

Complete Genome Sequence of *Streptococcus thermophilus* Strain MN-ZLW-002

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***Streptococcus thermophilus* MN-ZLW-002 was originally isolated from traditionally fermented Chinese dairy products. One of the strain-dependent characteristics of this bacterium is its ability to produce exopolysaccharides (EPSs). This study determined and analyzed the genome sequence of MN-ZLW-002. Its complete genome comprised 2,046 genes and 1,848,520 nucleotides with an average GC content of 39%. The EPS cluster of MN-ZLW-002 includes 25 open reading frames (ORFs), and some results indicate a horizontal gene transfer between MN-ZLW-002 and other lactic acid bacteria (LAB).**

Lactic acid bacteria (LAB) are a heterogeneous group of microorganisms that convert carbohydrates into lactic acid. *Streptococcus thermophilus* is an important lactic acid bacterium in the dairy industry worldwide and has long been used as a starter culture for fermented dairy products. *S. thermophilus* MN-ZLW-002 was originally isolated from a traditional fermented dairy food called Yogurt Block, originating from the Gannan region of Gansu province, China. MN-ZLW-002 has many good fermentation characteristics, but the most prominent is the ability to produce exopolysaccharides (EPSs).

EPSs produced by LAB in fermented milk or yogurt improve the viscosity, body, texture, and taste of the final product (2, 3). In addition, LAB-derived EPSs contribute to human health through their potential antitumor, antiulcer, immunomodulating, and cholesterol-lowering properties (4, 14).

Whole-genome sequencing of *S. thermophilus* strain MN-ZLW-002 was performed with a combined strategy of 454 sequencing (10) and Solexa paired-end sequencing technologies (1). Genomic libraries containing 8-kb inserts were constructed, and 188,861 paired-end reads and 64,276 single-end reads were generated using the GS FLX system, giving 45-fold coverage of the genome. The majority (97.4%) of reads were assembled into three large scaffolds, including 50 nonredundant contigs, using the 454 Newbler assembler (454 Life Sciences, Branford, CT). A total of 339,700,400 reads (500 bp library) were generated to reach a depth of 180-fold coverage with an Illumina Solexa GA IIx (Illumina, San Diego, CA) and mapped to the scaffolds using Burrows-Wheeler alignment (BWA) (8). The gaps between scaffolds were filled by sequencing PCR products using an ABI 3730 capillary sequencer. The genome analysis was performed as described previously (5, 6).

The complete genome sequence of MN-ZLW-002 contains a circular 1,848,520-bp chromosome with a GC content of 39%. There are 2,046 genes in total, including 1,910 coding genes, 5 rRNA operons, and 57 tRNAs in the MN-ZLW-002 genome.

EPSs produced by LAB benefit the health of host animals (9, 11, 13, 15). Recently, EPSs from LAB have been shown to enhance the immune responses of host animals (7, 12). These immunoregulatory effects of EPSs might be related to their chemical composition. In the present study, we analyzed the EPS cluster of MN-ZLW-002 bacteria to elucidate the underlying mechanisms by which the fermented milk prepared using MN-ZLW-002 affects the immune response of host animals.

The EPS cluster of MN-ZLW-002 comprises 20,358 nucleotides, including 24 open reading frames (ORFs) in the sense orientation; 1 ORF is oriented in the antisense direction. In front of the EPS cluster, there is a *deoD* gene encoding purine nucleoside phosphorylase (PNP). The first four genes, *epsA*, *epsB*, *epsC*, and *epsE*, are conserved among the four compared genomes. Behind the EPS cluster, there are 2 ORFs oriented in the antisense direction; these ORFs encode transposases, indicating a horizontal gene transfer between MN-ZLW-002 and other LAB.

Nucleotide sequence accession number. The sequence and annotation of the *Streptococcus thermophilus* MN-ZLW-002 genome are available from GenBank under accession number CP003499.

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