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Whole-Genome Sequence of the *Spodoptera frugiperda* Sf9 Insect Cell Line

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ABSTRACT The draft whole-genome sequence of the *Spodoptera frugiperda* Sf9 insect cell line was obtained using long-read PacBio sequence technology and Canu assembly. The final assembled genome consisted of 451 Mbp in 4,577 contigs, with 12,716× mean coverage and a G+C content of 36.53%.

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Spodoptera frugiperda cell lines and their derivatives are used to produce a variety of baculovirus-expressed biological products. The Sf9 cell line is known to produce low-level reverse transcriptase (RT) activity (1, 2), which might be associated with particles. Additionally, other endogenous viral genes related to a rhabdovirus (3) are also present in the Sf9 DNA (4). The availability of the Sf9 genome sequence can help identify and characterize endogenous viral sequences of interest and aid in chromosomal mapping and investigating factors regulating their expression. This paper presents a draft of the whole-genome sequence of the Sf9 cell line, which was obtained from American Type Culture Collection (CRL-1711, lot number 58078522; ATCC, Manassas, VA). The Sf9 cell line was cloned from the parent Sf21 cell line (IPLB-Sf-21-AE), which was derived from pupal ovarian tissue of the fall armyworm (*Spodoptera frugiperda*) (5).

Total cell DNA was extracted from Sf9 cells using the Qiagen Gentra Puregene cell kit (Qiagen, Gaithersburg, MD). The library was prepared by shearing DNA using g-TUBES (Covaris, Inc., Woburn, MA), targeting an average fragment size of 20 kb, and sequencing was done on the RSII (Pacific Biosciences, Menlo Park, CA) at the Institute for Genomic Sciences (University of Maryland, Baltimore, MD). The SMRTbell template preparation kit (Pacific Biosciences) was used to ligate hairpin adapters required for sequencing to the fragmented DNA. The library was size selected using BluePippin (Sage Science, Beverly, MA) and sequenced using PacBio's P6-C4 chemistry using 240-min movies. The total raw data generated was 47×. Reads were trimmed, corrected, and assembled using the Canu assembler version 1.2 (6). The final assembled genome consisted of 451 Mbp in 4,577 contigs, with 12.7× mean coverage. The largest contig size was 3,055,912 bp. Scaffolds (2,396) were generated using SSPACE-LongRead (7). The N_{50} of the contigs was 250,325 bases, and the N_{50} of the scaffolds was 606,288 bases. The G+C content of the Sf9 genome was 36.53%. The size of the Sf9 genome was in the range expected of lepidopteran genomes; however, it was larger than that of the Sf21 cell line (385 Mbp), which was obtained using Illumina short-read sequence technology (8).

Repeat elements were identified in Sf9 scaffolds using Repeat Masker version 4.0.7 (http://www.repeatmasker.org/) using Arthropoda as the query species, with default parameters. There were 4,096 retroelements, which consisted of non-LTR elements and LTR elements (0.98% of the genome) and 390 DNA transposons (0.03%). Additional retrovirus-related and other endogenous viral sequences will be identified using BLAST (9) and HMMER (10) searches against available virus and repeat family databases.

Furthermore, analysis is ongoing to predict chromosomal location and gene annotation.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. NJHR00000000. The version described in this paper is version NJHR01000000.

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