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GENOME SEQUENCES

Draft Genome Assembly of the Entomopathogenic Bacterium *Photorhabdus luminescens* subsp. *sonorensis* Caborca

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ABSTRACT *Photorhabdus luminescens* subsp. *sonorensis* strain Caborca is an entomopathogenic bacterium with a dual lifestyle, namely, as a mutualist of the *Heterorhabditis sonorensis* nematode and a pathogen to a wide range of insect species. The genome assembly, in 231 contigs, is 5.2 Mbp long and includes 25 putative gene clusters for secondary metabolism.

Photorhabdus luminescens subsp. *sonorensis* strain Caborca is the symbiont of the entomopathogenic nematode *Heterorhabditis sonorensis*, a native species from Caborca, Sonora State, Mexico (1). *P. luminescens* subsp. *sonorensis* and *H. sonorensis* form an insecticidal partnership that targets a wide range of insect hosts (2). Upon death, the insect cadaver serves as a suitable environment that enables the nematodes to mature and reproduce. *P. luminescens* subsp. *sonorensis* produces a variety of toxins and secondary metabolites with diverse antimicrobial properties. Mass spectrometry analysis of crude extracts of *P. luminescens* subsp. *sonorensis* cultures revealed 15 distinct compounds (3), 8 of which are unique compared with those of other *Photorhabdus* spp. These findings prompted further efforts to investigate this bacterium for potential applications in agriculture and medicine.

Two rounds of genome sequencing using the Ion Torrent next-generation sequencing technology were conducted. In the first round, genomic DNA (gDNA) was isolated from overnight cultures grown in Luria-Bertani medium inoculated from a primary phase colony, using the Thermo Scientific genomic DNA purification kit for bacterial gDNA isolation. The recovered gDNA was resuspended in 100 μl nuclease-free water and sequenced with Ion Torrent technology with a 200-bp chemistry on a 314 chip at the University of Arizona Genetics Core (UAGC). In the second round, gDNA was extracted from an identical culture using phenol/chloroform/isoamyl alcohol (25:24:1), followed by ethanol precipitation, and sequenced at the Pennsylvania Genomic Analysis Core (University of Pennsylvania) with Ion Torrent technology on an Ion S5 system with a 540 chip.

Raw sequencing data were checked for quality prior to trimming to ensure high-quality data for the assembly process using Sickle 1.0 (4) (quality threshold, 20; min length, 50) and Trimmomatic-programmable 0.36 (5) (LEADING, 25; TRAILING, 25; MINLEN, 50) launched from the University of Arizona Cyverse Discovery Environment (https://de.cyverse.org/de/). The quality of data was analyzed using FastQC 0.11.5 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/), also launched from the Cyverse Discovery Environment. *De novo* assembly was completed using the Geneious 11.1.5 software (https://www.geneious.com) with the plugin assembler SPAdes 3.10.0 (6) with different k-mer sizes to select the best assembly. The quality of the assemblies was assessed using QUAST (7). Table 1 displays a summary of the best assembly from each data set.

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TABLE 1 Summary of the assemblies from different data sets

Feature	Value for data set(s):		
	First	Second	Combined
No. of raw reads	395,197	7,801,769	8,196,966
No. of trimmed reads	314,277	6,288,858	6,603,135
No. of contigs	509	263	231
Length of contigs (bp)	135–70,803	202–262,598	202–431,332
G+C content (%)	42.4	42.5	42.5
Avg coverage (×)	9.4	252.2	272.0
Total length (bp)	5,145,620	5,216,436	5,225,282
N_{50} (bp)	19,121	70,534	88,967
L_{50}	82	19	16

The assembled genome from the combined data set was annotated with the NCBI Prokaryotic Genome Annotation Pipeline (8), resulting in the identification of a total of 4,657 genes, including 4,132 protein-coding sequences, 109 RNA-coding genes, 416 pseudogenes, and 7 to 13 partial rRNA sets. antiSMASH (9) analysis predicted 25 gene clusters that are potentially involved in secondary metabolism, including that for the canonical compound isopropylstilbene, which is produced by many *Photorhabdus* spp. (10), as well as those for novel compounds that await to be identified and tested for their antimicrobial properties.

Data availability. The raw reads have been deposited in the NCBI SRA under the accession no. SRS4934682. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. SBIJ00000000. The version described in this paper is the first version, SBIJ01000000.

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