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## Draft genome sequences and description new probiotic strain of *Lactobacillus rhamnosus* CLS17

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The genus *Lactobacillus* is the largest of the three genera in the family Lactobacillaceae and belongs to one of the dominant phylum Firmicutes, in the human microbiome. *Lactobacillus* spp. usually isolated from fermented foods, and is a key member of the human microflora. They colonize the oral cavity, gastrointestinal and urogenital tracts and breast milk. This genus is a symbiont to humans and has a high probiotic characteristic. One of the most studied and used probiotic strain *L. rhamnosus* GG isolated from the human intestine. Studies have shown that *L. rhamnosus* GG can modulate host immunity. Experiments *in vitro* have shown a decrease in the production of inflammatory cytokines in various eukaryotic cell lines induces the expression of mucin gene; and *in vitro* reduces the barrier dysfunction induced by inflammatory cytokines. Sequencing genomes should help to identify differences, genetic features that are important for specific probiotic strains. It was identified that strain *L. rhamnosus* has immunomodulatory functions. Level  $\gamma$ INF increased by 1.7 times ( $p < 0.01$ ). The concentration of IL-4 doubly decreased ( $p = 0.0005$ ). Antigenotoxic activity decreased, damage index of 1.9. Carried out works on sequencing bacterial strain *Lactobacillus rhamnosus* CLS 17. Obtained by 23 fold coverage of each nucleotide. Identified polymorphisms in genes responsible for the adaptive properties of the strain (transport of sugar and metabolism, heat shock proteins, regulators of intracellular pH, alkaline-shock proteins, bile salt, heat shock proteins, and heavy metal, adhesins). Identified polymorphisms in the genes encoding proteins related to oxidative stress such as (catalase, thiolperoxidase, glutathioneperoxidase, haloperoxidase, four thioredoxins, four glutathionereductases, five NADH-oxidases, and two NADH peroxidases, peptide methionine sulfoxide reductases, alkyl hydroperoxide reductase), intracellular accumulation of  $Mn^{2+}$  ions.

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