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Genome Sequences of *Lactococcus garvieae* TB25, Isolated from Italian Cheese, and *Lactococcus garvieae* LG9, Isolated from Italian Rainbow Trout

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***Lactococcus garvieae* is a fish pathogen and an emerging zoonotic opportunistic pathogen as well as a component of natural microbiota in dairy products. Here, we present the first report of a genome sequence of *L. garvieae* TB25, isolated from a dairy source, and that of *L. garvieae* LG9, isolated from rainbow trout.**

Lactococcus garvieae, one of the most important bacterial fish pathogens (12, 22), has also been isolated from cows and buffaloes with mastitis (8, 21) and from various human clinical specimens (6, 17). In the last years, *L. garvieae* has gained interest in the food industry because it has been isolated from vegetables (13) and meat (19) and it has also been found in dairy products produced from raw milk, associated with the natural fermentation of different artisanal cheeses (3, 9). Most of the characterization studies of *L. garvieae* strains have shown that the phenotypic and genetic diversity is related to the specific animal host or environment they colonize (14). Molecular genetic studies have revealed a low genetic relatedness between fish and dairy strains (11). In particular, a report (10) showed that the *L. garvieae* isolates of each origin can be differentiated by the ability to use lactose for the presence of a phospho-β-galactosidase (*lacG*) gene, detectable in all isolates of dairy origin but lacking in fish isolates. Recently, the entire genomes of four *L. garvieae* fish-derived strains have been sequenced (2, 18, 20), along with that of a strain isolated from human blood (1). However, no sequenced *L. garvieae* genomes from a dairy environment exist. A comparative genome analysis was performed to unveil the global genetic variations that may justify, at least in part, the registered phenotypic differences.

Here, we report the draft genome sequences of *L. garvieae* strain TB25, isolated from Italian cheese, and *L. garvieae* strain LG9, isolated in Italy from a diseased rainbow trout (*Oncorhynchus mykiss*). The genomic DNA was sequenced using a whole-genome shotgun strategy with an Illumina Genome Analyzer Hiseq1000. Quality-filtered reads were assembled using the Velvet software (version 1.1.04), which generated 140 and 92 contigs for the LG9 and TB25 strains, respectively. Open reading frames (ORFs) were predicted using Glimmer 3.02 (7). Functional annotation was done by merging the results obtained from the RAST (rapid annotation using subsystem technology) Server (5), BLAST (4), tRNAscan-SE 1.21 (16), and RNAmmer 1.2 (15).

The draft genome of the *L. garvieae* LG9 isolate includes 2,087,705 bases, with an average G+C content of 38.5%. It encodes 2,027 putative coding sequences (CDSs) and 43 predicted tRNAs. The genome of the *L. garvieae* TB25 isolate includes 2,014,328 bases, with an average G+C content of 38.1%, and it contains 1,977 CDSs and 41 tRNAs. The draft genomes of the LG9 and TB25 strains contain 305 and 318 subsystems (sets of related functional roles), respectively, according to the RAST Server. We used this information to reconstruct the metabolic network. A preliminary comparison of the genome contents of the strains TB25 and LG9 and of the *L. garvieae* strains previously sequenced (1, 2, 18, 20) shows differences in some additional features related to carbohydrate metabolism, including the *lacG* gene, found only in the dairy strain TB25, and genes involved in sucrose fermentation, identified only in strains TB25, 21881 (1), and 8831 (2). The availability of genome sequences of *L. garvieae* strains coming from different sources can provide a better background for the future understanding of genes that can be useful or necessary for the colonization of different habitats.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited in DDBJ/EMBL/GenBank under accession numbers AGQY00000000 (*L. garvieae* LG9) and AGQX00000000 (*L. garvieae* TB25). The versions described in this paper are the first versions, DDBJ/EMBL/GenBank accession numbers AGQY01000000 (LG9) and AGQX01000000 (TB25).

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