Genome Sequence of a Novel Archaeal Fusellovirus Assembled from the Metagenome of a Mexican Hot Spring
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Members of the *Fuselloviridae* family from the crenarchaeal order *Sulfolobales* have been characterized, and they are abundant in extreme geothermal environments (1, 2). They carry circular double-stranded DNA (dsDNA) genomes and exhibit spindle-shaped morphologies. Here, we report the consensus genome sequence of a novel fusellovirus recovered from aqueous sediments from Los Azufres, Mexico.

Samples were collected from a hot spring with a pH of 3.6 and a temperature of 65°C. DNA was purified using the UltraClean microbial and the UltraClean Mega soil DNA kits (MoBio Laboratories, Inc., Carlsbad, CA). Sequencing was performed on an Illumina GAIIx platform, producing 36-bp paired-end reads with 300-bp inserts representing 216 Mb. Reads were assembled using Velvet 1.2.07 (3). A set of contigs were predicted by BLASTX searches to be of fuselloviral origin. Gaps were closed iteratively by mapping and reassembling reads to these contigs using Maq. The average sequence coverage of the 14,847-bp circular dsDNA genome was 1,257-fold. We detected 57 candidate single nucleotide polymorphisms by Maq. The G+C content was 45.43%, higher than the 37.5 to 39.7% content of other fuselloviral genomes (1, 2, 7–9).

The genome has a strong coding-strand bias, not previously seen for fuselloviruses, with only the ubiquitous fuselloviral integrase encoded on one strand. The genome organization is also exceptional for fuselloviruses. The SMF1 genome shows exceptional properties, including a coding-strand bias and a high incidence of genes organized in operon structures, but nevertheless, it retains a large set of conserved fusellovirus genes, which lends further support to the exchange of genetic material over intercontinental distances (2, 10).

In conclusion, the SMF1 genome was recovered from a site widely separated geographically from the locations of other sequenced fuselloviruses. The SMF1 genome shows exceptional properties, including a coding-strand bias and a high incidence of genes organized in operon structures, but nevertheless, it retains a large set of conserved fusellovirus genes, which lends further support to the exchange of genetic material over intercontinental distances (2, 10).

**Nucleotide sequence accession number.** The genome sequence was deposited in GenBank under the accession no. KC618393.

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