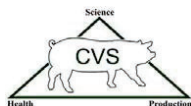


# Dr. Bob Morrison's Swine Health Monitoring Project

SHMP@umn.edu

September 13, 2019

These producers are willing to share their premises IDs and pathogen status in the interests of national disease control



Regional Projects:  
N212 MN, PA, SE IA, and Lyon Co

## National PRRS incidence/prevalence: July 2019 - June 2020

38 out of 38 systems contribute data to charts 1 and 4. 31 of these 38 follow or are adapted to the AASV PRRS classification and contribute data to charts 2 and 3. Chart 1 monitors the 2019-2020 cumulative incidence in **RED**. Chart 2 shows prevalence of herd statuses over time beginning July 2009. Chart 3 shows incidence rate of PRRS statuses per farm-week for the season 2019-2020. Chart 4 is the exponentially weighted moving average (EWMA) epidemic monitor. Numbers and geographic representation of herds change over time, so direct comparison across years should be made with caution. **Disclaimer: All companies report regularly but at different frequencies.**

Breaks	Number	Break status
New breaks	3	1, 2fvi, 2fvi
Previous breaks	2	
Systems reporting	30	

	1-2	1-2fvi	1-2vx	Status change	2-3	2fvi-2	2fvi-3	2vx-2	2vx-3	3-4
N week	0	1	0		0	0	0	0	0	0
N 19-20	4	22	18		2	0	0	1	1	1

Chart 1 – PRRS cumulative incidence beginning July 01, 2009

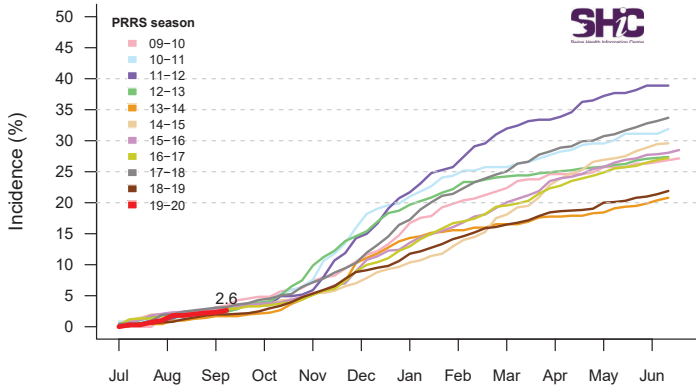


Chart 2 – PRRS prevalence of sow herd status beginning July 01, 2009

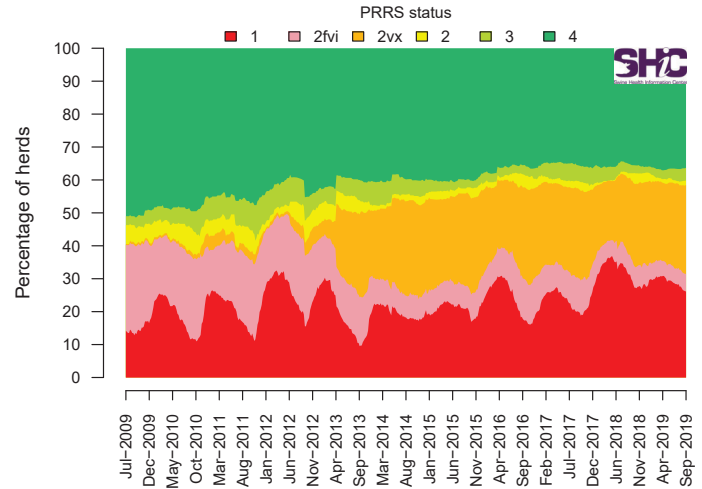
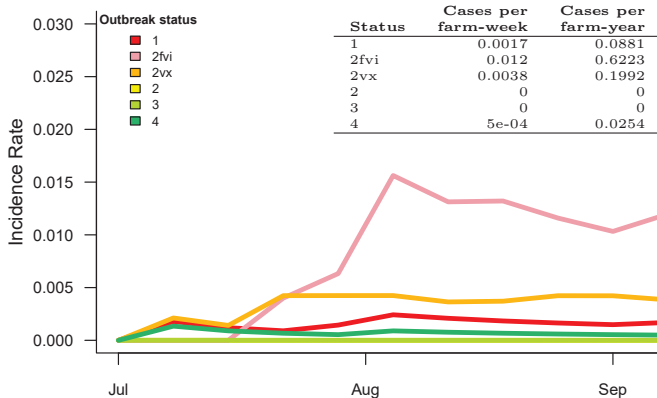


Chart 3 – PRRS incidence rate beginning July 1, 2019



Classification scheme
1 Positive Unstable
2fvi Positive Stable, field virus exposure
2vx Positive Stable, live virus vaccinated
2 Positive Stable
3 Provisionally Negative
4 Negative

Recent PRRS EWMA

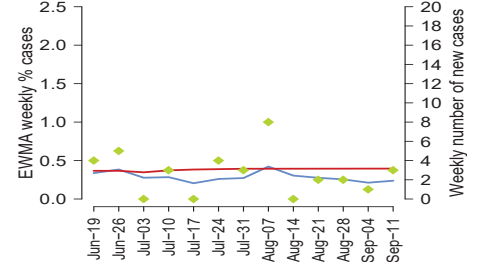
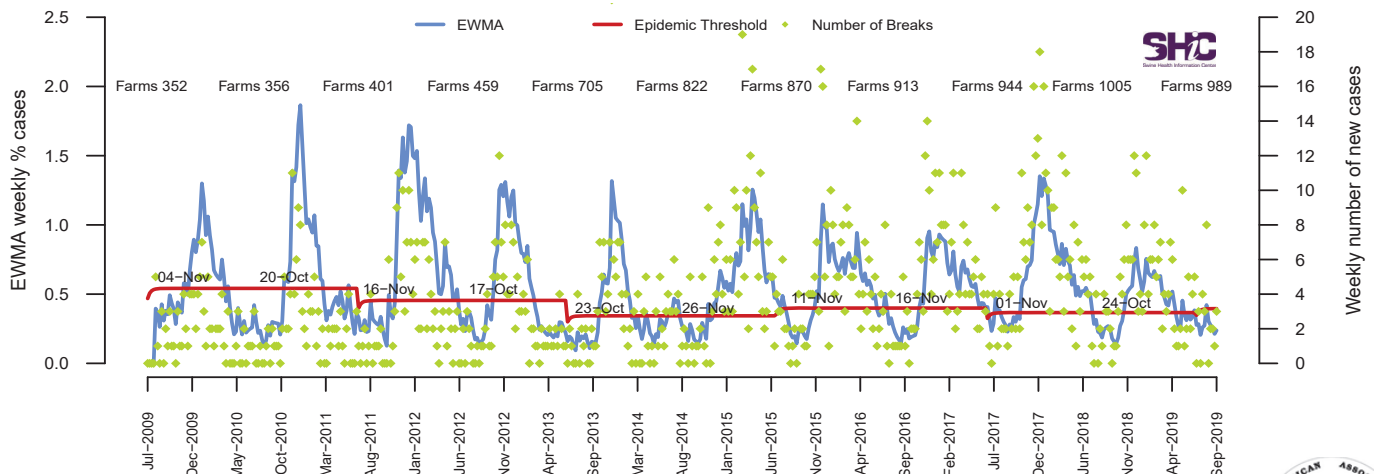


Chart 4 – PRRS EWMA analysis for years 2009 – 2019



## National Porcine Enteric Coronavirus incidence/prevalence: July 2019 - June 2020

37 out of 38 systems contribute data to charts 1, 3 and 4; and 34 of 38 systems to chart 2. Chart 1 monitors the 2019-2020 cumulative incidence of Porcine Epidemic Diarrhea (PED) in **RED**. Chart 2 shows the aggregate prevalence beginning May 2013. Chart 3 summarizes the outbreak history of farms that have had an outbreak during the current MSHMP season. Chart 4 is the exponentially weighted moving average (EWMA) epidemic monitor. Numbers and geographic representation of herds change over time, so direct comparison of values across years should be made with caution. **Disclaimer: All companies report regularly but at different frequencies.**

Breaks	Number	Break status
New breaks	0	
Previous breaks	0	
Systems reporting	30	

	Status change					
	1-2	1-2fvi	2-3	2fvi-2	2fvi-3	3-4
N week	0	0	0	0	0	0
N 19-20	1	8	0	0	0	0

Chart 1 – PED Cumulative incidence beginning May 01, 2013

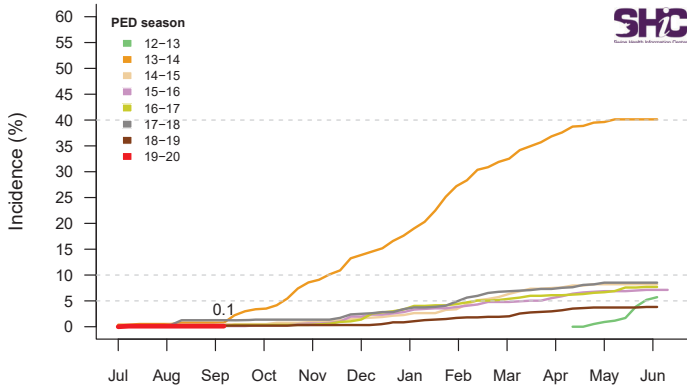


Chart 2 – PED prevalence of sow herd status beginning May 01, 2013

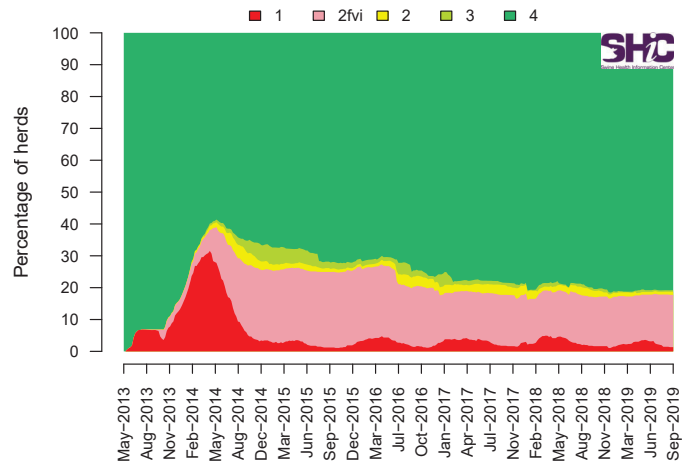
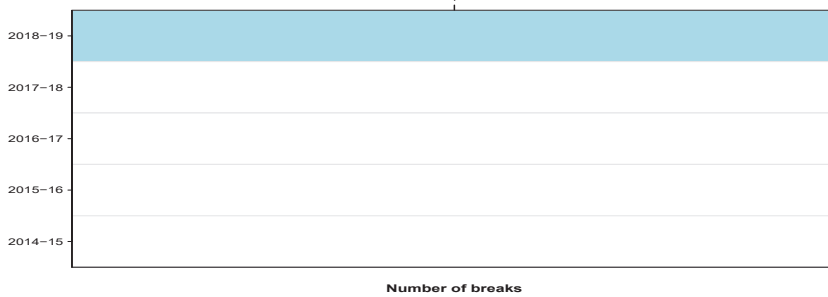


Chart – 3 PED history of farms that broke during the 2018-19 season



Classification scheme	
1	Positive Unstable
2fvi	Positive Stable, field virus exposure
2	Positive Stable
3	Provisionally Negative
4	Negative

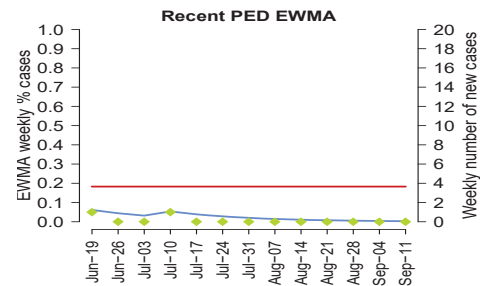
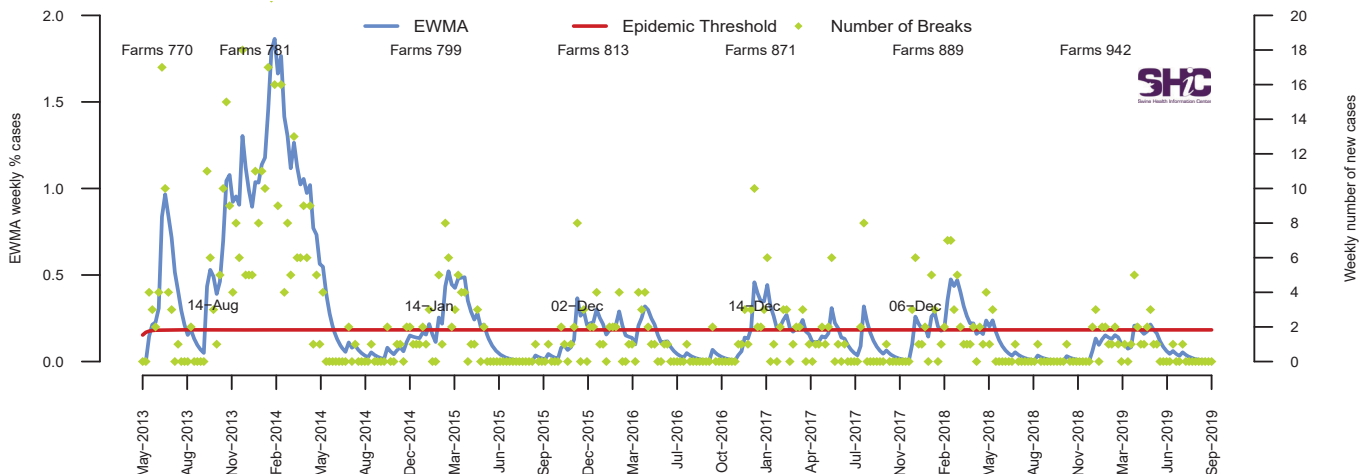


Chart 4 – PED EWMA analysis for years 2013 – 2019

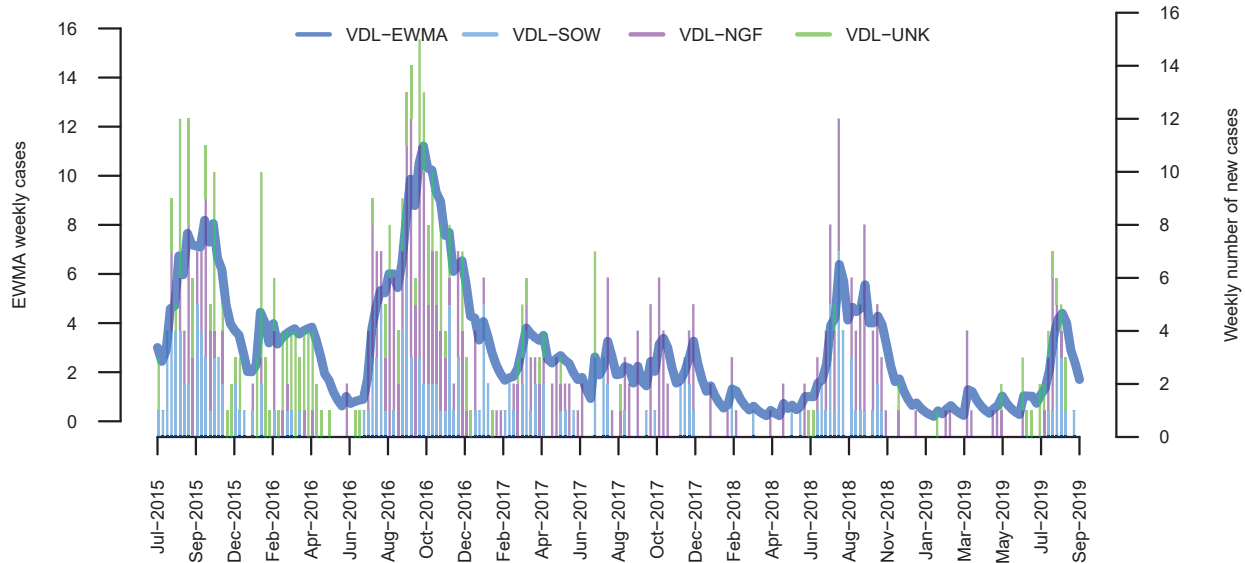


## Senecavirus A: Case updates

We requested ISU, SDSU, KSU and UMN diagnostic laboratories to report the number of Senecavirus A cases each week.

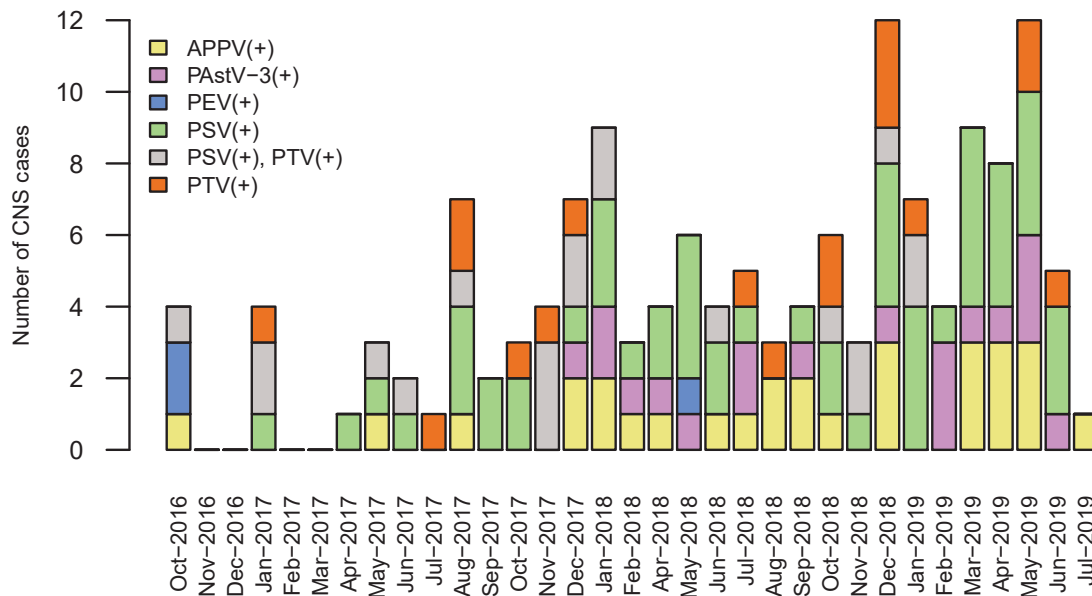
- 1 VDL case(s) (Sow x 1) last reported on the 04-September-2019.

Seneca Valley Virus frequency of VDL and SHMP cases by production type



## Atypical Central Nervous System Cases

The ISU, SDSU, KSU, and UMN diagnostic laboratories are coordinating with MSHMP and reporting atypical CNS cases each month. The diseases being tracked are atypical porcine pestivirus (AAPV), porcine enterovirus (PEV), porcine sapelovirus (PSV), porcine teschovirus (PTV), and porcine astrovirus (PAstV-3). Cases that show clinical signs, histological lesions compatible with viral infection and are PCR positive for one or more of the viruses are considered positive and reported here. Last month reported (July, 2019): 1 new CNS case(s) reported. Previous months update: 0.



## ***Streptococcus suis* strains circulating in the U.S. and their association with pathogenicity**

April A. Estrada<sup>1</sup>, Marcelo Gottschalk<sup>2</sup>, Stephanie Rossow<sup>1</sup>, Aaron Rendahl<sup>1</sup>, Connie Gebhart<sup>1</sup>, Douglas G. Marthaler<sup>3</sup>

<sup>1</sup>University of Minnesota, <sup>2</sup>University of Minnesota, <sup>3</sup>Kansas State University

### **Key Points:**

- *Streptococcus suis* isolates were classified into 20 different serotypes and 58 different Sequence types (ST)s.
- Serotypes 1 and 1/2 were associated with higher pathogenic frequency, while ST profiles 1 and 28 were associated with higher frequency of pathogenic isolates.
- The analysis of the association between pathotype, serotype, and ST showed that overall, STs were a better predictor of pathogenicity than serotypes.

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*Streptococcus suis* (*S. suis*) is a bacterium that may be classified into pathogenic, opportunistic or commensal strains. Pathogenic strains cause disease of importance to the swine industry, with clinical manifestations such as meningitis, arthritis, and septicemia. *S. suis* can be further classified into serotypes or sequence type (ST). ST classification is primarily based on multilocus sequence typing (MLST), a nucleotide sequence-based technique for subtyping bacteria, while serotype classification is traditionally done by coagulation test, although serotyping with PCR-based and whole-genome sequencing techniques is also possible.

The study by Estrada et al. (2019) aimed to describe current strains circulating in the U.S. and to evaluate if specific serotypes or STs are associated with pathogenicity. Briefly, a total of 203 *S. suis* isolates from over 20 U.S. states sent for routine diagnosis were obtained from the University of Minnesota Veterinary Diagnostic Laboratory (UMNVDL) and the Kansas State Veterinary Diagnostic Lab (KSVDL) and classified into serotypes and STs. An additional 4 isolates from Canada and 1 from Mexico were included in the analysis. Isolates were also classified into pathogenic (obtained from brain/meninges, joint, heart, or liver and reported as the primary cause of meningitis, arthritis, epicarditis, or septicemia), possibly opportunistic (from lung of pigs without signs of neurological or systemic disease), and commensal (from laryngeal, tonsil, or nasal samples from farms with no known history or current control methods for *S. suis*).

Most isolates (94.2%) were classified into 20 different serotypes. The most predominant were serotypes 1/2 (n=54) and 7 (n=23). Of those 20 serotypes, the frequency of pathogenic isolates varied from 56-100% for 14 serotypes and was 0% for 6 serotypes. Serotypes 1 and 1/2 were associated with higher pathogenic frequency, while serotype 21 was associated with higher frequency of commensal isolates. Isolates were also classified into 58 different STs (20 previously reported and 38 new), the most predominant being ST28 (n=52) and ST94 (n=18). The frequency of pathogenic isolates was 0% in 33 out of the 58 STs and ranged from 44-100% for the remaining STs. ST profiles 1 and 28 were associated with higher frequency of pathogenic isolates, while profiles 750 and 821 were associated with higher frequency of commensal isolates.

The authors discuss that the large number of new ST profiles might be due to the addition of possibly opportunistic and commensal isolates, which are not usually subjected to typing. They also conclude that ST appears to be a stronger predictor of pathogenicity than serotypes. The full article is published and publicly available at <https://jcm.asm.org/content/57/9/e00377-19.long>

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