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GENOME SEQUENCES

Foot-and-Mouth Disease Virus Serotype A Genome Sequence from Kenya in 2016

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ABSTRACT We report the genome sequence of a foot-and-mouth disease virus (FMDV) serotype A topotype Africa isolate collected from bovine vesicular epithelium from Kenya in 2016. This novel sequence updates the knowledge of FMDV diversity in eastern Africa and has important implications for FMDV epidemiology and molecular analyses.

Foot-and-mouth disease (FMD) is an economically important disease of livestock worldwide, caused by the highly diverse FMD virus (FMDV; *Aphthovirus*, *Picornaviridae*). The high morbidity associated with FMD manifests as characteristic vesicles predominantly on the feet and oral cavities, as well as fever and lameness (1). FMDV has been genetically and immunologically differentiated into seven distinct serotypes, A (FMDV-A), Asia1, C, O, SAT1, SAT2, and SAT3, which are further classified based on their VP1 sequence (2). All serotypes, except C and Asia1, circulate endemically in Africa, although some serotypes have regionally limited ranges (3).

In October 2016, a vesicular epithelium sample was collected from a cow in Subukia, Kenya, during a regional FMDV-A outbreak, and the virus designated A/KEN/K74/2016 was isolated on baby hamster kidney (BHK-21) cells in the Kenya FMD Laboratory (KFMDL). The viral isolate was sent to the Foreign Animal Disease Research Unit (FADRU) at the Plum Island Animal Disease Center for further characterization.

The isolated virus was propagated on LFBK-αVβ6 cells and confirmed using FMDV-specific real-time reverse transcription-PCR (rRT-PCR) (4, 5). Total RNA was extracted (MagMAX total RNA isolation kit; Thermo Fisher) and DNase treated (DNA-free DNase kit; Ambion). cDNA was generated using SuperScript II reverse transcriptase (Invitrogen) with random primers and an FMDV untranslated region (UTR)-specific primer, followed by double-strand generation with a NEBNext Ultra nondirectional RNA synthesis module. Double-stranded cDNA was purified with AMPure XP beads, and libraries were prepared with the Nextera XT kit and run on an Illumina NextSeq platform (6). All steps were performed as specified by the manufacturer. A total of 374,232 trimmed reads (average length, 147.6 nucleotides [nt]) were *de novo* assembled into contigs, and the contigs were examined using BLASTn. Reads were then aligned to the closest reference genome identified by BLASTn containing complete 5′ and 3′ UTRs (A/Zambia/90; GenBank accession number MH053307 [7]), and the consensus sequence was extracted for analysis. A total of 195,140 reads aligned to the reference, with an average coverage of 3,392.4 reads. Trimming, alignment, and analyses were performed in CLC Genomics Workbench version 11.0.

To our knowledge, this is the only FMDV serotype A genome from Kenya reported

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since 2005. The 8,168-nt genome encodes a 7,002-nt open reading frame flanked by a 1,071-nt 5′UTR and a 96-nt 3′UTR and has 53.6% GC content. The sequence reported herein, that of A/KEN/K74/2016, had 89.8% pairwise nucleotide identity to A/Zambia/90, obtained from a cow in Zambia in 1990 (7). Single-nucleotide insertions were identified at sites 21 and 474 (5′UTR). Additionally, three single-nucleotide deletions, two in the 5′UTR (sites 124 and 523) and one in the 3′UTR (sites 8144 to 8145), were present in A/KEN/K74/2016. The VP1 region was identical to the previously published VP1 sequence for this sample (GenBank accession number MH882567 [8]). Importantly, in the VP1 region, the identity to A/Zambia/90 was only 82.9%. The VP1 region was 95.4% identical to that of A/TAN/1/2013 (GenBank accession number MF592645 [9]), obtained from a cow in Tanzania in 2013.

Although FMDV is hyperendemic in eastern Africa and VP1 sequences are available, there is a substantial deficit of currently available complete genomes. Since 2005, no FMDV serotype A complete viral genomes have been published from eastern Africa. Considering the rapid evolution of FMDV, the addition of A/KEN/K74/2016 to the available genomes is critical for understanding molecular epidemiology and vaccine selection.

Data availability. The consensus sequence was deposited in GenBank under accession number MN116688. The deep sequencing reads were submitted to the NCBI Sequence Read Archive under accession number SAMN12167164.

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