Genome Sequence of *Leuconostoc inhae* KCTC 3774, Isolated from Kimchi[▽]

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***Leuconostoc inhae* strain KCTC 3774 is a Gram-positive, non-spore-forming, heterofermentative, spherical or lenticular lactic acid bacterium. Here we announce the draft genome sequence of *Leuconostoc inhae* KCTC 3774, isolated from traditional Korean kimchi, and describe major findings from its annotation.**

The fermentation of kimchi, a traditional Korean food, is initiated by various microbes originating from raw materials and the environment (4, 6, 11). Taxonomically diverse groups of lactic acid bacteria have been found during the fermentation process. Some important species responsible for the fermentation of kimchi are leuconostocs, such as *Leuconostoc mesenteroides*, *Leuconostoc pseudomesenteroides*, and *Leuconostoc lactis*, as well as lactobacilli, including *Lactobacillus brevis* and *Lactobacillus plantarum* (7, 10, 11).

The *Leuconostoc inhae* strain KCTC 3774, known to be present in kimchi (7, 8) based upon the Korean Collection for Type Cultures, was grown under standard conditions (lactobacilli MRS broth; 30°C and 200 rpm). Genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (3). In this report, we present the draft genome sequence of the *Leuconostoc inhae* strain KCTC 3774 consisting of 983 contigs. A whole-genome shotgun strategy using Roche 454 GS Titanium pyrosequencing was performed by the Genome Resource Center, Korea Research Institute of Bioscience and Biotechnology. The identified genome sequences were processed with Roche's software according to the manufacturer's instructions. Quality-filtered reads assembled *in silico* using the 454 Newbler assembler version 2.3 provided 983 contigs of >100 bp in size, 63 of which were >10,000 bp. Open reading frames (ORFs), predicted using the Glimmer 3.02 modeling software package (5) and RNAmmer 1.2 (9), were searched using clusters of orthologous group (COG) databases (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. All the data mining steps mentioned were carried out automatically with our rational database-driven tools written in Python scripts.

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 72% (2,020) of the ORFs were annotatable with known proteins. The genome contained 2,757 protein coding genes, one copy of the 5S rRNA gene, 47 tRNA genes, and two copies of long subunit-short subunit (LSU-SSU) ribosomal protein genes. There were 2,807 possible ORFs in 983 contigs with sizes ranging between 71 and 3,663 bp. There were not many ORFs longer than 2,000 bp (only 42); most were less than 1,500 bp. The genome contains putative permease genes of the major facilitator superfamily, membrane proteins, transcriptional regulators, glycerophosphoryl diester phosphodiesterase, and cellobiose-specific IIC components. There are 28 subsystems represented in the genome. This information was used to reconstruct the metabolic network (determined using the RAST server). There were many carbohydrate subsystem features, protein metabolism, and amino acid derivatives, including genes involved in methionine and histidine biosynthesis, SSU ribosomal bacteria, common pathways for synthesis of aromatic compounds (DAHP [3-deoxy-D-arabinoheptulosonic acid 7-phosphate] synthase to chorismate), pentose phosphate pathway, beta-glucoside metabolism, fatty acid biosynthesis, and C21 steroid hormone metabolism. Knowledge regarding the genome sequence will facilitate additional bioinformatic and experimental investigations intent upon elucidating the role of carbohydrates and amino acid derivative subsystems in kimchi fermentation.

Nucleotide sequence accession number. The draft genome sequence of *Leuconostoc inhae* KCTC 3774 is available in GenBank under the accession number AEMJ00000000.

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