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Complete Genome Sequence of *Weissella koreensis* DMW12 Isolated from Kimchi, Traditional Korean Fermented Vegetables

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Weissella koreensis **DMW12 was isolated from kimchi added Myeongtae (*Theragra chalcogramma*), and its complete genome sequence was determined. The complete genome of strain DMW12 includes a single circular 1,518,288-bp chromosome without plasmids. The G+C content of the genome is 35.6 mol%. Although strain DMW12 did not showed protease and lipase activities, the genome includes 33 protease- and 3 lipase-encoding genes. The genome of strain DMW12 does not include acquired antibiotic resistance genes against ampicillin, chloramphenicol, clindamycin, erythromycin, gentamicin, kanamycin, tetracycline, and streptomycin.**

Keywords: ***Weissella koreensis*****, genome, kimchi, protease, lipase, antibiotic-susceptibility**

Weissella koreensis was isolated from kimchi and first designated in 2002 [1]. *W. koreensis* is most often identified in kimchi and fermented foods [2, 3]. The strain of *W. koreensis*, which is dominant species in kimchi and heterolactic fermentation bacteria, has been suggested as a suitable candidate for the kimchi fermentation [4], and has been the subject of various studies for strain development [5]. Furthermore, genome studies have been conducted to elucidate the metabolic pathways contributed by *W. koreensis* during fermentation [6, 7]. While research on *W. koreensis* as a starter culture mainly focuses on its functionality [5], there is a lack of studies on enzyme activity related to fermentation in food.

We isolated *W. koreensis* species from commercial kimchi added Myeongtae (*Theragra chalcogramma*), and assessed the antibiotic-susceptibility and the enzymatic activity to select potential starter candidates in this study. Enzyme activity experiments for protease and lipase were conducted, but none of the strains showed enzyme activity (data not shown). Additionally, through antibiotic susceptibility testing, strain *W. koreensis* DMW12, which exhibited the lowest Minimum Inhibitory Concentration (MIC) values for 8 antibiotics (1 mg/l ampicillin, 4 mg/l chloramphenicol, 0.5 mg/l clindamycin, 0.5 mg/l erythromycin, 8 mg/l gentamicin, 8 mg/l kanamycin, 2 mg/l tetracycline, and 32 mg/l streptomycin), was identified. Despite the absence of enzyme activity, the strain DMW12 was selected as a safe candidate for a starter culture due to its lowest activity in antibiotic resistance experiments. To validate the strain for safety, genomic analysis was performed.

Whole-genome sequencing of *W. koreensis* DMW12 was performed using the PacBio Sequel 10K system at CJ Bioscience, Inc. (Republic of Korea). One contig was generated from the obtained sequencing reads (24,484 reads, 464× coverage) by SMRT Link (version 10.1.0, PacBio) and annotated by using the NCBI Prokaryotic Genome Annotation Pipeline (version 6.6). Functional

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Table 1. Genome features of *Weissella koreensis* DMW12.

Feature	Value
Genome size (bp)	1,518,288
G+C content (mol%)	35.6
Total number of genes	1,513
Protein coding genes (CDS)	1,440
rRNA genes	15
tRNA genes	57
Other RNA genes	1

categories of annotated gene were analyzed using the Clusters of Orthologous Groups (COG) database [8]. The complete genome of *W. koreensis* DMW12 consists of a circular 1,518,288-bp chromosome (Table 1). The G+C content of the genome is 35.6 mol%. The average nucleotide identity (ANI) for the genome sequence of *W. koreensis* DMW12 showed 100% and 99.9% similarity to *W. koreensis* SK, and *W. koreensis* JCM11263, respectively. It showed ANI homology of 95.7%, and 95.8% with *W. cibaria* CMS3, and *W. confusa* LM1 of the same genus, respectively. The genome was predicted to contain 1,513 open reading frames, 57 tRNA genes, and 15 rRNA genes. COG functionally categorized 1,266 genes and major COG categorizations except function unknown are related to translation, ribosomal structure and biogenesis (138 genes, 10.90%), transcription (94 genes, 7.42%), and replication, recombination and repair (92 genes, 7.27%). *Lactiplantibacillus plantarum* KM2 and *Bacillus velezensis* KMU01, involved in food fermentation, showed major COG categorizations in carbohydrate transport and metabolism, as well as amino acid transport and metabolism [9, 10]. This was presumed to be indicative of their roles as starter cultures for utilizing carbohydrates or proteins. However, the COGs profile of *W. koreensis* DMW12 predominantly displayed genes involved in the fundamental processes of life, such as replication, transcription, and translation, showing a different pattern with fermentation bacteria. Particularly, the lack of enzyme activity in *W. koreensis*, including *W. koreensis* DMW12, implies that it may not significantly contribute to the breakdown of macromolecules such as protein and lipid, and enhancement of sensory characteristics during the fermentation process. This suggests the need for further research on the role of *W. koreensis* in fermentation.

The genomic analysis of *W. koreensis* DMW12, which did not show protease and lipase activity in 2% skim milk (w/v) and tributyrin agar (Sigma-Aldrich, USA) supplemented with 1% glyceryl tributyrate (w/v), revealed the presence of 33 putative protease genes and 3 putative lipase genes. However, these genes are presumed to be involved in intracellular functions and not secreted into the extracellular environment for enzyme activity. In the evaluation of susceptibility to 8 antibiotics, *W. koreensis* DMW12, exhibiting the lowest MIC values among the strains, did not encode any antibiotic resistance-related genes in the genome. The results, confirmed through genomic analysis of enzyme activity and antibiotic susceptibility of *W. koreensis* DMW12 derived from kimchi, are expected to be utilized in future safety and enzyme activity analyses of *W. koreensis* strains. Furthermore, it is anticipated that these findings will be valuable in the selection of fermentation starter.

Nucleotide Sequence Accession Number

The complete genome sequence of *Weissella koreensis* DMW12 has been deposited in DDBJ/ENA/GenBank under accession number CP144279.

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Conflict of Interest

The author has no financial conflicts of interest to declare.

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