I. Project Title: Characterization of Seneca Valley virus circulating in the US and in Brazil (SHIC 15-192)

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II. Stated Objectives from original proposal

The overall goal of this study is to characterize contemporary SVA isolates to determine the genetic diversity of the strains circulating in the US and Brazil. Specific aims of the proposed project are:

Objective 1: To determine the complete genome sequence of SVA strains currently circulating in the US and in Brazil.

Objective 2: To compare SVA complete genome sequences and to identify genetic signatures that might affect the specificity of SVA diagnostic tests.

III. Project Update

To date we have screened 1517 samples for the presence of SVA by real-time PCR. These samples consisted of routine diagnostic samples submitted to the SD ADRDL and included oral fluids (n = 902), nasal swabs (n = 22), feces (n = 419), tissues (n = 20), semen (n = 5), feed (n = 8) and environmental samples (n = 141). These samples originated from 13 US states, including NE, IA, SD, ND, AZ, IL, OK, CO, MT, MO, MN, MI and TX. All samples tested negative for SVA corroborating other similar studies conducted in the US, and suggesting a low prevalence of SVA infection in swine.

Clinical samples submitted to the SD ADRDL for SVA diagnostic investigation were subjected to virus isolation in cell culture. This effort led us to obtain 17 contemporary US SVA isolates. The complete genome sequencing of 6 of these isolates were obtained and compared to the sequences of other isolates currently circulating in the US. They share 97-99% nucleotide identity with other contemporary US isolates. Complete genome sequences of the remaining isolates will be determined shortly and compared to the sequences of other SVA isolates. All virus isolates obtained in our project, were effectively detected by a standard SVA real-time PCR assay used at the SD ADRDL for routine detection of SVA in diagnostic specimens.

Our collaborators from Embrapa – Brazil, are working on optimizing the real-time PCR for SVA and will shortly screen their samples to evaluate the prevalence and distribution of SVA in Brazil. Embrapa has also obtained a few Brazilian SVA isolates and these will be sequence in the next couple of months.

In an attempt to identify potential risk factors associated with SVA infection in swine, we conducted an outbreak investigation and tested multiple environmental samples by SVA real-time PCR. Interestingly, SVA RNA was detected in mice fecal samples, a mouse small intestine and in houseflies. We were able to isolate SVA from mice fecal samples and the small intestine.

The houseflies samples were negative on virus isolation. Although the actual role and contribution of these pests on the epidemiology of the virus is not completely clear at this point, our findings suggest that they may represent potential risk factors for swine.