



Complete Genome Sequence of a Naturally Occurring Simian Foamy Virus Isolate from Rhesus Macaque (SFVmmu_K3T)

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ABSTRACT The full-length genome sequence of a simian foamy virus (SFVmmu_K3T), isolated from a rhesus macaque (*Macaca mulatta*), was obtained using high-throughput sequencing. SFVmmu_K3T consisted of 12,983 bp and had a genomic organization similar to that of other SFVs, with long terminal repeats (LTRs) and open reading frames for Gag, Pol, Env, Tas, and Bet.

Simian foamy viruses (SFVs) are highly prevalent in nonhuman primate species (1–4), and human infections can occur due to cross-species transmission (5–14). Although there is no known disease associated with SFV, infectious virus can persist life long due to the stable integration of viral DNA in the host genome (15–18). Therefore, studying the biology and gene regulation of naturally occurring SFVs may provide insight regarding the potential of the virus for cross-species transmission and human infection. Humans have frequent exposure to rhesus macaques in nonhuman primate research centers and in natural habitats in Asia. To date, there is no full-length genome sequence for SFV from rhesus macaques.

SFVmmu_K3T was isolated from a rhesus macaque (*Macaca mulatta* K3T), which was obtained from a domestic breeding colony in Morgan Island, SC, USA. At the FDA facility, animals were housed singly and maintained in accordance with the Guide for the Care and Use of Laboratory Animals (19) under an approved protocol by the Institute Animal Care and Use Committee. Monkey peripheral blood mononuclear cells (PBMC) were prepared by the Ficoll-Hypaque method (20) and cocultured with *Mus dunni* cells until extensive cytopathic effect was seen due to viral replication (21). Filtered supernatant containing high reverse transcriptase (RT) activity (passage 3) was collected, and aliquots were stored at -80°C . Ten milliliters of the virus stock was concentrated by ultracentrifugation through a 20% sucrose cushion at $141,000 \times g$ for 2 h. The resuspended pellet was treated with DNase I to reduce host cell DNA, and nucleic acid was prepared using the QIAamp viral RNA minikit (Qiagen, Gaithersburg, MD, USA). High-throughput sequencing was done using the Illumina MiSeq version 3 system in the single-read mode (CD Genomics, Shirley, NY, USA).

Read trimming and assembly were done in our laboratory using the CLC Genomics Workbench software, version 10.0.1 (CLC bio, Denmark). The total number of reads was 1,878,772, and the average read length was 151 bases. The 12,983-bp complete viral genome sequence was obtained by mapping the raw reads (using default parameters) to SFVmcy-1/FV21, a full-length genome from a Taiwanese macaque (*Macaca cyclopis*), which was used as a reference genome (GenBank accession number X54482). The long terminal repeats (LTRs) were mapped separately to generate the full-length consensus genome sequence of SFVmmu_K3T. Open reading frames were identified (<https://www.ncbi.nlm.nih.gov/orffinder/>). The genomic structure of SFVmmu_K3T was similar to that

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of other SFVs encoding Gag, Pol, Env, Tas, and Bet. Nucleotide sequence analysis using NCBI BLASTN indicated 93% to 96% sequence identity with the partial sequences available for SFVs isolated from Asian rhesus macaques in the United States (22) and Bangladesh (23, 24). Additionally, a nucleotide sequence comparison with full-length SFVs of other macaque species indicated 93% identity with a Japanese macaque SFV (SFVmfu_WK1.pJM356 [25], GenBank accession number AB923518), 86% to 87% with Taiwanese macaque SFVs (SFVmcy-1/FV21 [26] and SFVmcy-2/FV34 [27], GenBank accession numbers X54482 and KF026286, respectively), and 85% with a cynomolgus macaque SFV (SFVmfa_Cy5061 [28], accession number LC094267). Biological studies are needed to investigate whether the genomic diversity is associated with differences in viral replication and transmission.

Accession number(s). The SFVmmu_K3T sequence was deposited in DDBJ/ENA/GenBank under accession number [MF280817](#).

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