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Genome Sequence of *Lactobacillus animalis* KCTC 3501▽

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Lactobacillus animalis **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 *Lactobacillus animalis* type strain KCTC 3501 (1,882,795 bp, with a G+C content of 41.1%), which consists of 7 scaffolds.**

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) (9). The fermentation process involved in making kimchi has been studied extensively by microbiologists with respect to its ecology, proteomics, genetics, and physiology (8, 11, 14). Our laboratory received *Lactobacillus animalis* strain KCTC 3501, 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] at 30°C and 200 rpm). The genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (4). We then sequenced the genome of *Lactobacillus animalis* KCTC 3501; genome sequencing of this organism had not been completed when our sequencing project began, according to the Genomes OnLine Database (GOLD) (12).

Here, we report the genome sequence of *Lactobacillus animalis* KCTC 3501, obtained using a whole-genome shotgun strategy (6) consisting of Roche 454 GS FLX Titanium pyrosequencing by synthesis of the paired reads (236,113 reads, totaling ~68.4 Mb; ~36.3-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 paired reads were assembled using Newbler Assembler 2.3 (454 Life Science), which generated 7 scaffolds (GL573153 to GL573159). 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 (5), tRNAscan-SE 1.21 (13), and RNAmmer 1.2 (10). In addition, the contigs were searched against the KEGG (7), UniProt (3), and COG (Clusters of Orthologous Groups) (15) databases to annotate the gene description. The G+C mole percent measurements were calculated using the genome sequences.

The uncompleted draft genome includes 1,882,795 bases and is comprised of 1,836 predicted coding sequences (CDSs), with a G+C content of 41.1%. There are single predicted copies of the 16S and 23S rRNA genes, double predicted copies of the 5S rRNA genes, and 25 predicted tRNAs. There are 246 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, di- and oligosaccharide, 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. The CDSs annotated by the COG database were classified into 3 COG categories (K, R, and S) and 15 COG (COG0488, COG0488, COG0488, COG0488, COG0536, COG0779, COG1272, COG1399, COG1801, COG1939, COG2110, COG2110, COG2740, COG4123, and COG4478). There are 5 alcohol dehydrogenase enzymes (EC 1.1.1.1) and 3 galactose-1-phosphate uridylyltransferase enzymes (EC 2.7.7.10).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in GenBank under accession no. AEOF00000000. The version described in this paper is the first version, which can be found under accession no. AEOF01000000.

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REFERENCES

1. **Aziz, R. K., et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9:**75.
2. **Bae, J. W., et al.** 2005. Development and evaluation of genome-probing microarrays for monitoring lactic acid bacteria. Appl. Environ. Microbiol. **71:**8825–8835.
3. **Bairoch, A., et al.** 2005. The Universal Protein Resource (UniProt). Nucleic Acids Res. **33:**D154–D159.
4. **Birnboim, H. C., and J. Doly.** 1979. A rapid alkaline extraction procedure for screening recombinant plasmid DNA. Nucleic Acids Res. **7:**1513–1523.
5. **Delcher, A. L., K. A. Bratke, E. C. Powers, and S. L. Salzberg.** 2007. Iden-

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tifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics **23:**673–679.
6. **Fleischmann, R. D., et al.** 1995. Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. Science **269:**496–512.
7. **Kanehisa, M., S. Goto, S. Kawashima, Y. Okuno, and M. Hattori.** 2004. The KEGG resource for deciphering the genome. Nucleic Acids Res. **32:**D277–D280.
8. **Kim, M., and J. Chun.** 2005. Bacterial community structure in kimchi, a Korean fermented vegetable food, as revealed by 16S rRNA gene analysis. Int. J. Food Microbiol. **103:**91–96.
9. **Kim, Y. K., E. Koh, H. J. Chung, and H. Kwon.** 2000. Determination of ethyl carbamate in some fermented Korean foods and beverages. Food Addit. Contam. **17:**469–475.
10. **Lagesen, K., et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35:**3100–3108.
11. **Li, S. J., H. Y. Paik, and H. Joung.** 2006. Dietary patterns are associated with sexual maturation in Korean children. Br. J. Nutr. **95:**817–823.
12. **Liolios, K., et al.** 2010. The Genomes OnLine Database (GOLD) in 2009: status of genomic and metagenomic projects and their associated metadata. Nucleic Acids Res. **38:**D346–D354.
13. **Lowe, T. M., and S. R. Eddy.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25:**955–964.
14. **Nan, H. M., et al.** 2005. Kimchi and soybean pastes are risk factors of gastric cancer. World J. Gastroenterol. **11:**3175–3181.
15. **Tatusov, R. L., et al.** 2003. The COG database: an updated version includes eukaryotes. BMC Bioinformatics **4:**41.