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GENOME ANNOUNCEMENT

Genome Sequence of the Bacteriocin-Producing Strain *Lactococcus garvieae* DCC43

Christina Gabrielsen,[a] Dag A. Brede,[a] Pablo E. Hernández,[b] Ingolf F. Nes,[a] and Dzung B. Diep[a]

Department of Chemistry, Biotechnology and Food Science, Laboratory of Microbial Gene Technology and Food Microbiology, Norwegian University of Life Sciences (UMB), Ås, Norway,[a] and Departamento de Nutrición, Bromatología y Tecnología de los Alimentos, Facultad de Veterinaria, Universidad Complutense de Madrid (UCM), Madrid, Spain[b]

This work describes the draft genome sequence of *Lactococcus garvieae* DCC43. The 2.2-Mb draft genome contains 2,227 predicted protein-coding genes, among which is a region encoding the bacteriocin garvicin ML. No antibiotic resistance genes or capsule-related virulence genes were identified. Two plasmid replication regions indicate that this strain likely contains plasmids. Comparative genomics suggests that this strain displays a high degree of sequence variation from the previously sequenced *L. garvieae* strains.

Lactococcus garvieae DCC43, a producer of the potent circular bacteriocin garvicin ML (11), was isolated from mallard duck intestines (*Anas platyrhynchos*) (16). This bacteriocin displays antagonistic activity against a range of food spoilage and pathogenic bacteria, including *Listeria* and *Clostridium*, as well as related *L. garvieae* strains (5). *L. garvieae* is a well-known pathogen responsible for lactococcosis in fish (18) but has also been associated with infections in animals and humans (6, 17). However, *L. garvieae* is also part of the bacterial flora of various dairy products (9, 19) and is commonly found in animal samples (13, 16). To date, eight strains of *L. garvieae* have been sequenced (two complete and six draft genomes) (2, 3, 10, 12, 14, 15), but little is known about their virulence traits and underlying mechanisms. This ubiquitous bacterium is therefore of interest from a comparative genomics perspective as an emerging pathogen and as the producer of a bacteriocin which could potentially be used to combat such pathogens.

Here we report the genome sequence of *L. garvieae* DCC43. Total genomic DNA was extracted from a bacterial culture using a genomic-tip kit (Qiagen). A genomic library was generated and pair end sequenced on a HiSeq 2000 system (Illumina). The sequencing service was provided by the Norwegian Sequencing Centre (University of Oslo). Reads were trimmed based on quality (limit, 0.01) and ambiguous bases (none allowed), and reads below 50 bp were discarded, before *de novo* assembly was done using the software program CLC Genomics workbench 5.5 (CLC Bio); 13,705,987 reads were used, resulting in an approximately 500-fold average genome coverage. The minimum contig size was 200 bp, and minimum coverage was 100-fold. Genome annotation was performed using the RAST (Rapid Annotation using Subsystem Technology) server (4).

The draft genome of *L. garvieae* DCC43 consists of 68 contigs, ranging in size from 227 to 178,922 bp, constituting a total of 2,244,387 bp with a GC content of 37.8%. It contains 2,227 predicted protein-coding genes and 50 predicted tRNAs. The coverage ratio indicates the presence of at least 4 rRNA operons containing predicted single copies of 23S, 16S, and 5S rRNA genes, as well as one additional 5S rRNA gene. Among the protein-coding genes is a locus encoding the bacteriocin garvicin ML (5). No evident antibiotic resistance genes were found, and no similarity was observed to the capsule gene cluster of *L. garvieae* Lg2, which has been implicated in virulence in fish (12). However, the genome contains two predicted internalins and five predicted LPXTG-specific sortases, two of the latter having no known counterparts in other *L. garvieae* strains. The genome contains 2 or 3 complete prophage regions, as well as two plasmid replication regions on contigs which both show a high degree of similarity to *L. garvieae* 21881 plasmid pGL5 (1).

Comparative genomics analysis of the sequenced *L. garvieae* strains by Mauve progressive alignment (8) and genomic BLAST (7) shows that *L. garvieae* DCC43 displays high sequence variation despite >99% identical 16S rRNA gene sequences, actually forming a separate clade from the other strains. This could suggest that DCC43 may represent a novel *L. garvieae* subspecies.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. AMQS00000000. The version described in this paper is the first version, AMQS01000000.

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Address correspondence to Christina Gabrielsen, christina.gabrielsen@umb.no.

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