

I. Project Title:

Systematic epidemiological investigations of cases of Senecavirus A in United States swine breeding herds

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II. OBJECTIVES

The objectives of this project were to enhance the industry's knowledge of Senecavirus A's (SVA) spread and prevention by investigating new cases in a timely, efficient, and uniform manner and to determine the most common gaps in biosecurity that may have led to the introduction of SVA in farms we investigated.

Our long term goal, is to continue to refine this outbreak investigation program and service so that it can serve as a deployable asset to the Swine Health Information Center (SHIC), the National Pork Board (NPB), the American Association of Swine Veterinarians (AASV), and other industry stakeholders in the event of endemic, emerging, or transboundary disease outbreaks.

III. INDUSTRY SUMMARY

Late in summer 2015, producers in the United States began to see swine herds become infected with Senecavirus A (SVA). Little is known about the transmission and prevention of the disease. The objective of this study was to enhance the swine industry's knowledge of SVA's spread and prevention by investigating new sow farm cases in a timely, efficient, and uniform manner.

Materials from the PRRS Outbreak Investigation Program, funded by the Iowa Pork Producers Association (IPPA), were adapted for use on SVA. Each SVA case was evaluated using a standard SVA Outbreak Investigation Form that captured details on the clinical signs observed, swine movements, people movements, vehicles and deliveries, dead removal, other animal entry, manure removal, air and water, and operational connections with other SVA positive swine sites.

The form was used for each investigation to ensure that the same data was collected from each case.

The outbreak investigation team was notified of new SVA cases by the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL). If the SVA-positive breeding herd was willing to participate and was not part of a production system with a case previously investigated by the outbreak investigation team, an outbreak investigation was scheduled. During the investigation, the outbreak investigation facilitator and coordinator used the SVA Outbreak Investigation Form as a guide for an in depth discussion of the case and risk events that occurred in the four weeks prior to the SVA outbreak.

After the meeting, the outbreak investigation coordinator used information recorded in the SVA Outbreak Investigation Form and conversations with the outbreak investigation facilitator to complete a summary report identifying risk events most likely to have introduced SVA to the farm. A qualitative risk score of high, medium, or low was assigned to each event. The summary report was returned to the herd veterinarian, who shared and reviewed it with the producer.

From August to October 2015, six SVA outbreak investigations were conducted by the outbreak investigation team. All cases (6/6) reported increases in pre-weaning mortality and sow anorexia. Neonatal diarrhea was reported in half of the cases (3/6). Vesicular lesions on sows were reported in 4/6 cases and one case reported severe sow lameness. Risk events rated as high risk for SVA introduction by the outbreak investigation team were: on-farm employee entry (4/6), dead disposal (4/6), cull sow transport or housing (3/6), replacement gilt entry (2/6), and operational connections with known SVA positive premises (2/6). Non-swine domestic animals, rodents, other visitors, repairs outside of swine barns, feed, weaned pig removal, and semen delivery were given a high risk ranking in one of the six investigations.

From the analysis of these six cases, there does not appear to be a typical clinical presentation of SVA as the clinical signs reported varied widely across the cases. Outbreaks occurred on farms of all sizes in both swine dense and non-dense areas. Three of the farms investigated had relatively low levels of biosecurity, including the absence of showering procedures for employees. One of the farms investigated had relatively good biosecurity, but had a very high frequency of risk events due to the size of the farm. For the other two farms, the biosecurity was average but operational connections with other positive farms or major deviations from standard protocols were identified as likely responsible for the outbreaks.