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ANALYSIS OF O.OENI PROTEOME

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Oenococcus oeni is the most important Lactic Acid Bacteria (LAB) in the wine industry, because is responsible for the deacidification of the wine following the alcoholic fermentation by a process termed malolactic fermentation. Therefore, it is of industrial interest the knowledge of proteins involved in metabolic pathways and transport systems of this bacteria. To this end, in silico predictions inferred from the genome sequence could be complemented by proteomic data. In this work, we report on the characterization of the proteome of *O. oeni* ATCC-BAA1163. This strain was chosen, because the DNA sequence of its genome has been determined, and thus it is possible to tentatively identify its encoded proteins. Protein preparations of subcellular fractions from LAB have been standardized. The *O. oeni* ATCC BAA-1163 membrane and cytosolic protein preparations have been subjected to two- dimensional gel fractionation, by use of a no linear range of pH 3.0-11.0 during electrofocusing. A comparative analysis of both proteomes was performed with the aim to establish whether the identified proteins are present in both or only one. Protein spots of interest were excised from the gel and digested with trypsin for further analysis by MALDI-TOF/TOF spectroscopy. In the course of the study we have identified 115 different polypeptides, which have been classified by their putative function and subjected to bioinformatics analysis for prediction of subcellular location.