Assessing Senecavirus A shedding and transmission in growing pig populations

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Introduction

Senecavirus A (SVA) has been linked to vesicular disease outbreaks in pigs worldwide (1), and the number of cases appears to be increasing yearly. Several SVA outbreaks have been detected following stressful events for pigs, such as transportation (2) and farrowing (3,4). Moreover, intermittent viremia and shedding for up to 60 days post-infection after stress simulation have been reported (5). Virus transmission within farrowing rooms may persist for several weeks since processing fluids (PF) in breeding herds undergoing SVA outbreaks test SVA RNA positive for an average of ~12 weeks (6). However, there is scarce information on SVA shedding and transmission after weaning in pigs born during the outbreak (e.g. growing pig populations). This study aims to use molecular diagnostic tools to assess shedding and infection in different stages of the nursery-grow and finishing phases.

Materials and Methods

A breeding herd located in the Midwestern United States undergoing an SVA outbreak was conveniently selected for this longitudinal study. Five different cohorts of weaned piglets were being longitudinally tested for SVA at the time this abstract was being written. PF samples from cohorts 2, 3, 4, and 5 were collected 2-3 days after farrowing. After weaning, four oral fluid (OF) samples are being consecutively collected at weeks 1, 2, 3, 4, 9, 11, and 16 post-placement into a wean-to-finish barn, with one last OF sampling time-point one week before sending the pigs to market. Additionally, 60 blood samples were collected at week 2. All OF and blood samples are being tested for SVA through rRT-PCR to monitor virus shedding and viremia throughout the growing phase at the University of Minnesota Veterinary Diagnostic Laboratory.

Results

The cohorts of piglets being longitudinally tested were weaned at weeks 4, 7, 8, 9, and 10 after outbreak detection in the breeding farm (cohorts 1, 2, 3, 4, and 5, respectively). Viral RNA was found in PF samples from cohorts 2, 3, 4, and 5. Unfortunately, it was not possible to collect PF samples from cohort 1. Interestingly, preliminary results show that only cohort 1 (weaned four weeks after SVA outbreak detection in the breeding herd) was OF-positive by SVA rRT-PCR until three weeks post-placement, with suspect results at weeks 4 and 8 post-placement. Until this moment, all tested OF samples from cohorts 2, 3, 4, and 5 have tested negative even though, at farrowing, their respective PF samples tested positive. All 60 sera samples collected from each cohort at week two post-placement in a wean-to-finish barn tested negative for SVA rRT-PCR. All preliminary results are shown in Table 1.

Table 1. Preliminary results from oral fluid (OF) and sera testing by SVA rRT-PCR.

	Sample type / Week in the growing phase							
	PF	OF	Sera	OF	OF	OF	OF	OF
Cohort	--	1	2	2	3	4	8	11
1	--	P	N	P	P	S	S	N
2	P	N	N	N	N	N	N	--
3	P	N	N	--	--	--	--	--
4	P	N	N	--	--	--	--	--
5	P	--	N	--	--	--	--	--

*P = Positive - at least 1 out of 4 samples tested positive with a Ct. value of at least 36. S = Suspect - at least 1 out of 4 samples tested yielded a Ct. value ≥36 and <40. N = Negative - all four tested samples tested negative. Dashed lines are shown where no results are yet available.

Discussion and Conclusion

Preliminary results agree with earlier findings in that SVA RNA was found in PF samples from cohorts 2 to 5, which could mean that piglets weaned up until ten weeks after outbreak detection were exposed to SVA infection. However, SVA shedding in the growing phase has only been detected in cohort 1 (weaned four weeks after outbreak detection), suggesting that virus transmission may occur post-weaning. It is unknown whether our negative findings in sera are due to maternal immunity or because most pigs were already infected during the suckling period and viremia had ended at the time of sample collection, or even if transmission was not occurring at high levels in the second week of the growing phase and our sample size was not large enough to detect viremic pigs.
Preliminary results of this study shed light on the epidemiology of SVA in growing pigs as pigs clearly carry the virus into growing pig sites.

Acknowledgments

The authors would like to acknowledge participating veterinarians and pig farms staff for agreeing to participate in this study and help collect samples. This study was funded by the American Association of Swine Veterinarians Foundation.

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