

Senecavirus A: A Newly Emerging Picornavirus of Swine

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Senecavirus A (SVA) is a single-stranded positive sense RNA virus of the genus *Senecavirus*, family *Picornaviridae* [1]. SVA was originally identified as a cell culture contaminant [1,2]; however, subsequent sequencing of picorna-like viruses isolated from pigs in the US revealed the presence of the virus in the US swine population since 1988 [2-4]. In the past ten years, scattered reports have described the association of SVA with cases of swine idiopathic vesicular disease (SIVD) in Canada and the US [2,4-6].

Notably, since November 2014 there has been several reports of SVA associated with vesicular disease in swine in Brazil [7], and since March 2015 an increased number of cases of SVA associated with vesicular lesions and neonatal mortality in swine have been reported in the US [6-9]. According to the report of December of the Swine Health Monitoring Project, over 100 cases of SVA have been confirmed in the U.S. from March to December, 2015. This represents a significant increase in the incidence of SVA when compared to 2014, when only two cases were reported. The virus has spread across the U.S., being detected in states ranging from Alabama to Hawaii. In addition to the cases reported in Brazil and the US, a complete genome sequence of an SVA isolate obtained in China has been recently deposited on Genbank. These observations indicate the presence of SVA in major swine producing countries of the world.

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, including foot-and-mouth disease (FMD). FMD is a severe-, highly infectious disease and a positive diagnosis of FMD may result in the slaughter of millions of animals, causing a significant economic burden to producers. An even higher economic impact of an FMD outbreak results from agriculture trade bans and loss of export markets. Therefore, it is in the industry's best interest to rapidly diagnose, report and control any vesicular disease that might resemble FMD or other FADs.

Senecavirus A has been detected in pigs presenting idiopathic vesicular disease (IVD), which is clinically indistinguishable from FMD in swine [3,6,8]. Characteristic clinical signs associated with SVA, include vesicles in the snout, oral mucosa, hoofs and coronary bands [3,6,8]. Interestingly, in addition to its involvement with vesicular disease, *Senecavirus A* has also been associated with increased neonatal mortality (30-70%), usually affecting piglets less than seven days of age [7,9]. These observations underscore the potential economic impact that SVA may pose to the swine industry.

Although SVA has been present in the US swine population since the late 1980's [2], many aspects of its infection biology, pathogenesis and epidemiology remain unknown, including the origin of the virus, its natural reservoirs and transmission pathways. A serological survey conducted in the US revealed the presence of neutralizing antibodies against SVA in swine, cattle and mice [2], suggesting a potential role for these species in the epidemiology of the virus. However, to date, live SVA and/or its nucleic acid have been detected only in pigs and the role of other species in the ecology of the virus remain unknown.

As tools and reagents to study the virus and its interactions with the host become available, we will likely improve our understanding of SVA epidemiology and infection biology. A better understanding of SVA ecology, pathogenesis and immunity should allow the development of effective disease prevention and control strategies.

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Conflict of Interest

The authors declare no conflict of interest.

Bibliography

1. Hales Laura M., *et al.* "Complete Genome Sequence Analysis of Seneca Valley Virus-001, a Novel Oncolytic Picornavirus". *The Journal of general virology* 89.5 (2008): 1265-1275.
2. Knowles NJ., *et al.* "Epidemiology of Seneca Valley Virus: Identification and Characterization of Isolates from Pigs in the United States". EUROPIC 2006: XVIth Meeting of the European Study Group on Molecular Biology of Picornaviruses. Saariselka: (2006).
3. Corner S and Singh K. "Seneca Valley Virus and Vesicular Lesions in a Pig with Idiopathic Vesicular Disease". *Journal of Veterinary Science & Technology* 3.06 (2012): doi: 10.4172/2157-7579.1000123
4. Amass Sandra F., *et al.* "Case Report Peer Reviewed Idiopathic Vesicular Disease in a Swine Herd in Indiana Case Description". *Journal of Swine Health and Production* 12.4 (2004): 192-196.
5. Pasma Tim., *et al.* "Idiopathic Vesicular Disease in Swine in Manitoba". *The Canadian veterinary journal. La revue vétérinaire canadienne* 49.1 (2008): 84-85.
6. Zhang Jianqiang., *et al.* "Full-Length Genome Sequences of Senecavirus A from Recent Idiopathic Vesicular Disease Outbreaks in U.S. Swine". *Genome announcements* 3.6 (2015): e01270-15.
7. Vannucci FA., *et al.* "Identification and Complete Genome of Seneca Valley Virus in Vesicular Fluid and Sera of Pigs Affected with Idiopathic Vesicular Disease, Brazil". *Transboundary and emerging diseases* 62.6 (2015): 589-593.
8. Leme RA., *et al.* "Senecavirus A: An Emerging Vesicular Infection in Brazilian Pig Herds". *Transboundary and emerging diseases* 62.6 (2015): 603-611.
9. Linhares D and Vannucci F. "Epidemic Transient Neonatal Losses and Senecavirus A". (2015).

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