

**TITLE: Analysis partial genome sequence of *Lactobacillus rhamnosus* UFMG 156.4**

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**ABSTRACT:**

Probiotics are living microorganisms that benefit the health of the host when administered in the correct dose. *Lactobacillus rhamnosus* belongs to the group of lactic acid bacteria (LAB), and are found in the gastrointestinal tract, oral cavity, vaginal epithelium, and fermented dairy products. This work aimed to investigate the genome of *L. rhamnosus* strain UFMG 156.4 regarding the production of compounds with potential biological activity. For the partial analysis of the genome of strain UFMG 156.4, a potential probiotic microorganism, the bacterial DNA was subjected to extraction with Genra Puregene kit (Qiagen, Hilden, Germany). The draft genome sequence of *L. rhamnosus* UFMG 156.4 was determined using a 250-bp paired-end library with Illumina MiSeq technology (Illumina, USA). The assembled genome sequences were annotated using Prokka annotation pipeline (version 1.11). Subsequently, the sequences obtained were submitted to the RAST server (<https://rast.nmpdr.org/>) for the identification of the main subsystems and conserved genes associated with the synthesis of exopolysaccharides, bacteriocins, colicins, and phage-related sequences. The genome of *L. rhamnosus* UFMG 156.4 strain presented 2.947,335 base pairs, containing 46.7% CG. The 329 subsystem were identified, comprising 2969 coding sequence for proteins. A total of 14 genes related to production of the exopolysaccharides (EPS) were characterized. Moreover, among the *eps* loci, we identified genes predicted to encode α-L-rhamnose α-1,3-L-rhamnosyltransferase (*GenBank*, access nº WP-014569859.1) and galactofuranosyltransferase (*GenBank*, access nº WP-070552776.1). This indicates the presence of a heterogenic EPS composition. The identity of the proteins varied from 99% to 100%, with sequences deposited in the *GenBank*. The genome present genes for production of colicin V (*GenBank*, access nº WP-005685524) and pre-bacteriocin (*GenBank*, access nº WP-005686837.1). In addition, we detected 07 (seven) phages sequences, Indicating a low potential for lysis mediated by lysogenic cycle. *L. rhamnosus* UFMG 156.4 strain presented genes for molecules presenting antimicrobial and other

biological activities, represented mainly by bacteriocin and EPS. In turn, EPS produced by UFMG 156.4 strain may present a potential for immunomodulation assays.

Keywords: *Lactobacillus rhamnosus*, genome, exopolysaccharides, bacteriocins.