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**“Comparative analysis of gene expression and regulation of replicative aging associated genes in *S. cerevisiae*”**

There are many factors, known, unknown, interacting that contribute to aging. The effects of aging through DNA mutations, oxidative damage of DNA, and the many diseases that they cause, cannot be analyzed in mouse or mammal models due to their long life span. *S. cerevisiae* are used as aging models for higher organismal cells due to their ability to replicate and rejuvenate. They allow researchers to analyze and identify genes that regulate life span. Analysis of Short vs. Long-Lived genes shows differences in epigenetic modifications in aging of cells.

To analyze the effects of short vs. long-lived genes, the replicative lifespan of 564 deletion strains were measured and compared with wild type genes. The gene list was divided into four groups: single gene deletion strains having a mean lifespan greater than 36 generations (LL)-44 genes, single deletion strains having a mean lifespan of less than 20 generation (SL)-114 genes, and single deletion strains having a mean lifespan of less than 26 generations (NLL), and the non-significant strains, middle group, (MG)-406.The dataset was then expanded using protein-protein interaction to add 1st degree interactors: 167 unique protein interactors for long lived genes, 159 unique protein interactorsfor short lived genes, and 830 unique protein interactors for middle genes were added to the LL, SL and MG group and analyzed.

Analysis of the results were calculated from the P-value and boxplot, which identifies the middle 50% of the data, the median, and the extreme points, using the “R” statistical program. Additional expression analysis conducted included: comparison of dynamic properties (mRNA copy number, mRNAhalf-life, ribosome occupancy, protein half-life, protein abundance and noise), time course expression analysis (expression of genes associated with LLand SL groups changed with time during the growthof yeast), and evaluation of the differences in regulation of long lived andshort lived genes at the epigenetic level (comparison ofdifferent histone modifications-acetylation and methylation). Results convey that proteins that interact with short and long-lived genes affect the lifespan. Results also convey that LL genes have a higher epigenetic modification, but that SL and LL genes have differing time course gene expression, similar dynamic expression, and similar regulation at the transcription level.

Although histone modifiers (methyltransferase) have been identified as regulators of replicative aging of yeast, the association and molecular mechanisms remain poorly understood. Future studies in this research are being made and are needed to understand the molecular mechanisms and exact association of histone modifiers in the process of replicative aging of yeast.