

# Draft Genome Sequence of *Lactobacillus delbrueckii* subsp. *bulgaricus* LBB.B5

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***Lactobacillus delbrueckii* subsp. *bulgaricus* LBB.B5 originates from homemade Bulgarian yogurt and was selected for its ability to form a strong association with *Streptococcus thermophilus*. The genome sequence will facilitate elucidating the genetic background behind the contribution of LBB.B5 to the taste and aroma of yogurt and its exceptional protocoooperation with *S. thermophilus*.**

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*Lactobacillus delbrueckii* subsp. *bulgaricus* is invariably found in yogurt produced in the Balkan region in combination with *Streptococcus thermophilus* (1) and occasionally it has been also isolated from raw milk and plant material (2). *L. delbrueckii* subsp. *bulgaricus* strain LBB.B5 was originally isolated in 1969 in the village of Dalboki (Bulgaria, GPS coordinates 42.481258, 25.770522) from homemade yogurt and maintained in the culture collection of LB Bulgaricum PLC (Sofia, Bulgaria). The strain has been used in industry in combination with *S. thermophilus* to produce Bulgarian yogurt with its typical taste and aroma (3, 4). Strain LBB.B5 was chosen for industrial application for yogurt starters for its ability to form a strong association with selected *S. thermophilus* strains (5). Only very few other pairs of *L. delbrueckii* subsp. *bulgaricus* and *S. thermophilus* strains cultures proved to be able to form stable associations, pointing to the rareness of this phenomenon (5). Such continuously co-cultured starters were even assigned the term “symbiotic.” Complete understanding of the nature of protocoooperation between *L. delbrueckii* subsp. *bulgaricus* and *S. thermophilus* needs underpinning from genomic data. Also, there are very few genome-based analyses that point to the properties that make a given *L. delbrueckii* subsp. *bulgaricus* strain suitable for industrial application (6).

The genome sequence of strain LBB.B5 was determined using a 101-bp paired-end library with Illumina Hiseq 2000 technology (Illumina, San Diego, CA) at BaseClear (Leiden, the Netherlands). A total of 2,545,204 reads were generated and assembled by IDBA-UD 1.1.1 (7) into 129 contigs of which 101 contigs were larger than 500 bp. Functional annotations of the predicted genes were performed using the RAST annotation server (8). Sequencing of strain LBB.B5 led to a final draft genome sequence of 1,777,882 bp, which contains 1,841 open reading frames (ORFs). Five rRNA genes and 74 tRNA genes were identified next to 33 pseudogenes. The G+C content of the genome is 49.8%. Based on its genome sequence, strain LBB.B5 was predicted to synthesize serine and cysteine, two of the four important amino acid synthe-

sis pathways essential to the industrial application of a strain (9). Strain LBB.B5 was found to contain a complete set of genes for phosphate transport/homeostasis, peptide transport, and *de novo* fatty acids synthesis.

The genome information of *L. delbrueckii* subsp. *bulgaricus* LBB.B5 presented here will be useful for further studies into the genomic determinants for protocoooperation and fermentation performance.

**Accession number(s).** The sequence data for the genome described here have been deposited at GenBank under the accession number [LUGK00000000](https://ncbi.nlm.nih.gov/nucl/LUGK00000000) and RefSeq accession number [NZ\\_LUGK00000000](https://ncbi.nlm.nih.gov/RefSeq/record/NC_020411).

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