

Co-expression & protein interactions in important cellular complexes

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Many important cellular processes are driven by a vast array of protein complexes. The mechanisms controlling the regulation of the subunits of these complexes, and how they are assembled together are mostly unclear. Through the exploitation of gene expression data, the role of transcriptional regulation in this process can be considered. In this study, we investigate to what extent this regulatory mechanism is conserved evolutionarily in protein complexes across organisms; prior research has so far focused mainly on *S. cerevisiae*. Initially we conducted a detailed analysis of RNA polymerase II and its associated complexes in *H. sapiens*, *D. melanogaster*, *C. elegans*, *A. thaliana* and *S. cerevisiae*; followed by a high-throughput global analysis of 130 protein complexes, of which these organisms share 2 orthologous components. An ortholog component was defined by it sharing membership to an OrthoMCL group with a *S. cerevisiae* annotated MIPS protein complex subunit. Extensive publicly available microarray datasets containing between 162 to 5896 features were used to examine gene expression levels of these components over the 5 organisms being studied. The varying degrees of global and local co-expression for each complex were investigated statistically using an all-against-all approach for the corresponding components of each complex. We find that there is a coherent transcriptional response of many of these complexes across the organisms studied. In particular we note the significantly high levels of conserved co-expression amongst the components of the transcriptional machinery. Such a conserved response suggests that transcriptional regulation plays an important role in the assembly of its own machinery and that of other complexes. To our knowledge, this is the first time such an extensive analysis has been undertaken to provide evolutionary insights into the transcriptional regulation of protein complexes.