

Swine Disease Reporting System Report 11 (January 8th, 2019)

What is the SDRS?

SHIC-funded, veterinary diagnostic laboratories (VDLs) collaborative project, with goal to aggregate swine diagnostic data from participating reporting VDLs, and report in an intuitive format (web dashboards), describing dynamics of disease detection by pathogen or disease syndrome over time, specimen, age group, and geographical space.

For this report, data is from the Iowa State University VDL and South Dakota State University ADRDL. University of Minnesota VDL and Kansas State University VDL. Specifically, for PRRSV RFLP data, and syndromic information the results are from Iowa State University VDL.

For all “2018 predictive graphs”, the expected value was calculated using a statistical model that considers the results from 3 previous years. The intent of the model is not to compare the recent data (2018) to individual weeks of previous years. The intent is to estimate expected levels of percent positive cases based on patterns observed in the past data, and define if observed percentage positive values are above or below the expected based on historic trends.

Collaborators:

Iowa State University: Giovani Trevisan*, Leticia Linhares, Bret Crim; Poonam Dubey, Kent Schwartz, Eric Burrough; Rodger Main, Daniel Linhares**.

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

Kansas State University: Rob McGaughey, Jamie Henningson, Eric Herrman, Gregg Hanzlicek, Ram Raghavan, Douglas Marthaler.

South Dakota State University: Shivali Gupta, Jon Greseth, Travis Clement, Jane C. Hennings.

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** Daniel Linhares: Principal investigator. E-mail: linhares@iastate.edu.

Advisory Council:

The advisory group reviews the data to discuss it and provide their comments to try to give the data some context and thoughts about its interpretation: Clayton Johnson, Emily Byers, Hans Rotto, Jeremy Pittman, Mark Schwartz, Paul Sundberg, Paul Yeske, Pete Thomas, Rebecca Robbins, Tara Donovan, Matthew Turner.

This report is an abbreviated version of the dashboards that are available online.

To access the full data, use your computer, tablet, or phone to:



1) Scan the code below, or go to: www.powerbi.com

2) Login: sdrs@iastate.edu

3) Password: Bacon 100

4) On the left bar, click on ‘Apps’

5) Select your dashboard of interest (e.g. PRRS)

5) More information at the SDRS webpage <https://fieldepi.research.cvm.iastate.edu/swine-disease-reporting-system/>

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Page 1 – Detection of PRRSV RNA over time by rRT-PCR (1 of 2).

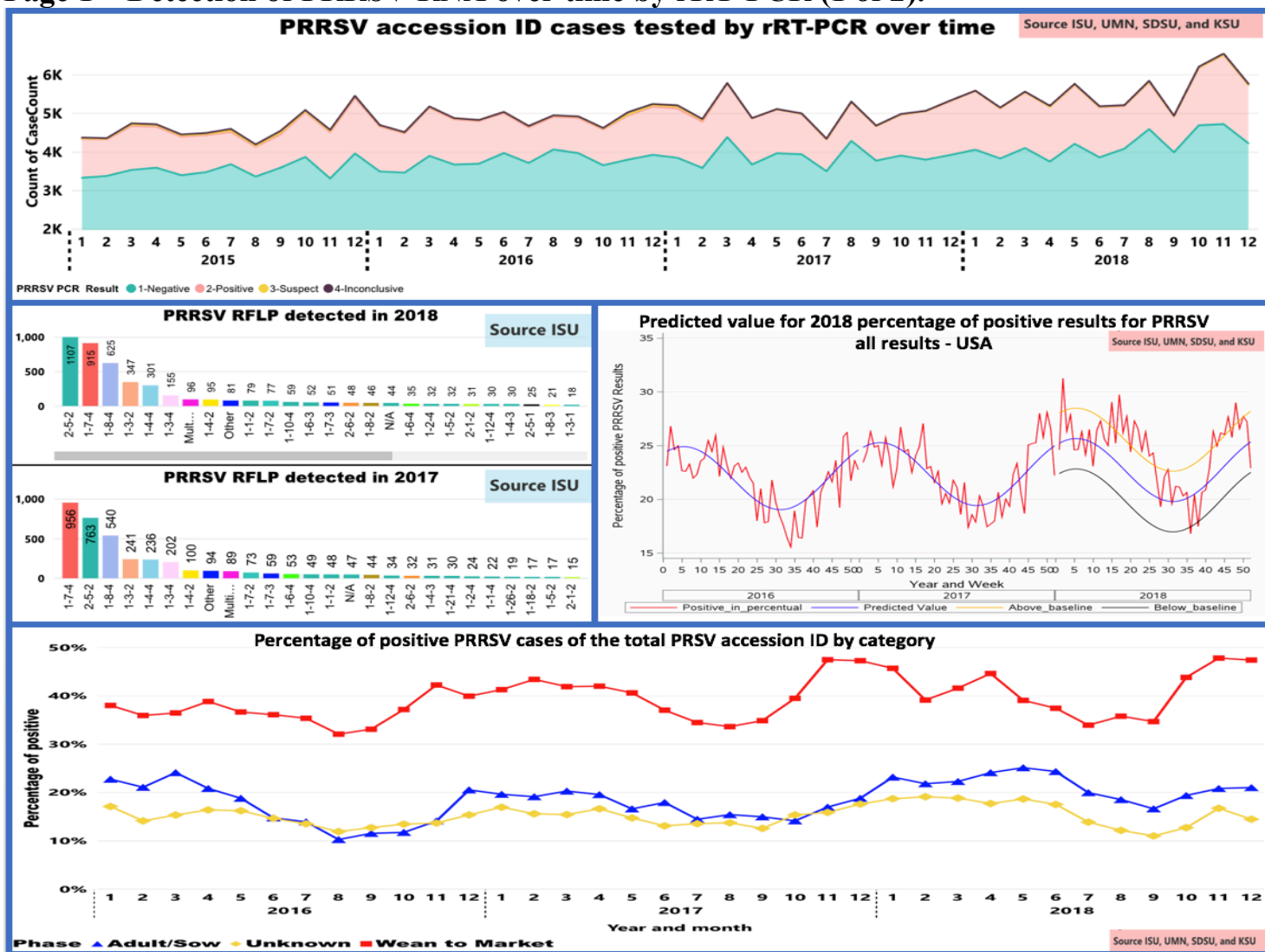


Figure 1 Top chart: Results of PRRS rRT-PCR cases over time. Middle right: expected percentage of positive results for PRRSV RNA by rRT-PCR, with 1 standard deviation above and below the expected value. Middle left: PRRS virus RFLPs detected on 2017, and 2018 for Winter, Spring, Summer, and Fall months. Bottom: Percentage of PRRS PCR-positive results, by 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.

SDRS Advisory Council highlights:

- Total accession ID cases tested by PCR decreased in December after two months of consecutive increase.
- Last PRRSV signal was at week 49, keeping within the predicted for the last three weeks of 2018.
- Percentage of positivity in wean-to-market, and adult/sow in December were similar to November results. Cases with unknown age category decreased from 16.75 to 14.49%.
- In 2018 there was a relative increase of RFLP 2-5-2, 1-8-4, 1-3-2, 1-4-4, 1-1-2, 1-10-4, 1-6-3, 2-6-2, and decrease of RFLP 1-7-4, and 1-3-4 compared to previous year.

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Page 1 – Frequency of detection of multiple PRRSV RFLP during 2018 (2 of 2).

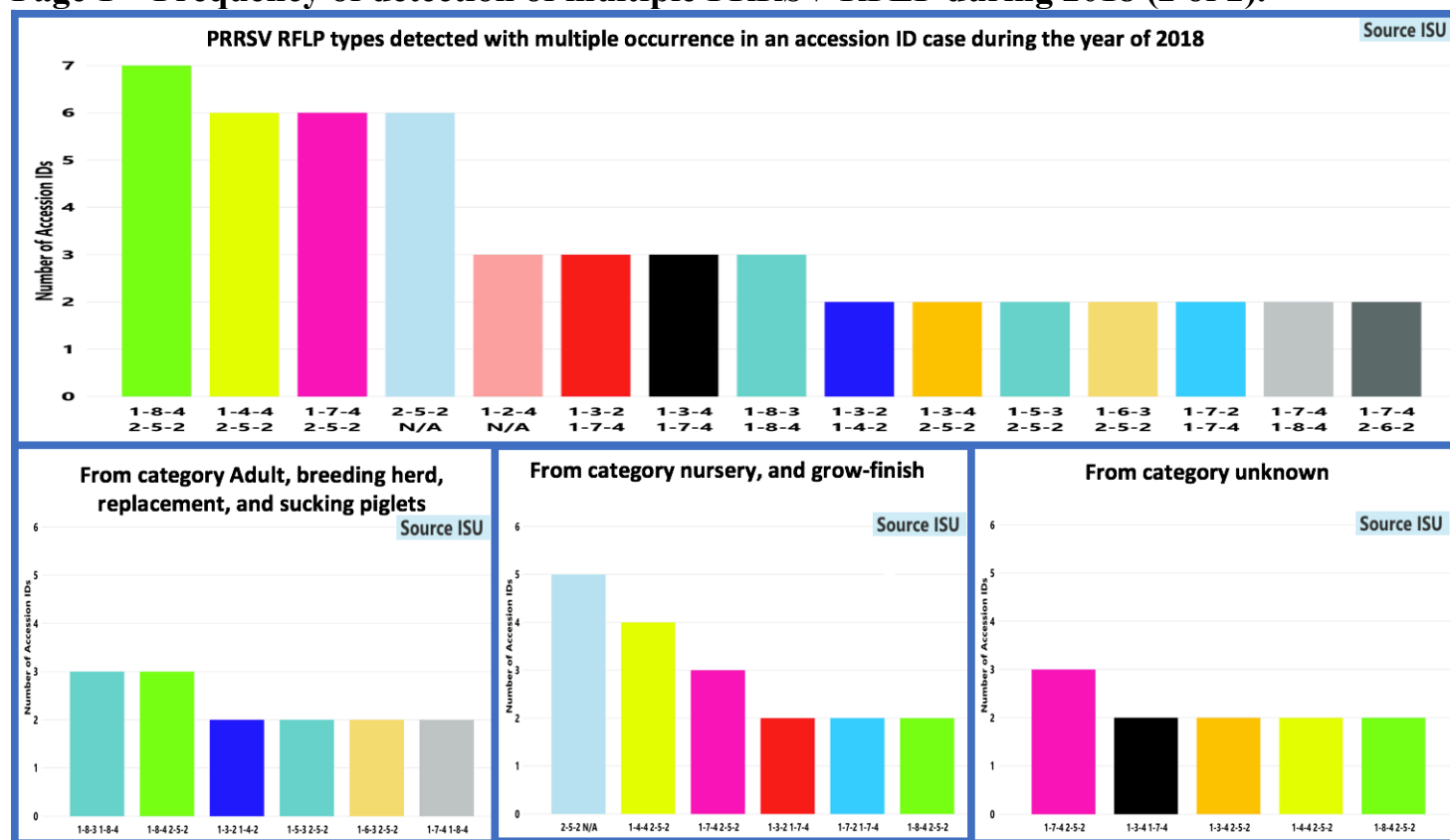


Figure 2 Multiple PRRSV RFLP detection during year of 2018. Each bar indicates a different combination of RFLP detected on the same accession ID case. RFLPs indicated as N/A represents not specified RFLP type or European PRRSV type sequence.

SDRS Advisory Council highlights:

- Detection of wild type PRRSV RFLP and a vaccine-like PRRSV RFLP in the same accession ID was the most common multiple RFLP combination detected during 2018.



Page 2 – Detection of enteric coronaviruses by rRT-PCR

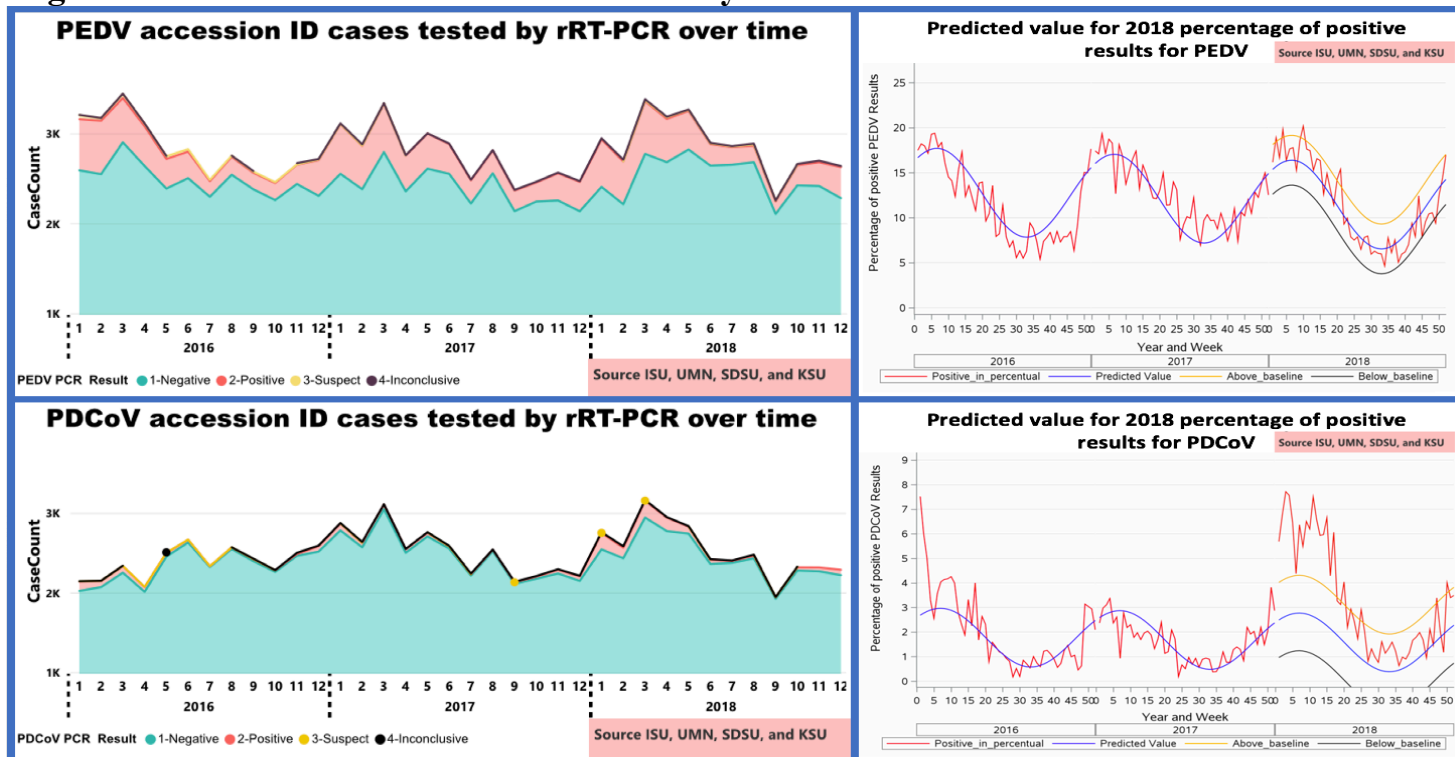


Figure 3 Left side: results of PEDV, and PDCoV rRT-PCR cases over time. Right side charts: expected percentage of positive results for PEDV, and PDCoV by rRT-PCR, with 1 standard deviation above and below the expected value, respectively.

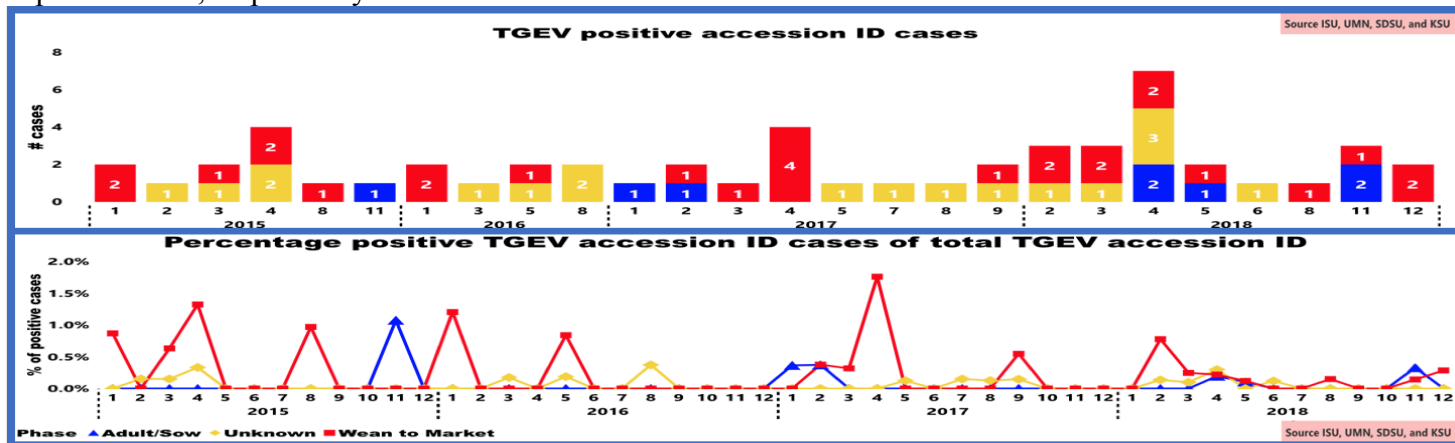


Figure 4 *Top*: number of positive accession ID results of TGEV by category. *Bottom*: percentage of positive results for TGEV by category. Each color represents one distinct category. Wean to market corresponds to nursery, and grow-finish. Adult/Sow correspond to adult, boar stud, breeding herd, replacement, and suckling piglets. Unknown corresponds to not informed site type or farm category.

SDRS Advisory Council highlights:

- Level of detection of PEDV by PCR continues to meet the expected value, indicating that the relative increase activity of the virus for this 'winter' was according to the expected based on previous years.
- There was a signal in the percentage of positivity for PDCoV PCR testing in the weeks 47, 48, and 50.
- There has been limited number of cases of TGEV, with only one detection in November 2018.

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Page 3 – Detection of pathogens associated with CNS disease

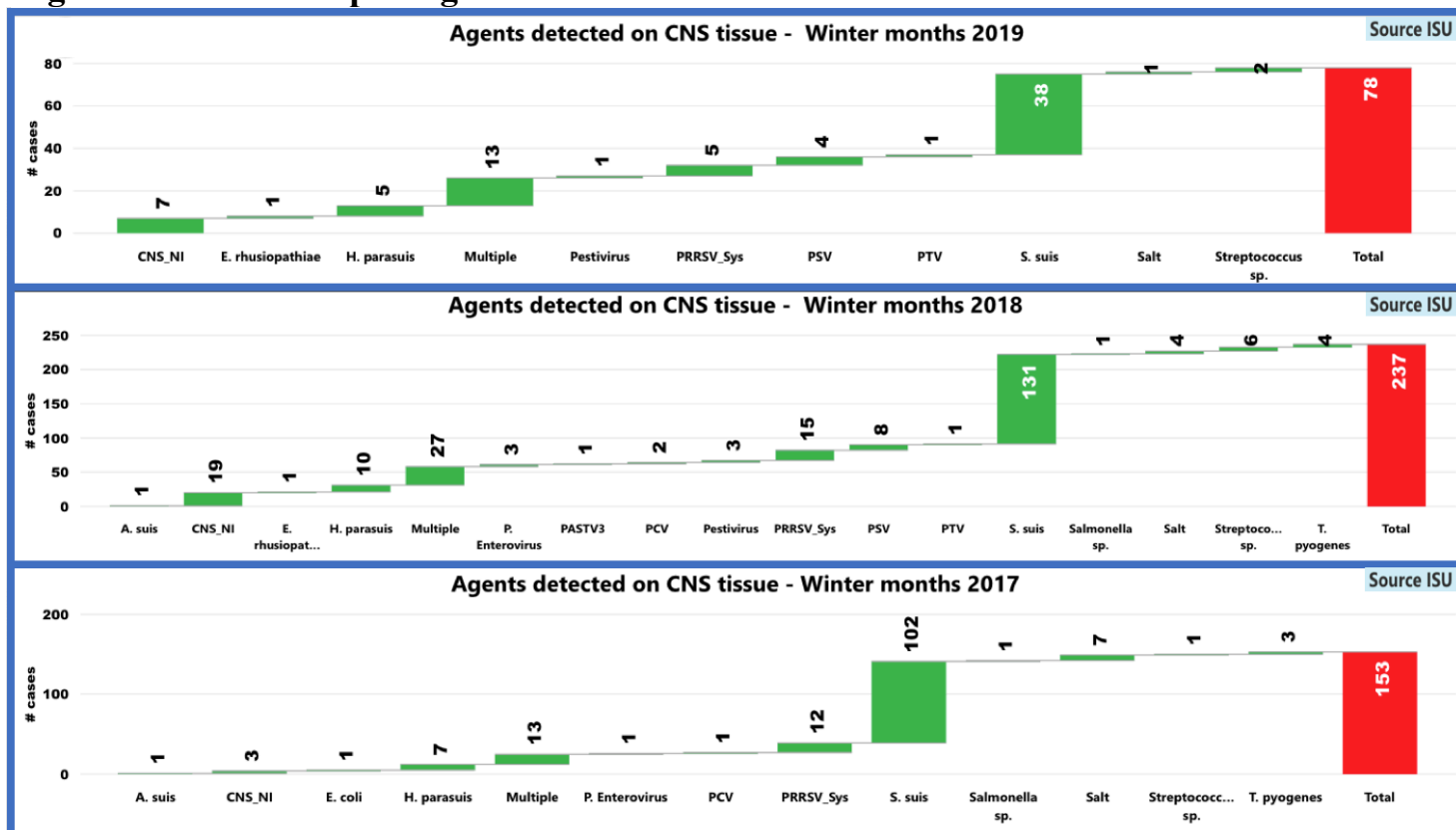


Figure 5 Pathogen detection on CNS tissue over time. Each green bar indicates a different agent or syndrome. The red bar accounts for the sum of the green bars. Bottom: winter months of 2017, middle winter months of 2018, top winter of 2019. Winter months contains results of December, January, and February. ‘Multiple agents’ represent cases with more than one pathogen detected on CNS tissues.

SDRS Advisory Council highlights:

- The number of cases per agent have similar distribution this Winter, compared to the same season of previous years. *Streptococcus suis* was still the major agent causing CNS.
- The number of *Haemophilus parasuis* detection on CNS tissue for December 2018 (2019 winter season) was similar to December 2017 (winter 2018).



Page 4 – Detection of pathogens associated with respiratory tissue disease over time (1 of 2)

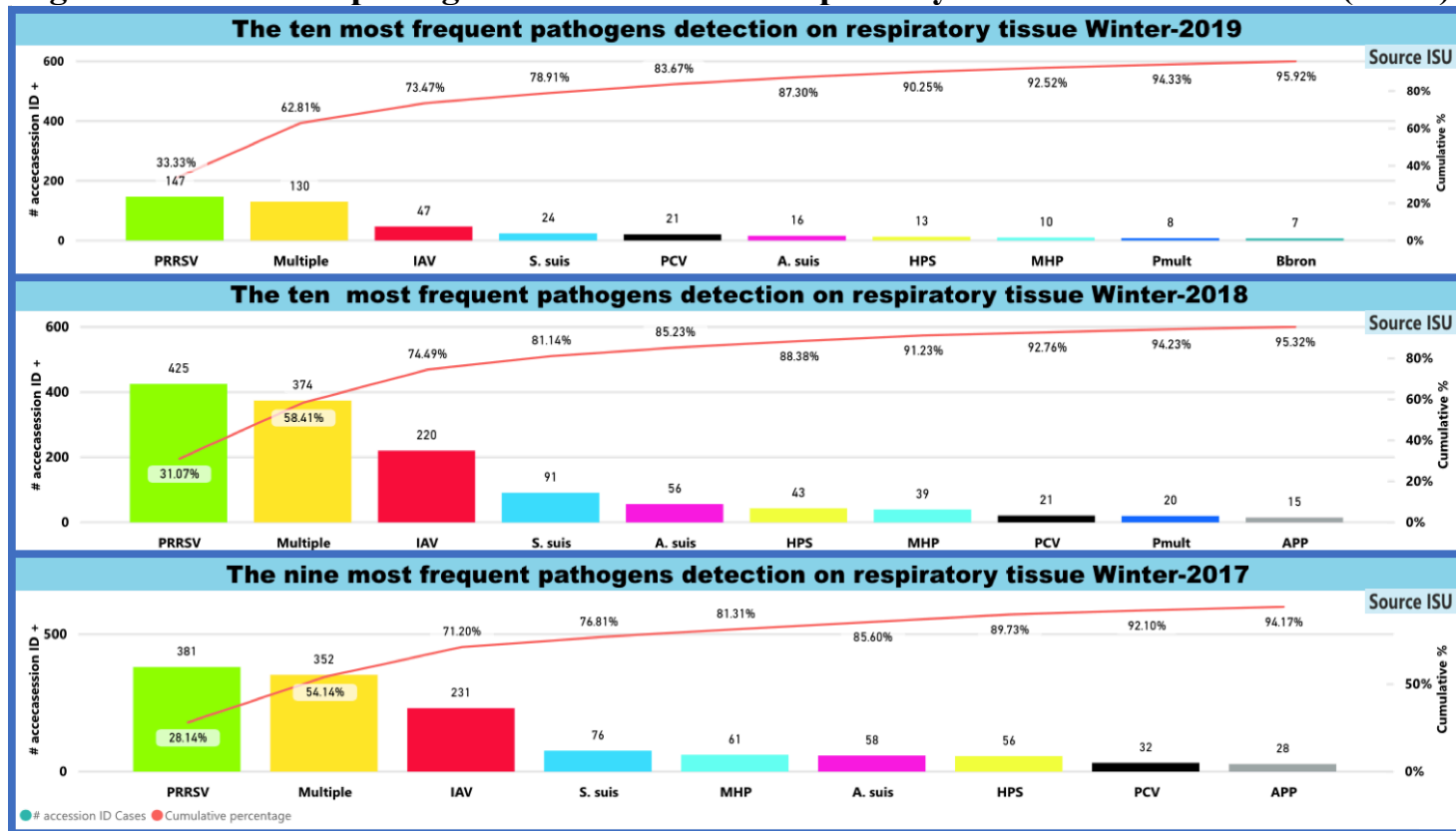


Figure 6 Pathogen detection on respiratory tissues over time. Each bar and color indicate a different agent or syndrome. The red line accounts for the cumulative percentage of the bars. Bottom: winter months of 2017, middle winter months of 2018, top winter months of 2019. Winter months include December, January, and February. ‘Multiple agents’ represents cases with more than one pathogen detected on respiratory tissues. Presented results are based on diagnostician interpretation.

SDRS Advisory Council highlights:

- For the beginning of 2019 winter Porcine Circovirus had greater percentage of detection, but similar number of cases, diagnosed as a single insulant, when compared with full winter season of previous years.
- Other agents had similar pattern of occurrence from previous winter season.



Page 4 – Detection of pathogens associated with respiratory disease over time (2 of 2)

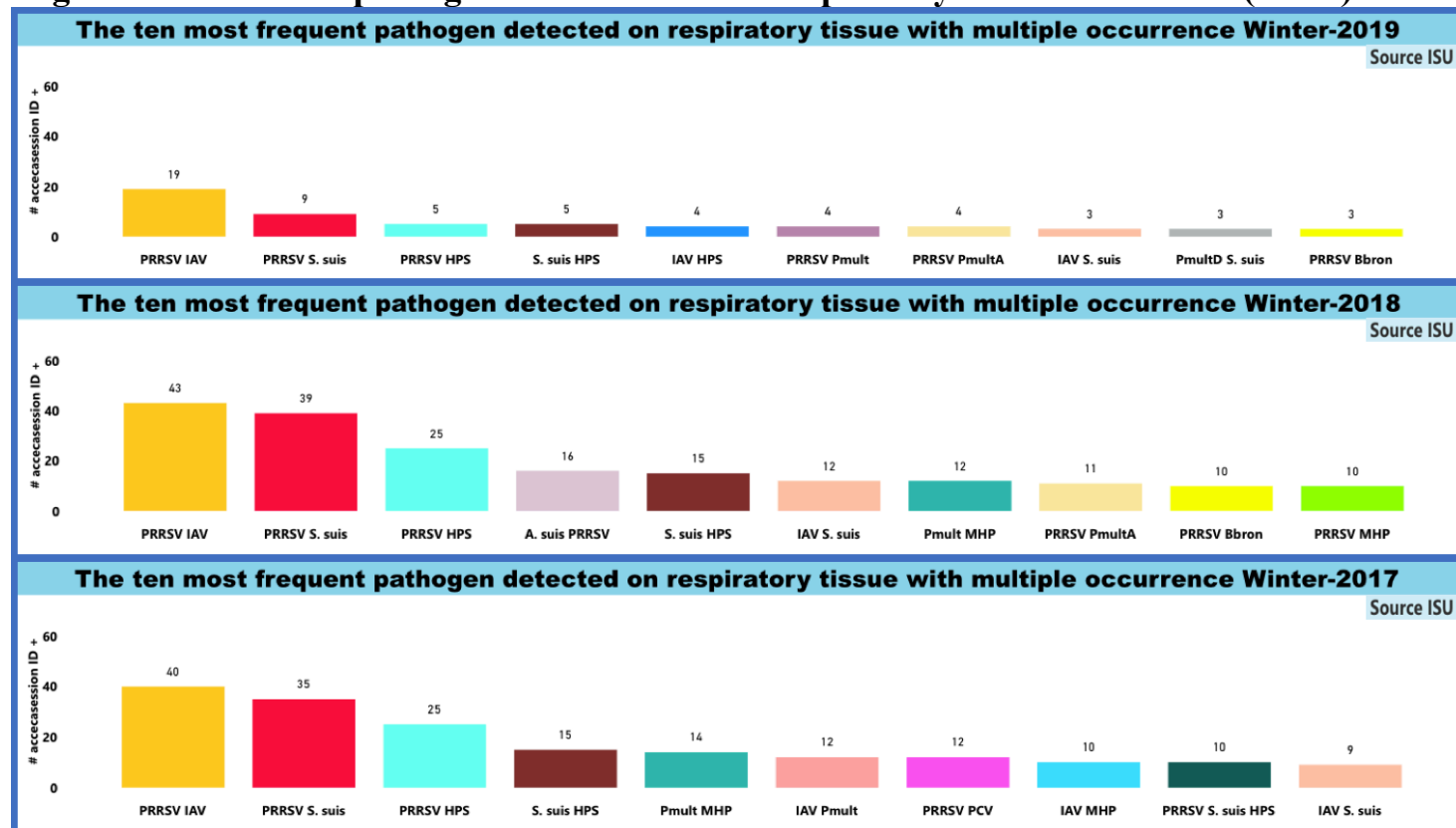


Figure 7 Multiple agents detected in respiratory tissue per accession ID case level. Each bar and color represent a combination of 2 or more agents. Presented results are based on diagnostician interpretation.

SDRS Advisory Council highlights:

- Association between PRRSV and Influenza A has been more frequent for the beginning of 2019 winter season. For the same winter season period of 2017, and 2016 there were 17, and 12 cases diagnosed with that combination.
- PRRSV and *Pasteurella multocida* (PRRS Pmult) has been more frequently reported in winter of 2019, when compared with previous years' winter season.



Page 5 – Detection of pathogens associated with enteric disease over time (1 of 2)

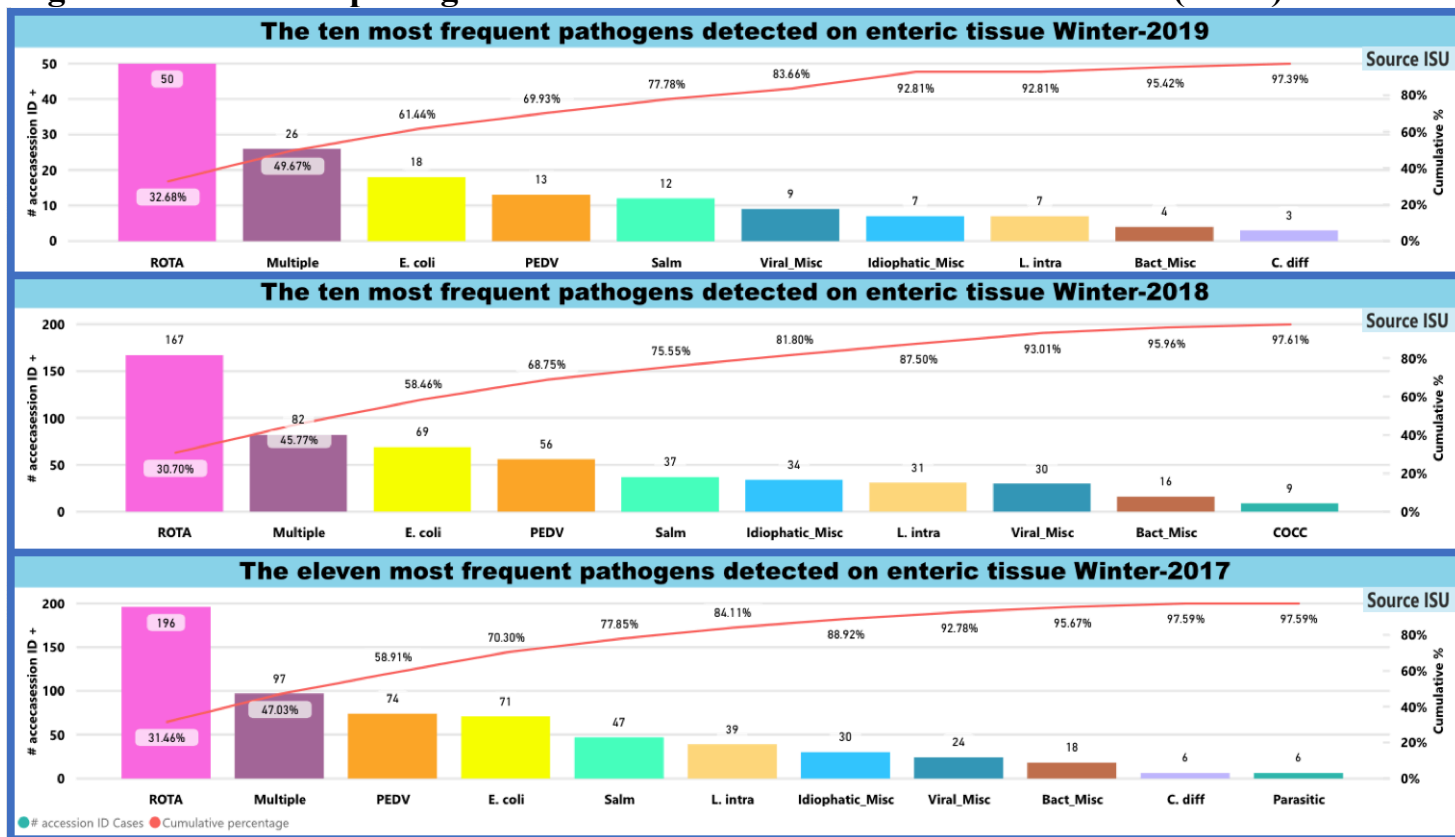


Figure 8 Pathogen detection on enteric tissues over time. Each bar and color indicate a different agent or syndrome. The red line accounts for the cumulative percentage of the bars. Bottom: winter months of 2017, middle winter months of 2018, top winter months of 2019. Winter months include December, January, and February. ‘Multiple agents’ represents cases with more than one pathogen detected on enteric tissues. Presented results are based on diagnostician interpretation.

SDRS Advisory Council highlights:

- Similar pattern of disease diagnosis on enteric submissions for winter of 2019 when compared with winter season of previous years.

Page 5 – Detection of pathogens associated with enteric disease over time (2 of 2)

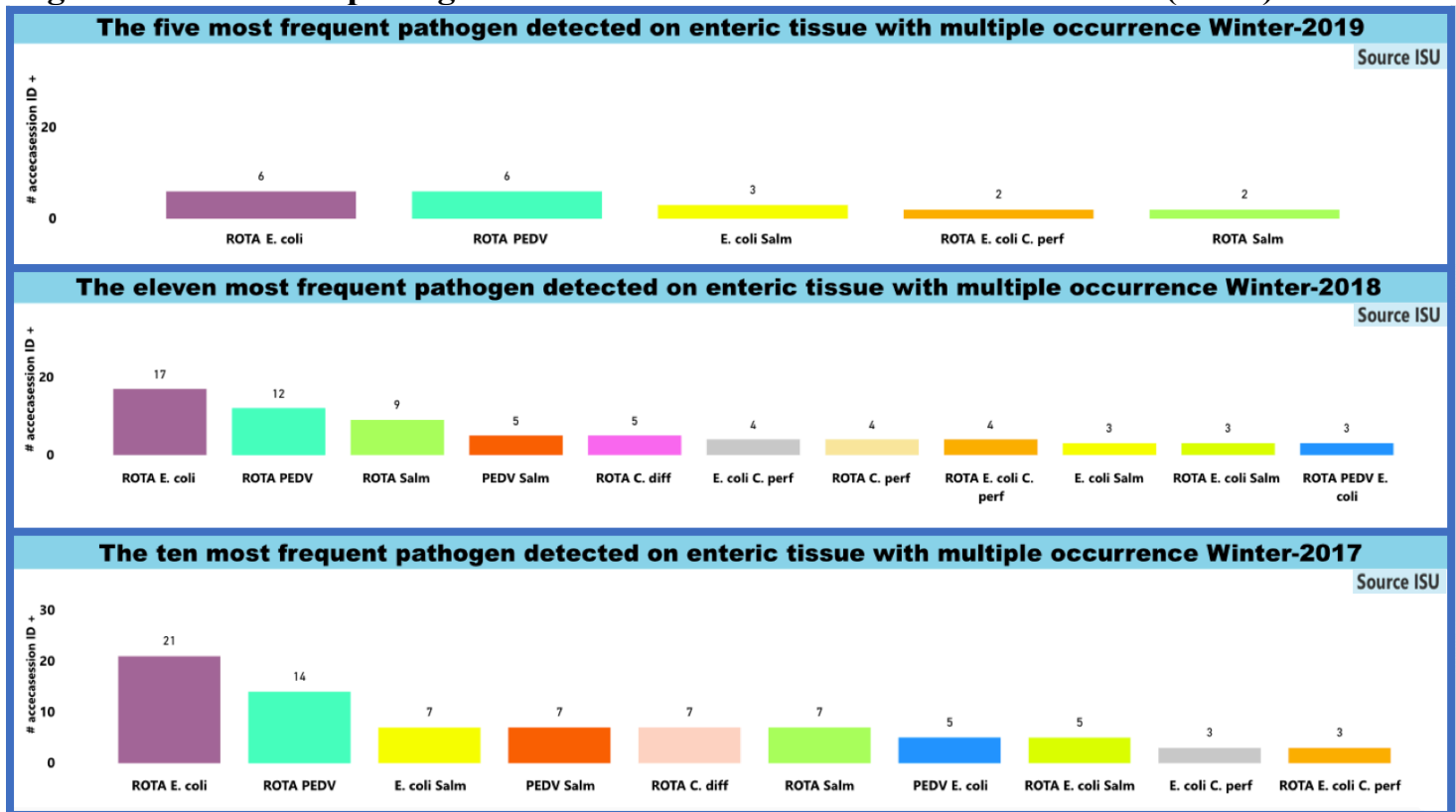


Figure 9 Multiple agents detected in enteric tissue per accession ID case level. Each and color bar represents a combination of 2 or more agents. Presented results are based on diagnostician interpretation.

SDRS Advisory Council highlights:

- Diagnosis of coinfection between Rotaviruses and PEDV (ROTA PEDV), *E. coli* and *Salmonella spp.*, (*E. coli* Salm), and Rotaviruses, *E. coli* and *Salmonella spp* (ROTA E.coli Salm) had similar number of diagnosis for the December of 2019 winter season as compared with previous years and season.
- Diagnosis of coinfection between Rotaviruses and PEDV (ROTA PEDV) were more frequent for the first month of winter-2019 than previous winter seasons.

Bonus page

Genetic diversity of ORF-5 from PRRSV classified as RFLP type 1-7-4 at the ISU-VDL in 2018

Giovani Trevisan, Aditi Sharma, Phillip Gauger, Daniel Linhares

The SDRS database demonstrates since 2015 the PRRSV RFLP type 1-7-4 has been the most common PRRSV wild type detected on cases submitted for ORF-5 sequencing at the ISU-VDL. The purpose of this analysis was to describe the nucleotide diversity of ORF-5 from PRRSV classified within the 1-7-4 RFLP.

Discriminant analysis of principal components (DAPC) [Fig. 1] was conducted for 769 PRRSV 1-7-4 ORF-5 sequences collected from January to November of 2018 from 15 states in the US. States with more than 10 sequences in the period were used in the analysis excluding sequences without a state designation. Iowa (IA) had the highest number of ORF-5 sequences in the database representing 40.6% of the total.

The DAPC plot [Fig. 1] demonstrates the genetic relatedness between IA, Minnesota-MN, Indiana-IN, Illinois-IL, and Ohio-OH. Missouri-MO had similar genetic diversity compared to the five previous states. In contrast, sequences from North Carolina-NC and Nebraska-NE were more genetically distant from all other states forming two distinct clusters [Fig. 1]. Distinct phylogenetic clusters in NC and NE could be due to the relative geographical and genetic isolation of the virus.

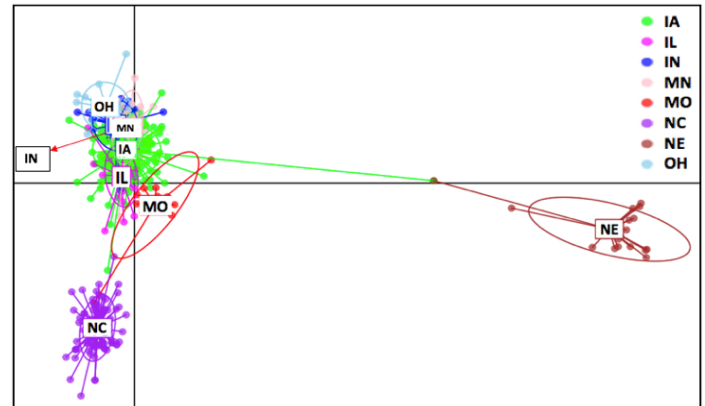


Figure 1 DAPC plot of ORF5 sequences for PRRSV RFLP type 1-7-4 for calendar year 2018 present at the SDRS database according to the state of origin. Each different color represents a different state. Each inertia ellipses shows a different cluster, while each dot represents individual sequences.

To further understand the genetic diversity among PRRSV sequences, pairwise nucleotide distances within and between states was calculated [Fig 2]. There is a considerable range of PRRSV 1-7-4 genetic diversity within and between states. The overall pairwise distances were ~ 2.8%. The most genetically distant PRRSV sequences differed by more than 8%. Interestingly, NE and MO had the lowest percent genetic diversity.

The RFLP is a historic method used to describe genetic relationships between PRRSV ORF5 sequences and are commonly reported by VDL's. This analysis using the SDRS database for PRRSV 1-7-4 demonstrates substantial genetic diversity within this RFLP type that can be above 8% on a nucleotide basis. PRRSV from different states formed separate clusters with the majority demonstrating genetic relatedness, which could reflect the movement of pigs and corresponding PRRSV to different geographic regions in the US. Conducting a phylogenetic analysis of PRRSV detected within production systems will help monitor genetic diversity and better understand if the same or different/new PRRSV is circulating in the population.

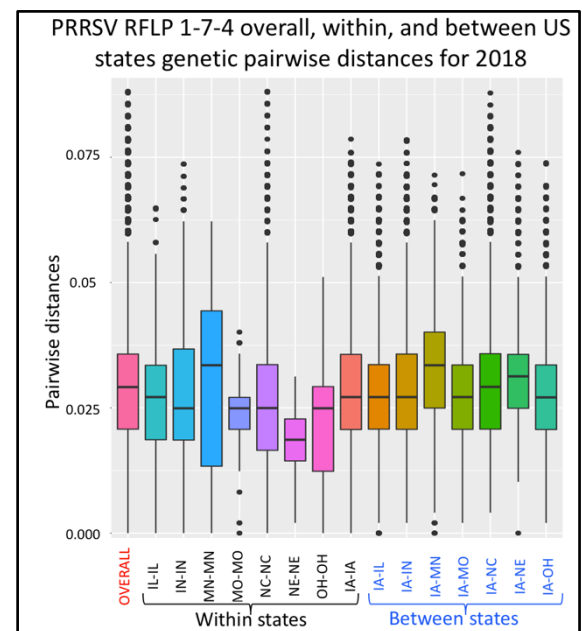


Figure 2: Box plot of pairwise ORF5 nucleotide distances for 769 PRRSV, within states, and between IA and other states. Each box-plot represents a different comparison. Box boundaries represent the second and third quartiles and the division inside the box the median. Lower and upper whiskers represent the first and fourth quartile. Open circles outside upper and lower whiskers represent outliers.

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