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Nearly Complete Genome Sequence of *Lactobacillus plantarum* Strain NIZO2877

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Lactobacillus plantarum **is a versatile bacterial species that is isolated mostly from foods. Here, we present the first genome sequence of *L. plantarum* strain NIZO2877 isolated from a hot dog in Vietnam. Its two contigs represent a nearly complete genome sequence.**

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Lactic 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.

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 K_2 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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