

Genome Sequence of *Lactococcus garvieae* 8831, Isolated from Rainbow Trout Lactococcosis Outbreaks in Spain[∇]

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***Lactococcus garvieae* is the etiological agent of lactococcosis, one of the most important disease threats to the sustainability of the rainbow trout farming industry. Here, we present the draft genome sequence of *Lactococcus garvieae* strain 8831, isolated from diseased rainbow trout, which is composed of 2,087,276 bp with a G+C content of 38%.**

Lactococcus garvieae is the etiological agent of lactococcosis, a septicemic infection affecting different wild and farmed fish species, although its major clinical significance is in the trout industry, where it is responsible for important economic losses. Moreover, it has also been isolated from clinical specimens in other animal species, and in human medicine is considered a potentially opportunistic zoonotic pathogen (12). Recently the genome of a human clinical isolate of *Lactococcus garvieae* has been sequenced (1). Since intraspecific heterogeneity in the genetic content of this species related to host specificity has been suggested (8), we have sequenced the genome of *Lactococcus garvieae* strain 8831, isolated from diseased rainbow trout and responsible for most of the lactococcosis outbreaks in Spain.

Lactococcus garvieae strain 8831 was sequenced by a whole-genome shotgun strategy performed as described before for strain 21881 (1), which generated 87 contigs larger than 200 bases. Open reading frames (ORFs) were predicted using Glimmer 3.02 (6). Functional annotation was done by merging the results obtained from the RAST (Rapid Annotation using Subsystem Technology) server (3), BLAST (2), tRNAscan-SE 1.21 (10), and RNAMmer 1.2 (9) and by searching the contigs against the UniProt (4) and COG (Clusters of Orthologous Groups) (11) databases. The uncompleted draft genome includes 2,087,276 bases with a G+C content of 38% and is composed of 1,969 predicted coding sequences (CDSs). There are 48 predicted tRNAs and single predicted copies of the 16S and 23S rRNA genes, and two copies of the 5S rRNA. The ORFs annotated by the COG database were classified into 20 functional COG groups. The draft genome contains 270 subsystems (sets of related functional roles) according to the RAST server, and we used this information to reconstruct the metabolic network. There are 20 virulence, disease, and defense features, most of them involved in resistance to antibi-

otics and toxic compounds. Likewise, we identified the gene involved in resistance to clindamycin, which has been described to be characteristic of this species (7). As expected for a *Lactococcus garvieae* strain virulent for fish (5), genes related to capsule biosynthesis were found.

Preliminary comparison of the genome content of strains 21881 (1) and 8831 (this work) shows a difference of approximately 0.1 Mb in their genome sizes. This difference is due to the lack of plasmids in the 8831 strain. The availability of the genome sequence of *Lactococcus garvieae* 8831 will allow deeper comparative genomic studies for the analysis of intraspecific variations in this ubiquitous bacterium, especially focused on the identification of genes potentially involved in virulence.

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number AFCD00000000. The version described in this paper is the first version, AFCD01000000.

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