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Genome Sequence of *Leuconostoc argentinum* KCTC 3773[∇]

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***Leuconostoc argentinum* is one of the most prevalent lactic acid bacteria present during the manufacturing
process of kimchi, the best-known traditional Korean dish. Here, we present the draft genome sequence of type
strain KCTC 3773 of *Leuconostoc argentinum* (1,720,683 bp, with a G+C content of 42.9%), which consists of
98 large contigs (>100 bp in size).**

Kimchi is a fermented vegetable product made of various vegetables, such as Chinese cabbage, radish, and cucumber, and a seasoning mixture (red pepper powder, garlic, ginger, and green onion) (7). The fermentation process involved in making kimchi has been studied extensively by microbiologists with respect to its ecology, proteomics, genetics, and physiology (6, 9, 12). Our laboratory received the *Leuconostoc argentinum* KCTC 3773 strain, which is known to be present in kimchi (2), from the Korean Collection for Type Cultures (KCTC), and it was grown under standard conditions (lactobacilli MRS broth [catalog no. 0881; Difco], 30°C, and 200 rpm). The genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (3). We then sequenced the genome of *Leuconostoc argentinum* KCTC 3773; genome sequencing of this organism had not been completed or initiated when our sequencing project began, according to the Genomes OnLine Database (GOLD) (10).

Here we report the genome sequence of *Leuconostoc argentinum* KCTC 3773, obtained using a whole-genome shotgun strategy (5) by Roche 454 GS (FLX Titanium) pyrosequencing (244,271 reads, totaling ~86 Mb; ~50-fold coverage of the genome) at the Genome Resource Center, KRIBB (Korea Research Institute of Bioscience and Biotechnology). Genome sequences obtained by pyrosequencing were processed by Roche's software, according to the manufacturer's instructions. All of the reads were assembled using Newbler Assembler 2.3 (454 Life Science), which generated 98 large contigs (>100 bp in size; AEGQ01000001 to AEGQ01000098). The annotation was done by merging the results obtained from the RAST (Rapid Annotation using Subsystem Technology) server (1), Glimmer 3.02 modeling software package (4), tRNAscan-SE 1.21 (11), and RNAmmer 1.2 (8). In addition, the contigs were searched against the KEGG, UniProt, and COG (Clusters of Orthologous Groups) databases to annotate the gene descriptions. The G+C mole percent measurements were calculated using the genome sequences. The DNA base composition was calculated using Java.

The uncompleted draft genome includes 1,720,683 bases and is comprised of 1,774 predicted coding sequences (CDSs), with a G+C content of 42.9%. There are single predicted copies of the 5S, 16S, and 23S rRNA genes and 48 predicted tRNAs. There are 28 subsystems that are represented in the genome, and we used this information to reconstruct the metabolic network (determined using the RAST server). There are many carbohydrate subsystem features, including genes involved in central carbohydrate, monosaccharide, and fermentation metabolism. There are also many protein metabolism features, including protein biosynthesis machinery such as the large subunit (LSU) and small subunit (SSU) of the bacterial ribosome. There are two predicted acetate kinase enzymes (EC 2.7.2.1) and an alcohol dehydrogenase enzyme (EC 1.1.1.1). There are also putative genes for the synthesis of all essential amino acids, including arginine, threonine, tryptophan, and valine, and of a number of essential vitamins, including biotin. In addition, there are 17 predicted genes related to fatty acids and to resistance to antibiotics and toxic compounds.

Nucleotide sequence accession number. The draft genome sequence of *Leuconostoc argentinum* KCTC 3773 is available in GenBank under the accession number AEGQ00000000.

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