Undergraduate Research Symposium May 18, 2012 Mary Gates Hall

Online Proceedings

POSTER SESSION 3

MGH 241, Easel 140

4:00 PM to 5:30 PM

Characterization of Replicate Evolutions of *S. cerevisiae* under Constant Sulfur-Limitation

Mei Huang, Junior, Extended Pre-Major
Anne Elisabeth (Annie) Young, Junior, Biology (Physiology)
Mary Gates Scholar
Bryony Marie (Bryony) Lynch, Senior, Biology (Molecular, Cellular & Developmental)
Mentor: Maitreya Dunham, Genome Sciences
Mentor: Aaron Miller, Genome Sciences

Chemostats are a continuous culture system in which cells are grown in a tightly controlled, chemically constant environment where culture density is constrained by limiting specific nutrients. Unlike batch cultures, the selective pressure imposed in a chemostat is constant. This has made them a desirable tool for evolution and competition experiments. Traditionally chemostat experiments with *S. cerevisiae* have been constrained due to the limited number of cultures that can be run at once. In order to solve this problem our team is working with a new culturing system that allows 64 chemostats to be run simultaneously. In our experiment we evolved 32 biological replicates of haploid *MAT*a yeast cells under constant sulfur-limitation for 250 generations. We are now using a variety of techniques including whole genome sequencing of evolved populations to characterize mutations that have been selected for during the course of these evolutions. Changes in the genome can be correlated to changes in relative fitness, which we assayed through competition with a GFP (a green fluorescent protein that exhibits bright green fluorescence when exposed to ultraviolet blue light) expressing ancestral strain every 50 generations. Ultimately it is our hope that higher replicate number will better reveal the spectrum of genes important for adaptive growth in a sulfur-limited environment. Furthermore we would like to use these methods to understand what genes are important in a wide variety of nutrient limited environments.

POSTER SESSION 3

MGH 241, Easel 139

4:00 PM to 5:30 PM

Using Plasmids as a Model for Gene Amplification in Yeast Competition Assays

Michael Joseph (Mike) Bocek, Senior, Biochemistry
Amgen Scholar
Mentor: Maitreya Dunham, Genome Sciences

The Dunham group studies the costs and benefits of changes in gene and chromosome copy number (aneuploidy) in *S. cerevisiae*. Gene copy number change is a common evolutionary mechanism, and is often seen in cancers. Previously, the lab carried out a series of experiments to determine the consequences of changing the copy number of every gene in the yeast genome. 4383 yeast strains, each carrying a plasmid containing a yeast gene and a unique barcode sequence, were competed in nutrient-limited continuous-culture environments. The relative success of each strain was found by performing high-throughput sequencing on the barcodes. Our project explored three assumptions of this experiment, using direct chemostat competition assays. First, we confirmed that fitness effects observed in the pooled experiment could be repeated in individual experiments. We performed competition experiments using 22 genes from the experiment that were found to either be beneficial in certain environments or potentially harmful when duplicated. We also found that the plasmid alone had a fitness effect, by competing a strain containing a plasmid without a gene insert against a wild-type strain. Finally we tested the fitness effects of Autonomously Replicating Sequences (ARSs), which are origins of DNA replication found in many of the loci we are investigating. In a competition between a strain transformed with a plasmid with two ARSs and a strain with a plasmid containing a single ARS, a fitness benefit was observed for the presence of an extra ARS on the plasmid. These data are important controls for the pooled experiments previously performed in the Dunham lab and will help to identify the precise molecular causes of fitness changes associated with aneuploidy, and, perhaps in the future, provide some new insights into cancer biology.