

Regulatory networks revealed by transcriptional profiling in the yeast

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ABSTRACT

Transcriptional regulation is achieved by transcription factors that can recognize specific DNA segments, called regulatory elements, in the gene promoter regions. We applied a method recently proposed by Buchermann et al.[1] to identify regulatory elements responsive to various conditions, as a first step towards deciphering the transcriptional networks.

We have identified about 250 motifs from about 220 microarray experiments using Bussemaker et al. algorithm[1]. These 220 microarray experiments include environmental stress response[2], sporulation[3], cell cycle[4], and phosphate metabolism[5]. We observed several motifs, such as general stress response element agggg/ccct, appear in most experiments while some motifs, such as the regulatory element recognized by GCN4, only appear in certain conditions. Specific appearances of regulatory elements under certain conditions imply that the corresponding transcription factors are activated only in specific pathways. Analysis of the global appearance profile for each gene can shed light on cross-talk between different regulatory pathways.

Further analysis of these data may provide many insights about the transcriptional regulation: A) Analyzing expression of a gene under different conditions and occurrences of different regulatory elements in its promoter region can suggest how different factors regulate the gene's expression in a combinatorial way; B) The occurrences of a regulatory element under different conditions suggest that the corresponding transcription factor is activated

under these conditions. A global view of different elements appearing under many different conditions should give us insight into cross-talk between different pathways.

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