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Molecular Genomics, Proteomic, and Bioinformatics

Gasch Paper Reflections

Genomic Expression Programs in the Response of

Yeast Cells to Environmental Changes

This purpose of this paper is to examine the internal environment of *Saccharommyces cerevisiae* in response to drastic environmental changes such as nutrient availability, temperature, osmolarity, acidity of environment, and the presence of noxious agents. Specifically, this study examines the genomic expression of yeast cells during extreme environmental conditions to further elucidate the network of regulators and stress responses and the details of their actions.

This study uses DNA microarrays to analyze changes in transcript abundance and to define stereotyped patterns of gene expression during adaptation to environmental changes. Microarray technology allows scientists to examine small samples of cell content for genes in a very short amount of time. This technology exploits that ability of mRNA to bind to the template DNA from which it originated in order to determine the expression levels of thousands of genes at once. Knowledge provided by DNA microarray allows the functions of genes to be more closely examined and characterized based on similarities between their expressions in stressful environments compared to the expression of genes whose functions are well known. The instrument itself consists of a glass microscope slide, silicon, or nylon membrane support onto which thousands of immobilized genes may be affixed in a specific order that allows scientists to easily identify genes.

Following the DNA microarray analysis, hierarchical clustering, which arranges genes according to similarity in expression profiles across all of the array experiments, was performed to organize transcripts levels detected during microarray. This type of clustering clusters genes with similar expression patterns together. Furthermore, the range of abundance in gene expression is depicted on a color scale. Shade of red represent increases and shades of green represent decreases in mRNA levels compared to unstressed cells. Black color represents undetectable transcript levels. A dendrogram, which further depicts the relationships between genes, organizes them into branches whose lengths represent the degree of similarity between genes based on their expression profile. Genes having similar expression over a multiple experiments will be grouped together on a common branch. Clustering helps to identify common sequence motifs, gene functions and links between sets of genes.

The results of the environmental stress response study revealed similar responses to the conditions tested. However, this regulation is not general, but it is dependent on many different signaling systems that act in a condition specific and gene specific manner. The results of the environmental stress response yielded to clusters of genes. One cluster consisted of genes involved in growth related processes which appeared to be correlated and the other cluster consisted of genes that encode ribosomal proteins. The results of this experiment showed repression of ribosomal genes and genes involved in RNA metabolism to be a general feature of environmental stress response.

The environmental stress response of cells is specific to conditions that are not optimal for growth and survival. Thus the researcher proposed that the ESR is an adaptive response to suboptimal environments. ESR protects the cells from potential harm. Furthermore, this study found that the ESR is a graded response meaning the amplitude of expression is dependent upon the severity of the environmental stress. In addition, this study illustrated that yeast cells detect many different signals and creates a genomic program to integrate them to allow the cell to customize its response to features of a new environment.

The data found in this paper can be used to estimate robustness because gene expression during environmental stress response give insight into the complexity of cellular networks and interactions.