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Bio 320: T/Th-1p

Gasch 2000 Summary

Saccharomyces cerveisiae response patterns to environmental changes

Yeast cells are used to analyze gene response patterns to environmental changes. In Gasch 2000, *Saccharomyces cerevisiae* response to environmental changes was used to analyze genomic expression patterns. Microarrays, clustering analysis and other techniques were utilized to measure cells response to temperature shocks, hydrogen peroxide, progression into the stationary phase, changes in the environmental stress response system and gene expression response system.

Clustering Analysis was used to examine coregulated genes and promoters and known transcription factors. Genes involved in similar cell processes are similarly expressed, so functions of the gene are clustered and suggest hypothetical functions for unspecified genes in the same cluster. Clustering analysis further allows an overview and better understanding of cellular responses elicited by factoring the known expression of genes and well as their function and regulation. A DNA microarray was used to measure changes in transcript levels over times for yeast genes as the cells response to temperature shocks, hydrogen peroxide, progression into the stationary phase, changes in the environmental stress response system and gene expression response system were measured.

Results from the study show that gene expression response systems in yeast are triggered by environment stress. ESR, Environmental Stress Response system, and regulatory systems contribute to cellular resistance to stressers, conserves energy by suppressing genes involved in protein synthesis and cellular growth, generates energy, defends the cell agains ROS (reactive oxygen species), but also threatens cellular viability. ESR is an adaptive system that is initiated when the cells is faced with conditions in which it is neither prepared nor able to adapt to. Yeast cell genomes have been identified to initiate ESR to protect and maintain critical internal cellular systems.

I believe that Qin’s proposal that data in this paper can be used to estimate robustness is supported by findings in this paper. Cellular aging is believed to be influenced by gene/protein networks. As Qin’s research proposal states it is hypothesized that cellular aging is proportional to gene/protein network robustness. Gasch 2000 further supports this proposal hypothesis because findings in the paper convey that gene/protein networks do have some correlation or effect on yeast cellular robustness, aging and ability to undergo cellular stressors. Robustness is identified as cellular endurance to Hsp90, TOR inhibitors, and oxidative stress, which influence Reactive Oxygen Species, ROS, in cells and their rate of death.

I believe that Qin’s proposal is a mathematical and computational analysis of robustness while Gasch 2000 identifies the theoretical approach of gene response networks and effects on robustness. Qin’s proposal identifies target genes and their influence on aging and network robustness and quantifies these variable using Gompertz equation, m = - 1/(s ) ds/dt = IeGt. After reading both the Gasch 2000 paper and Qin’s proposal I believe that robustness, gene/protein networks, reactive oxygen species and cellular stressors, and response systems are all correlated and interact to affect and influence one another. I also believe that all of these factors contribute to aging.