**244c Integrating Genomic, Transcriptomic and Proteomic Information to Understand Rhsa Function**

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We study the effects of overexpression of *rhsA* fragments, ORF-ex and dsORF-a1, in *E. coli* cells. Cell samples induced differentially with IPTG to express these fragments were studied at multiple time points after induction. *RhsA* expression resulted in a reduced growth rate. DNA microarray experiments revealed that many genes involved in translation and in protein post translational modifications had increased mRNA levels in induced cells. The genes coding for 50S and 30S ribosomal subunit proteins show a more than three folds upregulation in mRNA expression. Proteomic analysis using a shotgun approach suggests a lower overall level of protein expression in *rhsA* cells. However, proteins involved in translation have an increased expression suggesting an altered translation machinery in these cells. A genome-wide comparison of transcriptomic and proteomic data suggests a non-linear mRNA-protein relationship in *E. coli* cells. Further, this non-linearity increases with *rhsA* expression. Ribosome quantitation experiments are used to directly observe the effect of *rhsA* expression on translation machinery. Transcription factors showing a changed activity are identified using network component analysis. Further, the directionality of change in mRNA and protein expression of various genes, as expression of *rhsA* changes, is examined to better understand the function of *rhsA*.