Title:

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Abstract:

Cellular Aging is a fundamental key in science that many people are trying to understand. Two aims of this research are to examine the effects of genes on lifespan and to examine the robustness of cellular aging. Although there are two aims of this research, there is one goal which is to increase our knowledge of cellular aging. Under Dr. Hong Qin’s supervision, we biologically and computationally studied aging using caloric restriction and reactive oxidative species utilizing the model organism S. cerevisiae.

This summer we examined cellular aging and gene/protein interaction networks; as well as network robustness. The lifespan of yeast can be measured in replicative and chronological lifespans. Replicative lifespan (RLS) is the number of cell cycles that individual mother cells produce before they cease to divide and chronological lifespan (CLS) is how long cells can survive without dividing in stationary phase. Robustness is the ability to maintain homeostasis during environmental changes or mutational changes. Three proxies used to study robustness was morphological robustness, the variance of gene expression robustness, and competitive growth fitness robustness. A method known as flow cytometry was a big help in detecting the effect of DHR/DHE levels on hydrogen peroxide. Reactive oxygen species (ROS) are chemically active molecules containing oxygen. One form of reactive oxygen species involving aging is intracellular levels of H2O2, which was studied in order to understand caloric restriction.

Different yeast strain types were studied such as BY4743 and M5 at different DHR/DHE levels. We grew these yeast strains, restaged the cells, performed a hydrogen peroxide treatment, performed DHR and DHE labeling, then measured both DHR and DHE in calibur. The flow cytometer allowed us to count the cells and to compare the yeast strain types at different levels. These yeast strains were measured in the time frame of the day of the experiment, the next day of the experiment, two days after the experiment, and three days after the experiment. This allowed us something to actually compare and contrast. Plots were generated on a computer program called "R". "R" allowed us to visualize the differences in each yeast strain at different levels by viewing a graph.

There were many errors that occurred while performing these experiments due to the fact that this was the first time that we ever conducted an experiment as such. Some errors were not growing the yeast strains in the shaker for the allotted amounts of time, not spinning cells down all the way, pouring the cell pellet off as well as the supernatant, not point sonicating the cells, and simply adding too much liquid to the cells or not washing the cells. Our main issue came with the flow cytometer. Since the flow cytometer is a very old machine, we had many complications in such that sometimes our cells did not run at all. That made it harder for us to compare the yeast strain types at different levels.

Although it is too early for final results to be made, some results have been concluded. Some conclusions that can be gathered from the experiments is that hydrogen peroxide treatment can increase DHR signal, while hydrogen peroxide treatment can decrease signals in M5 and M13 in 2%D, M5 in 0.5%D.DHR/DHE double stain was performed to test the hypothesis that low DHE signals in higher hydrogen peroxide are due to inefficient cells. As we continue to perform these experiments, we will hopefully understand the cellular aging process better.