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GENOME SEQUENCES

Genome Sequences of Foot-and-Mouth Disease Virus SAT1 and SAT2 Strains from Kenya in 2014 to 2016

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ABSTRACT Here, we report the near-complete genomes of three Southern African Territories 1 (SAT1) serotype strains and one SAT2 serotype strain of foot-and-mouth disease virus (FMDV) recently isolated from Kenya. Viral isolates were obtained from bovine epithelial tissues collected in 2014 and 2016 following outbreaks of foot-and-mouth disease (FMD). These near-complete genome sequences provide a critical update of Kenyan FMDV molecular epidemiology.

Foot-and-mouth disease (FMD) is a high-consequence, transboundary disease affecting livestock that is caused by FMD virus (FMDV; *Picornaviridae*, *Aphthovirus*). FMD manifests clinically with characteristic vesicles on the feet and in the oral cavities of susceptible species (1). FMDV exists in seven distinct serotypes (Asia1, A, C, O, and Southern African Territories 1 [SAT1] to SAT3), genetically classified based upon the VP1 sequence (2). Southern African Territories serotypes (SAT1 to SAT3) are endemic in Africa (2).

In 2014 to 2016, vesicular epithelium was collected from cattle following an outbreak of vesicular disease in Kenya. At the Kenya FMD Laboratory, the FMD viruses designated SAT1/KEN/K14/2014, SAT1/KEN/K29/2014, SAT1/KEN/K75/2016, and SAT2/KEN/K137/2014 were isolated on baby hamster kidney (BHK-21) cells (3). Cell supernatants were collected and sent to the Foreign Animal Disease Research Unit (FADRU), Plum Island Animal Disease Center, for further characterization.

At FADRU, viruses were passaged once on LFBK-αVβ6 cells and verified by FMDV-specific real-time reverse transcription-PCR (4, 5). Passaged supernatants were analyzed by deep sequencing (6). Briefly, total RNA was extracted with the MagMax total RNA isolation kit (Thermo Fisher) and DNase treated using the DNA-free DNase kit (Ambion). First-strand cDNA was generated with random hexamers and FMDV-specific primers using SuperScript II (Invitrogen). Double-stranded cDNA was created (NEBNext Ultra nondirectional RNA second-strand synthesis module) and purified with AMPure XP beads. Libraries were prepared with the Nextera XT kit and run on an Illumina NextSeq instrument (Table 1). All steps were performed according to the manufacturer's instructions. Reads were trimmed and *de novo* assembled in CLC Genomics Workbench v11.0 using default parameters. A BLASTn search of the contigs in GenBank identified full-length reference genomes. Trimmed reads were mapped to the closest full-length reference to obtain near-complete genomes, and consensus sequences were extracted using CLC Genomics Workbench v11.0 with default parameters.

This study describes the first near-complete FMDV SAT1 and SAT2 strain genome sequences from Kenya since 1983 and 1960, respectively. The SAT1 strain genomes

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TABLE 1 Summary of deep sequence results from foot-and-mouth disease serotype SAT1 and SAT2 strain samples from Kenya

Virus name	Total no. of reads	No. of reads aligned to reference	Avg coverage	Avg read length (nt)	Sequence length (nt)	Genome GC content (%)	Indels[a]	VP1 accession no.	GenBank accession no.	SRA accession no.
SAT1/KEN/K14/2014	354,492	267,903	4,671.5	146.2	8,131	53.5	Insertions: 991, 8,046, 8,087, 8,088, 8,100; deletion: 160	MH882578	MN116689	SAMN12167191
SAT1/KEN/K29/2014	364,542	224,655	3,917.8	146.8	8,133	53.4	Insertions: 991, 8,046, 8,087, 8,100; deletion: 160	MH882580	MN116690	SAMN12167192
SAT1/KEN/K75/2016	575,140	533,832	9,501.9	145.5	8,145	53.6	Deletions: 159, 378, 544, 8,086	MH882581	MN116691	SAMN12167193
SAT2/KEN/K137/2014	594,734	469,955	7,669.9	130.5	8,151	53.1	Deletions: 989, 8071	MH882612	MN116692	SAMN12167194

[a] Positions of single-nucleotide indels compared to the reference genomes SAT1/TAN/22/2012 (SAT1) and SAT2/TAN/5/2012 (SAT2).

encode a 7,020 to 7,021-nucleotide (nt) open reading frame (ORF) flanked by a 1,002 to 1,005-nt 5′ untranslated region (UTR) and a 107 to 116-nt 3′ UTR, while SAT2/KEN/K137/2014 encodes a 7,008-nt ORF, a 1,001-nt 5′ UTR, and a 142-nt 3′ UTR. Indels were present in all sequences (Table 1).

The SAT1 strain nucleotide sequences are 88.3% to 94.5% identical to that of SAT1/TAN/22/2012 (GenBank accession number KM268899), and that of SAT2/KEN/K137/2014 is 92.3% identical to that of SAT2/TAN/5/2012 (KM268900) (7). The VP1 coding regions of the current viruses were identical to those of previously published VP1s for these samples (8). In the VP1 coding region, SAT1/KEN/K14/2014 and SAT1/KEN/K29/2014 had the highest identity (92.1% and 92.3%, respectively) to SAT1/K28/06 (HQ267529) (9). Similarly, the VP1 coding region of SAT1/KEN/K75/2016 was 89.7% identical to that of SAT1/T155/71 (HQ267519) (9). Finally, the VP1 nucleotide sequence of SAT2/KEN/K137/2014 was 94.1% identical to that of SAT2/TAN/6/2004 (KF561723) (10).

Despite the numerous SAT1 and SAT2 strain VP1 sequences from Eastern Africa, no near-complete SAT strain genomes have been reported from Kenya since 1983 (SAT1) or 1960 (SAT2). Considering the widespread endemicity and rapid mutation rate of FMDV, maintaining recent near-complete references is critical for understanding the regional molecular epidemiology. The near-complete genomes of SAT1 and SAT2 strains described here provide timely updates to our knowledge of FMDV genetic diversity in Kenya.

Data availability. The consensus sequences of near-complete genomes were deposited in GenBank under the accession numbers MN116689 to MN116692. Deep sequence data are available in the NCBI Sequence Read Archive (SRA) under BioProject accession number PRJNA551873.

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