



Fifty-Six Draft Genome Sequences of 10 *Lactobacillus* Species from 22 Commercial Dietary Supplements

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ABSTRACT Here, we present the genome sequences of 56 isolates of 10 species of the genus *Lactobacillus* that are considered beneficial components of the gut microbiota. The isolates examined were found in commercially available dietary supplements in the U.S. market.

Lactobacilli are Gram-positive, facultative anaerobic or microaerophilic, non-spore-forming rods with a DNA G+C content typically below 50%. They are one of the major constituents of the lactic acid bacteria group, whose primary fermentation end product is lactic acid (1). These bacteria are part of the normal human gastrointestinal (GI) microbiota, and they may also be found in the GI tract of other mammalian species (2, 3). The genus *Lactobacillus* is known to be highly diverse, with more than 80 recognized species and a complex phylogenetic history (2). Some *Lactobacillus* species have been attributed to have probiotic properties, which upon ingestion in sufficient quantities can provide health benefits to the consumer (4). As part of our ongoing work to expand the observed genomic diversity of the *Lactobacillus* group, we sequenced the genomes of 56 isolates of 10 species of the genus *Lactobacillus* found in commercially available dietary supplement products.

Pure cultures of each isolate were grown under microaerophilic conditions in MRS broth for 48 h at 37°C. Total genomic DNA was extracted from 1.2 ml of the 48-h culture using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany). DNA extractions were performed with the Qiagen QIAcube instrument using the manufacturer's protocol for Gram-positive bacteria. Sequencing libraries were prepared with 1 ng of DNA using the Nextera XT DNA sample prep kit (Illumina, San Diego, CA, USA) 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 version 3.11.1 (5) or CLC Genomics Workbench version 8.2.1 (CLC bio, Aarhus, Denmark).

Depths of coverage for the draft genomes ranged from 21× to 229×, with the genome sizes ranging from 1,956,319 to 3,301,350 bp. The number of contigs ranged from 22 to 309, while the N_{50} values ranged from 30,183 to 722,638 bp. The 56 *Lactobacillus* isolates were identified as belonging to 1 of the following 10 species: *L. acidophilus* (11), *L. rhamnosus* (10), *L. plantarum* (9), *L. casei* (8), *L. reuteri* (5), *L. salivarius* (4), *L. helveticus* (4), *L. fermentum* (2), *L. zeae* (2), and *L. brevis* (1). The average genome size and G+C content for each of the 10 species are as follows: *L. acidophilus*, 2.0 Mb, 34.6%; *L. brevis*, 2.2 Mb, 46.1%; *L. casei*, 3.2 Mb, 46.1%; *L. fermentum*, 2.0 Mb, 51.8%; *L. helveticus*, 2.0 Mb, 36.6%; *L. plantarum*, 3.2 Mb, 44.5%; *L. reuteri*, 2.0 Mb, 38.7%; *L. rhamnosus*, 2.9 Mb, 46.7%; *L. salivarius*, 2.0 Mb, 32.9%; and *L. zeae*, 3.0 Mb, 47.3%, respectively.

Accession number(s). The draft genome assemblies were deposited in DDBJ/ENA/GenBank under the accession numbers [QAGU00000000](#) to [QAHZ00000000](#) and

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QAZD00000000 to QBAA00000000 (BioProject number PRJNA336518). The versions described in this announcement are the first ones.

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