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Genome Sequence of *Lactococcus garvieae* 21881, Isolated in a Case of Human Septicemia▽

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***Lactococcus garvieae* is a Gram-positive bacterium considered an important opportunistic emerging human pathogen and also a well-recognized fish pathogen. Here, we present the draft genome sequence of *Lactococcus garvieae* strain 21881 (2,164,557 bp, with a G+C content of 37.9%), which represents the first report of a genome sequence on *Lactococcus garvieae*.**

In recent years, *Lactococcus garvieae* has gained recognition as an opportunistic human pathogen, due to the increasing number of clinical cases in which has been involved. In humans, the most common manifestation is infective endocarditis, but it has also been associated with septicemia and urinary and skin infections (7, 14). In addition, *Lactococcus garvieae* is an important fish pathogen, mainly in the trout industry (13). The genetic content of *Lactococcus garvieae* has been studied previously by genomic interspecies microarray hybridization (1). Here, we present the first-draft genome sequence of the *Lactococcus garvieae* species.

Lactococcus garvieae strain 21881, isolated from human blood (from a 74-year-old male affected with septicemia) (4), was grown statically at 28°C in brain heart infusion (BHI) broth (bioMérieux, Marcy l'Etoile, France). Cells were grown until the late exponential phase (optical density at 600 nm [OD_{600}], ~1) and harvested for purification of genomic DNA using a DNeasy blood and tissue kit (Qiagen, Hilden, Germany). A whole-genome shotgun strategy using Roche 454 GS Titanium pyrosequencing was performed. The identified genome sequences were processed with Roche's software. Quality-filtered reads were assembled *in silico* using the 454 Newbler Assembler, version 2.3 (454 Life Sciences), which generated 91 contigs of sizes ranging between 257 and 169,878 bp. Open reading frames (ORFs) were predicted using Genemark.hmm (11). The annotation was done by merging the results obtained from the RAST (Rapid Annotation using Subsystem Technology) server (5), BLAST (3), tRNAscan-SE 1.21 (10), and RNAmmer 1.2 (9). In addition, annotation of the proposed genes was done by searching the contigs against the KEGG (8), UniProt (6), and COG (Clusters of Orthologous Groups) (12) databases to annotate the gene description.

The uncompleted draft genome includes 2,164,557 bases, with a G+C content of 37.9%, and is composed of 2,141 predicted coding sequences (CDSs), with an average size of 723 bp. There are single predicted copies of the 16S and 23S rRNA genes, two copies of the 5S rRNA, and 42 predicted tRNAs. The CDSs annotated by the COG database were classified into 21 functional COG groups. Of these, 1,938 (90%) were assigned a predicted function. Genes not functionally identified yet could be well identified upon closure of the genome. The draft genome contains 273 subsystems (sets of related functional roles) according to the RAST server. We used this information to reconstruct the metabolic network. There are many carbohydrate and protein metabolism features, as well as many genes related to cell wall and capsule biosynthesis. As previously shown, the phospho-beta-galactosidase (*lacG*) gene was absent in this strain (2), but it carries the genes involved in the galactose metabolism. There are also 25 virulence, disease, and defense features, including proteins involved in adhesion and resistance to antibiotics and toxic compounds. Several phage-related genes and some insertion sequences were identified.

The availability of the genome sequence of *Lactococcus garvieae* will provide a better background for future understanding of this organism's pathobiology.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AFCC00000000. The version described in this paper is the first version, AFCC01000000.

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