Emergence and complete genome of Senecavirus A in pigs of Henan Province in China, 2017

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Abstract

Senecavirus A (SVA) the only member of the Senecavirus genus within the Picornaviridae family, is an emerging pathogen causing swine idiopathic vesicular disease and epidemic transient neonatal losses. Here, SVA strain (CH-HNKZ-2017) was isolated from a swine farm exhibiting vesicular disease in Henan Province of Central China. A phylogenetic analysis based on complete genome sequence indicated that CH-HNKZ-2017 was closely related to US-15-40381IA, indicating that a new SVA isolate had emerged in China.

Key words: Senecavirus A, vesicular disease, phylogenetic analysis

Introduction

Senecavirus A (SVA) (syn. Seneca Valley virus), the only member of the Senecavirus genus within the Picornaviridae family, is a non-enveloped, single-stranded RNA virus (Hales et al. 2008). The virus was first discovered in PER.C6 cell cultures in 2002, speculating that it is introduced into the cell culture via contaminated fetal bovine serum (FBS) or porcine trypsin (Hales et al. 2008). Initially, SVA does not cause any specific pathology and is considered to be a potential oncolytic virus against tumors in humans (Reddy et al. 2007, Hales et al. 2008). However, recent studies have provided evidence that SVA is associated with swine idiopathic vesicular disease (SIVD) and epidemic transient neonatal losses (ETNL) in newborn piglets (Oliveira et al. 2017). The clinical signs induced by SVA were indistinguishable from those caused by other economically more devastating transboundary pathogens that caused vesicular disease, including swine vesicular disease virus (SVDV), foot-and-mouth disease virus (FMDV) and vesicular stomatitis virus (VSV). Currently, SVA has emerged in swine in major swine producing countries around the world, including the US, Brazil, Cana-