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Article 2 Report

This article is a comparative review of other studies that have been done on yeast in trying to find out what causes aging. Specifically, the article is discussing studies that have conducted experiments on yeast to determine the effect of gene deletion on the longevity of lifespan. Extra data from a different but similar study was added. Personally I did not think that was a good idea to mix different data and then draw a conclusion from that information. Figure 1 shows the protein-protein interactions that took place between the different groups of proteins that were grouped in this experiment. Datasets were taken to compare the dynamic properties that the groups shared in common with one another. The data that I agree with the most that I think should have been the main focus of the paper was the time-course expression analysis. In this experiment they analyzed the expression of genes associated with two of the groups of proteins a different time intervals. Figure 2 shows that ribosome occupancy between long and short lived genes are at the same level. The article says that mRNA abundance is also the same between the two but when I look at the figure it doesn’t seem so at all. The comparative analysis of the two types of genes shows that there is no difference in stability. Figure 3 shows that the long lived genes are decreasing in the stationary phase of the growth curve and continue to decrease and time progresses, whereas the short lived genes decreased only a little bit as compared to the long lived. I am having a problem reading and understanding the graphs they are showing and how they are seeing a decrease and an increase, so I am taking their description as the truth as to what I see. I am also confused as to their conclusion of the replicative lifespan of yeast. They state that the reduced expression of long lived genes in the stationary phase is responsible for the replicative aging of yeast. Then the confusing part comes when they say “this evidence altogether strengthens the notion that the replicative lifespan of yeast can be enhanced by decreasing the expression of long lived genes in the stationary phase. A good finding of the paper was that the transcription factors most likely do not play a role in the differences in the gene expression based on gene regulation by transcription factors. A major finding in this paper was shown in figure 4. It showed that there was a higher trimethylation of a specific gene in long lived genes than in short lived genes. This result suggests that the differences in the expression of long and short lived gene-sets are due to differences in histone post translational modifications.