Genome Sequence of *Lactobacillus versmoldensis* KCTC 3814

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***Lactobacillus versmoldensis* KCTC 3814 was isolated from raw fermented poultry salami. The species was present in high numbers and frequently dominated the lactic acid bacteria (LAB) populations of the products. Here, we announce the draft genome sequence of *Lactobacillus versmoldensis* KCTC 3814, isolated from poultry salami, and describe major findings from its annotation.**

The lactic acid bacteria (LAB) play an important role in the ripening process of raw fermented sausages. In European raw fermented sausages, strains of *Lactobacillus sakei*, *Lactobacillus curvatus*, *Lactobacillus plantarum*, and *Lactobacillus pentosus* are widely used as starter organisms (7). In sausage fermentations performed at 18 to 23°C, the indigenous microflora is usually dominated by strains of *L. sakei* and *L. curvatus* (5, 6, 11). The genus *Lactobacillus* represents the largest group of rod-shaped organisms within the LAB.

The strain *Lactobacillus versmoldensis* KCTC 3814, known to be present in poultry salami (8) based upon the Korean Collection for Type Cultures, was isolated from poultry salami and grown under standard conditions. Genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (3). We then sequenced the genome of *Lactobacillus versmoldensis* KCTC 3814, 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 *Lactobacillus versmoldensis* KCTC 3814, consisting of 102 contigs (~33-fold coverage of the genome). A whole-genome shotgun strategy was used, and pyrosequencing using a Roche 454 Titanium sequencer was performed at the Genome Resource Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB). Genome sequences from pyrosequencing were processed by using Roche software according to the manufacturer's instructions. Quality filtered reads were assembled *in silico* using a 454 Newbler 2.3 assembler, giving 102 contigs of >100 bp in size and 53 contigs of >2,000 bp. Open reading frames (ORFs) were predicted using the Glimmer 3.02 modeling software package (4) and RNAmmer 1.2 (9) 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 noncoding rRNAs and tRNAs.

The percentage of GC content in all contigs was 38%. The predicted proteins were annotated by BLAST (1) and the RAST server (2). A total of 77% of ORFs (1,799) were annotatable with known proteins. The genome contained 2,355 protein-coding genes, 1 copy of the 5S RNA, 51 tRNA genes, and 3 copies of LSU-SSU ribosomal proteins. There were 2,355 possible ORFs in 62 contigs, with a size range of between 114 and 8,883 bp. There were not many ORFs with lengths of >2,000 bp (only 112); in fact, most were <1,500 bp.

The genome contains putative genes for permeases of the integral membrane protein, transcriptional regulator, 3- β -hydroxysteroid dehydrogenase, ABC transporter, and ATP-binding protein. 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 glycolysis and gluconeogenesis, heme and siroheme biosynthesis, folate biosynthesis, threonine and homoserine biosynthesis, and central carbohydrate metabolism. 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 numbers. The draft genome sequence of *Lactobacillus versmoldensis* KCTC 3814 is available in GenBank under accession numbers BACR01000001 to BACR01000102.

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