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GENOME SEQUENCES

Foot-and-Mouth Disease Virus Serotype O/CATHAY Genome Sequences from Five Outbreaks in Vietnam, 2017 to 2019

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ABSTRACT We report the genomes of five foot-and-mouth disease viruses (FMDVs) from distinct provinces in Vietnam. All five viruses were grouped within the O/CATHAY topotype. Sequences contain the full polyprotein coding sequence and partial untranslated regions. These genomes provide critical data on the spread and evolution of FMDVs in the region.

Foot-and-mouth disease virus (FMDV) (in the family *Picornaviridae* and the genus *Aphthovirus)*, the etiological agent of foot-and-mouth disease (FMD), is an economically devastating infectious disease of livestock. Acutely infected animals typically develop vesicles on the feet, mouth, and/or teats (1, 2). The seven FMDV serotypes (A, Asia 1, C, O, SAT 1, SAT 2, and SAT 3) are divided into topotypes, lineages, and sublineages based on VP1 sequence similarity (3). A distinct topotype of serotype O (O/CATHAY), characterized by a deletion within its 3A region (4) and low infectivity for cattle (5), was identified in 2001. The O/CATHAY topotype was responsible for a 1997 FMD outbreak in Taiwan, leading to the culling of over 4 million pigs and an economic loss of more than 6 billion dollars (6). O/CATHAY is currently endemic in Southeast Asia, including Vietnam (7, 8).

The viruses described herein were obtained from vesicular epithelium from pigs during FMD outbreaks in five provinces of Vietnam in 2017 to 2019 (Table 1). Samples were sent to the Foreign Animal Disease Research Unit (FADRU), Plum Island Animal Disease Center. At the FADRU, FMDV was confirmed by real-time reverse transcription-PCR (rRT-PCR) using FMDV-specific primers and by virus isolation on LFBK-$\alpha v\beta 6$ cells followed by rRT-PCR (9, 10). Total cell supernatant or tissue homogenate RNA was subjected to deep sequencing, as described previously (11, 12). Briefly, RNA was extracted from supernatant using the MagMAX total RNA isolation kit, and DNA was depleted using the DNA-free DNase kit (Ambion). Treated RNA underwent first-strand synthesis using the SuperScript first-strand synthesis system (Invitrogen) with random hexameric primers, a poly(T) primer targeting the 3′ untranslated region (UTR), and one FMDV-specific reverse primer (GCCCRGGGTTGGACTC), which improves sensitivity and ensures specificity (11, 13). Double-stranded cDNA was generated using the NEBNext Ultra II nondirectional RNA second-strand synthesis module (New England Biolabs). A sequencing library was constructed using the Nextera XT kit (Illumina) and sequenced on the NextSeq 500 platform. The NextSeq sequencing generated 310,360 to 3,023,414 total reads per sample. Using CLC Genomics Workbench 11.0, reads were trimmed and filtered for quality, which resulted in average read lengths of 133 to 148 nucleotides (nt)

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TABLE 1 Sampling locations, dates, sequencing metrics, and accession numbers for sequences in this report

Sequence identification no.	Location (province)	Yr	Total no. of reads	No. of mapped reads	Avg read length (nt)	Avg coverage (fold)	GC content (%)	GenBank accession no.	SRA accession no.	Genome length (nt)
O/VIT/17-19073/2017	Hồ Chí Minh City	2017	591,192	475,964	148	8,571	54.8	MN250314	SRX6653068	8,031
O/VIT/18-3766/2018	Tiền Giang	2018	3,023,414	2,884,218	138	48,339	54.9	MN250315	SRX6653067	8,032
O/VIT/18-5490/2018	Bình Phước	2018	1,859,748	1,397,414	147	24,970	54.9	MN250316	SRX6653066	8,020
O/VIT/18CD-1610.2/2018	Nghệ An	2018	1,842,842	1,497,510	147	26,722	54.8	MN250317	SRX6653065	8,023
O/VIT/19-005/2019	Hậu Giang	2019	310,360	81,075	133	1,276	55.1	MN250318	SRX6653064	8,026

(Table 1). Trimmed reads were mapped to a previously published contemporary sequence (GenBank accession number KU204894), and default parameters were used to extract the consensus sequence. Consensus sequences were annotated based on comparisons to the reference and BLASTn sequence results, and the 5′ UTR poly(C) tract was standardized to 12 nt, as described previously (14).

The 8,032- to 8,044-nt genomes encode a 6,966- to 6,969-nt open reading frame flanked by a 972- to 976-nt 5′ UTR and a 78- to 91-nt 3′ UTR, excluding the poly(A) tail. The sequences share 94.9 to 98.8% pairwise identity with each other, with O/VIT/19-005/2019 and O/VIT/18CD-1610.2/2018 being the most dissimilar. Additionally, they share 83.2 to 83.5% pairwise identity with a previously published 7,128-nt O/CATHAY genome from Vietnam (GenBank accession number KY657269). The closest BLASTn match was GD/CHA/JH12/2013 (GenBank accession number KU204894), a 2013 isolate from south China, with 94.8 to 95.3% sequence identity.

The O/CATHAY topotype appears sporadically throughout Southeast Asia, with no clear pattern of emergence and maintenance (5). This ambiguity and its endemicity in Southeast Asia create a need for detailed O/CATHAY sequences. The viruses described herein substantially update our knowledge of the molecular epidemiology of FMDVs in the region.

Data availability. The assembled FMDV genomes have been deposited in GenBank under accession numbers MN250314 to MN250318. The sequence data are available in the NCBI Sequence Read Archive (SRA) under accession number PRJNA558049.

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