A PROTEOMIC ANALYSIS OF THE SALMONELLA RCSCDB SYSTEM UNRAVELING POST-TRANSCRIPTIONAL REGULATION OF METABOLIC GENES

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The RcsCDB regulatory system of enteric bacteria has been shown to respond to signals as envelope stress and high osmolarity. The system is activated by a phosphorelay modulated by auxiliary proteins. An example is the *Salmonella enterica* membrane proteinIgaA, which acts as an attenuator of the system. In our previous studies, we defined by transcriptomics more than 70 genes differentially expressed in bacteria carrying *igaA* mutations. In this work, we have extended these observations to a proteomic analysis based on ICPL-protein labeling followed by LC-ESI MS/MS analysis. A total of 505 unique proteins were identified and quantified, with 15% exhibiting statistically significant changes in response to distinct activation states of the RcsCDB system. Divergent expression at the RNA and protein level was also observed in a few cases. This feature was observed in the metabolic genes *pckA*, encoding the gluconeogenetic enzyme phosphoenolpyruvate carboxykinase, and *metE*, involved in the cobalamin-independent synthesis of methionine. In both cases, opposite transcriptional and translational patterns were observed. These findings were further confirmed by RT-PCR and western-blot assays. Our proteomic and transcriptomic comparison therefore provided evidence for the existence of post-transcriptional regulatory phenomena implicating the RcsCDB system.