MOLECULAR IDENFICATION OF ACID LACTIC BACTERIA WITH PROBIOTIC POTENCIAL

Silva, T.N.L.<sup>1</sup>, Chaves, M. A. M.<sup>1</sup>, Granjeiro, P. A.<sup>1</sup>, Valadares, H. M.<sup>1</sup>, Lopes, D.O.<sup>1</sup>, Vinderola, C. G.<sup>2</sup>

Magalhães, J.T.<sup>1</sup>

<sup>1</sup>UFSJ - Universidade Federal de São João Del-Rei (400 Sebastião Gonçalves Coelho street,

Chanadour, Divinópolis, Minas Gerais, Brazil, Zip code 35501-296)

<sup>2</sup> UNL - Universidade Nacional del Litoral (Pellegrini 2750, Santa Fe, Argentina)

Probiotic are living microorganisms that are found in food supplements. These microorganisms are

able to induce beneficial effects in the host organism and favor the equilibrium of the native

microbiota. For security reasons, it is very important to identify the strains of microorganisms in the probiotic products by molecular tests, since the biochemical and phenotypical tests are not very

discriminatory and can present the same results for different species. Therefore, this work aimed to

identify 21 isolates of lactic bacteria with probiotic potential by molecular tests, as well to check if they

belong to different clones. Thus, the isolates were submitted to the PCR technique using specific

primers to a region of the rDNA 16S gene: 27F (5' AGATTTGATCCTGGCTCAG 3') e 1492R (5'

GGTTACCTTGTTACGACTT 3'). Then, the DNA samples that were previously amplified were

submitted to the sequencing technique and the found sequences were compared to other in gene

banks. The genetic diversity of the isolates were evaluated by the profile obtained by RAPD, which

used the following unspecific primers: M13 (5'-GAGGGTGGCGGTTCT - 3') e P2 (5'- GGTGACGCAG

- 3'). Phylogenetic tree were generated by the Treecon program. According to the results, the species

identified by PCR were Leuconostoc mesenteroides, Weissella paramesenteroides, Lactobacillus

plantarum, Lactobacillus paraplantarum, Lactobacillus pentosus, and Lactobacillus fermentum. The

analysis of the results generated by RAPD showed that 7 isolates belonged to the same clone.

Therefore, 14 of the 21 isolates were classified as the same and considered strains of lactic bacteria.

Lastly, the results were confirmed and organized using phylogenetic trees, which allowed the

visualization of the evolutionary distance among them. To sum up, these results identified and define

lactic bacteria strains, which will be used in future studies. The specie of L. plantarum was the most

representative, and it is highlighted among the other species since some studies reported some

important properties of this bacterium that intensify its probiotic potential.

**Keywords:** lactic bacteria, PCR, RAPD, probiotics

Acknowledgment: CNPq, FAPEMIG, UFSJ