Complete Genome Sequence of *Leuconostoc mesenteroides* subsp. *mesenteroides* Strain J18, Isolated from Kimchi

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*Leuconostoc mesenteroides* subsp. *mesenteroides* is one of the most predominant lactic acid bacterial groups during kimchi fermentation. Here, we report the complete genome sequence of *L. mesenteroides* subsp. *mesenteroides* J18, which was isolated from kimchi. The genome of the strain consists of a 1,896,561-bp chromosome and five plasmids.

Kimchi, a traditional Korean fermented food, is made by fermentation of vegetables such as Chinese cabbage and radish with assorted seasoning mixtures containing ingredients such as red pepper powder, garlic, ginger, green onion, and fermented seafood (jeotgal). Taxonomic studies using conventional and molecular methods have shown that various lactic acid bacteria (LAB) species, such as *Leuconostoc mesenteroides*, *Lactobacillus sakei*, and *Weissella koreensis*, are likely to be key players responsible for kimchi fermentation (1, 6, 9). Members of the genus *Leuconostoc* are heterofermentative LAB species that are typically dominant during the early and mid-phases of kimchi fermentation (2, 6) and are known to be among the LAB species that determine kimchi’s flavors (7, 10, 12). A strain of *L. mesenteroides* subsp. *mesenteroides*, designated J18, was isolated from baechu (Chinese cabbage) kimchi fermented at 4°C. Here, we report the complete genome sequence and annotation of *L. mesenteroides* subsp. *mesenteroides* J18.

The whole genome of strain J18 was sequenced at Chunlab (Republic of Korea). About 39.38 Mb (~19.5-fold coverage) with 203,962 paired-end reads containing 8-kb inserts and about 2,171.1 Mb (~1,076.7-fold coverage) with 25,902,870 paired-end reads containing 100-bp inserts were generated from the 454 GS FLX Titanium system (Roche) and a model IIx Illumina genome reads containing 100-bp inserts were generated from the 454 GS FLX Titanium system (Roche) and a model IIx Illumina genome reads containing 100-bp inserts were generated from the 454 GS FLX Titanium system (Roche) and a model IIx Illumina genome assembly and quality assessment. 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) for annotation. The tRNA and rRNA genes were annotated using the tRNAscan-SE (11) and RNAmmer (8) software programs, respectively. The genome of *L. mesenteroides* subsp. *mesenteroides* J18 is composed of one circular chromosomal genome of 1,896,561 bp (37.77% G+C content) and five circular plasmids (pKLE01, 37,252 bp; pKLE02, 35,425 bp; pKLE03, 24,548 bp; pKLE04, 19,293 bp; and pKLE05, 3,347 bp) (Table 1). The entire genome (2,016,426 bp) contains 1,942 predicted protein-coding sequences, i.e., 1,803 coding sequences with an average gene length of 930 bp and a coding intensity of 88.38% on the chromosome and 43, 46, 29, 19, and 2 coding sequences on plasmids pKLE01 to -5, respectively, as well as four complete tRNA operons and 71 tRNA genes coding 20 amino acids on the chromosome. The G+C content of the chromosome is 37.77%, while those of the five plasmids are in the range of 34.85 to 38.78% (Table 1).

**Nucleotide sequence accession numbers.** The genome information for the chromosome of *Leuconostoc mesenteroides* subsp. *mesenteroides* strain J18 was deposited in NCBI under GenBank accession number CP003101, and the accession numbers for the plasmids are listed in Table 1.

**ACKNOWLEDGMENTS**

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**REFERENCES**


**TABLE 1**

Sequence features of 5 plasmids in the *Leuconostoc mesenteroides* subsp. *mesenteroides* strain J18 genome.

<table>
<thead>
<tr>
<th>Plasmid name</th>
<th>Size (bp)</th>
<th>No. of coding gene sequences</th>
<th>Avg gene length (bp)</th>
<th>Coding density (%)</th>
<th>G+C content (%)</th>
<th>GenBank accession no.</th>
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