Systems-level evidence of transcriptional co-regulation of yeast protein complexes

J. William Lee¹, Tomasz Zemojtel², Eugene Shakhnovich¹

¹Dept. of Chemistry and Chemical Biology, Harvard University, Cambridge, MA 02138, USA; ²Dept. of Computational Molecular Biology, Max Planck Institute for Molecular Genetics, 14195 Berlin, Germany

Protein complexes are functional units in the cell whose formation is regulated by a number of mechanisms. Previous studies have suggested that transcriptional co-regulation of protein components play a minor role in assembly of individual complexes. Recent developments in experimental approaches and bioinformatic analyses offer an opportunity to investigate the cell at a global or systems level with better quality. Here we show that, using genome-/proteome-wide yeast data of protein complexes and protein-DNA interactions in normal growth conditions, a contribution of transcriptional co-regulation to global formation of protein complexes is statistically significant at a systems level. A significant fraction of proteins that form complexes shares common transcription factors on a global scale. We provide evidence for the significant contribution by quantifying transcriptional co-regulation of complexes as a global topological pattern of an integrated network. Our co-regulation measure for a complex takes into account both the absolute fraction of co-regulated protein components and their probabilistic scores from the hypergeometric distribution for all transcription factors. Biological relevance is examined by functional analysis of highly co-regulated complexes. Our finding indicates that there exists linear causality at a systems level between transcriptional co-regulation of genes and formation of multi-protein complexes in the unicellular organism.

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