

Genome Sequence of *Brevibacillus laterosporus* Strain GI-9

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We report the 5.18-Mb genome sequence of *Brevibacillus laterosporus* strain GI-9, isolated from a subsurface soil sample during a screen for novel strains producing antimicrobial compounds. The draft genome of this strain will aid in biotechnological exploitation and comparative genomics of *Brevibacillus laterosporus* strains.

Brevibacillus laterosporus is a unique species of the genus *Brevibacillus* because of its characteristic physiology, spore formation, and ecology and its use as a biocontrol agent (2, 6, 7). The strain GI-9 was isolated from a subsurface soil sample obtained from a farmland in Chandigarh, located in northern India. This strain was identified during a screen for bacteria displaying antimicrobial activities. The presence of endospores, the phenotypic properties of the strain, and 16S rRNA gene sequence BLAST analysis (GenBank accession no. [FR686596](#)) assigned strain GI-9 to the genus *Brevibacillus*. It has high similarity (99%) to *Brevibacillus laterosporus* DSM25, the type strain. However, it shows differences in phenotypic properties, including growth at 50°C, a positive reaction in the Voges-Proskauer test, and urea hydrolysis, compared to *B. laterosporus*.

To gain further insights into its phylogeny and taxonomy and to study the genomic determinants of its useful activities, we sequenced the genome of GI-9 using the Roche 454 GS (FLX Titanium) pyrosequencing platform (Macrogen, Seoul, Republic of Korea). The shotgun sequencing yielded 764,215 reads, amounting to 308,006,351 bases and ~61-fold coverage. The GS de novo assembler (version 2.6) yielded 61 contigs (over 500 bp) with an average contig size of 84.995 kb and a largest contig of 512.124 kb. The proportion of Q40+ bases (bases with a quality score of 40 or above) was 99.97%. The genome of strain GI-9 has a G+C content of 40.8% and annotation using the RAST (Rapid Annotation using Subsystem Technology) pipeline (5), RNAmmer 1.2 (4) with further manual inspection revealed 4,775 predicted coding regions (CDSs) and 101 tRNA and 3 rRNA genes.

Earlier diversity studies failed to identify variation in a collection of *Brevibacillus laterosporus* strains (1, 7). In our case, strain GI-9 was isolated from a unique location (subsurface soil) and is of Indian origin. The genome of GI-9, along with the already available genome of another of *Brevibacillus laterosporus* strain, LMG 15441, a pathogen of invertebrates (3), will help in mapping the genetic determinants of its valuable properties and also identify-

ing molecular markers in diverse strains for their systematic exploitation in agriculture and medicine.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at EMBL under accession numbers [CAGD01000001](#) to [CAGD01000061](#).

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