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## The metabolic potential of *Escherichia coli* BL21 in defined and rich medium

Zhaopeng Li<sup>1,2</sup>, Manfred Nimtz<sup>1</sup> and Ursula Rinas<sup>1,2</sup>

<sup>1</sup>Helmholtz Centre for Infection Research, Braunschweig, Germany

<sup>2</sup>Leibniz University of Hannover, Technical Chemistry-Life Science, Hannover, Germany

### Abstract:

**Background:** The proteome reflects the available cellular machinery to deal with nutrients and environmental challenges. The most common *E. coli* strain BL21 growing in different commonly employed media was evaluated using a detailed quantitative proteome analysis.

**Results:** The presence of preformed biomass precursor molecules in rich media such as Luria Bertani supported rapid growth concomitant to acetate formation and apparently unbalanced abundances of central metabolic pathway enzymes, e. g. high levels of lower glycolytic pathway enzymes as well as pyruvate dehydrogenase, and low levels of TCA cycle and high levels of the acetate forming enzymes Pta and AckA. The proteome of cells growing exponentially in glucose-supplemented mineral salt medium was dominated by enzymes of amino acid synthesis pathways, contained more balanced abundances of central metabolic pathway enzymes, and a lower portion of ribosomal and other translational proteins. Entry into stationary phase led to a reconstruction of the bacterial proteome by increasing e. g. the portion of proteins required for scavenging rare nutrients and general cell protection. This proteomic reconstruction during entry into stationary phase was more noticeable in cells growing in rich medium as they have a greater reservoir of recyclable proteins from the translational machinery.

**Conclusion:** The proteomic comparison of cells growing exponentially in different media reflected the antagonistic and competitive regulation of central metabolic pathways through the global transcriptional regulators Cra, Crp, and ArcA. For example, the proteome of cells growing exponentially in rich medium was consistent with a dominating role of phosphorylated ArcA most likely a result from limitations in reoxidizing reduced quinones in the respiratory chain under these growth conditions. The proteomic alterations of exponentially growing cells into stationary phase cells were consistent with stringent-like and stationary phase responses and a dominating control through DksA-ppGpp and RpoS.

**Keywords:** *Escherichia coli*, growth rate control, metabolic balance, overflow metabolism, proteome, stationary phase response, transcriptional control, two-dimensional gel electrophoresis