




First Complete Genome Sequence of a Simian Foamy Virus Infecting the Neotropical Primate *Brachyteles arachnoides*

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ABSTRACT The complete genome sequence of a simian foamy virus infecting the neotropical primate *Brachyteles arachnoides* (SFVbar) was obtained using next-generation sequencing and genome walking. The full-length SFVbar genome is composed of 11,994 bp and shows a genomic organization similar to that of other neotropical SFVs.

Simian foamy viruses (SFV) naturally infect a wide diversity of nonhuman primates, including Old World primates (OWP) (1–3) and New World primates (NWP) (4–7) and can be transmitted to exposed humans, mainly through contact with saliva (8–15). Although no disease has been associated with SFV infection in natural hosts (16), a study of SFV-infected Cameroonian hunters evidenced mild to moderate hematological abnormalities (17). Humans exposed to NWP SFV were found positive by serological assays, but no viral sequence was detected (6, 18). While SFV was detected in a wide diversity of NWP (4, 5, 7), only four complete genome sequences of SFV from NWP are available (19–21). Novel NWP SFV sequences are useful for developing screening assays to study SFV infection in humans.

A saliva sample was collected from a *Brachyteles arachnoides* hosted at the Primate Center of Rio de Janeiro by following the national guidelines and provisions of Instituto Brasileiro do Meio Ambiente e dos Recursos Naturais Renováveis, Brazil, under permanent license number 11375-1, which included animal welfare standard operating procedures. The project was approved by the Ethics Committee on the Use of Animals of Universidade Federal do Rio de Janeiro (037/14). Nucleic acids (both DNA and RNA) were extracted from saliva using a QIAamp MinElute virus spin kit. Following reverse transcription-PCR (RT-PCR) and library preparation using the Nextera XT DNA library preparation kit (Illumina), deep sequencing was conducted using the Illumina MiSeq V2 600-cycle kit. FASTq reads were loaded in DNAnexus, and after removal of human and known microbial contaminant reads with the viral-ngs-human-depletion tool from the Broad Institute and trimming of low-quality reads using bbmap (Joint Genome Institute), *de novo* assembly was carried out using MEGAHIT version 0.3.3. Four contigs of 595, 826, 543, and 548 bp comprising 21 reads with lengths of >150 nucleotides (nt) mapped to a spider monkey foamy virus sequence (GenBank accession number EU010385). These contigs were used to design specific primers, and genome sequence walking was performed with Sanger sequencing to obtain the virus' complete genome using genomic DNA from saliva.

An 11,994-bp full-length genome of SFV infecting *B. arachnoides* was assembled. The virus was named SFVbar in accordance with the nomenclature recently published

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(22). The GenBank ORFfinder tool was used to determine the location and size of SFVbar open reading frames (ORFs). The genomic structure of SFVbar was similar to that of other foamy viruses (FV) (23), with ORFs encoding the essential proteins Gag, Pol, and Env and the accessory proteins Tas and Bet, flanked by two long terminal repeats. Additionally, the SFVbar sequence was aligned with the four NWP SFV genome sequences available from GenBank (SFV_{sxa}, accession number [KP143760](#); SFV_{cja}, accession number [GU356395](#); SFV_{asp}, accession number [EU010385](#); and SFV_{spp}, accession number [GU356394](#)) using MUSCLE in MEGA version 7.021. A phylogenetic tree inferred using the neighbor-joining method, the Kimura 2-p model, and 1,000 bootstrap replicates grouped SFVbar with SFV_{asp}, both infecting NWP species of the Atelidae family. These findings corroborate the FV-host cospeciation hypothesis (24). A nucleotide sequence comparison using the pairwise distance tool of MEGA showed that SFVbar is more similar to SFV_{asp} in the *pol* gene (75.7% sequence identity) but less in *env* (68.8%) and in *gag* (55.8%).

Data availability. The SFVbar genome sequence was deposited in DDBJ/ENA/GenBank under accession number [MH368762](#).

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