Comparative proteomics of oxidative stress response of Lactobacillus acidophilus NCFM reveals effects on DNA repair and cysteine de novo synthesis

Probiotic cultures encounter oxidative conditions during manufacturing, yet protein abundance changes induced by such stress have not been characterized for some of the most common probiotics and starters. This comparative proteomics investigation focuses on the response by Lactobacillus acidophilus NCFM to H2O2, simulating an oxidative environment. Bacterial growth was monitored by BioScreen and batch cultures were harvested at exponential phase for protein profiling of stress responses by 2D gel-based comparative proteomics. Proteins identified in 19 of 21 spots changing in abundance due to H2O2 were typically related to carbohydrate and energy metabolism, cysteine biosynthesis, and stress. In particular, increased cysteine synthase activity may accumulate a cysteine pool relevant for protein stability, enzyme catalysis and the disulfide-reducing pathway. The stress response further included elevated abundance of biomolecules reducing damage such as enzymes from DNA repair pathways and metabolic enzymes with active site cysteine residues. By contrast, a protein-refolding chaperone showed reduced abundance, possibly reflecting severe oxidative protein destruction that was not overcome by refolding. The proteome analysis provides novel insight into resistance mechanisms in lactic acid bacteria against reactive oxygen species and constitutes a valuable starting point for improving industrial processes, food design or strain engineering preserving microorganism viability.

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