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CHARACTERIZING OF PROTEOME DYNAMICS AT DIFFERENT GROWTH RATES IN CONTINUOUS CULTURES

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Quantitative characterization of metabolism of microorganism requires cultivation techniques where physiological state of cells is precisely controlled. Continuous cultivation method A-stat, which is a modified chemostat with smooth change of dilution rate, enables precise determination of metabolic switch points.

Changes of proteomes in A-stat continuous cultures at different growth rates were measured and analyzed. Two widely used micro-organisms *Escherichia coli* and *Lactococcus lactis* were studied under strictly controlled glucose limited conditions in the specific growth rate range of 0.1 – 0.6 h^{-1}. Two different labelling approaches were used for detection of relative protein amounts. *E. coli* proteome changes were monitored by using ^{15}N labelled batch culture as a comparison. For *L. lactis* chemical labelling by isobaric tag for relative quantification (*iTRAQ)* was used.

For *E. coli* 50% of the proteome was covered and 40% of the proteome was quantified with metabolic labelling for five samples over the growth rate.

For *L. lactis* 40% of the proteome was covered and 32% of the proteome was quantified with chemical labelling for four samples over the growth rate.

Changes of proteomes observed for both organisms showed very good correlation with global transcriptome analysis from the same experiments. The data obtained demonstrated the need to use controlled cultivation procedures in order to collect quantitatively reliable and fitting omics data.