

Complete Genome Sequence of the Probiotic *Lactobacillus plantarum* ST-III[∇]

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Received 28 September 2010/Accepted 19 October 2010

***Lactobacillus plantarum* strain ST-III, a probiotic strain with several functions, was isolated from kimchi. Here we report the complete genome sequence of ST-III and compared it with two published *L. plantarum* genomes.**

Lactobacillus plantarum is a flexible and versatile species that is encountered in a variety of environmental niches (5) and can be used as probiotic supplements both in dairy products and other foods. *L. plantarum* strain ST-III, originally isolated from kimchi, has many probiotic properties, such as cholesterol removal (8) and strong adhesion to the Caco-2 cells (2).

Whole-genome sequencing of ST-III was performed with a combined strategy of Roche 454 and Solexa paired-end sequencing technology. A genomic library containing an 8-kb insert was constructed, and 186,059 paired-end reads and 58,975 single-end reads were generated using the GS FLX system, giving 28.04-fold coverage of the genome. Using the 454 Newbler (454 Life Sciences, Branford, CT), about 97% of the reads were assembled into two large scaffolds, including 51 contigs. A total of 11,548,718 reads (3-kb library) were generated to reach a depth of 262-fold coverage with an Illumina Solexa GA IIx (Illumina, San Diego, CA) and mapped to the scaffolds using the Burrows-Wheeler alignment (BWA) tool (6). Most of the gaps within the scaffolds were filled by local assembly of 454 and Solexa reads. Remains and the gaps between scaffolds were filled by sequencing PCR products by using an ABI 3730 capillary sequencer. Comparative genomic analysis was performed with the published *L. plantarum* genomes of strains WCFS1 (5) and JDM1 (11) as described previously (3, 4).

The complete genome sequence of ST-III is composed of a circular 3,254,376-bp chromosome and a 53,560-bp plasmid

named pST-III, with mean GC contents of 44.58% and 38.69%, respectively. There are 3,013 coding genes, five rRNA operons, and 64 tRNAs in the chromosome and 44 coding genes in the plasmid.

Compared with WCFS1 and JDM1, ST-III carries most of the core genes and pathways of *L. plantarum*, with no known pathogenic genes identified. More than 100 genes were lost in ST-III, including those coding molybdenum cofactor biosynthesis and rhamnase biosynthesis. Loss of these genes likely has led to increased fitness of ST-III in the kimchi but a decreased capacity to inhabit other ecological niches (1).

There are more than 200 unique genes in ST-III compared with the other two genomes. Notably, a cluster of *ssuACB* genes was identified in ST-III. They encode an ABC-type transporter for aliphatic sulfonates (10), which can be used as sulfur sources. Many aliphatic sulfonates, such as taurocholate, taurodeoxyolate (9), or their mixture, bile salt (7), can increase the cholesterol removal ability of *Lactobacillus* strains.

In conclusion, the comparative analysis revealed that ST-III altered its genome to adapt the environmental niches and the *ssu* genes in ST-III might have contributed to its ability of cholesterol removal. The genome sequence proves the safety and stability of ST-III in commercial use and gives us a basis to further elucidate the functional mechanisms of its probiotic properties.

Nucleotide sequence accession number. The complete nucleotide sequence of the *Lactobacillus plantarum* ST-III chromosome has been deposited in GenBank under the accession number CP002222.

This work was supported by the National Natural Science Foundation of China (grant no. 30871952, 20836003) and the National Science & Technology Pillar Program in the Eleventh Five-Year Plan Period (2009BADCB1B02, 2009BADB9B05).

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∇ Published ahead of print on 29 October 2010.

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