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GENOME SEQUENCES

Complete Genome Sequence of an Alphabaculovirus from the Southern Armyworm, *Spodoptera eridania*

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ABSTRACT We report the complete genome sequence of a baculovirus from the moth *Spodoptera eridania*, the southern armyworm. The genome sequence is 149,090 bp and exhibits the greatest degree of sequence similarity with genomes from alphabaculoviruses isolated from other moths of the genus *Spodoptera*.

The southern armyworm, *Spodoptera eridania* (*Lepidoptera*: *Noctuidae*), is found in Central and South America and the southeastern United States (1). The larvae of this moth are defoliating pests that attack a broad range of vegetable, fruit, and ornamental crops. Genome sequences have been reported for baculoviruses from other moth species of the genus *Spodoptera*, including *S. exigua* (2), *S. frugiperda* (3), *S. litura* (4), and *S. littoralis* (5). To date, there has been no published description of a baculovirus from *S. eridania*.

An isolate of a *S. eridania* baculovirus, *Spodoptera eridania* nucleopolyhedrovirus-251 (SperNPV-251), had been provided by Howard R. Bullock (U.S. Department of Agriculture-Agricultural Research Service [USDA-ARS]) and deposited in an insect virus collection at the USDA-ARS Insect Biocontrol Laboratory in Beltsville, Maryland, in October 1974. The isolate deposit consists of viral occlusion bodies that were suspended and lyophilized in a lactose solution. To characterize this virus's genome and its relationships to other *Spodoptera* spp. baculoviruses, viral DNA was isolated from the lyophilized material by solubilizing occlusion bodies in 0.1 M Na_2CO_3, pelleting occluded virions by centrifugation through a 25% wt/wt sucrose pad, and extracting DNA from the purified virions using previously described procedures (6). Viral DNA (100 ng) was used to construct a library with the QIAseq FX DNA library kit, and the library was sequenced on an Illumina MiSeq system using a MiSeq reagent kit v. 2 (300 cycles). Quality end trimming and assembly of sequencing reads were performed with DNASTAR Lasergene SeqMan NGen v. 14 using default parameters.

From an initial 2,012,800 generated reads, 1,696,216 reads with an average length of 154 bp were assembled into an initial contig with overlapping termini, indicating that the complete circular genome was obtained. The initial contig was edited into a final contig of 149,090 bp with a coverage of 1,755×. The first nucleotide was set at the start codon adenine of the polyhedrin (*polh*) open reading frame (ORF). The genome possessed a 45% G+C nucleotide distribution. ORFs were annotated if they were identified as homologs of previously identified baculovirus ORFs with BLASTx, as implemented in DNASTAR Lasergene GeneQuest v. 14. Additional ORFs with no sequence similarity to other baculovirus ORFs were annotated if they were 50 or more codons, predicted to encode proteins with both the fgenesV (http://linux1.softberry.com/berry.phtml) and GeneMarkS (7) algorithms, and did not overlap larger ORFs by more than 75 bp. There were 146 ORFs annotated by these criteria, including ORFs for the 38 core genes of *Baculoviridae* (8, 9). In addition, three homologous regions (*hr*), putative origins of baculovirus DNA replication (10), were detected using Tandem

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Repeats Finder (11). These *hrs* contained multiple copies of a conserved 72-bp direct repeat.

BLAST queries with the amino acid sequences of translated ORFs indicated that SperNPV-251 was most closely related to the unclassified baculovirus isolate *Spodoptera litura* nucleopolyhedrovirus-II (SpltNPV-II, GenBank accession number EU780426). A Martinez/Needleman-Wunsch alignment of the SperNPV-251 and SpltNPV-II genomes, carried out with Lasergene MegAlign using default parameters, indicated that they share 94.7% sequence identity, with 767 gaps inserted to optimize the alignment. Alignment of the SperNPV-251 sequence with the genome sequences of *Spodoptera exigua* nucleopolyhedrovirus-US1 (2) and *Spodoptera frugiperda* multiple nucleopolyhedrovirus-3AP2 (3) yielded sequence identities of 78.9% (with 2,043 gaps) and 70.2% (with 2,809 gaps), respectively. Pairwise comparisons with *Spodoptera litura* nucleopolyhedrovirus and *Spodoptera littoralis* nucleopolyhedrovirus genomes (4, 5) were characterized by lower sequence identities and genomic inversions.

Data availability. The sequence reads generated for this study are available at the NCBI Sequence Read Archive under BioProject number PRJNA505607. The assembled and annotated genome sequence for this baculovirus was deposited in GenBank under the accession number MH320559.

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