Molecular Genomics, Proteomics and Bioinformatics (Did not identify major problems)

Kinnari Matheson

Dhami Paper Review

2/2/12

In a “Comparative analysis of gene expression and regulation of replicative aging associated genes in S. cerevisiae”, Baker’s yeast is used as a model for understanding molecular mechanisms of aging due to the short lifespan and ability to manipulate and study the genome of the organism with high throughput techniques. Specifically, genes involved in the lengthening of replicative lifespan (RLS), the number of daughter cells produced by a progenitor, were analyzed in contrast to genes that decrease lifespan. Previously, deletion of genes in the TOR pathway was shown to increase RLS in yeast. In the current paper, the 564 gene deletions from the Kaeberlein *et al.* are classified into long lived (44 genes), short lived (114 genes) and middle group (406 genes). Protein interaction data from a paper published by Krogan *et al.* is incorporated to extend the scope of the Kaeberlin data set and include first degree interactors that are unique. A Venn diagram of these relationships is shown in Figure 1.A Wilcoxon/ Man-U Whitney test was done in R to generate a boxplot, to identify the median, quartiles and outliers of the data set. A comparative analysis was done to compare the stability of the long lived and short lived genes by comparing ribosome occupancy and protein and mRNA abundance and half life data with the Wilcoxon test and boxplot. The regulation of genes over time is measured at a given optical density (660) at time point zero. Also, the expression of histone methylase and demethylase was determined in the log phase and stationary phase over 24 hours. Epigenetic effects were quantified by histone modification. The same statistical analysis was done on these data sets.

The results of these analyses show similarities between the dynamic expression and transcription factors of long lived and short lived genes, but significant differences in the other categories of comparison. There is reduced expression of long lived genes in the stationary phase of growth and higher epigenetic modification in the long lived genes. Though the authors emphasize the importance of histone modification, future directions should explore the effect of various conditions on the replicative lifespan of yeast.