Swine Disease Reporting System:
Overview

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

Swine Disease Reporting System
Report # 39 (May 4, 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 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: Mark Schwartz, Paul Yeske, Rebecca Robbins, Tara Donovan, Deborah Murray, Scott Dee, Melissa Hensch, Brigitte Mason, Peter Schneider, and Sam Copeland.

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 April 30, 2021.

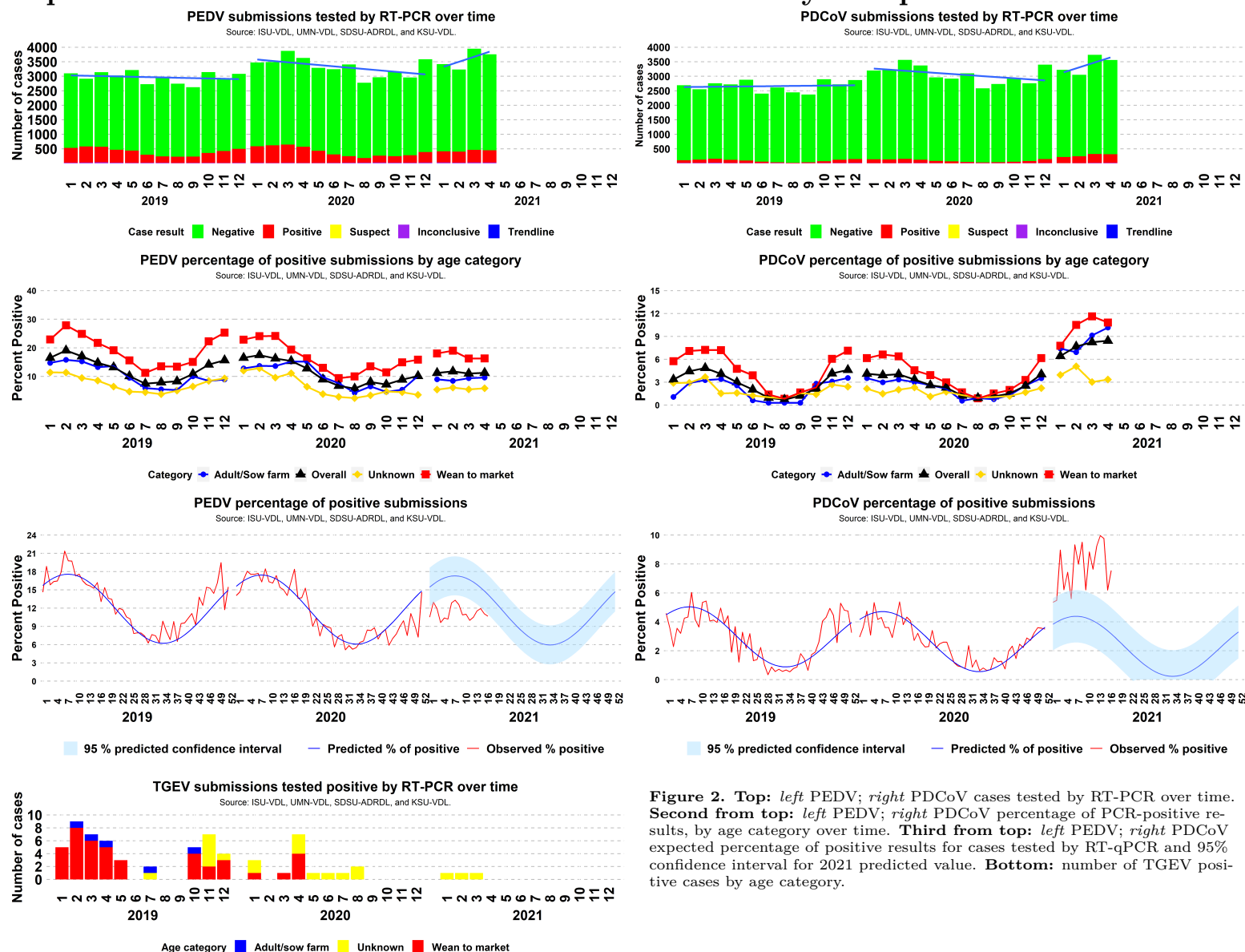# Topic 1 – Detection of PRRSV RNA over time by RT-qPCR.
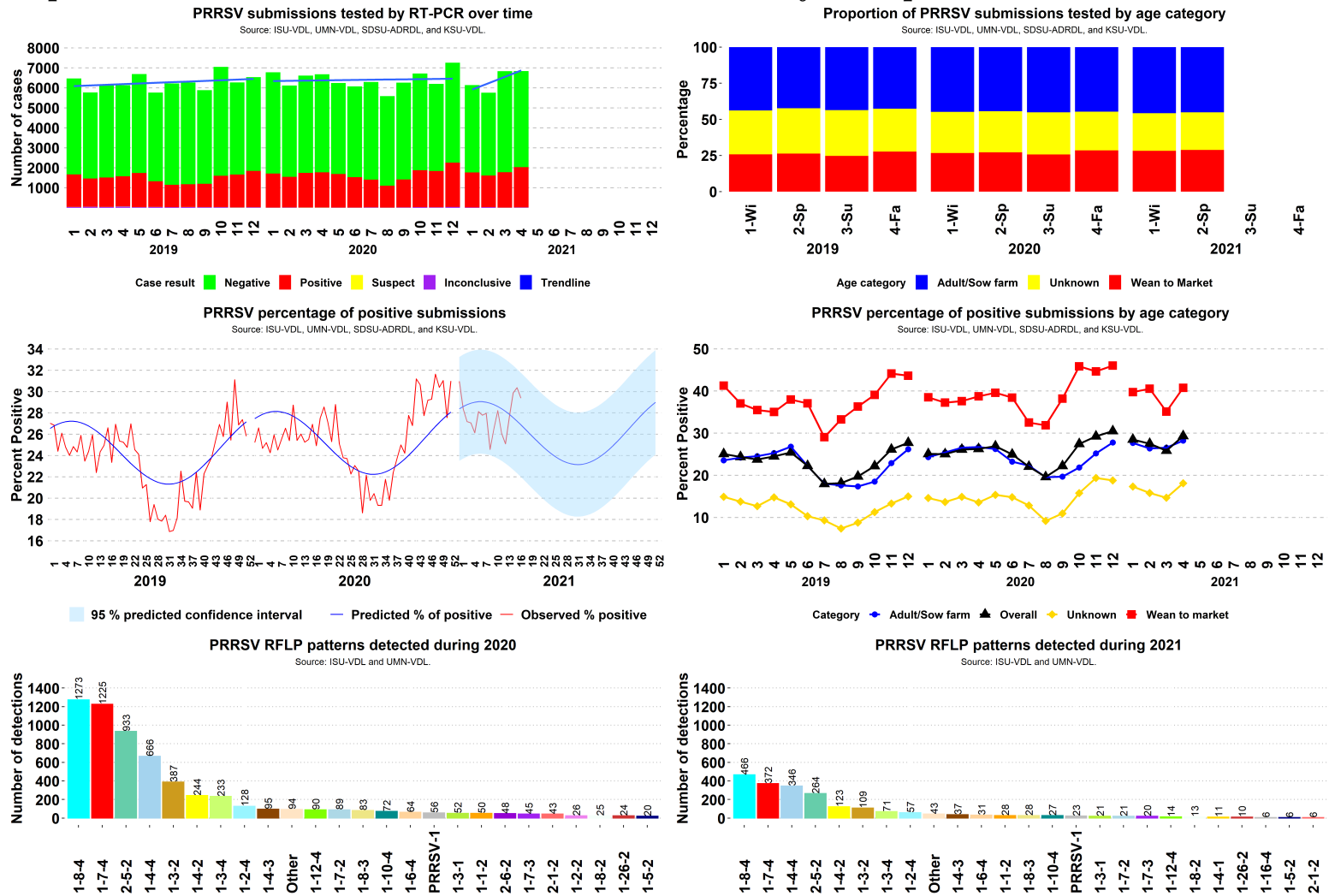
Figure 1. Top: *left*: Results of PRRSV RT-PCR cases over time. *Right*: Proportion of accession ID cases tested for PRRSV by age group per year and season. **Middle**: *Left* expected percentage of positive results for PRRSV RNA by RT-qPCR, with 95% confidence interval band for predicted results based 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, 29.33% of 6,843 cases tested PRRSV-positive in April, a moderate increase from 25.84% of 6,834 in March;
  - The overall PRRSV detection was within the forecasted levels during March;
  - Positivity in adult/sow category in April was 28.23% (855 of 3,029), similar to 26.55% (833 of 3,138) in March;
  - Positivity in wean-to-market category in April was 40.77% (830 of 2,036), a substantial increase from 35.11% (671 of 1,911) in March;
  - Overall PRRSV-percentage of positive cases was 3 standard deviations from state-specific baselines NC, NE, and OH;
- The advisory group pointed out that increased detection of PRRSV observed in April is partly a reflection of finishing breaks those were contributed by the placement of positive pigs derived from sow farms that broke with PRRSV during past winter;
- Additionally, the increased detection of PRRSV in NE and OH is associated with higher monitoring due to PRRSV breaks in those regions this past winter and positive finishing pigs placement;
- Update on the PRRSV 1-4-4 Lineage 1C variant situation. Based on PRRSV detection, ORF-5 sequences, and disease diagnosis, this strain's initial and rapid spread across breeding heds has been contained. Based on the advisory group's input, farms that first broke with this strain are now at low prevalence stages. New breaks were observed in less magnitude and will continue to occur as long as this strain finds the opportunity to infect other herds that have not seen it before. We should keep vigilant in the upcoming fall and winter for a potential re-emergence of this strain.

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

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

Case result: Negative Positive Suspect Inconclusive Trendline

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

Case result: Negative Positive Suspect Inconclusive Trendline

PEDV 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

PDCoV 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

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

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

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

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

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

Age category: Adult/sow farm Unknown Wean to market

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.
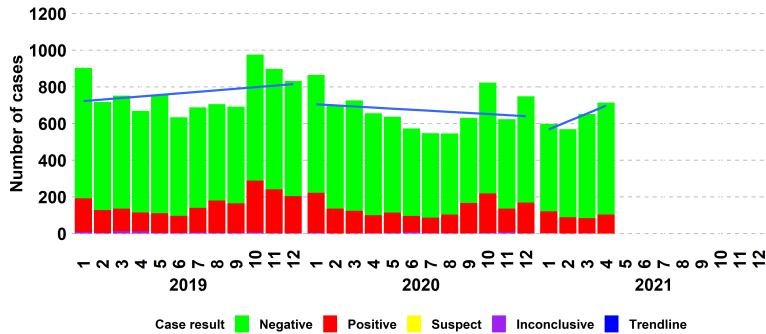
SDRS Advisory Group highlights:

- Overall, 11.26% of 3,757 cases tested PEDV-positive in April, similar to 11.02% of 3,949 in March;
  - Positivity in adult/sow category in April was 9.61% (112 of 1,165), similar to 9.39% (108 of 1,150) in March;
  - Positivity in wean-to-market category in April was 16.31% (248 of 1,521), similar to 16.25% (262 of 1,612) in March;
  - The overall PEDV-percentage of positive cases was 3 standard deviations from state-specific baselines in IL;
- Overall, 8.42% of 3,561 cases tested PDCoV-positive in April, similar to 8.24% of 3,738 in March;
  - The overall PDCoV detection was outside of the upper boundaries of the forecasted levels since January;
  - Positivity in adult/sow category in April was 10.15% (112 of 1,103), similar to 9.13% (98 of 1,073) in March;
  - Positivity in wean-to-market category in April was 10.82% (153 of 1,414), similar to 11.63% (175 of 1,505) in March;
  - Overall PDCoV-percentage of positive cases was 3 standard deviations from state-specific baselines in OK, KS, MO, and NC;
- There was 0 positive case for TGEV RNA in April, 2021 over a total of 3,452 cases tested. During the last year (5/1/2020 to 4/30/2021) 36,083 cases, 117,999 samples have been tested for TGEV, and only 8 cases had a TGEV positive result;
- The advisory group pointed out that the increased detection of PDCoV is associated with increased testing following outbreaks observed in sow farms. Also, the increased PDCoV activity observed since January explains the increased viral activity in grow-finish animals.

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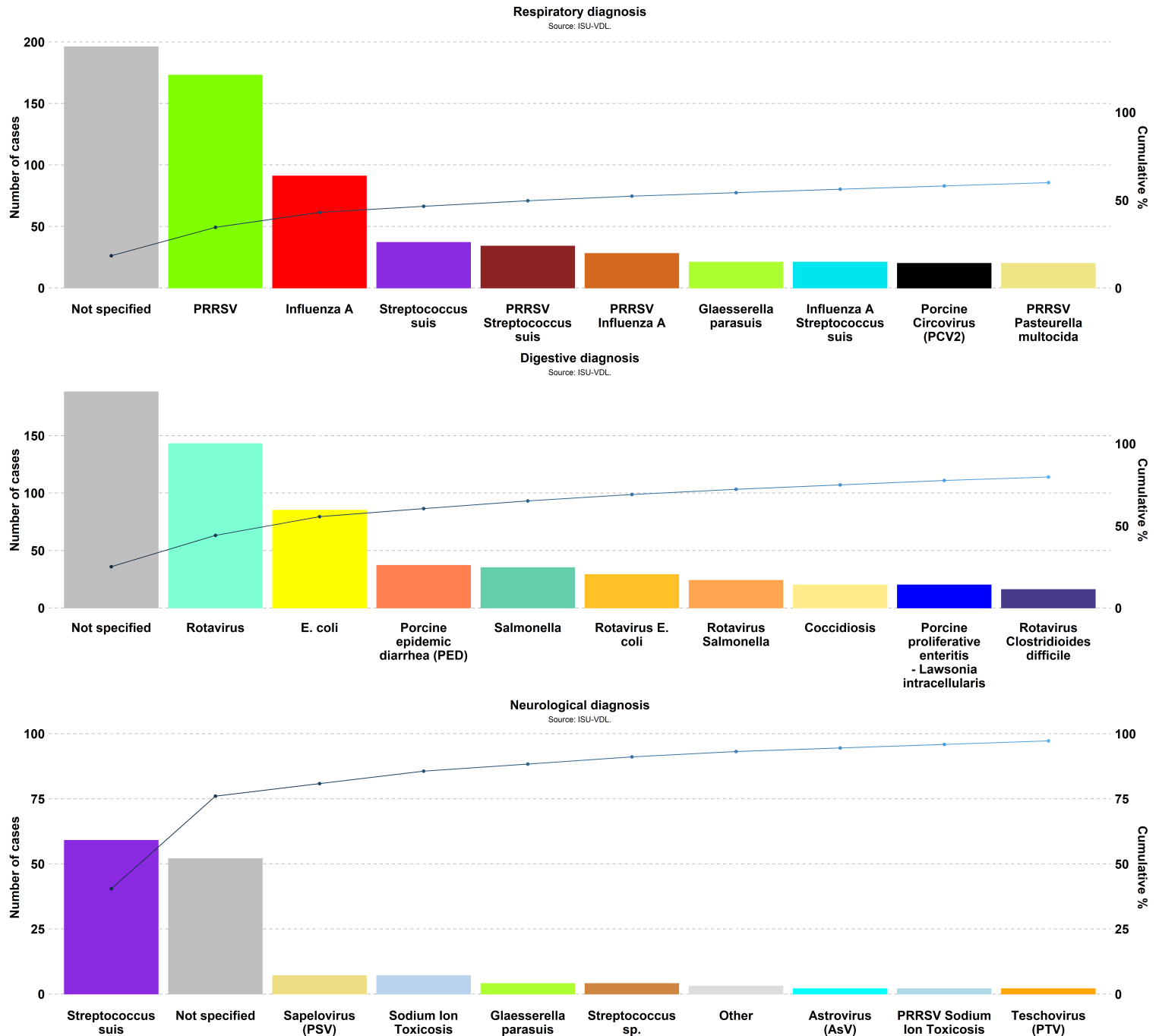# Topic 3 – Detection of *Mycoplasma hyopneumoniae* (MHP) DNA by PCR.
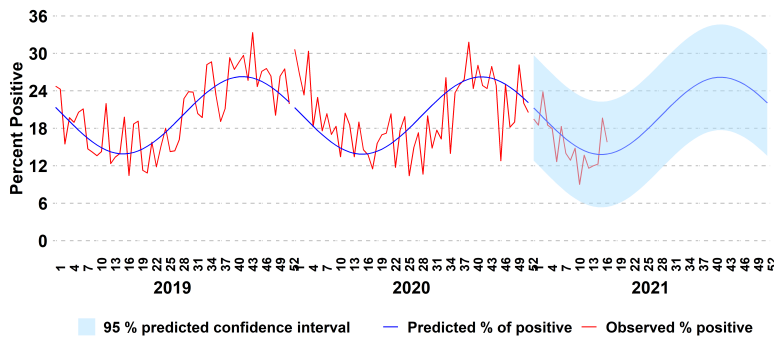
Figure 3. *Left top*: results of MHP PCR cases over time. *Right top*: percentage of MHP PCR-positive results, by category over time. *Bottom*: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2020 predicted value, based on weekly data observed in the previous 3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

SDRS Advisory Group highlights:

- Overall, 14.57% of 714 cases tested *M. hyopneumoniae*-positive cases in April, similar to 12.75% of 651 in March;
    - Positivity in adult/sow category in April was 22.99% (20 of 87), a moderate increase from 18.57% (13 of 70) in March;
    - Positivity in wean-to-market category in April was 14.69% (57 of 388), similar to 13.53% (46 of 340) in March;
    - Overall MHP-percentage of positive cases was within 3 standard deviations from state-specific baselines in all 11 monitored states;
- 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.

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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 March 1, 2021 to April 17,2021.

SDRS Advisory Group highlights:

• After not specified (196 of 1069), PRRSV (173 of 1,069) continues to lead the number of respiratory diagnoses. After not specified (188 of 748), Rotavirus (143 of 748) continues to lead the number of digestive diagnoses. *Streptococcus suis* (59 of 146) continues to lead the number of neurological diagnosis;

• During March 29 - April 3, there was a significant increase (signal) in the diagnosis of agents classified as respiratory, urogenital and musculoskeletal.

• During March 29 - April 17, there was a significant increase (signal) in the diagnosis Influenza A and Porcine Circovirus-2 .

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

Novel human-seasonal H3 influenza A virus spillover into US swine

Aditi Sharma[1], Michael A. Zeller[1], Carine K. Souza [2], Tavis Andersonb[2], Amy L. Vincent[2], Karen Harmon[1], Ganwu Li[1], Jianqiang Zhang[1], Phillip C. Gauger[1]

1 - Iowa State University, Ames, Iowa, USA. 2 - Virus and Prion Research Unit, National Animal Disease Center, USDA-ARS, Ames, Iowa, USA.

In March 2017, a novel H3N2 influenza A virus (IAV) was detected in a diagnostic case from Oklahoma received at the Iowa State University Veterinary Diagnostic Laboratory. The HA gene was sequenced followed by next-generation sequencing to obtain the whole genome. Pairwise comparison between these detections in swine and the most similar human seasonal H3 revealed 99.9% nucleotide identity with 2016-2017 strains, suggesting this IAV was of human origin and was subsequently transmitted to pigs. As more cases were identified, these H3 genes formed a monophyletic clade with the initially detected sequence, and a clade designation of "H3.2010.2" was assigned to indicate the second human seasonal H3 in the 2010 decade spillover. Genetic and antigenic characterization of the H3.2010.2 H3N2 was performed to understand the origin of this novel virus.

A total of 45 HA and 26 neuraminidase (NA) sequences from 2017-2020 as well as 11 whole genome sequences (WGS) were utilized in the study.
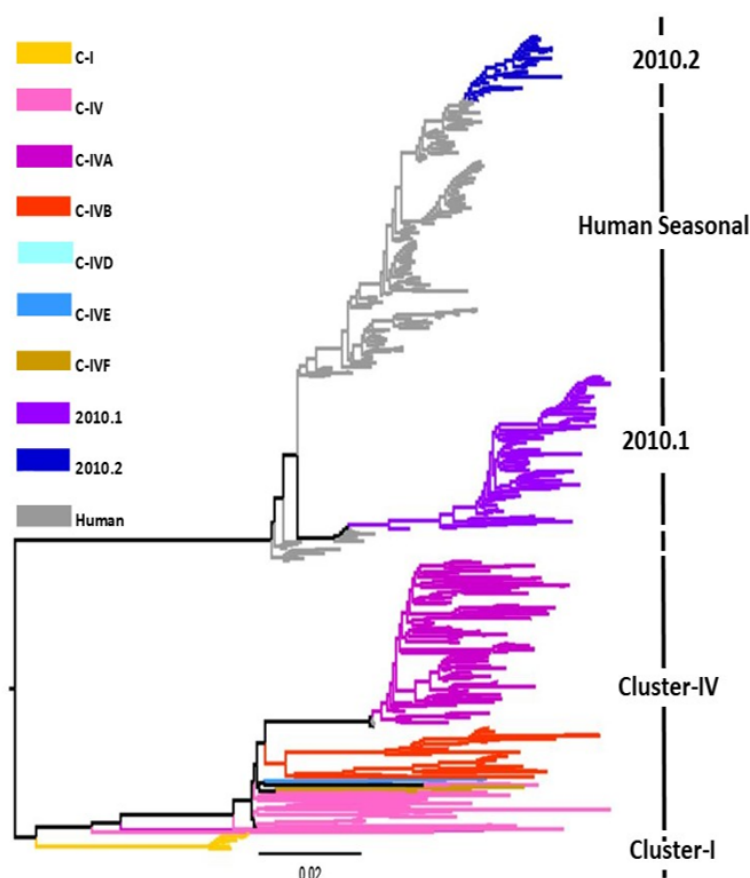
Time to most recent common human ancestor (MRCA) based on the HA gene was estimated between August-September, 2016. As a result of reassortment, the internal genes (PB2, PB1, PA, NP, M and NS) were of swine origin while the surface protein genes (HA and NA) remained of human seasonal H3N2 origin with the exception N2 gene in one strain. The internal gene segments from WGS consisted of matrix genes originating from the 2009 pandemic H1N1 and the additional 5 internal genes of triple reassortant swine origin (TTTTPT). K189N substitutions at one of the 6 amino acid positions (145, 155, 156, 158, 159 and 189), collectively referred to as "antigenic motif", were identified as a difference from pre-2018 and post-2018 sequences. A loss of glycosylation was also observed at two predicted sites compared to the putative human seasonal ancestor, 133 and 165, from late 2017 to 2020, although their significance is unknown. The H3 antigenic motif and glycosylation data suggest adaptive changes made by 2010.2 IAV while circulating in swine (Fig. 1).

Pigs experimentally infected with H3.2010.2 demonstrated efficient nasal shedding and replication in the lungs, mild pneumonia, minimal microscopic lung lesions and transmitted the virus to indirect contact swine. The antigenic phenotype of the H3.2010.2 viruses were closer to human seasonal vaccine strain A/Hong Kong/4801/2014 compared to the H3.2010.1 viruses that were first detected in swine in 2012. However, continued antigenic evolution away from current human seasonal H3N2 vaccine strains is likely and thus, these swine 2010.2 may become a zoonotic threat in the future. Monitoring and detecting novel human to swine IAV spillovers aids in vaccine antigen selection and could impact pandemic preparedness.

Figure 1. H3-HA maximum likelihood phylogenetic tree demonstrating different H3 lineages circulating in the US swine population. The novel H3 IAV designated "2010.2" is colored in blue

Highlights:

- A novel novel H3 influenza A strain was detected in 2017 in pigs;

- The strain was designated as "2010.2";

- The antigenic evolution of these swine 2010.2 strain may become a zoonotic threat in the future.

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