The widespread procedure of kimchi processing includes brining of cabbage, blending of brined cabbage with spices and ingredients, aging, and fermentation. Kimchi fermentation is initiated by various microbes originating with raw materials and the environment (5, 11). Among the *Leuconostoc* species, *Leuconostoc mesenteroides* is well known as a dominant species in kimchi, while other *Leuconostoc* species, including *Leuconostoc lactis*, have also been isolated from kimchi (4, 5, 9, 11). The strain *Leuconostoc gelidum* KCTC 3527, known to be present in kimchi (7), from the Korean Collection for Type Cultures, was isolated from kimchi and grown under standard conditions (Lactobacilli MRS broth, 30°C, 200 rpm). Genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (3). We then sequenced the genome of *Leuconostoc gelidum* KCTC 3527, since genome sequencing of this organism had not been completed or initiated when our project was proposed according to the Genomes OnLine Database (GOLD) (10). In this report, we present the draft genome sequence of strain *Leuconostoc gelidum* KCTC 3527, consisting of 43 contigs. A whole-genome shotgun strategy using Roche-454 Titanium pyrosequencing was performed by the Genome Resource Center, Korea Research Institute of Bioscience and Biotechnology (KRIIB). Genome sequences from pyrosequencing were processed by Roche’s software according to the manufacturer’s instructions. Quality filtered reads were assembled in silico using the 454 Newbler 2.3 assembler, giving 43 contigs, with a size range between 99 and 2,000 bp. Open reading frames (ORFs) were predicted using a Gimmer 3.02 modeling software package (6) and RNAmmer-1.2 (8) and searched using the Clusters of Orthologous Groups database (12). The draft genome sequence was also uploaded into the RAST (Rapid Annotation using Subsystem Technology) server to check the annotated sequences and screen for non-coding rRNAs and tRNAs.

The percentage of GC content in all contigs was 36%. The predicted proteins were annotated by BLAST (1) and the RAST server (2). A total of 79% (3,541) of ORFs were annotatable with known proteins. The genome contained 1,930 protein coding genes, 1 copy of the 5S rRNA gene, 4 tRNA genes, 21 copies of large subunit-small subunit (LSU-SSU) ribosomal proteins, and 24 copies of RNA genes. There were 1,930 possible ORFs in 43 contigs, with a size range between 99 and 5,862 bp. There were not many ORFs with lengths of >2,000 bp (only 104); in fact, most were <1,500 bp.

The genome contains putative genes for permeases of the major facilitator superfamily, transcriptional regulator, integral membrane protein, 3-oxoacyl protein, and glycerolphosphoryl diester phosphodiesterase. There were 28 subsystems represented in the genome, and we used this information to reconstruct the metabolic network. There are many amino acid derivatives and carbohydrate subsystem features, including genes involved in methionine biosynthesis, arginine biosynthesis extended, the pentose phosphate pathway, beta-glucoside metabolism, and L-ascorbate utilization. Genes not yet conclusively identified in the inventory include those encoding the capacity of carbohydrate and amino acid derivative subsystems. These features may well be identified upon closure of the genome.

**Nucleotide sequence accession number.** The draft genome sequence of *Leuconostoc gelidum* KCTC 3527 is available in GenBank under the accession number AEMI0000000.

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**Leuconostoc gelidum** KCTC 3527 is found mainly in vegetables and plays an important role in vegetable fermentation, including that of Korean traditional kimchi. Here we announce the draft genome sequence of *Leuconostoc gelidum* KCTC 3527, isolated from Korean traditional kimchi, and describe major findings from its annotation.


