Draft Genome Sequence of *Brevibacillus panacihumi* Strain W25, a Halotolerant Hydrocarbon-Degrading Bacterium

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Brevibacillus panacihumi strain W25 was isolated from hydrocarbon-contaminated saline soil. Here, we report the 5.5-Mb draft genome sequence of this strain, which may provide insights into the mechanism of microbial hydrocarbon degradation in saline environments.

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Microbial degradation plays a crucial role in the natural attenuation of hydrocarbon-contaminated saline environment, which has attracted increasing attention (1, 2). *Brevibacillus panacihumi* W25 was isolated from petroleum-contaminated saline soil in China, which can degrade crude oil in the presence of 40 g/liter NaCl. Although several strains belonging to the genus of *Brevibacillus* have been sequenced (3–9), the genome of *B. panacihumi* is still unavailable. Here, the draft genome sequence of *B. panacihumi* W25 is presented for the first time, helpful to gain a deeper understanding of the mechanisms of microbial hydrocarbon degradation in saline environments.

Genomic DNA was extracted from a 2-day culture growing in tryptic soy broth using a commercial DNA isolation kit, and was sequenced using the Illumina HiSeq 2000 platform (San Diego, CA). The shotgun sequencing yielded 10,458,934 read pairs (6,863,516 100-bp paired-end reads with an insert size of 500 bp and 3,595,418 100-bp mate-pair reads with an insert size of 6 kb). Filtered sequencing data were assembled using SOAPDeNovo v 2.04 (10) and were scaffolded and gap filled with SSPACE v 2.0 (11) and GapFiller v 1.10 (12). Final assembly consisted of 18 contigs with an N_{50} length of 1,095,539 bp, which were assembled into 11 scaffolds with an N_{50} length of 1,760,181 bp. The sequences were annotated using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The genome consists of 5.5 Mb with a G+C content of 50.1%. A total of 5,294 coding sequences (CDS), 115 pseudogenes, 135 tRNA genes, 1 noncoding RNA (ncRNA), and 11 rRNA operons were identified. One clustered regularly interspaced short palindromic repeat (CRISPR) element with 75 spacers was detected using CRISPR Finder (13). Eighty-seven tandem repeats was detected using Tandem Repeats Finder v 4.07 (14). One intact prophage sequence was identified using PHAST (15). The IS3 family dominates the insertion sequence (IS) elements, as revealed by ISFinder (16). Average nucleotide identity (ANI) analysis (17) revealed that *B. panacihumi* W25 is phylogenetically related to *B.*

agri BAB-2500 (74.2%) (6), *B. borstelensis* AK1 (71.6%), *B. brevis* FJAT-0809-GLX (72.2%) (3), *B. brevis* NBRC100599 (72.5%), *B. brevis* X23 (72.3%) (4), *B. laterosporus* DSM 25 (66.4%), *B. laterosporus* GI 9 (67.4%) (9), *B. laterosporus* LMG 15441 (67.6%) (5), *B. laterosporus* PE36 (67.6%), *B. massiliensis* phR (69.2%) (8), *Brevibacillus* sp. BC25 (72.2%), *Brevibacillus* sp. CF112 (74.3%) and *B. thermoruber* 423 (72.6%) (7).

Seven genes were identified as involved in hydrocarbon degradation, including 1 alkanal monooxygenase gene and 6 ring-cleavage dioxygenase genes. Moreover, 7 genes were identified as involved in compatible solute synthesis and uptake, including 1 ectoine synthase gene, 1 betaine-aldehyde dehydrogenase gene and 5 glycine/betaine ABC transport genes, which may enhance the tolerance to NaCl stress. Information about the genome sequence of *B. panacihumi* W25 will improve our understanding of microbial hydrocarbon degradation in saline environment.

Nucleotide sequence accession number. The draft genome sequence of *B. panacihumi* W25 has been deposited in GenBank under the accession number AYJU00000000. The version described in this paper is the first version.

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