The Role of the Nuclear Genes KU70 and KU80 in the Stability of the Mitochondrial Genome in *Saccharomyces cerevisiae.*

Amber Blidy ablid1@u.brockport.edu (716) 352-0575

Mentor: Dr. Rey Sia rsia@brockport.edu

The College at Brockport, State University of New York, Department of Biology

The purpose of this research is to determine the role of the nuclear genes, *KU70* and *KU80*, in maintaining mitochondrial DNA stability in the budding yeast, *Saccharomyces cerevisiae*. The mitochondrion is an organelle in eukaryotes that produces much of the ATP used by a cell. Mitochondria have their own genomes, separate from nuclear DNA, which encodes many proteins needed for cellular respiration. Mutations can occur in the mitochondria of humans that could result in decreased or loss of mitochondrial function, which leads to neuromuscular or neurodegenerative diseases. The KU heterodimer consists of the Ku70p and Ku80p proteins. The complex has been shown to function during DNA double-strand break (DSB) repair through non-homologous end-joining (NHEJ) and telomere maintenance in the nuclear genome. The goal of this lab is to determine the effects caused by the loss of *KU70* and *KU80* genes on mitochondrial DNA stability. The major focus of this research is to investigate at what frequency *ku70*Δ and *ku80*Δ deletion strains will lose the ability to respire that directly relates to the loss of mitochondrial function. These strains will also be used to monitor the affect loss of these genes have on homologous recombination in the mitochondrial genome. By completing two different assays, respiration loss and direct repeat-mediated deletion (DRMD), the role of these genes can be determined. In regard to *KU70,* the respiration loss assay showed a 1.4 fold decrease in spontaneous respiration loss compared to the wild type strain. Likewise, *KU80* was found to have a 1.5 fold decrease. The rate of DRMD events in the nuclear and mitochondrial genomes showed an increase in the *KU70* mutant strain compared to the wild type; however, more trials of this assay must be completed to verify the validity of the results.

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