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GENOME SEQUENCES

First Report of Near-Complete Genome Sequences of Foot-and-Mouth Disease Virus Serotype O Strains from Kenya

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ABSTRACT This is the first report of two near-complete genome sequences of foot-and-mouth disease virus (FMDV) serotype O from Kenya. The viruses were isolated from bovine epithelium collected in 2014 and 2016 from local FMD outbreaks. These full-genome sequences are critical for improving the understanding of regional FMDV molecular epidemiology.

Foot-and-mouth disease virus (FMDV; *Picornaviridae*, *Apthovirus*) is a positive-sense single-stranded RNA virus. FMDV is the causative agent of foot-and-mouth disease (FMD), one of the most economically significant livestock diseases, which manifests as fever, lameness, and vesicular lesions largely on the feet and oral cavities (1). The seven immunologically distinct serotypes (Asia1, A, C, O, SAT1, SAT3, and SAT3) are genetically classified by the VP1 coding sequence, of which FMDV-O has the highest prevalence worldwide (2).

Following a vesicular disease outbreak in 2014, vesicular epithelium (VES) was collected from a cow in Nakuru, Kenya, and the virus designated O/KEN/K60/2014 was isolated on baby hamster kidney (BHK-21) cells at Kenya FMD Laboratory (3). The virus designated O/KEN/K19/2016 was obtained similarly from a cow in Nyandarua, Kenya, in 2016. VES from O/KEN/K60/2014 and BHK-21 cell supernatant of O/KEN/K19/2016 were sent to the Foreign Animal Disease Research Unit (FADRU) at the Plum Island Animal Disease Center.

At FADRU, the virus isolates were analyzed using FMDV-specific real-time reverse transcription (rRT)-PCR and passaged on LFBK-αVβ6 cells (4, 5). Tissue culture supernatants were subjected to deep sequencing (6). Briefly, total RNA (MagMax total RNA isolation kit) was depleted for contaminating DNA (DNA-free DNase kit; Ambion), first-strand cDNA was generated with random hexamers (SuperScript II; Invitrogen) and FMDV-specific untranslated region (UTR) primers, double-stranded (ds) cDNA was created from the first-strand cDNA (NEBNext Ultra nondirectional RNA second-strand synthesis module), and ds cDNA was purified (AMPure XP beads; Beckman-Coulter). The purified cDNA libraries were prepared with the Nextera XT kit and run on an Illumina NextSeq instrument (Table 1). All preparation steps were completed as specified by the manufacturer. *De novo* assembled contigs were analyzed via BLASTn, identifying O/UGA/3/2002 (GenBank accession number MH053318) (7) as the closest full-genome reference (92.8% to 93.2% identity). Trimmed reads for each sample were aligned to O/UGA/3/2012, and consensus sequences were extracted.

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TABLE 1 Overview of deep sequence results from foot-and-mouth disease serotype O samples from Kenya

Virus name	Total no. of reads	No. of reads aligned to reference	Avg coverage (no. of reads)	Avg read length (nt)	Sequence length (nt)	Deletion sites compared to MH053318	VP1 accession no.	GenBank accession no.	SRA accession no.
O/KEN/K60/2014	602,902	497,863	8,893.5	145.5	8,158	457, 978, 1040	MH882574	MN116693	SAMN12167188
O/KEN/K19/2016	716,924	615,915	11,072.7	146.1	8,152	111, 184, 345, 457, 1040, 1122–1124	MH882573	MN116694	SAMN12167189

Trimming, assembly, and analyses were executed using default parameters in CLC Workbench v11.0.

Here, we report the first near-complete FMDV-O sequences from Kenya. The O/KEN/K60/2014 and O/KEN/K19/2016 genomes include a 6,996- to 6,999-nucleotide (nt) open reading frame (ORF) flanked by a 1,053- to 1,055-nt 5′ UTR and a 104- to 105-nt 3′ UTR, respectively. The nucleotide sequences have 53.9 to 54% GC content and are 91.4% identical to each other and 92.8% to 93.2% identical to O/UGA/3/2002, which was collected in 2002 in Uganda from an unknown source (7). The VP1 nucleotide sequences are 100% identical to the available VP1s from these samples (8). In the VP1 region, O/KEN/K60/2014 and O/KEN/K19/2016 are only 89.7% and 91.6% similar to O/UGA/3/2002, respectively. The VP1 sequence of O/KEN/K60/2014 had the highest identity (96.8%) to O/K47/2011 (GenBank accession number KF207884), which was isolated from a cow in Kenya in 2011 (9). In contrast, O/KEN/K19/2016 had equal similarity (96.7%) to O/CVL-2010-0144 (GenBank accession number KJ947831) (9), a bovine isolate from Tanzania in 2010, and O/KEN/16/2011 (GenBank accession number KF135293) (10), a bovine isolate from Kenya in 2011.

Despite the availability of VP1 sequences from Kenya and the endemic status of FMDV-O in eastern Africa, near-complete FMDV-O genomes from Kenya are lacking. Nearly complete references are crucial for many molecular epidemiological analyses and vaccine selection. The addition of the O/KEN/K60/2014 and O/KEN/K19/2016 genomes updates useful FMDV data availability.

Data availability. The consensus genomes were deposited in GenBank under the accession numbers MN116693 and MN116694. The deep sequence reads were deposited in the NCBI Sequence Read Archive (SRA) under BioProject number PRJNA551797.

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