

Draft Genome Sequence of *Weissella koreensis* KCTC 3621^T

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***Weissella koreensis* is a Gram-positive, rod-shaped, nonmotile, and facultative anaerobic species belonging to the lactic acid bacteria (LAB). The members of this species have been repeatedly isolated from kimchi (a traditional Korean fermented food) and are known for their beneficial effects on human and animal intestinal microflora through producing various clinically important amino acids such as γ -aminobutyric acid and ornithine. Here we report the genome sequence of the type strain of *W. koreensis* (KCTC 3621^T) to provide taxonomic and functional insights into the species.**

Weissella koreensis is a Gram-positive, non-spore-forming, heterofermentative, and nonmotile short-rod bacterium belonging to the family *Leuconostocaceae* (10, 11). The members of this species have been repeatedly isolated from kimchi (a traditional Korean fermented food), which is composed of various kinds of vegetables (2, 3, 9). Kimchi is well known for human health-promoting properties such as anticarcinogenic, immunomodulatory, antimicrobial, antidiarrheal, and antiallergy activities (13, 15), for which lactic acid bacteria (LAB) in kimchi may be responsible. Recently, the antiobesity effect of *W. koreensis* was found to be due to the production of various clinically important amino acids, including γ -aminobutyric acid and ornithine (13). In order to provide biological insights and understand the evolutionary relationships of *W. koreensis*, the genome of the type strain (KCTC 3621^T) was sequenced through the use of the GS 454 and Illumina platforms.

The whole-genome sequencing was performed by a combination of a 100-bp single-end Illumina Genome Analyzer IIx system (29,722,442 reads; 1,735-fold coverage) and a Roche 454 GS FLX Titanium system (220,167 reads) with an 8-kb paired-end library. The draft hybrid assembly was constructed using Newbler assembler 2.6 (Roche), CLC genomics wb 4.8 (CLCbio), and Codon-Code Aligner (CodonCode Co.). Gene prediction was carried out by Glimmer 3 (5), and gene annotation was performed using the Clusters of Orthologous Groups (COG) and SEED databases (6, 14). Comparative genomics was achieved according to the method of Chun et al. (4).

The genome of KCTC 3621^T consists of one chromosome (17 contigs; 1,729,728 bp; 35.5% G+C ratio) and has 1,672 coding sequences (CDS), 61 tRNA genes, and 5 rRNA loci. Among protein-coding genes, 397 (23.4%) open reading frames (ORFs) matched hypothetical protein sequences in a public database and 129 genes (7.7%) were present only in strain KCTC 3621^T and not in other *Weissella* genomes (1, 8, 11).

A phylogenetic tree based on average nucleotide identity (ANI) (7) showed that KCTC 3621^T was most closely related to *W. koreensis* KACC 15510, with 98.76% and 99.48% similarity values, confirming that the two belong to the same species. Strain KACC 15510, which has a 1.42-Mb genome and 1,335 CDS, was also isolated from kimchi (11).

Recently, a strain of *W. koreensis* designated OK1-6 was reported to produce ornithine from arginine, implying its functional role in reducing obesity (13). However, the mechanism of ornithine production has not been elucidated. In the genome of

KCTC 3621^T, six genes related to ornithine metabolism were found, including those encoding acetylornithine deacetylase (*argE*) and ornithine carbamoyltransferase (*argF*). In addition, five genes related to arginine metabolism were identified, including one encoding arginine deiminase (*arcA*). When the KCTC 3621^T genome was searched against the Antibiotic Resistance Genes Database (ARDB, version 1.1) (12), six antibiotic-resistance-related genes were found, including genes encoding bacitracin resistance protein (*bacA*) and virginiamycin A acetyltransferase (*vat*). The genome sequence of *W. koreensis* KCTC 3621^T will serve as a valuable reference for understanding the taxonomical and biological details of *W. koreensis*, a key player in kimchi fermentation (9).

Nucleotide sequence accession numbers. The sequence from this whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [AKGG00000000](https://www.ncbi.nlm.nih.gov/nuccore/AKGG00000000). The version described in this paper is the first version, AKGG01000000.

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