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GENOME SEQUENCES

First Detection and Genome Sequence of Senecavirus A in Vietnam

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ABSTRACT In 2018, senecavirus A was detected for the first time in Vietnam. This report contains the first complete genome of a senecavirus A isolate collected from pigs in Kon Tum Province, Vietnam. This novel incursion has substantial implications for regional control of vesicular transboundary diseases.

Senecavirus A (SVA; genus *Senecavirus*, family *Picornaviridae*) causes a vesicular disease in pigs characterized by lethargy, anorexia, fever, lameness, and vesicles on the snout and coronary bands (1, 2). The disease is clinically indistinguishable from other transboundary vesicular diseases, including foot-and-mouth disease (FMD), vesicular stomatitis, and swine vesicular disease (1). Clinical disease attributed to SVA was first reported in pigs in Canada in 2007 and in the United States in 2012 (3). In 2015, the virus was confirmed outside North America, with reports in Brazil and China, followed by reports from Colombia and Thailand in 2016 (1, 3).

An outbreak of a vesicular disease was reported during January 2018 in pigs in Kon Tum Province, Vietnam, and provincial field veterinarians made a presumptive diagnosis of FMD based on clinical signs. Vesicle epithelial samples were subjected to FMD virus (FMDV) serotyping by antigen ELISA at Vietnam's Department of Animal Health, as previously described (4). One sample (clarified tissue homogenate), positive for FMDV serotype O with antigen ELISA, was subsequently sent to the Foreign Animal Disease Research Unit (FADRU), Plum Island Animal Disease Center in New York, for further testing.

At FADRU, virus isolation was performed using LFBK-αVβ6 cells, and RNA was extracted from the passaged sample as previously described (5). The recovered virus was negative with FMDV real-time reverse transcription-PCR (rRT-PCR) (6, 7) and pan-serotypic RT-PCR primers that amplify the FMDV P1 region (8). Next, RT-PCR primers designed to detect FMDV clinical differentials were applied to amplify the complete SVA genome (9). The purified amplicons were processed with the Nextera XT DNA library kit (Illumina, catalog no. FC131-1096) and sequenced on an Illumina NextSeq 500 instrument. CLC Genomics Workbench v11.0.1 was implemented for read quality filtering and *de novo* assembly. The average read length was 147.8 nucleotides (nt), and 3,810,443 total reads were assembled, with an average coverage of 75,505.72 reads. The consensus sequence consisted of 7,289 nt, with a GC content of 51.8%.

Here we report the complete sequence of the novel SVA isolate SVA/VIT/3187/2018, obtained from a pig in Vietnam. The sequence codes for the complete genome,

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including the 6,546-nt open reading frame, 667-nt 5′ untranscribed region (UTR), and 76-nt 3′ UTR. Annotations were based on comparisons of the nucleotide and inferred amino acid sequences with published SVA sequences and protease cleavage sites (10). This sequence had 98.5% to 99% homology with isolates collected in China in 2015 and 2016 (GenBank accession no. KX173339, KX173338, KX173340, and KY038016).

This detection of SVA in Vietnam is highly important as a demonstration of further spread of this (recently) geographically constrained pathogen. The cocirculation of FMDV and SVA in Southeast Asia hinders control efforts for both viruses and could potentially lead to emergence of novel viruses through recombination. Additional surveillance is needed to determine the spread of SVA in Southeast Asia, and rapid diagnostic tests are needed to differentiate SVA and FMDV. Until adequate methods are available to effectively differentiate SVA and FMDV infections, substantial resources will be misdirected toward SVA cases, including premise quarantines, animal movement restrictions, FMDV vaccinations, and, potentially, trade restrictions.

Data availability. The complete genome nucleotide sequence of SVA/VIT/3187/2018 described herein has been deposited in GenBank under the accession no. MH704432. The version described in this paper is the first version, MH704432.1. The raw sequencing reads are available in the Sequence Read Archive (SRA) under the accession no. PRJNA497427.

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