



Draft Genome Sequence of *Bacillus velezensis* Lzh-a42, a Plant Growth-Promoting Rhizobacterium Isolated from Tomato Rhizosphere

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ABSTRACT The plant growth-promoting rhizobacterium *Bacillus velezensis* strain Lzh-a42, which has antimicrobial activity, was isolated from tomato rhizosphere. Here, we report its genome sequence, which includes several predicted functional genes related to secondary metabolite biosynthesis, antimicrobial activity, and bio-film synthesis.

Bacteria associated with the rhizosphere are generally referred to as plant growth-promoting rhizobacteria (PGPRs) (1). Various bacterial species have been reported as PGPRs, including some *Bacillus* species (2). For example, *B. velezensis* is a widespread PGPR in rhizosphere soil, and it was reported that *B. velezensis* G341 could secrete bacillomycin L and fengycin A with antifungal activity (3). *B. velezensis* ZJ20 (4), *B. velezensis* YJ11-1-4 (5), *B. velezensis* GQJK49 (6), and *B. velezensis* 2A-2B (7) were also found to exert antifungal effects on plant-pathogenic fungi.

B. velezensis strain Lzh-a42 was isolated from tomato rhizosphere soil samples from the city of Dezhou, Shandong Province, China. This PGPR strain had antimicrobial activity toward some plant pathogens, including *Fusarium moniliforme*.

From this study, we report the draft genome sequence of *B. velezensis* Lzh-a42. Whole-genome DNA was extracted and then sequenced using the PacBio and Illumina MiSeq systems, respectively. The raw data were filtered and assembled with SPAdes version 3.9.0 (8) and A5-miseq version 20150522 (9), which generated 1,237 Mb of total clean data with a genome coverage of 278.0×. Two scaffolds were finally obtained, and the total length of the genome was 4,246,605 bp, with a GC content of 45.99%, which is similar to those of *B. velezensis* subsp. *plantarum* YAU B9601-Y2 (99%) (GenBank accession no. HE774679), *B. velezensis* Y2 (99%) (CP003332), and *B. velezensis* CN026 (99%) (CP024897).

A total of 4,402 open reading frames, 4,074 functional genes, 86 tRNAs, and 27 rRNAs were predicted in the genome of *B. velezensis* Lzh-a42. Moreover, 2,888 of the 4,074 genes (70.9%) were classified into 22 classes of Clusters of Orthologous Groups of proteins (COG) functional categories, and 118 genes (including 19 polyketide synthases and 10 nonribosomal peptide synthetases) were predicted to be involved in secondary metabolism biosynthesis and catabolism. Gene clusters for synthesizing secondary metabolism with antagonistic action were also found in the genome. For example, there were genes coding for the antibiotics bacilysin (*bacABCDE*; CXP43_RS19760 to CXP43_RS19740) (10), fengycin (*fenEDCBA*; CXP43_RS10610 to CXP43_RS10630) (11), bacillomycin (*bmyCBAD*; CXP43_RS10480 to CXP43_RS10495) (12), and surfactin (*srfAACD*; CXP43_RS01800 to CXP43_RS01810) (11). Genes coding for the

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antibacterial polyketides bacillaene (CXP43_RS08875 to CXP43_RS08920) (13) and diffridin (CXP43_RS12585 to CXP43_RS12655) (12) were also predicted.

B. velezensis Lzh-a42 also possesses the ability to synthesize biofilm. The genes for biofilm synthesis (14), including *tapA* (CXP43_RS13100), *sipW* (CXP43_RS13095), *tasA* (CXP43_RS13090) operon, *bslA* (CXP43_RS15835), and *epsABCDE* (CXP43_RS18010 to CXP43_RS18030) were identified, as were their regulators, Spo0A (GenPept accession no. WP_003153177), SinR (WP_003153104), and SlrR (WP_007407395).

The genome sequence of *B. velezensis* Lzh-a42 presented here will help us to understand the strain's mechanisms for antimicrobial activity and biofilm synthesis and its potential use as a biocontrol agent for disease management and enhancing agricultural productivity.

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession no. [CP025308](#).

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