1 to 7. The ORF5 is comprised of 603 bp and represents 4% of the whole-PRRSV genome and has been mainly genome portion used to compare different PRRSV strains in the US. As ORF5 is limited to only one fragment of the whole-PRRSV genome, there is a need to understand better PRRSV genetic variability based on the whole-PRRSV genome. This study objective was to investigate different PRRSV strains circulating in the breeding herds using the whole-PRRSV genome.

A total of 20 breeding herds that recently faced a PRRSV outbreak by a wild-type PRRSV (wt-PRRSV) strain and adopted measures like load, closure, and exposure, or all of them to eliminate the virus from the herd were enrolled. Weekly processing fluid (PF) samples were collected and tested on a weekly pool for PRRSV by reverse quantitative polymerase chain reaction (RT-qPCR). PF and, for farms that used live virus inoculation (LVI) as an exposure method, an aliquot of the LVI material was submitted for whole-genome sequencing (WGS). Selection of PF for WGS sequencing was based on 3-time points after the break: a) 2-3 weeks into the break; b) around 10 weeks; c) last PF samples having Ct < 30 before 8 consecutive weeks with negative for PRRSV on RT-qPCR results were obtained. A recovered whole-PRRSV genome from each farm was set as the reference strain for additional comparisons. When only PRRSV genome fragments, named as contigs, were recovered, they were compared with the farm-referent strain. A Blast technique was applied to determine contig position within the whole-PRRSV genome and similarity level. Whole-PRRSV sequences available in PubMed and having country identified as "USA" were downloaded and used to compare the recovered strains to investigate potential recombination events. Contigs and whole-PRRSV strains were compared with the commercial modified live virus (MLV) vaccine strains. Four of 20 enrolled farms reached 8 weeks with consecutive negative results for PRRSV in PF, and 1 went through depopulation. A total of 45 samples (8 serum, 4 lung/lung homogenate, and 33 processing fluid) from 15 farms were submitted for WGS. For 13 farms, a wt-whole-PRRSV genome has been recovered and set as farm referent strain. For 4 farms, the comparison between contigs and referent strain revealed at least 2 wt-PRRSV strains. A vaccine like strains was detected in 2 farms at 11 and 22 weeks after the farm closure. Recovered vaccine-like strains were similar to the vaccine used during gilt acclimation or herd exposure. There was supportive evidence for 4 strains with recombination events between wt-PRRSV strains and one involving a wt-PRRSV strain and a vaccine-like strain.

This study preliminary results are promising and show that diverse PRRSV strains are potentially co-circulating in a farm. Veterinarians should make efforts to recover at least one whole-PRRSV genome to characterize at least one farm-specif strain allowing them to make further comparisons. Additionally, recombination between wt-PRRSV strains may be frequent in the field. This study still ongoing, and the next steps will investigate the influence of encountered viral diversity and recombination events on time to stability and baseline production.

Highlights:
- Breeding herds infected with PRRSV should have at least 1 wt-PRRSV strain known;
- Using processing fluids, diverse PRRSV strains were detected and co-circulating in 6 breeding herds;
- wt-PRRSV strains recombinations may often occur in the field.