Characterization of Seneca Valley virus circulating in the US and in Brazil (SHIC 15-192)

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Industry Summary:

Senecavirus A (SVA) or Seneca Valley virus (SVV) is a picornavirus that was originally identified as a cell culture contaminant in the US in 2002. Subsequent sequencing of unidentified picornaviruses viruses isolated from pigs with a variety of clinical presentations revealed the presence of SVV in the US swine population since 1988. In the past ten years, scattered reports have described the association of SVV with cases of swine idiopathic vesicular disease (SIVD) in New Zealand, Australia, Canada, and the US. Most importantly, since November 2014 there have been increased reports of SVV associated with vesicular disease in swine in Brazil and since July 2015 in the US. The significance of this newly emerging virus lies on its association with vesicular lesions that are indistinguishable from those observed in other high consequence foreign animal diseases (FAD) of swine (i.e foot-and-mouth disease virus, FMDV). Thus, any evidence of vesicular disease in pigs requires a complete diagnostic investigation to rule out the possibility of a FAD. In spite of being present in the US since late 1980's, there is very limited information on SVA epidemiology. Most importantly, the prevalence of SVV infection and the genetic diversity of viral strains currently circulating in the field remain largely unknown.

The Swine Health Information Center (SHIC) has requested research proposals focusing on the characterization of SVA isolates circulating in the US and in Brazil, "in order to determine genetic differences among isolates that would affect specificity of diagnostic tests and/or be associated with more severe clinical presentation".

Before we started our project there were only two SVA complete genome sequences available on GenBank (original SVV-001 and a more recent isolate from NVSL – 2013). **Thus, the overall goal of our study was to characterize contemporary SVV isolates to determine the genetic diversity of the strains circulating in the US and Brazil.** Specific aims of the proposed project were:

Specific aim 1: To determine the complete genome sequence of SVV strains currently circulating in the US and in Brazil.

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

The complete genome sequence of 21 contemporary SVA isolates circulating in the US or in Brazil were obtained. To assess the genetic diversity and relationship between SVA isolates currently circulating in different parts of the world we performed complete genome comparisons between the isolates obtained here and other sequences available in public databases. Results of our study demonstrate a close relationship between current SVA isolates circulating in different parts of the world

(US, Brazil and China). The isolates that are now circulating in the U.S. and Brazil are very similar, and they are similar to the SVV that is circulating in China. Interestingly, these recent SVA isolates present marked genetic differences when compared to SVA isolates obtained in the US or Canada prior to 2015. Whether these genetic differences contributed to an increased virulence and/or pathogenicity of current SVA isolates that led to the spike in the number of cases observed since 2015 remains to be determined.

We also assessed whether the genetic differences between current isolates and the ones obtained prior to 2015 would affect the detection efficacy of the SVA diagnostic test in use at the SD Animal Disease Research and Diagnostic laboratory (ADRDL). For this, the real-time PCR assay currently in use at the ADRDL was tested against several US SVA isolates obtained in 2015 and 2016 and against nine SVA isolates obtained between 1988 and 2002. This PCR assay which targets a conserved region of SVA genome efficiently detected all SVA isolates. Results from our study provide an improved understanding of genetic diversity of contemporary SVA isolates recently associated vesicular disease in the US and in Brazil.

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