Genome Sequence of a Novel Archaeal Fusellovirus Assembled from the Metagenome of a Mexican Hot Spring
Servin-Garciduenas, L. E.; Peng, Xu; Garrett, Roger Antony; Martinez-Romero, E.

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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 G+C content was 45.43%, higher than the 37.5 to 39.7% content of other fuselloviruses. The SMF1 genome shows exceptional coding-strand bias and a reduced set of fuselloviral core genes.

The genome has a strong coding-strand bias, not previously seen for fuselloviruses, with only the ubiquitous fuselloviral integrase encoded on one strand. The gene organization is also exceptional for fuselloviruses, with a high incidence of genes arranged in operons, which are also likely to encode cofunctional proteins.

Twenty-four genes were predicted, 22 of which are arranged in five operons. Fourteen genes have putative fuselloviral homologs, consistent with SMF1 being a member of the *Fuselloviridae* family. Most gene products show 30 to 70% amino acid sequence similarity to the best fuselloviral matches. Previous studies identified thirteen genes conserved in all fusellovirus genomes (2), and nine of these were localized in a “core” genomic region of SMF1. The core genes encode a DnaA-like protein, the integrase, one VP1-like structural protein, a putative helix-turn-helix (HTH) transcriptional regulator, and five proteins with unknown functions.

Five additional putative gene products shared with other fuselloviruses include a second VP1-like protein, a VP2-like structural protein, a putative end-filament protein, a regulatory protein, and a hypothetical protein. Three further nonconserved ORF products showed sequence similarities to putative regulatory proteins.

The host of SMF1 is likely to be a member of the order *Sulfolobales*. Fuselloviruses can replicate in both *Acidianus* and *Sulfolobus* species of the order *Sulfolobales* (2), and they are predicted to have an extended host range that may include as-yet-uncultured species (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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