

Draft Genome Sequence of *Lactobacillus sakei* Strain FBL1, a Probiotic Bacterium Isolated from *Mukeunji*, a Long-Fermented Kimchi, in South Korea

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This report describes the 2,032,158-bp draft genome sequence of *Lactobacillus sakei* (*L. sakei*) strain FBL1, isolated from *mukeunji* purchased at the Gwangju World Kimchi Culture Festival in 2012, South Korea. The total draft genome size was 2,032,158 bp with a G+C content of 41.2%.

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Lactobacillus sakei (*L. sakei*) is a facultative heterofermentative and Gram-positive anaerobic lactic acid bacterium (LAB). This bacterium, originally described in rice alcohol or sake, is commonly found in fresh meat and fish and is used as a starter culture (1). The complete genome sequence of *L. sakei* 23K (GenBank accession no. CR936503.1) was reported in 2005 (2). It consists of the circular chromosome containing 1,884,661 bp and 1,883 protein coding genes.

The genome sequence of *L. sakei* strain FBL1 with bile acid tolerance, isolated from *mukeunji*, a long-fermented kimchi (3), was analyzed in this study. *L. sakei* FBL1 was isolated from commercial *mukeunji* and showed 99% identity with the *L. sakei* strain DGH5 (KF469177.2) 16S rRNA gene. Comparative genomic analysis revealed 84% similarity with *L. sakei* 23K.

Genomic DNA was extracted with the G-spin genomic extraction kit (Intron Biotechnology Co., Republic of Korea) and quality was evaluated by the Agilent 2100 bioanalyzer with the high-sensitivity DNA kit. Draft genome sequencing was performed using an Ion Torrent Personal Genome Machine (PGM) system (Life Technologies, Germany) and a 318 semiconductor chip with 400-bp sequencing reads. A total of 4,048,495 reads, with an average read length of 320 bp, were generated. Reference-based assembly was carried out using SPAdes version 3.1.0, with *L. sakei* 23K as the reference genome. Assembly of the reads resulted in 44 contigs (≥ 500 bp, 541 to 287,097 bp, N_{50} length 116,042 bp). The total draft genome size was 2,005,160 bp with a G+C content of 41.0%. A total of 1,972 coding sequences, 76 RNA genes, and 296 subsystems were revealed by the RAST server (4, 5). The genome includes the production of a colicin V synthesis protein, adhesion and multidrug resistance efflux pumps, as well as those containing resistance genes, beta-lactam antibiotics, bile salt (choloylglycine hydrolase), and fluoroquinolones. Compared to the *L. sakei* 23-K

genome, about 32 genes are missing. Importantly, phage proteins, choline binding protein, beta-galactosidase, phosphotransferase systems, and cobalt-zinc-cadmium resistance protein existed in *L. sakei* strain FBL1.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number [LSFF00000000](https://www.ncbi.nlm.nih.gov/nuclink/LSFF00000000). The version described in this paper is the first version, LSFF01000000.

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