

Genome Sequence of the Naturally Plasmid-Free *Lactobacillus plantarum* Strain NC8 (CCUG 61730)

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***Lactobacillus plantarum* is a highly versatile lactic acid bacterium found in various ecological niches, such as fermented vegetable, meat, and dairy products and the gastrointestinal tract. We sequenced the genome of *L. plantarum* NC8, a naturally plasmid-free strain, which has been used as a model strain in many laboratories worldwide.**

Lactic acid bacteria (LAB) are important in several fermentation processes and as commensals/symbionts in the gastrointestinal (GI) tract (3, 20). One of the most versatile LAB species is *Lactobacillus plantarum* (16). Strains of *L. plantarum* can colonize the GI tract (1, 10) as well as dominate many fermentations of food and feed products (7, 11). The versatility and metabolic capacity make *L. plantarum* interesting for industrial applications, and some strains are marketed as starter cultures or probiotics (7, 9, 22). *L. plantarum* WCFS1 was the first *Lactobacillus* strain to be genome sequenced (6) and was recently resequenced and reannotated (15). Presently, three additional *L. plantarum* genomes are publically available (17, 21, 23).

L. plantarum strain NC8 (CCUG 61730) was isolated in the 1980s from grass silage and identified as naturally plasmid free, an unusual property among *L. plantarum* strains. NC8 has been used as a model strain in the development of genetic tools, such as conjugation (14), transformation (2), and expression vectors (18, 19), in lactobacilli. It has also been used in studies of bacteriocin production (8), general fermentations (4), and metabolic engineering (13). Here, we report the genome sequence of *L. plantarum* NC8.

Whole-genome sequencing was performed (GATC, Konstanz, Germany) with a combined strategy using 454 single-end sequencing (500,381 reads totaling ~220 Mb; ~69-fold coverage) on a GS FLX platform and Illumina paired-end sequencing with an insert length of 300 bp. The initial assembly of 454 reads was with Newbler, and contigs were further assembled using paired-end reads together with mapping to the reference genome of *L. plantarum* WCFS1 (6, 15). The assembled draft genome, consisting of 10 contigs with a total length of 3,207,224 bp and 44.5% GC content, has 2,868 predicted protein-coding sequences (CDS), 64 pseudogenes, 5 rRNA operons, 70 tRNA genes, and no plasmids. Automatic annotation was done with the Institute for Genome Sciences (IGS) pipeline (<http://ae.igs.umaryland.edu/cgi/index.cgi>) and curated using the highly homologous curated genome of *L. plantarum* WCFS1 (15). New CDS were manually annotated using NCBI BLAST and InterProScan (12).

Comparison with published genomes of *L. plantarum* strains WCFS1 (6, 15), ATCC 14917 (GenBank accession number NZ_ACGZ00000000.2), JDM1 (23), and ST-III (21) shows that all of the genomes are highly colinear with the exception of the type and location of prophages; some prophages of NC8 are novel,

while others are present in strain WCFS1 or JDM1. Most of the orthologous genes of strains NC8, WCFS1, and ATCC 14917 have >98% nucleotide sequence identity. Exceptions include gene clusters for extracellular polysaccharide (EPS)/capsular polysaccharide (CPS) biosynthesis which are variable in gene content and nucleotide sequence identity in all *L. plantarum* genomes (17); strain NC8 shares some of these EPS/CPS genes with other strains but also has a novel EPS/CPS cluster of 10 genes. An NC8 cluster of 12 genes encodes a type III restriction-modification system not present in the other genomes. Only strains NC8 and ATCC 14917 encode a tannase (tannin acyl hydrolase), which is produced by some microorganisms to assist in the degradation of plant-derived tannins into gallic acid (5).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AGRI00000000](https://www.ncbi.nlm.nih.gov/nuccore/AGRI00000000). The version described in this paper is the first version, AGRI01000000.

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