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Short communication

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-

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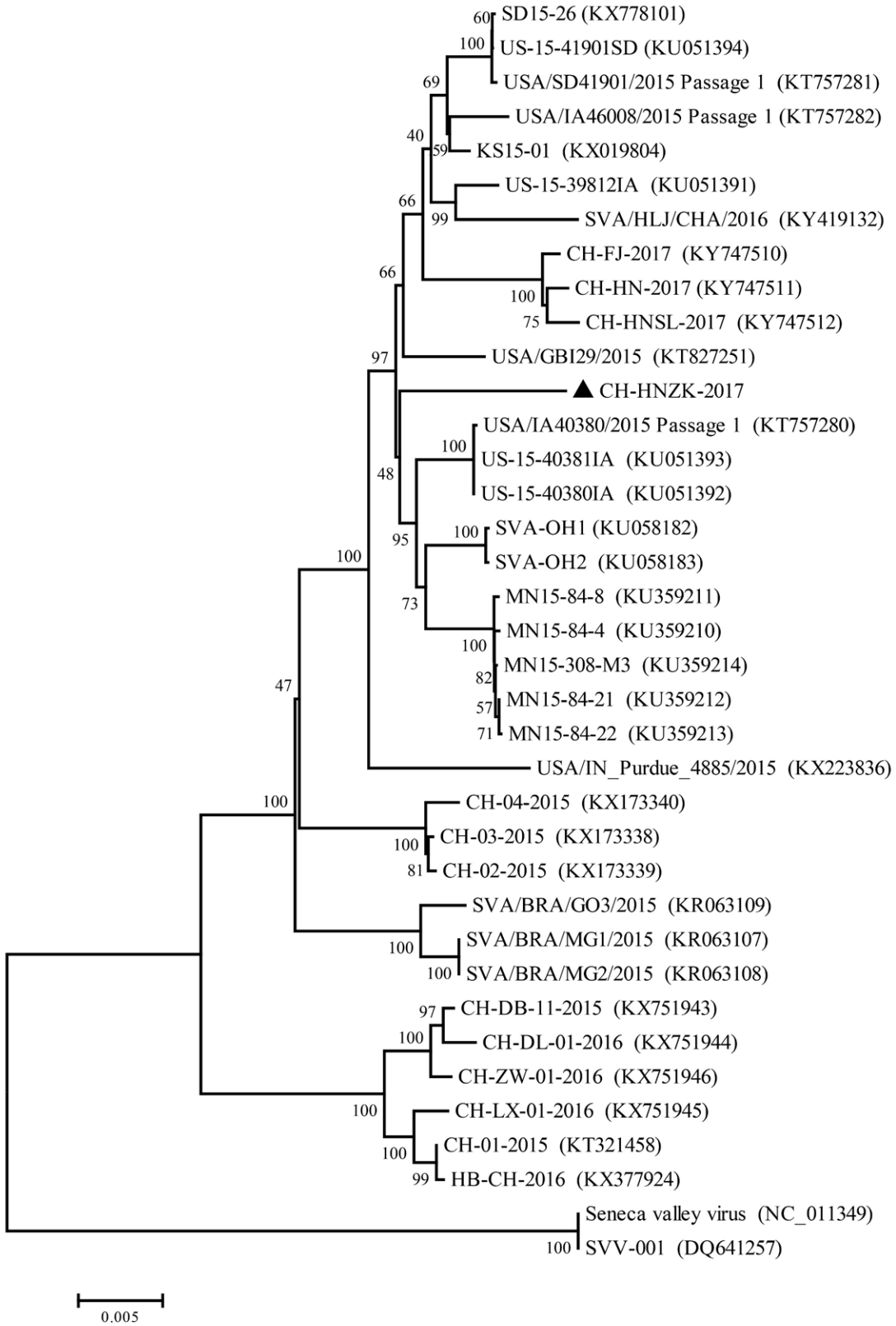

Fig. 1. Genetic relationships of CH-HNZK-2017 with other SVA isolates available from SVA database inferred by MEGA 6.0.

da, Thailand and China, posing a serious problem for the farming industry (Hause et al. 2016, Wu et al. 2016, Leme et al. 2017, Saeng-Chuto et al. 2017, Sun et al. 2017). In China, an increasing number of cases of SVA infection have been reported, including Guangdong, Hubei, Fujian, Henan and Heilongjiang province (Qian

et al. 2016, Wu et al. 2016, Wang et al. 2017, Zhu et al. 2017). In this study, we isolated and characterized the complete genome sequence of SVA strain from a swine farm in Henan Province.

Materials and Methods

In March 2017, 300 finishing pigs displayed erosions and vesicles on the snout and coronary bands on a swine farm (total population was 12,000) vaccinated against FMDV in Henan province, suggesting that this might be an outbreak of a novel disease. Organization of pig production and biosecurity was strictly implemented according to the Law of the People's Republic of China on Animal Epidemic Prevention and Henan animal epidemic prevention regulations. The pigs were reared on a modern intensive farm in a good environment according to the animal care and use committee, Henan Provincial Animal husbandry and Veterinary Bureau. In order to control the disease, measures had been taken, including separation of sick pigs from the rest of the herd and disinfection every day. The affected pigs were 12 weeks old and fully recovered within 15 days without mortality. Vesicle fluid and vesicular lesion swab samples were collected and stored at -80°C for subsequent experiments. The genomic RNA was extracted from the tissue homogenate using TRIzol reagent (Invitrogen). To determine the pathogen, the extracted RNA was respectively detected using specific primers of VSV, FMDV, SVDV and SVV as previously described (Qian et al. 2016).

Porcine kidney (PK-15) cells were used for virus isolation. The cells were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% (v/v) FBS, 100 U/ml penicillin (Invitrogen), and 10 μg/ml streptomycin sulfate (Invitrogen). The PK-15 cells were incubated vesicle fluid. The plates were incubated for 2-3 days at 37°C in a humidified 5% CO_2 incubator and observed for cytopathic effect (CPE). The cultured cells and supernatants were harvested when 70% of the cells had CPE. The complete genome of SVA was amplified with seven overlapping fragments as previously described (Wu et al. 2016). The seven fragments of SVA were manually assembled into a complete genome. A phylogenetic tree was implemented in MEGA 6.0 as previously described (Liu et al. 2018).

Results and Discussion

In the present study, the SVA strain (designated as CH-HNZK-2017) was successfully isolated. Genetic analysis revealed that the highest nucleotide sequence identity was 98.6% between CH-HNZK-2017 and US-15-40381IA, suggesting that CH-HNZK-2017 was closely related to US-15-40381IA, while the lowest minimum genome identity was 93.7% between CH-HNZK-2017 and SVV-001. In order to discover the genetic relationship, a phylogenetic tree was constructed using the complete genome of the SVA CH-HNZK-2017 strain and other representative SVA strains (Fig. 1). In the tree, CH-HNZK-2017 clustered with the strains from the United States, not with recent SVA strains from China, revealing that CH-HNZK-2017 was closely related to US-15-40381IA. These results confirmed that the recent outbreaks of SVA infection in Henan province were not caused by previous Chinese strains.

SVA infections in pigs have been reported in some provinces in China (Qian et al. 2016, Wu et al. 2016, Wang et al. 2017, Zhu et al. 2017). When compared with all other Chinese strains, CH-HNZK-2017 strains shared 96.6–97.9% nucleotide identity. Interestingly, recently deposited Chinese SVA isolates SVA/HLJ/ /CHA/2016 from Harbin (Wang et al. 2017), CH-FJZZ-2017 from Fujian (Zhang et al. 2017) and six SVA strains from Guangdong (Liu et al. 2018) as with the isolate (CH-HNSL-2017) of the present study, were closely related to US strains, instead of other previous Chinese strains. In line with previous studies this indicates that the SVA isolates reported after 2016 were more closely related to the United States strains, while isolates before 2016 shared higher nucleotide identities with Canadian and Brazilian strains (Zhang et al. 2017). At present, SVA infection has only been identified in finishing pigs, and no clinical manifestations have been identified in piglets, consistent with other Chinese strains reported in 2017 (Wang et al. 2017, Zhang et al. 2017, Liu et al. 2018). However, the strains reported in 2015 can cause neonatal losses in piglets with strains closely related to Brazilian strains (Wu et al. 2017). These results suggest that the reemergence of new SVA strains and different SVA strains have been spreading in China. Unfortunately, it remains obscure how these SVA strains were introduced into China, and given that five provinces have reported outbreaks of SVA, a higher national prevalence of SVA is possible. Consequently, epidemiological investigations should be carried out in countries that have not been reported, and proper control strategies should be taken carefully to avoid the virus transmitting across the country.

In conclusion, an SVA strain (CH-HNKZ-2017) was isolated from swine in Henan Province of Central China in the present study. A phylogenetic analysis based on the complete genome sequence indicated that CH-HNKZ-2017 was closely related US-15-40381IA, indicating that a new SVA isolate had emerged in China.

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