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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Bacillus cereus* Strain LCT-BC244

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***Bacillus cereus* is a prevalent, soil-dwelling, Gram-positive bacterium. Some strains are harmful to humans and cause food-borne illness, while other strains can be beneficial as probiotics for animals. To gain insight into the bacterial genetic determinants, we report the genome sequence of a strain, LCT-BC244, which was isolated from CGMCC 1.230.**

Bacillus cereus is a Gram-positive, rod-shaped, aerobic or facultatively anaerobic, spore-forming bacterium. *B. cereus* is an opportunistic pathogen causing food poisoning by producing emetic toxin and three different enterotoxins that cause emetic syndrome and diarrheal illness (3, 5, 6). The genomic revolution has expanded knowledge of *B. cereus*, like many other bacteria, and there is a large number of fully sequenced genomes for *B. cereus* strains (4, 11), allowing for thorough comparative genomic analyses. Strain LCT-BC24 originated from the China General Microbiological Culture Collection Center (CGMCC) as CGMCC 1.230. The entire genome of strain LCT-BC244, which shares 100% similarity of 16S rRNA gene sequence with *B. cereus* 14579, was sequenced for a better understanding of its biology and function.

Whole-genome shotgun (WGS) sequencing of *Bacillus cereus* LCT-BC244 was performed with a strategy of Solexa paired-end sequencing technology at BGI-Shenzhen, Shenzhen, People's Republic of China. For the 350-bp PCR-free index library, 90 base pairs was set, while 65 base pairs was set for the 6,000-bp index library. The 3,058,387 paired-end reads of the 350-bp PCR-free index library and 2,233,099 paired-end reads of the 6,000-bp index library were combined into 5,291,486 paired-end reads which were generated to reach 163-fold coverage with an Illumina Hiseq 2000. About 99.06% of the reads of the 350-bp PCR-free index library and about 99.78% of the reads of the 6,000-bp index library were assembled into 7 scaffolds using the SOAP *de novo* release V1.05 (8) and SOAPaligner/soap2 (9).

The total length of the draft genome shotgun sequence of *B. cereus* LCT-BC244 is 5,156,879 bp, and the mean GC content is 35.37%. Its sequence contains 39 contigs with ~5.11 Mb, and these contigs were constructed into 7 scaffolds. The sequence contains 5,263 protein-coding genes that were predicted by Glimmer version 3.02 (2), and 3,295 of these genes encoded proteins in 22 functional COG (clusters of orthologous groups of proteins) groups. One rRNA operon was predicted by RNAmmer (7), 55 tRNA genes were predicted by tRNAscan-SE 1.21 (12), and 4 small RNA (sRNA) genes were predicted by Infernal 1.0.2 (10). In addition, by aligning the sequence with those in the DBETH database (1), we found 4 exotoxin genes.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJGQ00000000. The version described in this paper is the first version, AJGQ01000000.

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