



Draft Genome Sequences of *Bifidobacterium* Strains Isolated from Dietary Supplements and Cultured Food Products

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ABSTRACT Here, we present the genome sequences of 23 *Bifidobacterium* isolates from several commercially available dietary supplements and cultured food products. Strains of this genus are natural inhabitants of the mammalian mouth, gastrointestinal tract, and vagina. Some species are considered beneficial to human health.

Bifidobacterium species are Gram-positive non-spore-forming anaerobic bacteria. Although they produce lactic acid during fermentation, they are not part of the lactic acid group due to genetic unrelatedness between species (1). These species have been isolated from the stool of breast-fed infants (2, 3) and are the predominant species in their gut microflora (4). *Bifidobacterium* species have been identified as nonpathogenic bacteria, as evidenced by their natural gut colonization and use in fermented foods. Over 45 species of *Bifidobacterium* are currently recognized, with *Bifidobacterium longum* and *Bifidobacterium animalis* being the most commonly used in dietary supplements (1, 3). Due to the high degree of similarity among species (87.7 to 99.5% based on 16S rRNA gene sequencing), *Bifidobacterium* species have often been taxonomically misclassified by existing identification methods (5–7). However, using whole-genome sequencing, it is now possible to reliably distinguish unique subspecies within the genus (8, 9). As more products containing *Bifidobacterium* species become available on the market, the need for a genomic reference collection becomes necessary for the identification and phylogenetic comparison of the different strains being consumed. Therefore, 23 genomes of *Bifidobacterium* species isolated directly from dietary supplements were sequenced and classified using phylogenetic methods.

Pure culture isolates from various products were grown anaerobically for 48 h in Lactobacilli MRS broth at 37°C. DNA extractions were performed with the QIAcube instrument (Qiagen) using the manufacturer's Gram-positive bacterium protocol. Sequencing libraries were prepared with 1 ng of DNA using the Nextera XT DNA sample prep kit (Illumina, San Diego, CA) and sequenced on either the Illumina MiSeq or NextSeq platform. The resulting paired-end reads were quality controlled using FastQC (Q > 30) and *de novo* assembled using SPAdes 3.8.2 (8) or CLC Genomics Workbench 8.2.1 (CLC bio, Aarhus, Denmark).

Depth of coverage for the draft genomes ranged from 28.6× to 290.9×, with genome sizes ranging from 1,916,859 to 2,448,259 bp. The number of contigs ranged from 13 to 417, while the N_{50} values ranged from 23,859 to 1,021,771 bp. The GC content varied from 58.9 to 62.9%. The sequences of these 23 *Bifidobacterium* isolates were submitted to GenBank and included 10 *B. animalis* subsp. *lactis*, 6 *B. animalis* subsp. *longum*, 6 *B. bifidum*, and 1 *B. breve* strain.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under BioProject number PRJNA336518 and accession numbers [QDIF00000000](https://doi.org/10.1128/genomeA.00610-18) to [QDJB00000000](https://doi.org/10.1128/genomeA.00610-18). The versions described in this paper are the first versions.

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