Complete Genome Sequence of *Bifidobacterium longum* subsp. *longum* KACC 91563[▽]

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***Bifidobacterium longum* strains predominate in the colonic microbiota of breast-fed infants. Here we report the complete genome sequence of *B. longum* subsp. *longum* KACC 91563, isolated from feces of neonates. A single circular chromosome of 2,385,301 bp contains 1,980 protein-coding genes, 56 tRNA genes, and 3 rRNA operons.**

Members of the genus *Bifidobacterium* are prevalent in the human colon and represent up to 90% of all bacteria in fecal samples of breast-fed infants and 3 to 5% of adult fecal microbiota (7, 8). Currently the genus harbors 32 species (2), and among these, *B. longum* strains often predominate in the colonic microbiota of breast-fed infants (4, 5). Many studies suggest that *Bifidobacterium longum* provides potential health benefits to human over a wide range of health conditions, for example, cholesterol reduction (11) and cancer prevention (9). Here we report the complete genome sequence, including its two plasmids, of *B. longum* subsp. *longum* KACC 91563, isolated from feces of healthy neonates.

The entire genome and two plasmids of *B. longum* KACC 91563 were sequenced using a Roche 454 Life Sciences GS FLX sequencer with paired-end and shotgun libraries (222× coverage) at the National Instrumentation Center for Environmental Management (NICEM, Seoul National University, Seoul, Republic of Korea). The obtained sequences were assembled using Newbler, and the gaps between contigs were closed by sequencing direct PCR products using BigDye chemistry and an ABI3730 capillary sequencer (Applied Biosystems). PCR products containing long repetitive areas were cloned using a pEZSeq cloning kit (Lucigen Corp.). The obtained clones were sequenced using a template generation system kit (Solgent). The viewing and editing of the sequences were done using Consed (6).

The protein-coding sequence was predicted using a Glimmer 3.0 (3). Protein functions were annotated by using a sequence similarity search using BLAST programs (1) against the proteins of the other *B. longum* strains and the nonredundant protein database of the NCBI. tRNA genes were predicted by tRNAscan-SE (10). rRNA genes were searched by BLASTN analysis using rRNA sequences.

We assembled the sequences into a single circular chromosome of 2,385,301 bp and two circular plasmids of 4,233 bp and 6,230

bp. The overall G+C content is 59.8%. The main genome contains 1,980 protein-coding genes, 56 tRNA genes, and 3 rRNA operons. One of the plasmids contains 6 protein-coding genes, while the other contains 9 protein-coding genes. In the main genome, protein functions have been annotated for 1,574 coding sequences (CDSs) (79.5%), whereas 406 (20.5%) of the CDSs were classified as corresponding to hypothetical proteins. In the plasmids, 8 CDSs were assigned protein functions and 6 CDSs were annotated as corresponding to hypothetical proteins.

Nucleotide sequence accession numbers. The complete genome and two plasmid sequences of *B. longum* KACC 91563 are available in GenBank under accession numbers CP002794 to CP002796.

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