Invitation to participate in an AASV-Foundation Funded Project – Assessing Senecavirus A shedding and transmission in growing pig populations

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Vesicular disease outbreaks due to Senecavirus A (SVA) continue to cause stress and economic burden to U.S. swine producers and production companies. This virus is responsible for the staggering and constantly increasing number of foreign animal disease (FAD) investigations performed by the USDA. During 2019, 1,845 out of 2,517 (73.3%) FAD investigations were due to swine vesicular diseases, mainly caused by SVA.

Previous research from the University of Minnesota Swine Group, funded by the American Association of Swine Veterinarians (AASV) Foundation, showed that SVA-infected breeding herds have SVA RT-PCR positive processing fluids for up to 21 weeks after the initial virus detection. However, there is no data on whether these piglets will serve as carriers of SVA into the growing pig site and lead to further transmission. Considering that many SVA outbreaks occur following stressful events for pigs, such as transportation and farrowing, it is crucial to better understand the epidemiology of this disease in growing pig sites.

The goal of the proposed study is to use molecular diagnostics (i.e., PCR assays) to assess shedding and infection in pigs in different stages of the nursery-finishing phases, using a strategic blood and consecutive oral fluid sampling strategy.

We are currently seeking a production system that would like to enroll in this study. Specifically, we are seeking one sow farm with an ongoing SVA outbreak. The sampling protocol includes collecting processing fluids from five cohorts of piglets, which will later be followed over time in the nursery-finish stages of production. Samples to be collected in each cohort of weaned piglets are a one-time-only blood collection and consecutive oral fluids collection in different weeks. Testing and shipping costs will be covered by the AASV-Foundation grant and data generated from this project will be shared with you as results become available.

If you detect SVA signs in your breeding herd and are interested in understanding how SVA is circulating in your downstream production flow, please email us! We can work together with the industry and increase our knowledge to control this endemic vesicular disease.

Table 1: Classification of week positivity/negativity by SVA RT-qPCR. Results by participating farm are represented in each row, while the columns are representing the weeks after the detection of the SVA outbreak in each farm.

Week	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Farm 1	P	P	P	P	P		N		P	N	S		S			N	N		N		N	
Farm 2	P	P	P	N	P	P	P	P	P	P	P	P	P	P	S	P	S	P	S	N	N	S
Farm 3	S	P	P	P	S	N	S	S	S	N	N	P	N	N	N	S	N	N	N	N		
Farm 4		S	N		N	N		N	N	N	N	N	N	N	N	N	N	N	N	N		
Farm 5	P	N	N	N	N	N	N	N	N	N	N	S	N	N	N	N	N	N	N			
Farm 6	N	S	P	P	P	P	S	N	N	N	N	N	N	S	S	N	N	N	N	N		
Farm 7	N	P	P	P	P	P	P	S	S	N	N	P	N	S	N	S	N	N				
Farm 8	P	P	P	P	N	N	N	S	N	S	N	N	N	N	N	N	N					
Farm 9	P	P	S	S	N	S	S	N	S	S	N	S	N	N	N	N	N					
Farm 10				P	S	P	P	P		S	N	N	N	N	N	N	N	N	N			

* "P" and "S" cells are considered as positive weeks for the purposes of this study. "P" was assigned when at least one processing fluid (PF) sample had a Ct value <36 (positive test result); "S" when >=36 (suspect test result); and "N" when no SVA RNA was detected (negative test result). Weeks when no samples were collected/tested are filled in black.

If you are interested in participating, please contact us: Dr. Guilherme Preis, Graduate Research Associate (milan060@umn.edu)
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