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Draft Genome Sequence of *Lactobacillus curvatus* FLEC03, a Meat-Borne Isolate from Beef Carpaccio Packaged in a Modified Atmosphere

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ABSTRACT In this study, we present the draft genome sequence for *Lactobacillus curvatus* FLEC03. This strain was isolated from beef carpaccio packaged in a modified atmosphere. The draft genome will contribute to understanding the role of *L. curvatus* strains in food products (fermentation, biopreservation, or spoilage) through comparative genomics with other strains.

Lactobacillus curvatus is a lactic acid bacterium that was first described in the 1970s and was first associated with fermented meat products (1, 2). The species *L. curvatus* is phylogenetically related to *L. sakei*, *L. fuchuensis*, and *L. graminis* (3), which belong to the *L. sakei* clade of psychrotrophic *Lactobacillus* spp. To date, three complete genome sequences and seven draft genome sequences of *L. curvatus* strains are available in GenBank. All of these strains originate from a wide variety of food products, including fermented sausage (4), sushi (5), milk (6), vegetable marinade (7), and kimchi (8).

L. curvatus FLEC03 was isolated in 2008 from a slice of beef carpaccio after 7 days of storage at 8°C, a type of food product and storage condition where this species is often identified (9). This strain was found dominant in the meat slice, having reached a population level of 10^7 CFU g⁻¹, although the meat did not show any characteristics of spoilage. The genome sequencing of this strain was undertaken for the purpose of genomic comparison with other strains, in order to get better insight into the genomic repertoire of the *L. curvatus* species in relation to meat fermentation, biopreservation, or spoilage.

The whole-genome sequencing of *L. curvatus* FLEC03 was carried out by Eurofins MWG Operon Laboratories (Ebersberg, Germany) using Illumina MiSeq 2 × 150-bp paired-end libraries. The 1.45 million reads were assembled *de novo* using Velvet software (10) after choosing the best *k*-mer value of 85. The draft assembly resulted in 46 contigs from 1,717 to 307,439 bp (N_{50} of 85,282 bp). The contigs were aligned against the *L. sakei* 23-K complete genome using progressiveMauve (11) to give two high-quality scaffolds. The first scaffold (1,854,704 bp, coverage of 62×), comprising 40 contigs with an overall G+C content of 41.82%, was for the chromosome sequence. The second scaffold (46,973 bp, coverage of 116×), comprising 6 contigs with a G+C content of 37.87%, was for the plasmid pFLEC03A1 sequence. Annotation performed using the MicroScope platform (12) detected 1,926 coding sequences (CDSs), 40 pseudogenes, 3 rRNAs, and 30 tRNAs for the chromosome and 59 CDSs for the plasmid. Manual curation of the annotated sequences confirmed the presence in the chromosome of one prophage region of 32,532 bp and one CRISPR-Cas system of type II. Bacteriocin cluster genes were not detected using Bagel version 3.0 (13), indicating that the preservative potential of this strain is not correlated to bacteriocin production.

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Unlike other *L. curvatus* strains sequenced so far, strain FLECO3 is also characterized by the presence of 8 cell-surface multicomponent complexes (14) similar to those present in *L. sakei* strain 23K (15) and whose functions are related to bacterial adhesion and complex carbohydrate molecule scavenging. The FLECO3 strain has been deposited in the CIP Culture Collection under the reference CIP 110935.

Accession number(s). This whole-genome shotgun project has been deposited in ENA under BioProject number PRJEB20186 and the assembly under the accession numbers [FXDK01000001](https://doi.org/10.1093/bioinformatics/btq000) to [FXDK01000046](https://doi.org/10.1093/bioinformatics/btq000). The versions described in this paper are the first versions.

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