Complete Genome Sequence of the Endophytic Biocontrol Strain *Bacillus velezensis* CC09

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Bacillus velezensis is a heterotypic synonym of *B. methylotrophicus*, *B. amyloliquefaciens* subsp. *plantarum*, and *Bacillus oryzicola*, and has been used to control plant fungal diseases. In order to fully understand the genetic basis of antimicrobial capacities, we did a complete genome sequencing of the endophytic *B. velezensis* strain CC09. Genes tightly associated with biocontrol ability, including nonribosomal peptide synthetases, polyketide synthetases, iron acquisition, colonization, and volatile organic compound synthesis were identified in the genome.

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*B*acillus velezensis was first described by Wang et al. in 2008 (1) as a heterotypic synonym of *B. amyloliquefaciens*. Recently, *B. methylotrophicus*, *B. amyloliquefaciens* subsp. *plantarum*, and *B. oryzicola* were reclassified as heterotypic synonyms of *B. velezensis* based on comparative genomics and DNA-DNA relatedness calculations (2). The distinctive characteristics of *B. velezensis* include methanol utilization, plant-growth promotion, biocontrol of phytopathogens, and induced systemic resistance of the host (2–4). Many *B. velezensis* strains are used as plant-growth promoters and antagonists of plant pathogens in agriculture performances, and some of them have already been commercialized for increasing crop yield (2, 5–7).

B. velezensis CC09 was isolated from *Cinnamomum camphora* leaf tissue, which can be used to improve plant growth and prevent fungal diseases in plants caused by *Glomerella glycines*, *Rhizoctonia solani*, and *Alternaria alternate* by producing bioactive compounds (8, 9). Here, we report the complete genome of strain CC09, to better understand the expression, regulation, and transportation of proteins related to iturin A biosynthesis and the properties of other biocontrol behaviors.

Genomic DNA was extracted using the DNAiso reagent kit (TaKaRa, Japan), and a 250-bp paired-end insert library was sequenced on an Illumina MiSeq platform. The sequences were quality-filtered, resulting in 393 Mbp comprising 1,572,192 high-quality reads and representing a 94-fold coverage of the genome. The high-quality reads were then assembled by SPAdes assembler (10) to generate 20 contigs (≥500 bp; total length, 4,134,483 bp; N_{50} length, 690,639 bp). The obtained contigs were ordered into a draft genome with gaps (11), which was further defined by high-fidelity PCR (TaKaRa Prime STAR) to construct the complete genome. The genome size was 4,167,153 bp with an average GC content of 46.1%. A total of 4,021 coding sequences (CDSs) and 97 structural RNAs (73 tRNAs) were predicted by rapid annotation using PGAAP (genomes at http://ncbi.nlm.nih.gov) (12). Among the CDSs, 3,882 (96.54% of total) were protein-coding sequences,

of which 2,143 (53.29%) were distributed over 26 functional gene categories in RAST (13).

Moreover, a total of 340.05 kb CDSs in the genome of CC09 (8.2% of the genome) encoding the proteins responsible for the synthesis of polyketide and nonribosomal peptides such as surfactin, iturin A, fengycin, bacillibactin, as well as genes associated with iron acquisition, colonization, and volatile organic compounds synthesis, which play important roles in the biocontrol processes of biocontrol agents like *B. velezensis* (2–4), were found in the genome of CC09. Without a doubt, these genome features make the endophytic strain CC09 an excellent candidate for biocontrol agents.

Accession number(s). This complete genome has been deposited at GenBank under the accession number CP015443. The strain has been deposited at the China Center of Industrial Culture Collection under the accession number CICC 24093.

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