



Complete Genome Sequence of *Lactobacillus acidophilus* Strain ATCC 53544

Scott N. Dean,^a  Gary J. Vora,^b  Scott A. Walper^b

National Research Council Research Associateship Program, Washington, DC, USA^a; Center for Bio/Molecular Science & Engineering (Code 6900), U.S. Naval Research Laboratory, Washington, DC, USA^b

ABSTRACT Here we present the complete genome sequence of *Lactobacillus acidophilus* ATCC 53544. The assembly contains 1,991,906 bp and is 99.7% similar to *L. acidophilus* NCFM. This strain was isolated from a rectal swab specimen of an infant and has previously been used as a feed supplement for animals.

The ATCC 53544 strain of *Lactobacillus acidophilus* (<https://www.atcc.org/en/Products/All/53544.aspx>) was originally isolated from a human infant rectal swab specimen (1). This strain has been shown to attach to human intestine cells, with improved adherence in the presence of calcium (1, 2). In addition, it has been found to inhibit growth of clinical toxic shock syndrome strains of *Staphylococcus aureus*, produce hydrogen peroxide, and degrade oxalate and bile salts (3–5).

The genome was sequenced on a Pacific Biosciences RS II sequencing platform using a 20-kb insert library and one single-molecule real-time (SMRT) sequencing cell. The genome assembly was carried out using the Pacific Biosciences Hierarchical Genome Assembly Process 2.0 (HGAP 2.0), and consensus polishing was performed with SMRTpipe Quiver. Glimmer v 3.02 was used to predict coding sequences (CDSs) and open reading frames (ORFs). Blastall was used for the alignment of ORFs and Blast2GO was used for annotation. rRNAs and tRNAs were predicted using RNAmmer 1.2 and tRNAscan-SE 1.4. The ATCC 53544 genome was aligned against other *L. acidophilus* genomes using progressiveMauve (6). The final assembly was composed of a single 1,991,906-bp chromosome with a mean G+C content of 34.7%. The genome contains one clustered regularly interspaced short palindromic repeat (CRISPR) array. The annotation predicted 1,892 CDSs, 12 rRNAs, and 61 tRNAs, and 1,482 of the annotated genes were categorized into 29 different functional Gene Ontology Consortium (GO) terms.

Comparative genome analysis revealed a 99.7% similarity with *L. acidophilus* NCFM (7), 99.9% similarity with *L. acidophilus* La-14 (8), and 98.6% similarity with *L. acidophilus* ATCC 4356 (9). In comparison with *L. acidophilus* NCFM, 245 single nucleotide polymorphisms (SNPs) and 121 gaps were found. One large chromosomal inversion was found (between 479,341 and 485,108 bp), where homologs of surface layer protein A (*slpA*), *LBA0170*, *LBA0171*, *LBA0173*, and *slpB* are in reverse complement orientation. Large regions that lack any detectable homology contain two 23S rRNAs and one 16S rRNA. Additionally, regions containing the majority of SNPs and gaps are near rearrangement sites, such as within gene homologs of a putative surface protein, *LBA1654*, previously identified as a potential strain-specific cell-surface protein in a differential BLAST analysis study in *L. acidophilus* (10), and hypothetical proteins *LBA1655* and *LBA1656*. In comparison with the type strain *L. acidophilus* ATCC 4356, 201 SNPs and 219 gaps were found and several large chromosome inversions and rearrangements were identified. Of note were significant regions that lack detectable homology or many SNPs, including within the homologs of a putative cellobiose phosphotransferase, *ERR203994_01916*, a

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Address correspondence to Scott A. Walper, scott.walper@nrl.navy.mil.

surface protein-encoding *ERR203994_01916*, *slpB*, and other surface proteins that are variable in *L. acidophilus* strains, including *LBA1654*. The *L. acidophilus* ATCC 53544 genome demonstrates similarities among the *L. acidophilus* strains sequenced so far and offers an opportunity to perform research to investigate how small genomic variations, in particular changes in genes encoding cell-surface proteins, may impact cell adherence, cell-host interaction, and other probiotic functionalities within the species.

Accession number(s). The genome sequence reported here has been deposited in GenBank under the accession number [CP022449](#) and is a component of BioProject number PRJNA394684. The version described in this paper is CP022449.1.

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