Genome Sequence of the Bacteriocin-Producing Lactobacillus curvatus Strain CRL705

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Lactobacillus curvatus is one of the most prevalent lactic acid bacteria found in fermented meat products. Here, we present the draft genome sequence of Lactobacillus curvatus CRL705, a bacteriocin producer strain isolated from an Argentinean artisanal fermented sausage, which consists of 1,833,251 bp (GC content, 41.9%) and two circular plasmids of 12,342 bp (pRC12; GC, 43.9%) and 18,664 bp (pRC18; GC, 34.4%).

Lactobacillus curvatus is a lactic acid bacterium commonly associated with meat environments, representing one of the major populations associated with fermented meat products, vacuum-packaged refrigerated meat, and to a lesser extent ready-to-eat meat, fish, and poultry products (4, 14, 15). L. curvatus is used in starter cultures for sausage fermentation (3, 6) and in biopreservative cultures for fresh and processed meat and fish (10). This species is phylogenetically closely related to Lactobacillus sakei, Lactobacillus fuchuensis, and Lactobacillus graminis, species that are also associated with meat environments (2, 9, 16). To date, only the genome of L. sakei (strain 23K) has been completely sequenced and annotated (7).

Here, we report the draft genome sequence of L. curvatus CRL705, a strain isolated from an Argentinean artisanal fermented sausage and known to produce the two-component lactocin 705 bacteriocin and “AL705,” a bacteriocin with antilisterial activity (5, 17). The L. curvatus CRL705 genome was sequenced (23-fold coverage) by using a whole-genome shotgun (WGS) strategy (198,804 total reads; ~80 Mb) with a 454 GS Titanium pyrosequencer at INDEAR, Argentina. The assembly was performed using a 454 Newbler 2.5.3 assembler, giving 128 large contigs. The draft genome is a single circular chromosome of 1,833,251 bases, with a mean GC content of 41.9%, and two circular plasmids, pRC12 (12,342 bp) and pRC18 (18,664 bp; accession number AF200347.3), which have GC contents of 43.9 and 34.4%, respectively. Genome annotation was performed according to standard operating procedures (SOPs) for prokaryotic annotation from ISGA (11), the RAST annotation server (1), Glimmer 3.02 modeling software package (8), tRNAscan-SE 1.21 (13), and RNAmmer 1.2 (12). A total of 1,830 coding sequences (CDS), 53 structural tRNAs, and 1 rRNA operon were predicted. Additionally, no functional prophages were identified, although several genes for transposases and two clusters of regularly interspaced short palindromic repeats (CRISPRs) and two potential CRISPRs were found.

There are 270 RAST subsystems represented in the chromosome. Comparative genome analysis of L. curvatus CRL705 with the closely related L. sakei 23K strain revealed that they are highly similar. However, 52 protein-encoding genes were unique in L. curvatus CRL705; among them are genes for proteins and enzymes involved in the metabolism of carbohydrates (dihydroxyacetone kinases, galactose-6-phosphate isomerase, tagatose aldolase and kinase, β-phosphoglucosaminate, and multiple sugar ABC transporters and galactose-specific and lactose-specific phosphotransferase systems), DNA (3 CRISPR-associated proteins and a restriction-modification system), and fatty acids (heptaprenyl dipiphosphate synthase), as well as in the stress oxidative response (coenzyme A-disulfide reductase) and in bacteriocin production (lactocin 705, sakacin P, sakacin Q, sakacin X, and sakacin T). On the other hand, L. curvatus CRL705 lacks several gene clusters, mainly those containing fatty acid biosynthesis FASII, sucrose utilization, the arginine deiminase pathway, and citrate metabolism. This is the first report on the genome of a technologically relevant L. curvatus strain.

Nucleotide sequence accession number. The data from this whole-genome shotgun project were deposited in GenBank under the accession number AGBU01000000.

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REFERENCES