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Draft Genome Sequence of the Probiotic *Bifidobacterium longum* subsp. *longum* Strain MC-42

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Here, we report the draft genome sequence of *Bifidobacterium longum* subsp. *longum* strain MC-42 isolated from the feces of a healthy infant, and which was used in the commercially available probiotic product Biovestin.

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Bifidobacteria, belonging to the *Actinobacteria* group, are Gram-positive bacteria with high G+C content that are commonly found in the human gastrointestinal tract (1). Members of genus *Bifidobacterium* are usually used as probiotic organisms, which provide a health benefit to the host (2). *Bifidobacterium longum* is widely used as a probiotic due to its resistance to the high acidic environment during the gastric transit (3, 4). Here, we present the draft genome sequence of *B. longum* subsp. *longum* strain MC-42 isolated from the feces of a healthy infant, and which was used in the commercially available probiotic product Biovestin.

Genomic DNA of *B. longum* was isolated from cultured cells by using a GeneJET genomic DNA purification kit (Thermo Scientific) according to the manufacturer's instructions. Then, genomic DNA was sheared in a microTUBE AFA fiber snap-cap tube using a Covaris S2 instrument (Covaris) with a medium size distribution of fragments of about 500 bp. The paired-end library was prepared using a NEBNext Ultra DNA library prep kit for Illumina (NEB). Whole-genome sequencing of the *B. longum* library was conducted on a MiSeq genome sequencer (2 × 300 cycles, Illumina) in the SB RAS Genomics Core Facility (ICBFM SB RAS, Novosibirsk, Russia). The entire genome was assembled *de novo* with CLC Genome Workbench software v8.5 (CLC Bio). The automatic functional annotation results were obtained using the NCBI Prokaryotic Genome Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

A total of 924,022 reads were generated from the *B. longum* genome. Reads were assembled to a draft genome of 2,287,827 nucleotides at 80-fold coverage with 59.8% G+C content. The genome sequence consists of 29 contigs. The *B. longum* MC-42 genome contains 1,827 coding sequences, four rRNA operons, and 51 tRNA genes. A total of 46 pseudogenes, three noncoding RNA (ncRNA) genes, two clusters of regularly interspaced short palindromic repeat (CRISPR) systems, and 22 frameshifted genes were predicted using PGAAP.

Accession number(s). The whole-genome shotgun project of *B. longum* has been deposited in GenBank under the accession number LNCM00000000.

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