Genome of *Bacillus macauensis* ZFHKF-1, a Long-Chain-Forming Bacterium

Lin Cai and Tong Zhang

Environmental Biotechnology Laboratory, Department of Civil Engineering, The University of Hong Kong, Hong Kong SAR, China

Here, we report the draft genome sequence of *Bacillus macauensis* ZFHKF-1, a novel long-chain bacterium previously isolated and identified by us (Zhang T, Fan XJ, Hanada S, Kamagata Y, Fang HHP, J. Syst. Evol. Microbiol. 56:349–353, 2006). The genome provides basic genetic information to understand this particular species and explore the potential mechanism of long-chain formation. The type strain is ZFHKF-1 (= JCM 13285 = DSM 17262).

Members of the *Bacillus* genus are Gram-positive, rod-shaped, and spore-forming bacteria with low GC contents and can live in various environments (3). They can be obligate aerobes or facultative anaerobes. At this time, more than 226 *Bacillus* species have been well identified and 111 of them have had their whole genomes released in GenBank. Most *Bacillus* species grow as single cells, but only a few of them can form long chains, including *B. anthracis* (3), *B. mycoides* (5), *B. macauensis* (9), and *B. funiculus* (1, 2). The whole genomes of strains belonging to *B. anthracis* and *B. mycoides* have been widely released in GenBank because of their pathogenic properties. However, no attention has been paid to the genomes of the potentially pathogenic *B. macauensis* and *B. funiculus*. *B. macauensis* ZFHKF-1 was isolated from the influent of a drinking water plant in China (9). It is resistant to chlorination and may tolerate up to 1.6 mg/liter of free chlorine. Single cells of this strain are 2.0 to 5.0 μm in length and 0.8 to 1.2 μm in diameter, but the length of a long chain can reach over 100 μm (9).

A BLAST search using the 16S rRNA gene of *B. macauensis* ZFHKF-1 indicated that *Bacillus solisalsi* YC1 (6), *Bacillus barbaricus* V2-BIII-A2 (8), *Bacillus gelatini* LMG 21880 (4), and *Bacillus arsenicus* Con a/3 (7) showed 16S rRNA gene identities of 98%, 97%, 95%, and 95%, respectively. The other *Bacillus* species shared identities of 94% or less. Although *B. macauensis*, *B. solisalsi*, *B. barbaricus*, *B. gelatini*, and *B. arsenicus* have been well identified (4, 6–9), especially for their particular evolutionary positions and biochemical and physiological properties, none of their genomes have been announced and deposited in a public database until now. Hence, a whole-genome sequencing project of *B. macauensis* ZFHKF-1 was performed in this study.

Genome sequencing of *B. macauensis* ZFHKF-1 was carried out by BGI (Beijing Genomics Institute) using the Illumina high-throughput sequencing platform. In total, ~3.05 Gb of clean data (30,489,924 paired-end reads with a 100-bp length) were obtained for assembly after filtering out the low-quality reads. CLC Genomics Workbench 4.9 was employed for *de novo* assembly and analyses. The draft genome of *B. macauensis* ZFHKF-1 was finally assembled into 55 contigs with a 3,736,359-bp genome size and more than 800-fold genome coverage. Ninety-nine percent of the clean reads were mapped into the assembled 55 contigs, and the N50 value was 213,431 bp. The draft genome was then submitted to NCBI Prokaryotic Genomes Automatic Annotation Pipeline for annotation (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). The results indicate that the genome has 3,905

genes, including 3,850 protein coding genes, 52 tRNA genes, and 3 rRNA genes, and its GC content is 40.6%.

Nucleotide sequence accession numbers. The draft genome sequence of *B. macauensis* ZFHKF-1 has been deposited at DDBJ/EMBL/GenBank under accession number [AKKV00000000](#). The current version described in the present study is the first version, AKKV01000000.

ACKNOWLEDGMENTS

Lin Cai thanks The University of Hong Kong for the postdoctoral fellowship. We thank the Hong Kong General Research Fund (7198/10E) for the financial support of this study.

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Received 12 June 2012 Accepted 20 June 2012

Address correspondence to Tong Zhang, zhangt@hku.hk.

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doi:10.1128/JB.01049-12