

TITLE: SIMILARITY SEARCHING AND PHYSICOCHEMICAL PROPERTIES OF HYPOTHETICAL PROTEINS OF *Lactobacillus fermentum*

AUTHORS: FRANÇA, H.L.; MONTEIRO-NETO, V.; HOLANDA, R.A.

INSTITUTION: UNIVERSIDADE CEUMA, SÃO LUÍS, MA (RUA JOSUÉ MONTELLO, 1, CEP 65075-120, SÃO LUÍS-MA, BRAZIL).

ABSTRACT:

Sequencing of deoxyribonucleic acid (DNA) was a landmark for the study of genomes and their products. Bioinformatics has allowed to increase the knowledge about the nature, composition, conformation, interaction and biological functions of biomolecules in microorganisms. The genus *Lactobacillus* comprises lactic bacteria (BAL) that confer balance and protection to the intestinal and vaginal mucous membranes of mammals. These bacteria have been extensively studied with the aim of characterizing their probiotic properties. Some proteins in the genome of *Lactobacillus fermentum* remain unknown as to the annotation and its physicochemical properties. In this sense, *in silico* analysis of annotation and prediction of the physicochemical properties of uncharacterized proteins of *Lactobacillus fermentum* ATCC 23271 were performed. The online BLASTp and ProtParam servers were used to annotate and predict the physical-chemical characteristics of the sequences of hypothetical proteins, respectively. Of the 50 submitted polypeptide sequences, practically one hundred percent (100%) presented high similarity with sequences corresponding to *L. fermentum* proteins present in the BLASTp database, although without functional annotation. According to ProtParam, eleven (11) sequences are said to be unstable proteins while thirty-nine (39) were considered stable, according to the hydrophobicity index, sixteen (16) proteins were characterized as hydrophobic while thirty four (34) were considered hydrophilic, the hypothetical proteins also obtained half-life time greater than 10 hours. The polypeptide sequences will be further subjected to other computational analyzes, such as those of cell localization and anti-microbial activity. *In silico* analyzes are important to guide the characterization of new biomolecules.

Keywords: *Lactobacillus fermentum*, hypothetical protein, physicochemical properties.

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