Lactobacillus plantarum is a versatile facultative heterofermentative lactic acid bacterium (LAB) that is encountered in a variety of environmental niches (1–3) and commonly used as a probiotic. L. plantarum strain ZJ316, originally isolated from healthy infant fecal samples, has many probiotic properties, such as significant improvement of pig growth and pork quality and antimicrobial activity against various pathogens in vitro, such as Micrococcus luteus, Bacillus subtilis, Staphylococcus aureus, Escherichia coli, Salmonella enterica, Listeria monocytogenes, and others (4). Here, we report the genome sequence of L. plantarum strain ZJ316.

Whole-genome sequencing of L. plantarum strain ZJ316 was performed (BGI-Shenzhen, Shenzhen, China) with a shotgun strategy. A total of 857 Mb of next-generation Illumina paired-end 90-bp reads was generated by sequencing genome shotgun libraries of different fragment lengths (500 bp, 2 kb, and 6 kb) that covered 267.5-fold of the genome. The assembly, performed by SOAPdenovo (5, 6), consisted of 239 contigs and 61 scaffolds and accounted for approximately 99.99% of the estimated L. plantarum strain ZJ316 genome. Contigs were further assembled using paired-end reads together with mapping to the reference genome of L. plantarum strain WCFS1 (1, 7), resulting in the assembled draft genome with a superscaffold and 2 contigs. Physical gaps were filled through sequencing of PCR products that spanned these regions. To evaluate the single-base accuracy of the assembled genome sequence, we realigned all the usable sequencing reads onto the scaffolds using SOAPalignter/soap2 (8).

L. plantarum strain ZJ316 has one circular chromosome of 3,203,964 bp, with a G+C content of 44.65%, and three plasmids, pLP-ZJ101 (15,167 bp with 40.18% G+C), pLP-ZJ102 (39,116 bp with 38.69% G+C), and pLP-ZJ103 (41,508 bp with 39.50% G+C). There are 3,159 protein-coding genes, 15 tRNA operons, and 61 tRNAs in the chromosome and 117 coding genes in the plasmid.

Compared with the published genomes of L. plantarum strains WCFS1 (1, 7), ATCC 14917 (GenBank accession number NZ_ACGZ00000000.2), JDML (9), ST-III (10), and NC8 (11), most of the orthologous genes of ZJ316 have >93% nucleotide sequence identity. Some prophage sequences and locations of ZJ316 are novel. There are more than 200 unique genes that are present in ZJ316. These include RNA-directed DNA polymerases and clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein genes, which encode enzymes involved in the DNA repair pathway. There are also new candidates, which contain the genes for glucarate dehydratase, tagatose 1,6-diphosphate aldolase 1, gluconate transport protein, the phosphotransferase system (PTS) family cellobiose porter, and other carbohydrated-related proteins, involved in carbohydrate metabolism.

Many sugar metabolism and transport genes in WCFS1 and other L. plantarum strains were lost in ZJ316, such as gene clusters for biosynthesis and transport of arabinose, rhamnose, mannose, and other carbohydrates.

In conclusion, the genes specific to L. plantarum strain ZJ316 may reflect niche differences between L. plantarum strain ZJ316 and the other L. plantarum strains, suggesting that L. plantarum strain ZJ316 may have different carbohydrate utilization to adapt to the human gastrointestinal tract. The genome sequence 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 ZJ316 chromosome has been deposited in GenBank under the accession number CP004082.

ACKNOWLEDGMENTS

This project was funded by the National Natural Science Foundation of China (numbers 31071513 and 31271821), the National Science Foundation of Zhejiang Province (number Z3110399), the National High Technology Research and Development Program (“863” Program) of China (2012AA022105B), and the International Science & Technology Cooperation Program of China (2013DFA32230).

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