

Draft Genome Sequence of Probiotic Strain *Lactobacillus rhamnosus* R0011

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***Lactobacillus rhamnosus* R0011 is a commercially available probiotic that is widely used in human dietary supplements and pharmaceutical products. We prepared a draft genome sequence consisting of 10 contigs totaling 2,900,620 bases and a G+C content of 46.7% for this strain.**

Lactobacillus rhamnosus R0011 (also known as R or Rosell-11) was deposited at the Institut Pasteur Collection Nationale de Cultures de Microorganismes as I-1720. It was isolated in 1976 by Edouard Brochu at Institut Rosell, Inc., in Montreal, Canada, from a dairy starter culture that was specifically for use in the dietary supplement industry. The strain has been extensively used as a probiotic in a number of commercial products (1).

The sample was prepared for sequencing by growing *L. rhamnosus* R0011 aerobically overnight at 37°C in deMan-Rogosa-Sharpe broth (Oxoid, catalog no. CM0361). Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, catalog no. 69504) according to the manufacturer's recommended protocol for Gram-positive bacteria. The quantity of DNA obtained was determined using a NanoDrop ND-1000 spectrophotometer, and typically 1 to 5 µg of DNA was sent to Genome Quebec (Montréal, QC, Canada) for sequencing according to their specifications.

The genome was sequenced with the 454 GS FLX Titanium, yielding 393,658 reads with an average raw size of 246 bases and a total of 94.6 Mb (a 32-fold coverage of the genome). These reads were assembled with version 2.1 of the Newbler software, yielding 51 contigs larger than 10 kb. A plausible ordering of these contigs was postulated based on comparisons with the genomes of *L. rhamnosus* LMS2-1 (accession no. NZ_ACIZ000000000), *L. rhamnosus* HN001 (accession no. NZ_ABWJ000000000), and *L. rhamnosus* Lc 705 (accession no. NC_03199). Primers were designed to join those contigs that were within PCR distance of each other. Thus, we were able to reduce the number of contigs from 51 to 10.

The 10 contigs were annotated with the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). This revealed a total of 2,782 genes, including 63 RNA coding regions.

R0011 contains the genes in *L. rhamnosus* strain GG that encode the soluble proteins p75 and p40, which were described by Yan et al. (5) as promoting intestinal epithelial homeostasis by decreasing cytokine-induced apoptosis and increasing proliferation. This appears to be mediated by an epithelial growth factor receptor (6). In addition, R0011 contains the SpaFED pilus gene cluster but lacks the SpaCBA cluster and therefore is not expected to produce the functional pili that were described by Kankainen et al. (2). It is unknown how this may impact the mucosal adhesion

properties of the strain that were described by von Ossowski et al. (4), but the lack of pili may reduce the chance of opportunistic bacteremia which has been reported for strain GG (3).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number [AGKC000000000](https://www.ncbi.nlm.nih.gov/nuccore/AGKC000000000). The version described in this paper is the first version, accession number [AGKC010000000](https://www.ncbi.nlm.nih.gov/nuccore/AGKC010000000).

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