APPLICATION OF COMPREHENSIVE PROTEOMICS TO MAP METABOLIC PATHWAYS OF STARVED *LACTOBACILLUS CASEI* GCRL163

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Introduction. Comprehensive proteomic analysis using one dimensional liquid chromatography/tandem mass spectrometry approach known as (1D-LC-MS/MS) provides the means to analyse bacterial proteomes in greater detail then gel-based methods. This approach was used to perform metabolic mapping to understand the survival of non-starter lactic acid bacterial (NSLAB) strain *Lactobacillus casei* GCRL163 under conditions where it is carbohydrate limited and starved.

The goal of the research is to more thoroughly understand the responses of a typical NSLAB cheese strain under carbohydrate starvation in order to develop eventually more effective ways to deliver food-associated probiotic microorganisms.

Methods. The global proteomic response of *L. casei* strain GCRL163 under carbohydrate limitation was analysed quantitatively using gel-based and 1D-LC-MS/MS with spectral counting in cells grown with different levels of lactose (0%, 0.2% and 1% lactose).

Results. Carbohydrate starvation leads to suppression of the lactose transporters and catabolic pathway as well as nucleotide and protein synthesis. Enzymes of the glycolysis/gluconeogenesis pathway, amino acid synthesis, pyruvate metabolism, citrate metabolism became more abundant as well as other carbohydrate catabolic pathways suggesting increased optimisation of intermediary metabolism and scavenging.

Conclusions. We applied the technology of one-dimensional capillary liquid chromatographic separation coupled with tandem mass spectrometry, to identify proteins involved in many metabolic pathways. The simplicity and power of this method enables a depth of analysis that will facilitate thorough characterization of physiological response.