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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Bacillus endophyticus* 2102

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***Bacillus endophyticus* 2102 is an endospore-forming, plant growth-promoting rhizobacterium isolated from a hypersaline pond in South Korea. Here we present the draft sequence of *B. endophyticus* 2102, which is of interest because of its potential use in the industrial production of algaecides and bioplastics and for the treatment of industrial textile effluents.**

Bacillus endophyticus was first isolated from the inner tissues of cotton plants (8). The randomly amplified polymorphic DNA pattern of *B. endophyticus* differs from that of other bacilli commonly isolated from plant tissues (8). *B. endophyticus* is an aerobic, Gram-positive, nonmotile, rod-shaped, endospore-forming bacterium (8). Multiple *Bacillus* species have been identified as plant growth-promoting rhizobacteria (PGPR) that promote growth by producing antibiotics, inhibiting plant ethylene synthesis, and inducing plant systemic resistance to pathogens (3, 4). However, *B. endophyticus* UCMB 5715^T, which inhibits the growth of *Alternaria brassicae*, does not protect oilseed rape against pathogens such as *A. brassicae*, *Botrytis cinerea*, *Leptosphaeria maculans*, and *Verticillium longisporum*, indicating that it produces antibiotic substances that are different from the algaecide bacillamide A, B, and C produced by *B. endophyticus* (2, 10). Recently, the fact that *B. endophyticus* strains produce copolymers of polyhydroxybutyrate and polyhydroxyvalerate was also highlighted (6); it was also able to decolorize textile effluents, a function applicable to the control of water pollution (7). Thus, *B. endophyticus* is of interest not only as a PGPR but also as a potential industrial microorganism; this led us to sequence the whole genome of this microorganism.

Genome sequencing was performed using an Illumina HiSeq 2000 system (101-nucleotide paired-end read sequencing from a 500-bp genomic library). Preprocessing of reads and *de novo* assembly were performed using the CLC Genomics Workbench version 4.8. We assembled 34,352,786 reads (achieving ~663-fold coverage [3.39 Gb]) into 54 contigs of >200 bp. The total contig length, average contig length, and N50 were 5,107,189 bp, 94,577.6 bp, and 446,113 bp, respectively (36.4% G+C). The draft genome sequence was subjected to automated annotation using the RAST server (1). A total of 5,186 putative protein-coding sequences were predicted, 43% of which were assigned a subsystem. While the *B. endophyticus* type strain was reported to be closest to *B. smithii* DSM 4216^T (8), RAST analysis suggested that *B. megaterium* DSM319 was actually the closest neighbor in terms of sequence similarity. Average nucleotide identity analysis using BLAST showed that, of all of the related *Bacillus* species, *B. megaterium* QM B1551 was closest to strain 2102 (70.9% sequence identity and 31.3% alignment when strain 2102 draft sequences were used as the query) (9).

Consequently, we identified a 40-kb gene cluster from the draft sequence that encodes five nonribosomal peptide synthesis-related polypeptides and a bacillibactin synthetase-like gene, which might be involved in the biosynthesis of secondary metabolites related to the production of algaecide bacillamides and antifungal compounds. Another feature of strain 2102 is its ability to decolorize azo dyes to treat textile industrial effluents (7, 11). Based on our data, several flavin mononucleotide-dependent NADH-azoreductases were identified, together with an NADPH-dependent azoreductase that is responsible for the transformation of azo dyes into colorless compounds (11). Genes involved in polyhydroxybutyrate metabolism were also identified (5). Thus, the draft genome sequence of *B. endophyticus* 2102 will not only provide insights into the molecular mechanisms underlying the function of secondary metabolites but also facilitate further study of its application to the treatment of industrial effluents.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. ALIM00000000. The version described in this paper is the first version, ALIM01000000.

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