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Complete Genome Sequence of *Bifidobacterium longum* subsp. *longum* BBMN68, a New Strain from a Healthy Chinese Centenarian▽

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***Bifidobacterium longum* subsp. *longum* BBMN68 was isolated from the feces of a healthy centenarian living in an area of BaMa, Guangxi, China, known for longevity. Here we report the main genome features of *B. longum* strain BBMN68 and the identification of several predicted proteins associated with the ecological niche of longevity.**

Bifidobacteria are Gram-positive bacteria which naturally inhabit the human gastrointestinal tract and vagina and play vital roles in maintaining human health (7, 14). *Bifidobacterium longum* subsp. *longum* BBMN68 (CGMCC 2265) is a new strain isolated from the feces of a centenarian living in an area of BaMa, Guangxi, China, known for longevity (15, 16). We determined the complete genome sequence of strain BBMN68 by a whole-genome shotgun strategy using both Roche's 454 next-generation sequencing and ABI's SOLiD platforms. After achieving 38X coverage raw reads, we assembled them into 166 contigs with Newbler and closed gaps by sequencing PCR products on an ABI 3730XL DNA analyzer. Genome finishing was carried out using the Phred/Phrap/Consed software package (http://www.phrap.org) (4, 5, 6). Protein-coding genes were predicted by Glimmer and Genemark (3). Artemis was used for final verification of the annotation results (12).

B. longum subsp. *longum* BBMN68 has one circular chromosome of 2,265,943 bp and is composed of 59.95% G+C without any plasmid. This genome size is smaller than those of *B. longum* ATCC 15697 (2.83 Mb), *B. longum* JDM301 (2.48 Mb), and *B. longum* DJO10A (2.38 Mb; NC_010816) and is slightly larger than the complete genome of *B. longum* NCC2705 (2.26 Mb; NC_004307). The BBMN68 genome contains 1,814 predicted protein-coding sequences, 16 rRNA operons, and 57 tRNAs. In addition, a total of 42 insertion sequence (IS) elements were found. Among these ISs, we detected a new IS*1595* family which encodes an aminoglycoside nucleotidyltransferase (BBMN68_1166) (1). No functional phages were identified in the genome sequence.

Genome annotation with clusters of orthologous groups revealed that about 10.7% of the total predicted protein-coding genes were in the carbohydrate transport-metabolism category, more than in the genomes of both *B. longum* NCC2705 (13) and DJO10A (11). The sugar transporters and hydrolases are organized into nine distinct gene clusters, including at least 10 ABC-type MalEFG sugar transporters and three Na^+/sugar symporters. Several genes involved in oligo- or polysaccharide synthesis (BBMN68_1004, BBMN68_1297) and sugar efflux (BBMN68_78, BBMN68_188, BBMN68_1664, BBMN68_1684) were found in the genome.

A gene encoding a serine protease inhibitor (BBMN68_154) with almost 100% similarity to that of other *B. longum* species was identified (10). Genes for a conjugated bile acid hydrolase (BBMN68_536) and an Na^+/bile acid symporter (BBMN68_849) were uncovered that belong to the bile acid metabolic pathway and are involved in a specific hydrolase or exclusion system (8). Furthermore, genes for a phage lysine-like lysozyme (BBMN68_552) and a bacteriolytic endo-β-*N*-acetylglucosaminidase D with a secretory signal peptide (BBMN68_222) were determined. Through BAGEL (2) and BACTIBASE (9) analyses, genes for two bacteriocins (BBMN_68_146, encoding colicin M, and BBMN68_67, encoding epicidin 280) were also found in *Bifidobacterium* for the first time. Finally, the major prokaryotic DNA recombination pathway encoded by *recA* (BBMN68_305), *recB* (BBMN68_1116), and *recD* (BBMN68_1757) was identified in the genome; this is lacking in that of *B. longum* NCC2705 (13). The genome sequence of BBMN68, from the lower gastrointestinal tract niche of a centenarian, indicates that this strain is endowed with a new characteristic associated with long survival competence.

Nucleotide sequence accession number. The complete nucleotide sequence of the *B. longum* subsp. *longum* BBMN68 chromosome was deposited in GenBank under accession number CP002286. More detailed annotations are available from GenBank.

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