

Genome Sequence of the Aerobic Bacterium *Bacillus* sp. Strain FJAT-13831

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***Bacillus* sp. strain FJAT-13831 was isolated from the no. 1 pit soil of Emperor Qin's Terracotta Warriors in Xi'an City, People's Republic of China. The isolate showed a close relationship to the *Bacillus cereus* group. The draft genome sequence of *Bacillus* sp. FJAT-13831 was 4,425,198 bp in size and consisted of 5,567 genes (protein-coding sequences [CDS]) with an average length of 782 bp and a G+C value of 36.36%.**

The genus *Bacillus* consists of aerobic, facultatively anaerobic, Gram-positive, spore-forming, or rod-shaped bacteria that are ubiquitous in nature. The species can be found in desert sands (9), hot springs (8), forest soils (2), freshwater (1), marine sediments (5), and an ancient tomb (4). In this paper, *Bacillus* sp. strain FJAT-13831 was isolated from the no. 1 pit soil of Emperor Qin's Terracotta Warriors in the People's Republic of China and incubated on nutrient agar (NA) medium at 30°C under aerobic conditions. Based on the polyphasic taxonomic studies of morphological and physiological tests, 16S rRNA gene and *gyrB* gene sequencing, DNA-DNA relatedness, and fatty acid testing, strain FJAT-13831 was maybe a novel species of the genus *Bacillus*. Therefore, here, we sequenced the genome sequence of FJAT-13831 to confirm whether it was a novel strain of the genus *Bacillus*.

The genome sequence of *Bacillus* sp. FJAT-13831 was determined by a whole-genome shotgun using Illumina Solexa technology with 500-bp and 2,000-bp paired-end sequencing and performed by the Beijing Genomics Institute (BGI; Shenzhen, China). All generated reads were assembled into 88 contigs using SOAPdenovo (7) v1.05.

Open reading frames (ORFs) were predicted using Glimmer 3.02 (3), and rRNA operons were predicted using RNAmmer 1.2 (6). The draft genome sequence of FJAT-13831 consisted of a circular 4,425,198-bp chromosome with a G+C value of 36.36%. The chromosome consisted of 5,567 genes (protein-coding sequences [CDS]) with an average length of 782 bp, and the CDS density was 80.79%.

Prediction of protein-coding genes and assignment of functions were done using the NCBI-NR, COG, and Swiss-Prot databases. The 5,333 CDS annotated can be classified into 2,863 COG categories by NR, and 2,969 CDS can be classified by Swiss-Prot. A total of 66.54% (3,549) of the ORFs were annotatable as known proteins in NR.

Nucleotide sequence accession numbers. This whole-genome shotgun project for *Bacillus* sp. FJAT-13831 has been deposited at DDBJ/EMBL/GenBank under the accession number [AKCS00000000](https://doi.org/10.1128/JB.01072-12). The version described in this paper is the first version, AKCS01000000.

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