

Characterization of the proteome of four strains of *Lactococcus lactis* with biotechnological relevance

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Lactococcus lactis is one of the utmost studied organisms considering lactic acid bacteria. Due to its role on both human and animal diet, these bacteria gained prominence in the dairy industry. Moreover, *L. lactis* can be used as probiotic or as vehicles for the heterologous expression of molecules of interest in the human body. So, *L. lactis* is of great importance for the pharmaceutical industry. Given this biotechnological potential, a great variety of structural and functional studies of this bacterium genome was performed. However, no study to date has been performed in order to determine the core-proteome of *L. lactis*. Know the core-proteome of *L. lactis* will provide valuable information about a set of conserved proteins that may play vital physiological functions in the adaptive process of this specie and, consequently, contribute to biotechnological optimization. Thus, in order to expand our knowledge of the physiological molecular basis of *L. lactis* and to complement previous structural and functional studies of the genome of this bacterium, the present work used high-throughput proteomics to characterize the proteome of four *L. lactis* strains with great biotechnological relevance. NCDO2118, IL1403, MG1363 and NZ9000 were grown in primary medium of synthetic cultivation for such bacteria. The four strains were grown in M17 medium supplemented with 0,5% glucose, at 30°C, for 16 hours, with no shaking. After obtaining proteins from total bacterial lysate, they were digested with trypsin. The tryptic fragments generated were subjected to proteomic analysis by LC / MS. From the proteome of the four strains, a total of 1109 *L. lactis* non-redundant protein were identified. Comparing this result with the in silico data of *L. lactis* core-genome, it was able to validate 56% (946 proteins) of the ORF encoding the predicted core genome. According to the analysis of Blast2Go tool (predicting biological processes), the proteins that comprise the core proteome were grouped into 20 biological processes. The processes with the highest number of proteins were: translation (96 proteins), amino acid metabolism (37 proteins), nucleotide metabolism (34 proteins) and carbohydrate metabolism (32 proteins). The core proteome was also analysed by KEGG database to assess which metabolic pathways were active and enrichment analysis showed the following processes: Ribosome (P = 0.0110), carbon metabolism (P = 0.0336) and pyruvate metabolism (P = 0.04280). The results obtained to date demonstrated the key proteins and the metabolic processes that contribute to the growth of *L. lactis* in M17.