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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Leuconostoc gelidum* Strain JB7, Isolated from Kimchi

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A strain of *Leuconostoc gelidum*, designated strain JB7, was isolated from kimchi, the representative Korean traditional fermented food. Here we announce the complete genome sequence of *L. gelidum* strain JB7, consisting of a 1,893,499-bp circular chromosome with a G+C content of 36.68%, and provide a description of its annotation.

Kimchi, the representative Korean traditional fermented food, is made through fermentation of vegetables such as Chinese cabbage and radish with seasoning ingredients, including red pepper powder, garlic, ginger, green onion, and fermented seafood (jeotgal) at low temperatures. Kimchi fermentation usually relies upon the growth of various naturally occurring microorganisms, especially lactic acid bacteria (LAB) (3). Taxonomic studies using conventional and molecular methods have shown that the genera *Leuconostoc*, *Lactobacillus*, and *Weissella* are likely to be key players responsible for kimchi fermentation (5, 6), and their members have been frequently isolated (7, 9, 10). A strain of *Leuconostoc gelidum*, designed JB7, was isolated from Chinese cabbage (baechu) kimchi. Here we report the complete genome sequence and annotation of *L. gelidum* JB7.

The whole genome of strain JB7 was sequenced at Chunlab (Republic of Korea). A sequence of 36.83 Mb (about 19-fold coverage) with 206,458 paired-end reads containing 8-kb inserts and a sequence of 4,626.6 Mb (about 2,443-fold coverage) with 45,807,807 paired-end reads containing 100-bp inserts were generated by using the 454 GS FLX Titanium system (Roche) and a model IIx Illumina genome analyzer, respectively. The resulting sequences were assembled into one large scaffold, including 39 contigs, using GS Assembler 2.6 (Roche Diagnostic, Branford, CT) and CLC Genomics Workbench 5.5 (CLC bio, Denmark). All the intrascaffold and interscaffold gaps were closed by sequencing of PCR products. The Phred/Phrap/Consed software (1, 2, 4) was used for sequence assembly and quality assessment, and the final whole-genome sequence was further validated by Sanger sequencing of uncertain regions such as mononucleotide runs and segments with low quality scores or low coverage in sequencing data. The complete sequence was submitted to the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP). The tRNA and rRNA genes were annotated using the tRNAscan-SE (11) and RNAmmer (8) software programs, respectively. Strain JB7 has a circular chromosomal genome of 1,893,499 bp with a G+C content of 36.68% and no plasmid. The genome contains 1,796 predicted protein coding sequences, 4 complete rRNA operons, and 67 tRNA genes coding 20 amino acids on the chromosome. The coding density of the genome was 86.45%, with an average gene length of 911 bp.

Nucleotide sequence accession number. The genome information for the chromosome of *Leuconostoc gelidum* strain JB7 was deposited in NCBI under GenBank accession number CP003839.

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