Complete Genome Sequence of *Leuconostoc carnosum* Strain JB16, Isolated from Kimchi

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Leuconostoc carnosum strain JB16 was isolated from kimchi, the traditional Korean fermented food. Here, we report the complete genome sequence of *L. carnosum* strain JB16, consisting of a 1,645,096-bp circular chromosome with a G+C content of 37.24% and four plasmids.

Kimchi, an emblematic traditional fermented food in Korean culture, is made through fermentation of a variety of vegetables with seasoning ingredients, including red pepper powder, garlic, ginger, green onion, and fermented seafood (jeotgal). Taxonomic studies have shown that kimchi preparation without the sterilization of raw materials leads to the growth of various lactic acid bacteria (LAB). Analyses of the kimchi microbial community have shown that members of the genera *Leuconostoc*, *Lactobacillus*, and *Weissella* play important roles in kimchi fermentation (5, 6). *Leuconostoc mesenteroides* is well known as one of the predominant *Leuconostoc* species during kimchi fermentation (5, 7), and some other *Leuconostoc* species, including *Leuconostoc citreum*, *Leuconostoc gelidum*, *Leuconostoc carnosum*, *Leuconostoc kimchii*, *Leuconostoc inhae*, and *Leuconostoc hozapfelii*, have also been frequently isolated from kimchi (1, 5, 9). A strain of *Leuconostoc carnosum*, designated JB16, was isolated from Chinese cabbage (baechu) kimchi. Here, we report the complete genome sequence and annotation of *L. carnosum* JB16.

The whole genome of strain JB16 was sequenced at Chunlab (Republic of Korea). A sequence of about 38.25 Mb (~21.6× coverage) with 216,235 paired-end reads containing 8-kb inserts was generated from the 454 GS FLX Titanium system (Roche). A sequence of 3,957 Mb (about 2,231× coverage) with 39,179,152 paired-end reads containing 100-bp inserts was also generated from an Illumina genome analyzer (Solexa). The resulting reads were assembled into five large scaffolds, including 36 contigs, using GS Assembler 2.6 (Roche Diagnostic, Branford, CT) and CLC Genomics Workbench 5.0 (CLC bio, Denmark). All the intrascaffold and interscaffold gaps were closed by sequencing of PCR products. The Phred/Phrap/Consed software (2, 3, 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 low-quality/depth segments. The complete sequence was submitted to the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). The tRNA and rRNA genes were annotated using the tRNAscan-SE (10) and RNAmmer (8) software programs, respectively.

The genome of *L. carnosum* strain JB16 is composed of one circular chromosomal genome of 1,645,096 bp and four circular plasmids (pKLC1, 21,990 bp; pKLC2, 29,615 bp; KLC3, 40,165 bp; pKLC4, 36,602 bp) (Table 1). The entire genome (1,773,468 bp) contains 1,693 predicted protein-coding sequences, i.e., 1,548 coding sequences with an average gene length of 932 bp and a coding intensity of 87.77% on the chromosome and 19, 38, 46, and 42 coding sequences on plasmids pKLC1 to pKLC4, respectively, as well as four complete rRNA operons and 66 tRNA genes encoding 20 amino acids on the chromosome. The G+C content of the chromosome is 37.24%, while those of the four plasmids are in the range of 34.93% to 38.03% (Table 1).

Nucleotide sequence accession numbers. The genome information for the chromosome of *Leuconostoc carnosum* strain JB16 was deposited in NCBI under GenBank accession number CP003851, and the information for the plasmids pKLC1 to pKLC4 was deposited under GenBank accession numbers CP003852 to CP003855, respectively.

TABLE 1 Sequence features of four plasmids present in the *Leuconostoc carnosum* strain JB16 genome

Plasmid name	Size (bp)	No. of coding gene sequences	Avg gene length (bp)	Coding density (%)	G+C content (%)	GenBank accession no.
pKLC1	21,990	19	734	63.4	38.03	CP003852
pKLC2	29,615	38	528	67.7	35.50	CP003853
pKLC3	40,165	46	775	88.8	35.29	CP003854
pKLC4	36,602	42	792	90.9	34.93	CP003855

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