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Comparative analysis of gene expression and regulation of replicative aging associated genes in *S. cerevisae*

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The single-celled eukaryote, S*accharomyces cerevisiae,* is used as a model of understanding the mechanism of lifespan regulation. *S. cerevisiae* is an ideal model due to its: simple and short life span, easy genetic manipulation, well studied genome and functional characterization and established methods for high throughput studies. Yeast genes have been shown to have orthologs in the human genome, including some aging related disease-causing genes (e.g. Werner syndrome), which makes yeast a suitable candidate for the study of aging. The replicative lifespan of yeast has been used as a model to understand the lifespan of dividing cells in higher eukaryotes, while chronological lifespan is related to non-dividing cells of eukaryotes. It is important to identify those genes whose modification can modulate lifespan, in order to determine how gene expression and their regulatory controls modulate with age. This study showed that LL and SL (long lived and short lived) groups of replicative aging associated genes have different patterns of gene expression and their regulation can be distinguished only at the epigenetic level. Krogan et al. measured the replicative lifespan of 564 deletion strains and compared it with the wild type. The authors have divided this gene list further into four groups: those single gene deletion strains having a mean lifespan greater than 36 generations are grouped as long lived (LL), single deletion strains having a mean lifespan of less than 20 generations are grouped as short lived (SL), single deletion strains having a mean lifespan of less than 26 generations are grouped as not long lived (NLL) and the rest as no significant change. Then, they expanded the dataset by adding unique 1st degree interactors to all three groups using protein–protein interaction data from Krogan et al. A Comparative analysis of dynamic properties, time-course expression analysis, and epigenetic regulation was done. They found that long lived and short lived genes have similar dynamic expression, long lived and short lived genes show differing time course gene expression, long lived and short lived genes have a common set of transcription factors controlling them, long lived and short lived genes have a common set of transcription factors controlling them, and long lived and short lived genes have a common set of transcription factors controlling them. This study found that the long lived and short lived gene-sets are significantly different in their time course expression levels, but does not show any significant difference in their dynamic properties at the mRNA level or at protein level as seen in the figures. New research should focus on direct involvement of histone methylases in modulation of aging in mammals.