



Complete Genome Sequence of the African Green Monkey Simian Foamy Virus Serotype 3 Strain FV2014 (SFVcae_FV2014)

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ABSTRACT The full-length sequence of simian foamy virus serotype 3 (SFV-3) strain FV2014, an African green monkey (*Chlorocebus aethiops*) isolate, was obtained using high-throughput sequencing. SFVcae_FV2014 consisted of 13,127 bp and had a genomic organization similar to those of other SFVs but was distinct from SFV strain LK3, isolated from the same monkey species.

Simian foamy viruses (SFVs) are ancient retroviruses that have cospeciated with their hosts (1–6) and are highly prevalent in all nonhuman primate (NHP) species (1, 3, 4, 7). Human infections with SFV have occurred due to cross-species transmission from infected Old World primates, including Asian and African monkeys, chimpanzees, and apes (8–17), and more recently there is serological evidence of potential zoonotic transmissions originating from New World primates (18, 19). Widespread SFV infection in NHPs most likely occurs via saliva (20, 21); however, there is no evidence of transmission in humans. Although there is no known disease associated with SFV, infectious virus can persist lifelong due to stable integration of viral DNA in the host genome (22–25). Availability of SFV sequences from diverse NHP species can facilitate development of virus-specific assays and serological reagents for detection and further investigation of virus transmission and persistence in humans.

SFV type 3 strain FV2014, which was isolated from the kidney of an African green monkey (*Chlorocebus aethiops*) (26), was obtained from American Type Culture Collection (ATCC, Manassas, VA; catalog number VR-218). A virus stock was prepared in our laboratory by infecting *Mus dunni* cells, and nucleic acid was extracted using a QIAamp viral RNA minikit. High-throughput sequencing was done using Illumina MiSeq V3 150-cycle chemistry and run in paired-end 150-base mode (CD Genomics, Shirley, NY).

The total number of paired-end reads was 19,978,602, and the average read length was 151 bases. Read trimming and assembly were done in our laboratory using the CLC Genomics Workbench software, version 10.0.1 (CLC bio, Denmark). The 13,127-bp full-length sequence of SFVcae_2014 was obtained (GenBank accession number MF582544) by mapping the raw reads to the available SFVcae-LK3 full-length genome as a reference (27) (NCBI RefSeq accession number M74895) and generating a consensus sequence. Open reading frames were identified (<https://www.ncbi.nlm.nih.gov/orffinder/>). The genomic structure of SFVcae_FV2014 was similar to that of other simian foamy viruses and contained long terminal repeats (LTRs), an internal promoter, a primer binding site utilizing tRNALys1,2, and open reading frames encoding Gag, Pol, and Env structural proteins and Tas and Bet accessory proteins (28).

The SFVcae_FV2014 full-length genome sequence is distinct from the currently available sequence of the SFV isolate LK3 (currently designated SFVcae_LK3), which was isolated from the same monkey species, with an overall 70% to 90% nucleotide sequence identity according to NCBI BLASTN (29).

Received 16 November 2017 **Accepted** 29 November 2017 **Published** 18 January 2018

Citation Nandakumar S, Bae EH, Khan AS. 2018. Complete genome sequence of the African green monkey simian foamy virus serotype 3 strain FV2014 (SFVcae_FV2014). *Genome Announc* 6:e01437-17. <https://doi.org/10.1128/genomeA.01437-17>.

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Accession number(s). The SFVcae_FV2014 sequence was deposited in DDBJ/ENA/GenBank under accession number [MF582544](https://www.ncbi.nlm.nih.gov/nuccore/MF582544).

ACKNOWLEDGMENT

We declare no conflicts of financial or personal interests.

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