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Actic acid bacteria are Gram-positive bacteria that have extensively been used in the food industry (1). Lactobacillus plantarum is one of the most important and widespread members of the genus Lactobacillus, and it is mainly isolated from plant- and meat-derived foods. L. plantarum is also used as a probiotic because of its beneficial effects on human and animal health (2, 3). Here, we report the draft genome sequence of L. plantarum strain NIZO2877 isolated from a hot dog in Vietnam. Its two contigs represent a nearly complete genome sequence.

Total DNA from L. plantarum NIZO2877 was extracted and subjected to 150-bp paired-end sequencing using Illumina MiSeq technology (Illumina, San Diego, CA) at ProfileXpert (Lyon, France). A total of 1,820,816 reads were obtained and assembled using Ray (4) in 23 contigs. Gap closing was conducted using Sanger sequencing. Twenty-three pairs of primers were designed between contigs using the Primer3 software (5). The endpoint PCRs were conducted on a Veriti Applied Biosystems thermocycler (Life Technologies, Carlsbad, CA). Twenty-two gaps were closed, and the resulting assembly consisted of 2 chromosomal contigs (1,275,359 bp and 1,956,412 bp). The total genome length is 3,231,771 bp. The G+C content is 44.49%, which is consistent with the results reported for other L. plantarum genomes (44.5 to 44.7%). Annotation was performed using the RAST annotation server (6). A total of 3,165 protein-coding sequences (CDSs) were identified; defined biological functions were assigned to 2,424 CDSs. Six hundred seventy-five CDSs were homologous to sequences encoding hypothetical proteins in other organisms, and 66 CDSs did not have a database match. The genome contains 68 tRNA genes and 14 rRNA genes.

While exploring the specific features of L. plantarum NIZO2877, we found that it has a truncated hepB2 gene (EC 2.5.1.30, heptaprenyl diphosphate synthase), which converts farnesyl diphosphate to heptaprenyl diphosphate in the vitamin K2 biosynthesis pathway. This feature is present in only one other L. plantarum strain, ATCC 14917 (7). However, the two strains bear a complete copy of the hepB1 gene that has the same function as hepB2, hinting that the truncated copy of hepB2 does not result in a loss of function.

The majority of L. plantarum genome sequences were derived from dairy product or plant isolates. The availability of the genome sequence of L. plantarum NIZO2877, isolated from a meat product, increases our knowledge of other food-derived L. plantarum strains and will assist in a better understanding of its ecology.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LKHZ00000000. The version described in this paper is version LKHZ01000000.

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