

### Swine Disease Reporting System Report #15 (May 7, 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 "2019 predictive graphs," the expected value was calculated using a statistical model that considers the results from three previous years. The intent of the model is not to compare the recent data (2019) 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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### **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, Mark Schwartz, Paul Sundberg, Paul Yeske, Rebecca Robbins, Tara Donovan, Matthew Turner, Deborah Murray.

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

To access the full data and hear the podcast for the reports, use your computer, tablet, or phone and go to: <u>https://fieldepi.research.cvm.iastate.edu/swine-disease-reporting-system/</u>

and explore the dashboard corresponding to each pathogen or syndrome.

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**Figure 1. A**: Results of PRRS rRT-PCR cases over time. **B**: Proportion of accession ID cases tested for PRRSV by age group per year and season. **C**: expected percentage of positive results for PRRSV RNA by rRT-PCR, with 95% confidence interval band for predicted results. **D**: percentage of PRRS 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. **E**: RFLP type detected during year of 2019. **F**: RFLP type detected during year of 2018. RFLPs indicated as N/A represents not detected or European PRRSV type.

SDRS Advisory Council highlights:

- PRRSV activity remains within the predicted values for 2019. On week 16 (April 14 to 20) there was
  an increase in detection coming from wean-to-market age category;
- From January to March of 2019 there was a 1.59% increase in detection in adult/sow farm. The slight
  increase in detection of PRRSV in this age category coincides with the curve for outbreaks detection
  reported from the MSHMP project for the year of 2018/2019;
- The overall number of cases with RFLP detection decreased by 16.01% in 2019 compared with the same period of 2018. Mostly associated, according to advisory group inputs, with less outbreaks in the field and which requires less sequencing;
- The three most frequent detected RFLP types 1-7-4, 2-5-2 and 1-8-4 had a decrease in detection of 114, 120, and 69 detection respectively. The RFLP type 1-3-2, 1-12-4, and 1-4-4 had higher occurrence detection of 84, 40, and 29 respectively. Most of the increased detection of RFLP 1-3-2 was related with vaccine like sequences. RFLP 1-12-4 and 1-4-4 has been detected in SDRS since 2010 as wild type strains and seems like there is some increased detection of this wild type strains.

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**Figure 2. A**: results of PEDV rRT-PCR cases over time. **B**: expected percentage of positive results for PEDV by rRT-PCR and 95% confidence interval for 2019 predicted value. **C**: percentage of PEDV PCR-positive results, by category over time. **D**: results of PDCoV rRT-PCR cases over time. **E**: expected percentage of positive results for PDCoV by rRT-PCR and 95% confidence interval for 2019 predicted value. **F**: percentage of PDCoV PCR-positive results, by age category over time. **G**: number of PCR-positive accession ID results of TGEV by age category. **H**: percentage of PCR-positive results for TGEV by age category. Each color represents one distinct age category.

SDRS Advisory Council highlights:

- Level of detection of PEDV by PCR is within the expected value for April. There was an overall decrease in the percentage of positive results from 17.12% in March to 14.12% during April. All age categories had decreased detection during this period;
- Level of detection of PDCoV was above expected during week 16 (April 14th to 20th). This week had the highest percentage of positive results of PDCoV in adult/sow for the year of 2019 at 7.10%. Additionally, the detection in wean-to-market increased by 2.12% in the first 2 weeks of April to last 2 weeks of April moving from 6.17% to 8.29%. According to advisory member inputs some sow farms experiencing PDCoV outbreaks experienced clinical signs.

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### Page 3 – Detection of MHP by PCR





**Figure 3. A**: results of MHP PCR cases over time. **B**: expected percentage of positive results for MHP by PCR and 95% confidence interval for 2019 predicted value. **C**: percentage of MHP PCR-positive results, by category over time.

### Page 3 – Detection of pathogens associated with CNS disease



**Figure 4.** 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. **A:** spring months of 2019. **B**: Table for agents detected in CNS tissue during spring months of 2017, 2018 and 2019. Spring months contains results of March, April, and May. 'Multiple agents' represent cases with more than one pathogen detected on CNS tissues.

SDRS Advisory Council highlights:

- Level of detection of MHP by PCR is within the expected value for April of 2019;
- Even though *Streptoccoccus suis* (S. suis) continues to be the major agent detected on CNS tissue, 2019 Spring months of March and April had increased number of Pestivirus (Shaking pig syndrome), Porcine Sapelovirus (PSV), and salt intoxication (Salt) detected on CNS tissue when compared with Spring season of 2018 and 2017. Salt intoxication pathogenesis and lesions are clearly characterized far back in time, which leads to speculate that the increased salt intoxication in the field is real. However, regarding increased detection of PSV and Pestivirus, it is not clear if the increased detection reflects increased clinical disease in the field, as opposed to more intense monitoring for those viruses.

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### Page 4 – Detection of pathogens in respiratory tissue over time.



**Figure 5.** Pathogen detection on respiratory tissues over time. **A**, **B**, and **C** each bar and color indicate a different agent or syndrome. The red line accounts for the cumulative percentage of the bars. **A**: spring months of 2019. **B**: winter spring of 2018. **C**: spring months of 2017. Spring months include March, April, and May. 'Multiple agents' represent cases with more than one pathogen detected on respiratory tissues. **D**: Multiple agents detected in respiratory tissue per accession ID case level. Each bar and colour bar represent a combination of 2 or more agents. Presented results are based on diagnostician interpretation.

### SDRS Advisory Council highlights:

• For the Spring of 2019 months there was an increase in detection of the following respiratory insultants *Haemophilus parasuis* (HPS) 16 cases, *Actinobacillus pleuropneumoniae* (APP) 8 cases, *Pasteurella multocida* (Pmult) 8 cases, *Mycoplasma hyorhinis* (MHR) 5 cases, when compared with same period of 2018 Spring months at ISU-VDL. These increased detections of bacterial agents have been linked as part of measures been taken to improve herd health by better detecting the agent and or agent strain circulating in the farm or herd population for further use in development and or update in autogenous vaccine for better control of the disease.

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### Page 5 – Detection of pathogens in enteric tissue over time.



**Figure 6.** Pathogen detection on enteric tissues over time. **A**, **B**, and **C** each bar and color indicate a different agent or syndrome. The red line accounts for the cumulative percentage of the bars. **A**: spring months of 2019. **B**: spring months of 2018. **C**: spring months of 2017. Spring months include March, April, and May. 'Multiple agents' represent cases with more than one pathogen detected on respiratory tissues. **D**: Multiple agents detected in enteric tissue per accession ID case level. Each bar and colour represent a combination of 2 or more agents. Presented results are based on diagnostician interpretation.

### SDRS Advisory Council highlights:

- Number of enteric diseases cases for Spring Months of March and April increased by 12.11% (n=463) when compared with the same spring months of 2018 (n=413);
- The most significant increase was represented by 27 cases reported as having multiple insultants, and 14 cases classified as viral miscellaneous (Viral\_Misc). Viral miscellaneous definition accommodates cases where enteritis atrophic was observed and could not be clear linked to a specific insultant, and/or was linked to insulants that are less frequent detected in swine as Adenovirus and or Enterovirus;
- The 4 most frequent combination of multiple insultant agents involved the 4 major insultants rotaviruses (ROTA), PEDV, *Escherichia coli* (E. coli), and *Salmonella sp.* (Salm). These 4 insultants were also diagnosed as major single insultant.

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### **Bonus Page**

### Genetic diversity of ORF-5 from PRRSV classified as RFLP type 1-8-4 at the ISU-VDL in 2018 and 2019 Giovani Trevisan, Aditi Sharma, Phillip Gauger, Daniel Linhares

The SDRS database demonstrates that since 2016, the PRRSV RFLP type 1-8-4 has been the second most common PRRSV wild type detected on cases submitted for ORF-5 sequencing at the ISU VDL (behind 1-7-4). The purpose of this analysis was to describe the nucleotide diversity of ORF-5 from PRRSV classified within the 1-8-4 RFLP.

To understand the genetic diversity among the 764 PRRSV sequences collected between January 2018 to March 2019, pairwise nucleotide distances within and between states was calculated [Figure 1]. The overall pairwise median distance was 10.28%, and the most genetically distant sequences differed by 17.89%. There was a large range of PRRSV 1-8-4 genetic diversity within and between states.

States with more than 10 sequences during the period were used for a discriminant analysis of principal components (DAPC) [Fig. 2], which included 612 sequences from seven states. Sequences without a state designation were excluded. Missouri had the highest number of 1-8-4 type in the database representing 41.01%, followed by Iowa with 37.58%.

The DAPC plot [Figure 2] demonstrates the genetic relatedness between Iowa, Minnesota, and Illinois had similar genetic diversity. In contrast, sequences from

Missouri, Oklahoma, Ohio, and Indiana were more genetically distant from all other states forming three distinct clusters [Figure 2]. Genetically distinct phylogenetic clusters could be due to the relative geographical distribution and genetic evolution of the virus.

The RFLP is a historic method used to describe genetic relationships between PRRSV ORF5 sequences and are commonly reported by VDLs. This analysis using the SDRS database for PRRSV 1-8-4 demonstrates substantial genetic diversity within this RFLP type that can exceed 17% on a nucleotide basis.

PRRSV from different states formed distinct clusters, which could reflect the movement (or lack of movement) of pigs, and corresponding PRRSV, to different geographic regions. PRRSV 1-8-4 was introduced in Minnesota in the early 2000s and is currently not frequently detected in some swine exporting states like North Carolina.

Movement of infected swine and geographic restriction of the virus can play a major role on PRRSV evolution. The presence of distinct phylogenetic clusters and the high genetic pairwise diversity within this RFLP type across different states demonstrates that further genetic analysis (i.e., comparing ORF-5 or whole-genome sequences) is necessary

to conduct molecular epidemiology analysis involving RFLP 1-8-4. The diversity observed among 1-8-4 is significantly higher than what has been observed among 1-7-4 (n=1,105, median difference 2.43%, range 0 – 11.95%), and the 2-5-2 (n=1,303, median difference 0%, range 0 – 4.1%).



Figure 1: Box plot of pairwise ORF5 nucleotide distances for 764 PRRSV, within states, and between 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



Figure 2 DAPC plot of ORF5 sequences for PRRSV RFLP type 1-8-4 for January 2018 to March 2019 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.

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