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Genome Sequence of *Lactococcus garvieae* UNIUD074, Isolated in Italy from a Lactococcosis Outbreak▽

Pilar Reimundo,[1]* Miguel Pignatelli,[2] Luis David Alcaraz,[3] Giuseppe D'Auria,[3,4] Andrés Moya,[3,4] and José A. Guijarro[1]

Área de Microbiología, Departamento de Biología Funcional, Facultad de Medicina, IUBA, Universidad de Oviedo, 33006 Oviedo, Spain[1]; EMBL-European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, United Kingdom[2]; Unidad Mixta de Investigación en Genómica y Salud—Centro Superior de Investigación en Salud Pública (Generalitat Valenciana)/Instituto Cavanilles de Biodiversidad y Biología Evolutiva (Universitat de Valencia), Valencia, Spain[3]; and CIBER en Epidemiología y Salud Pública, Valencia, Spain[4]

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Lactococcus garvieae **is the etiological agent of lactococcosis disease, affecting many cultured fish species worldwide. In addition, this bacterium is currently considered a potential zoonotic microorganism since it is known to cause several opportunistic human infections. Here we present the draft genome sequence of the *L. garvieae* strain UNIUD074.**

Lactococcus garvieae is a serious fish pathogen responsible for lactococcosis, a bacterial disease that produces hyperacute and hemorrhagic septicemia in various cultured fish species the world over (17). First isolated in 1983 as a mastitis agent in bovines (5), this bacterium has also been isolated from a wide variety of dairy environmental and animal samples (1, 6, 11, 12, 15, 18). Additionally, *L. garvieae* has recently been associated with an increasing number of human infections, such as endocarditis (7–9, 13, 19–23), septicemia (20), liver abscess (14), secondary peritonitis (20), spondylodiscitis (4, 10), and diverticulitis (20). Thus, this ubiquitous bacterium is considered at present as a potential zoonotic agent with an increasing relevance in both veterinary and human medicine. Despite the importance of *L. garvieae* as a bacterial pathogen, little is known about its precise virulence mechanisms.

In the present study, we report the genome sequence of *L. garvieae* strain UNIUD074, isolated in Italy from a lactococcosis outbreak in rainbow trout. Total genomic DNA was extracted from a cultured bacterial strain (brain heart infusion broth at 28°C; Difco) according to the user manual of the UltraClean Mega soil DNA kit (MO-BIO Laboratories, Inc.). Genomic DNA was subsequently sequenced through a whole-genome shotgun strategy using Roche 454 GS-FLX Titanium pyrosequencing. As a result, 395,244 single-end reads and 79,811 paired-end reads (3-kb fragments) were obtained (totaling ~160 Mb; ~70-fold coverage of the genome). Quality-filtered reads were assembled using the 454 Newbler v2.3 (454 Life Sciences) and the Celera v6.1 (SourceForge) software assemblers into 25 large contigs (>1,000 bp). Screening for rRNAs and tRNAs, as well as prediction and annotation of protein-coding sequences (CDSs), were carried out through the RAST (rapid annotation using subsystem technology) server (2). Identification of insertion sequences (IS) and tandem repeat regions was carried out using IS finder (http://www-is.biotoul.fr) (16) and IR finder (3), respectively. The draft genome of *L. garvieae* UNIUD074 includes 2,171,966 bp and contains 2,101 CDSs, with a G+C content of 38.7%. There are at least nine rRNA operons constituted by single-copy genes predicted for 5S, 16S, and 23S rRNAs, at least six pseudo-tRNAs, and at least 60 tRNAs covering all amino acids except for serine. In addition, nine IS and 215 tandem repeat regions were identified. An estimated 78.15% of the CDSs were predicted to encode proteins with a known function in other bacterial species. A comparison was made between both *Lactococcus lactis* IL1403 and *L. garvieae* UNIUD074 genome sequences, concluding that 18.6% of all the protein-coding genes are specific to the *L. garvieae* genome. The majority (61.8%) of these specific CDSs were annotated as hypothetical proteins. We hope that the whole-genome sequencing of *L. garvieae* strain UNIUD074 will allow scientists to gain insights into the molecular basis of the virulence mechanisms of this important bacterial pathogen.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AFHF00000000. The version described in this paper is the first version, AFHF01000000.

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* Corresponding author. Mailing address: Área de Microbiología, Departamento de Biología Funcional, Facultad de Medicina, IUBA, Universidad de Oviedo, 33006 Oviedo, Spain. Phone: 34985104218. Fax: 34985103148. E-mail: reimundomaria@uniovi.es.

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