Genome Sequence Data of *Bacillus* sp. Strain LP16S, Which Is Capable of Inhibiting the Growth of Multiple Sorghum Fungal Pathogens

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Funding

This work was supported by the United States Department of Agriculture Current Research Information System project number 3091-22000-034-00D and Department of Energy grant award #DE-SC0014172.

Genome Announcement

Biological control by numerous *Bacillus* strains is well-established. Here, we present the genome of a *Bacillus* sp. strain, LP16S, capable of suppressing the propagation of several fungal pathogens of sorghum, a grain of worldwide significance. The information will contribute to decoding the biocontrol mechanism.

Bacillus species are gram-positive prokaryotes that include disease and biocontrol agents (Cawoy et al. 2015; Islam et al. 2012; Oyedele and Ogunbanwo 2014; Thakaew and Niamsup 2013). *Bacillus thuringiensis* encode Bt toxins that are used for biocontrol. The Bt toxins have previously been successfully engineered into agricultural crops for protection against insect pests (Palma et al. 2014). Recently, we showed that *Bacillus* sp. strain LP16S is capable of inhibiting both mycelial growth and sporulation of several significant fungal pathogens (*Colletotrichum*, *Bipolaris*, *Curvularia*, and *Fusarium* sp.) of sorghum (*Sorghum bicolor*) (Prom et al. 2017). Globally, sorghum is the fifth most important cereal with multiple uses; as a result, identification of potent nonsynthetic chemical agents that control its microbial infection is vital (Frederiksen and Odvody 2000; Ngugi et al. 2002; Thakur et al. 2007). The presented annotated whole-genome sequence of strain LP16S was generated to provide insight on the associated genes used by the bacterial strain to either inhibit or minimize the growth of sorghum pathogens.

Strain LP16S was isolated from panicles harvested from sorghum plants grown at the Texas A&M University AgriLife Research Farm in Burleson County, Texas. Seeds from the threshed sorghum panicles were placed in Petri dishes containing half strength potato dextrose agar (1/2 PDA) (Beckson Dickinson, Sparks, MD, U.S.A.). After 7 days of incubation at 27°C, fungal colonies within a plate were separated by a clear zone. The prokaryote responsible for the zone of fungal inhibition was subcultured, purified, and stored. Purified bacterial cultures were routinely propagated at 27°C on 1/2 PDA plates and were putatively identified as a *Bacillus* sp. using 16S ribosomal DNA sequence analysis (Prom et al. 2017). Genomic DNA was extracted using a Qiagen DNeasy kit (Valencia, CA, U.S.A.) according to manufacturer instructions. Following the strategy described by Medrano et al. (2014), a comprehensive draft whole-genome sequence of strain LP16S was generated with a Roche 454

Keywords

bacterial pathogenesis, *Bacillus* sp. strain LP16S, biocontrol, sorghum

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The author(s) declare no conflict of interest.

Accepted for publication 16 November 2021.

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GS-Junior. A Roche Titanium shotgun library was prepared, and three runs were conducted, resulting in over 145.3.4 Mb calculated from 32.4 Mb (105,134 reads, average length 433 bases), 44.9 Mb (138,847 reads, average length 438 bases), and 68.0 Mb (297,758 reads, average length 703 bases). Employing the same genomic DNA stock, a 3-kb paired-end Titanium library was constructed and was twice pyrosequenced, producing 35 Mb (157,540 reads with 20,292 paired reads) and 32 Mb (144,456 reads with 18,654 paired reads).

In addition, Illumina sequencing was conducted at Medgenome (Foster City, CA, U.S.A.) on a contract basis. MiSeq v2 sequencing using a 2 × 150 bp read strategy (300 cycle kit) generated 19 million total reads per sample (9.5 million paired reads) with a mean read length of 151 bp. Using FastQC v0.119, read quality was assessed. The Trimmomatic v0.36 program was employed to discard ends of the Illumina reads and remove the adaptors. The mean read quality had a Phred score of 37.3 and contigs were assembled into scaffolds as described below. The Roche and Illumina data were used concurrently to construct the genome, using the GS De Novo Assembler 454 v2.7 and CLC Genomics Workbench Linux platform v3.5, generating scaffolds equaling 3.2 Mb ($N_{50} = 195,288$ bp). Putative coding sequences were identified with the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline-4.13 program (Li et al. 2021) and were manually curated.

Predicted coding DNA sequences totaled 3,070 with 23 ribosomal RNA operons and 19 transfer RNAs. The GC content was 46.2% for the chromosome (around 4 Mb) with 100× coverage. Putative antifungal agents identified included fusaricidin synthetase, surfactin synthetase, bacillomycin, and mycosubtilin. Using the methods described by Ciufu et al. (2018), an average nucleotide identity (ANI) test that compared the LP16S genome to genomes of both type and proxy type strains was conducted. Results of the analysis best characterized the LP16S strain as *B. velezensis* with an ANI of 99.117% when compared with the *B. velezensis* type strain LMG 22478. Although other *B. velezensis* strains have been sequenced (Choi et al. 2021; Liu et al. 2021; Nifakos et al. 2021), this is the first to both be isolated from sorghum and demonstrated to inhibit pathogens of this cereal plant.

Data Availability

Raw sequencing data were deposited in the NCBI Sequence Read Archive database under accession number SRX5801078. This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number SSKM00000000.1.

Acknowledgments

Thanks are due to R. M. Hernandez and Y. Hara for technical assistance in sequencing. R. Ramirez was critical to the manual annotation of the genome.

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