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► **To cite this version:**

Laurent Marché, Taous Saraoui, Benoit Remenant, Monique Zagorec, Hervé Prévost, et al.. Complete Genome Sequence of *Lactococcus piscium* CNCM I-4031, a Bioprotective Strain for Seafood Products. *Genome Announcements*, 2017, 5 (4), pp.e01510-e01516. 10.1128/genomeA.01510-16 . hal-01543872

**HAL Id: hal-01543872**

**<https://hal.science/hal-01543872v1>**

Submitted on 21 Jun 2017

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# Complete Genome Sequence of *Lactococcus piscium* CNCM I-4031, a Bioprotective Strain for Seafood Products

Laurent Marché,<sup>a</sup> Taous Saraoui,<sup>a,b\*</sup> Benoit Remenant,<sup>a\*</sup> Monique Zagorec,<sup>a</sup> Hervé Prévost,<sup>a</sup> Christine Delbarre-Ladrat,<sup>b</sup> Françoise Leroi,<sup>b</sup> Marie France Pilet<sup>a</sup>

UMR1014 SECALIM, INRA, Oniris, Nantes, France<sup>a</sup>; Ifremer, Laboratoire Ecosystèmes Microbiens et Molécules Marines pour les Biotechnologies (EM<sup>3</sup>B), Nantes, France<sup>b</sup>

**ABSTRACT** *Lactococcus piscium* CNCM I-4031 is a psychrotrophic foodborne lactic acid bacterium showing potential interest for the biopreservation of seafood products due to its inhibition properties toward pathogenic and spoilage bacteria. The analysis of its genome will provide a better understanding of the mechanisms of interaction between these bacteria.

*Lactococcus piscium* is a psychrotrophic species first isolated in 1990 from rainbow trout (1). Studies have reported the presence of this species in a large variety of food products, including meat, seafood, and vegetables (2, 3). *L. piscium* CNCM I-4031 (also named EU2241), isolated from raw salmon packs (4), might present interests for seafood biopreservation: it improves the sensory quality of seafood and limits the growth of spoilage (*Brochothrix thermosphacta* and *Serratia proteamaculans*) or pathogenic (*Listeria monocytogenes*) bacteria (5–7). Although the mechanisms of growth inhibition have not yet been elucidated, a previous study suggested the requirement for a contact between *L. piscium* CNCM I-4031 and the target-inhibited strain as well as putative involvement of quorum sensing (8).

The whole-genome sequencing of *L. piscium* CNCM I-4031 was carried out by Eurofins MWG Operon laboratories (Ebersberg, Germany) using GS FLX/FLX+ technologies with shotgun and 8-kbp-long paired-end libraries. The genome sequencing coverage is 63×. The assembly realized with Newbler 2.6 (9) showed an  $N_{50}$  of 144,750 bp for 31 contigs. The final assembly gave two scaffolds with seven contigs and a genome size of 2.26 Mbp, in accordance with results obtained by pulsed-field gel electrophoresis (PFGE) (data not shown). The first scaffold (2.06 Mb), composed of six contigs, is the complete sequence of the chromosome, with a G+C content of 38.74%. The second scaffold (one contig) formed a 20-kb plasmid with a G+C content of 34.36%. Automatic annotation and manual curation were performed on the whole genome thanks to the MicroScope platform (10, 11) (Genoscope, Évry, France). The results showed that *L. piscium* CNCM I-4031 chromosome contains 2,205 predicted coding DNA sequences (CDSs), as observed in *Lactococcus lactis* genomes (around 2,500).

Thirty-one percent of the predicted CDSs were assigned to proteins of unknown functions, 40% were predicted as enzymes, 6% as transcriptional factors, and 4% as proteins of cell structure. The remaining proteins are involved in diverse cell processes (including carriers, lipoproteins, receptors, and other membrane proteins) or from an extrachromosomal origin. Seventy-five genes (3.4%) were manually curated as carbohydrate-active enzymes (CAZymes) that degrade or modify carbohydrates or create glycosidic bonds.

Received 14 November 2016 Accepted 22 November 2016 Published 26 January 2017

**Citation** Marché L, Saraoui T, Remenant B, Zagorec M, Prévost H, Delbarre-Ladrat C, Leroi F, Pilet MF. 2017. Complete genome sequence of *Lactococcus piscium* CNCM I-4031, a bioprotective strain for seafood products. Genome Announc 5:e01510-16. <https://doi.org/10.1128/genomeA.01510-16>.

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Address correspondence to Marie France Pilet, [marie-france.pilet@oniris-nantes.fr](mailto:marie-france.pilet@oniris-nantes.fr).

\* Present address: Taous Saraoui, Laboratoire de Biologie, Clermont Université, Université d'Auvergne, IUT Aurillac, Clermont-Ferrand, France; Benoit Remenant, Laboratoire de la Santé des Végétaux (LSV), Anses, Angers, France.

The plasmid encompasses 26 CDSs, including a complete ribose gene cluster, *rbsRKDACB*. The *rbs* genes are involved in ribose utilization but have also been reported to be responsible for internalization of autoinducer II (AI-2) involved in quorum sensing (12, 13).

The comparison of *L. piscium* CNCM I-4031 genome with that of *L. piscium* MKFS47, a spoiler strain of meat products (14), revealed 384 *L. piscium* CNCM I-4031-specific genes.

**Accession number(s).** This whole-genome shotgun project has been deposited in ENA under the accession no. [FLZT01000001](https://ena.ebi.ac.uk/ena/record/FLZT01000001) to [FLZT01000007](https://ena.ebi.ac.uk/ena/record/FLZT01000007). The versions described in this paper are the first versions.

## ACKNOWLEDGMENTS

The LABGeM (CEA/IG/Genoscope & CNRS UMR 8030) and the France Génomique National infrastructure (funded as part of Investissement d'Avenir Program managed by Agence Nationale pour la Recherche, contract ANR-10-INBS-09) are acknowledged for support within the MicroScope annotation platform. Taous Saraoui was the recipient of a Ph.D. fellowship program from the French Ministry of Higher Education and Research. This study was financially supported by the Région des Pays de la Loire, France within the context of the COM-BACT research program (contract 2014 07957).

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