Draft Genome Sequence of *Bacillus paranthracis* Strain DB-4, Isolated from Nukadoko, Fermented Rice Bran for Japanese Pickles

Daisuke Fukuda,[a] Cirilo Nolasco-Hipolito[b]

aVaccine and Infectious Disease Area, Medical Affairs, Merck Research Laboratories, MSD K.K., Chiyoda-ku, Tokyo, Japan
bInstitute of Biotechnology, Universidad del Papaloapan Campus Tuxtepec, Tuxtepec, Oaxaca, México

ABSTRACT *Bacillus paranthracis* strain DB-4 was isolated from nukadoko in Japan. We report the draft genome sequence of this strain to provide insights into the survival mechanisms of lactic acid bacteria in fermented rice bran.

The *Bacillus cereus* group, also known as *B. cereus sensu lato*, comprises at least 21 related species (1). Members of the *B. cereus* group, including *Bacillus paranthracis*, are Gram-positive, facultatively anaerobic, and spore-forming. Due to their variety of lifestyles and genetic diversity, some strains of the *B. cereus* group are considered to be beneficial for human and animal health (2, 3). *Bacillus* spp. may also protect lactic acid bacteria in fermented foods from reactive oxygen species through their catalase activity (4, 5). To clarify the physiological role of *Bacillus* spp. in fermented foods, we analyzed the genome of *B. paranthracis* DB-4, isolated from homemade nukadoko, fermented rice bran used as a bed for making Japanese pickles.

B. paranthracis DB-4 was first discovered in homemade nukadoko in Yokohama, Japan. Strain DB-4 was isolated by spreading serially diluted nukadoko onto MRS agar (Difco) at 30°C for 2 days. A single colony of strain DB-4 was picked for culturing prior to DNA isolation.

Strain DB-4 was cultured in MRS broth (Difco) at 30°C for 15 h (late log phase). Then, genomic DNA was extracted from *B. paranthracis* DB-4 and purified using the GeneJET genomic DNA purification kit (Thermo Fisher), following the instruction manual. After the quality and quantity of the genomic DNA obtained were checked using a Synergy LX microplate reader (BioTek, USA) and the QuantiFluor double-stranded DNA (dsDNA) system (Promega), respectively, the sequence library was prepared using a Nextera XT library preparation kit (Illumina). The quantity and quality of the library were verified using the Agilent fragment analyzer and dsDNA 915 reagent kit (Advanced Analytical Technologies). Whole-genome sequencing was performed using the Illumina MiSeq sequencer with 2×250-bp paired-end reads. The sequences were processed to remove low-quality bases using Cutadapt ver. 1.9.1 (6) and Sickle ver. 1.33 (https://github.com/najoshi/sickle). Sequencing resulted in 5,085,667 paired-end reads. *De novo* genome assembly was performed using the SPAdes ver. 3.13.2 genome assembler (5, 7) with default parameters.

The assembly yielded 57 contigs covering a total of 5,424,208 bp, with an N_{50} value of 498,305 bp and a G+C content of 35.2%. The genome sequence was annotated using the DFAST ver. 1.14.5 annotation pipeline (8, 9), which revealed 5,595 coding DNA sequences (CDSs), 103 tRNA genes, 13 rRNA genes, 1 CRISPR, and a coding ratio of 84.0%. The average nucleotide identity (ANI) was analyzed using the JSpeciesWS online service (10), which showed 98.9% and 91.96% identities with the genomes of *B. paranthracis* Mn5T (GenBank accession number GCA_001883995.1) and *B. cereus* ATCC

14579^T (GCA_000007825.1), respectively. These ANI scores indicate that strain DB-4 belongs to the species *B. paranthracis*.

Five catalase genes, including vegetative catalase genes and a manganese catalase gene, were identified in the genome of *B. paranthracis* DB-4. A putative heme-dependent peroxidase gene and three superoxide dismutase genes were also identified in the genome of DB-4. These may contribute to eliminating reactive oxygen species in fermented nukadoko.

The whole-genome sequence, assembly, and annotation of *B. paranthracis* DB-4 will support our understanding of the physiological roles of *B. cereus* group bacteria in fermented foods, lactate fermentation processes, and human health (7, 11).

Data availability. The genome sequence was deposited in the DDBJ/ENA/GenBank under accession number BPLB00000000.1. The draft genome project data have been submitted under BioProject accession number PRJDB11683, DRA accession number DRR294728, and Sequence Read Archive (SRA) accession number DRX284184.

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