

Genome Sequences of the Ethanol-Tolerant *Lactobacillus vini* Strains LMG 23202^T and JP7.8.9

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We report on the genome sequences of *Lactobacillus vini* type strain LMG 23202^T (DSM 20605) (isolated from fermenting grape musts in Spain) and the industrial strain *L. vini* JP7.8.9 (isolated from a bioethanol plant in northeast Brazil). All contigs were assembled using gsAssembler, and genes were predicted and annotated using Rapid Annotation using Subsystem Technology (RAST). The identified genome sequence of LMG 23202^T had 2,201,333 bp, 37.6% G+C, and 1,833 genes, whereas the identified genome sequence of JP7.8.9 had 2,301,037 bp, 37.8% G+C, and 1,739 genes. The gene repertoire of the species *L. vini* offers promising opportunities for biotechnological applications.

Lactobacillus vini is present in fermenting grape musts in France and Spain and is a homofermentative lactic acid species capable of fermenting pentoses (5). *L. vini* is one of the most abundant lactic acid bacteria (LAB) in the ethanol process in several refineries in northeast Brazil (3). JP7.8.9 appeared to be one of the most common strains found during the harvest season, when ethanol concentration exceeds 5% in the distillery Japungu (Santa Rita, Paraíba State) (3). Both strains JP7.8.9 and LMG 23202^T (DSM 20605^T) tolerate an ethanol concentration of 10% in test tube assays (3). Those features stimulated us to sequence their genomes. Some cellular and genomic features that allow for ethanol tolerance have recently been disclosed for different types of microbes (2, 6). Genomes were obtained by pyrosequencing using Roche 454 GS FLX Titanium (4). All reads were assembled using gsAssembler 2.3, which generated 260 contigs for LMG 23202^T and 734 contigs for JP7.8.9, and the annotation was performed using Rapid Annotation using Subsystem Technology (RAST) (1). The annotated genome of LMG 23202^T includes 2,201,333 bases (G+C content of 37.6%). It comprises 1,833 predicted genes, including 53 predicted RNA genes (one rRNA and 52 tRNAs). We found 107 genes in the cell wall and capsule subsystem and 55 genes in the stress response. The JP7.8.9 genome contains 2,301,037 bases (G+C content of 37.8%) and comprises 1,739 predicted genes, including 52 predicted RNA genes (1 rRNA and 51 tRNAs). We found 115 genes in the cell wall and capsule subsystem and 35 genes in the stress response in the JP7.8.9 genome.

Both genomes (LMG 23202^T and JP7.8.9) have the cellobiose metabolism operon, genes coding for beta-glucosidase (EC 3.2.1.21), xyloside transporter XynT, and the heat-inducible transcription repressor HrcA. The importance of *Lactobacillus vini* in the ethanol process is highlighted by the presence of these genes. LMG 23202^T contains genes coding for L-arabinose isomerase (EC 5.3.1.4), and L-arabinose-proton symporter. The gene repertoire of the species *L. vini* offers promising opportunities for biotechnological applications.

Nucleotide sequence accession numbers. The genome shotgun projects of LMG 23202^T (DSM 20605^T) and JP7.8.9 have been

deposited at DDBJ/EMBL/GenBank under accession numbers AHYZ00000000 and AHZA00000000, respectively. The versions described in this paper are the first versions, AHYZ01000000 and AHZA01000000.

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