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Draft Genome Sequence of *Brevibacillus brevis* DZQ7, a Plant Growth-Promoting Rhizobacterium with Broad-Spectrum Antimicrobial Activity

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***Brevibacillus brevis* DZQ7 is a plant growth-promoting rhizobacterium (PGPR) isolated from tobacco rhizosphere. Here, we report the draft genome sequence of *B. brevis* DZQ7. Several functional genes related to antimicrobial activity were identified in the genome.**

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Brevibacillus brevis (formerly *Bacillus brevis*), the type species of *Brevibacillus*, is considered a plant growth-promoting rhizobacterium (PGPR) (1–3) and organic pollutant degradation strain (4, 5). *B. brevis* is widespread in the soil and sediment, and it has been widely used in agriculture and environmental remediation because of its multiple potential functions (6, 7). *B. brevis* DZQ7 was isolated from the soil of tobacco rhizosphere in Guizhou, China. It showed broad-spectrum antimicrobial activity to pathogens of soilborne plant diseases, such as *Ralstonia solanacearum*, *Phytophthora nicotianae*, and *Fusarium* spp., and has been widely used in biological control of soilborne plant diseases.

Here, we report the draft genome sequence of *B. brevis* DZQ7. Genomic DNA was extracted and sequenced using the Illumina HiSeq 2500 platform. The whole-genome shotgun sequencing produced 1,243,319 paired-end reads with an average insert size of 500 bp (over 96-fold coverage). Another mate-paired (MP) library containing 5-kb inserts was constructed, and 5,041,325 paired-end reads (read length, 125 bp) were produced. The filtered reads were assembled by SOAPdenovo (8, 9) (http://soap.genomics.org.cn/soapdenovo.html) to generate scaffolds. All reads were used for further gap closure. Final assembly consisted of 3 scaffolds (length, $\geq$500 bp) with an N_{50} length of 6,158,809 bp, average length of 2,144,406 bp, and largest length of 6,158,809 bp. The genome sequence was annotated using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The genome consists of 6.43 Mb, with a G+C content of 47.42%, which is similar to those of *B. brevis* NBRC 100599 (47.3%) (NCBI reference sequence NC_012491), *B. brevis* FJAT-0809-GLX (47.3%) (GenBank accession no. AHKL00000000), and *B. brevis* X23 (46.8%) (GenBank accession no. AKYF00000000). A total of 5,762 coding sequences (CDS), 44 pseudogenes, 120 tRNA genes, and 29 rRNA genes were identified. As expected, many of the genes involved in the antimicrobial activity of *B. brevis* DZQ7 were identified in the genome, such as tyrocidine-synthetic gene, bacteriocin-synthetic gene, fusaricidin-synthetic gene, polyketide-synthetic (PKS) gene, chalcone-synthetic gene, nonribosomal peptide synthetic (NRPS) gene, and chitinase gene, and so on. In addition, *B. brevis* DZQ7 possesses genes with likely relevance to the degradation of organic pollutants, such as the phenylacetic acid degradation, phenylacetate degradation, and ethyl tert-butyl ether degradation genes.

The genome sequence of *B. brevis* DZQ7 and its curated annotation provides deeper insights into understanding the antimicrobial mechanism of *B. brevis*, which is critical for the development of a genetically engineered biocontrol agent. Also, it provides abundant genetic information regarding useful functions in bioremediation.

Nucleotide sequence accession numbers. The whole-genome shotgun project of *B. brevis* DZQ7 has been deposited in DDBJ/ENA/GenBank under the accession number LDZV00000000. The version described in this paper is the first version, LDZV00000000.1.

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