

# Complete Genome Sequence of *Weissella koreensis* KACC 15510, Isolated from Kimchi

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***Weissella koreensis* KACC 15510 was isolated from kimchi, a representative traditional Korean fermented food. Here, we announce the complete genome sequence of *W. koreensis* KACC 15510, consisting of a 1,422,478-bp chromosome and one 18,992-bp plasmid, and provide a description of their annotation.**

Kimchi, a representative Korean fermented food, is fermented from a variety of vegetables, such as Chinese cabbage or radish, with seasoning ingredients, including red pepper powder, garlic, and salts. In recent years, kimchi's health-promoting characteristics have been recognized (1, 11). Taxonomically diverse groups of lactic acid bacteria (LAB) have been isolated from fermented kimchi (6). Heterofermentative LAB, such as *Leuconostoc mesenteroides*, *Lactobacillus sakei*, and *Weissella koreensis*, have been known to be key players in kimchi fermentation, and LAB usually determine kimchi's particular flavors (5, 7). Members of the genus *Weissella*, placed within the family of *Leuconostocaceae*, are Gram-positive, non-spore-forming, heterofermentative, and nonmotile short-rod bacteria (9). *Weissella koreensis* KACC 15510 was isolated from Chinese cabbage kimchi.

This genomic sequence was determined using Roche 454 technology. The total sequence (107 Mb [about 77× coverage] with 1,404,581 paired-end reads containing 3-kb inserts) was generated from a 454 GS FLX Titanium system, and the resulting sequences were assembled initially into 11 large scaffolds, including 57 contigs, using the Newbler program. All the intrascaffold and interscaffold gaps were closed by sequencing PCR products. 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/low-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. *W. koreensis* KACC 15510 has a circular chromosomal genome of 1,422,478 bp (35.48%

G+C) and one circular plasmid of 18,992 bp (36.7% G+C). The chromosomal genome contains 1,335 predicted protein-coding sequences, 5 complete rRNA loci, and 56 tRNA genes, and its coding density is 85.1%, with an average gene length of 906 bp. The plasmid contains 23 predicted protein-coding sequences, with an average gene length of 632 bp.

**Nucleotide sequence accession numbers.** The genome information for the chromosome of *Weissella koreensis* KACC 15510 was deposited in NCBI under GenBank accession number CP002899. The plasmid of strain KACC 15510 is available in GenBank under accession number CP002900.

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