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Honors Senior Thesis Abstract Draft

The effects of the environmental stress of cold shock on *Saccharomyces cerevisiae* have not been extensively studied. Cold shock causes changes in gene expression, but which transcription factors regulate this response is still unknown. To determine which factors are involved, we screened nine transcription factor deletion strains for impaired growth at different temperatures on solid media, and found that the *∆phd1* and *∆gcr2* strains were impaired for growth at all temperatures (15°C, 20°C, 30°C and 37°C), the ∆nrg1 strain was impaired for growth at warm temperatures (30°C and 37°C) and enhanced for growth at cold temperatures (15°C and 20°C), and the ∆*ash1*, ∆*swi4*, and ∆*hap4* strains were impaired for growth only at cold temperatures. We then subjected yeast cells deleted for the Swi4, Hap4, and Ash1 transcription factors to cold shock at 13°C, followed by recovery at 30°C. Samples were collected before cold shock (t0), after 15, 30, and 60 minutes of cold shock (t15, t30, t60), and after 30 and 60 minutes (t90, t120) of recovery after 60 minutes of cold shock. Then, total RNA from these cell samples was purified and aRNA was synthesized and indirectly labeled with the Cy3 and Cy5 dyes, followed by hybridization to DNA microarrays. A total of 4 replicates was completed for each strain and timepoint. An ANOVA test showed that 2233 out of 6189 (36%) genes had a significant change in gene expression at any time point at an adjusted p value < 0.05 for the *∆swi4* strain, while 1749 genes (28%) were significantly changed in the *∆hap4* strain. Both strains showed patterns of expression where genes were up-regulated during cold shock and down-regulated during recovery or vice versa. Genes showing these patterns of expression belong to the ribosome biogenesis and glycogen metabolic processes, respectively, processes used by the cell to survive cold shock. In addition, we have just begun microarray analysis on the *∆ash1* strain.