SESSION 1Q

EVOLUTION, FROM AEDES TO ZEBRAFISH

Session Moderator: Maitreya Dunham, Genome Sciences
JHN 175
12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

The Role of Transposable Elements in Hybrid Adaptation

Erica Alcantara, Senior, Biology (Molecular, Cellular & Developmental)
Mary Gates Scholar
Mentor: Maitreya Dunham, Genome Sciences
Mentor: Caiti Smukowski Heil, Genome Sciences

Understanding the genetic changes by which organisms adapt to novel and extreme environments is a central goal of evolutionary biology. One mechanism that may offer a rapid path to adaptation is hybridization: the union of two genetically distinct populations or species. Hybridization may transport beneficial genetic variation from a related species or may stimulate new variation to form within genomes, such as the mobilization of transposable elements (TEs). Transposable elements are large, repetitive sequences that can independently move around the genome, and thus mediate a cascade of large-scale changes in chromosome structure, gene expression, and gene content. I am interested in studying whether TE insertions occur more frequently in hybrid species vs. parental species and identifying the types of genomic changes TE insertions facilitate in hybrids. To do this, I am using a two-part approach in the model system of budding yeast, *Saccharomyces cerevisiae*. First, I am performing fluctuation assays to assess the rate of transposition in *S. cerevisiae*, its relative *Saccharomyces uvarum*, and an interspecific hybrid of the two. Second, I am using sequencing to identify novel TE insertions in hybrids evolved in nutrient-limited environments. If TEs do play a role in hybrid adaptation, I would expect to map transposition events with sequencing data and identify associated chromosome rearrangements and/or gene disruptions that may confer a fitness benefit. I also hypothesize finding higher transposition rates in the *S. cerevisiae* x *S. uvarum* hybrid clones compared to the non-hybrid parental clones. In doing so, I hope to gain a deeper understanding on the genetics of hybrid adaptation, which has yet to be studied in greater detail in the field of experimental evolution.

POSTER SESSION 3

Balcony, Easel 115
2:30 PM to 4:00 PM

Identifying Essential Genes in Different Yeast Species under Varying Conditions

Azhar Khandekar, Senior, Biochemistry
Mentor: Monica Sanchez, Molecular and Cellular Biology
Mentor: Maitreya Dunham, Genome Sciences

Phenotypes of mutant alleles in a given environment can be used to determine which processes depend on the normal function of a gene. Although genes involved in specific biosynthesis pathways are well characterized in the model organism *Saccharomyces cerevisiae*, there are genes involved in these processes that still have uncharacterized function. The interaction between gene function and the environmental condition is complex, and requires a comparative approach across yeast species to identify the function of uncharacterized genes in a variety of conditions. We have used a Tn7 transposon insertion mutagenesis system in *Saccharomyces uvarum* to randomly mutate genes across the genome and pooled all resulting insertional mutants together. We used deep sequencing to identify the insertion sites, and previously predicted 809 genes to be essential for growth in standard laboratory conditions in *S. uvarum*. Using these same methods, we will apply different selective pressures to libraries of mutant yeast, and aim to understand which genes are critical for growth under specific conditions, such as glucose, phosphate, and sulfate limiting media. We expect that it will be more common to find genes that were non-essential in normal growth media to be essential in more limiting conditions, whereas most genes that were essential in normal growth media should also be essential in limiting conditions. Studying yeast in conditions where they are naturally found (such as grape-must) can provide insight into new, critical genes. This information can be used to make commercial processes such as fermentation more efficient by optimizing metabolic pathways. Additionally, this data can be used to improve gene annotations and increase our knowledge of the biochemical pathways that underlie these essential processes. Thus, acquiring phenotypic information of mutant genes across species and conditions can even help discover genes involved in previously well-

studied pathways.

POSTER SESSION 3

Balcony, Easel 111

2:30 PM to 4:00 PM

Determining the Genetic Mechanisms of Cell Aggregation in Evolved Strains of *Saccharomyces cerevisiae*

Kolena Dang, Junior, Biochemistry
Mentor: Maitreya Dunham, Genome Sciences
Mentor: Elyse Hope, Genome Sciences

The model yeast, *Saccharomyces cerevisiae*, can evolve the ability to clump, a trait called flocculation that protects the yeast cells from stress factors including antimicrobial treatments. Understanding the genetics behind this trait could give us insight into treatment options for biofilm-related complications in hospitals as well as targets for microbe engineering in the case of industrial production. In this project, we are interested in identifying the mutations that occur when yeast evolve flocculation. We evolved *S. cerevisiae* from a non-flocculent ancestor strain for 300 generations in miniature chemostats, multiplexed culture devices that maintain a constant environment. Strains that flocculate have a selective advantage in these devices, and 35% of our final populations evolved this trait. In backcrossing these flocculent strains with their ancestor and dissecting the tetrads into four spores, 20 out of 22 strains segregated the flocculation trait with a 2:2 ratio, indicative of a mutation in a single gene causing the trait. We identified causal alleles using bulk segregant analysis, a pooling and sequencing approach, including a causal transposable element insertion in the promoter of *FLO1*, a gene known to control flocculation. We hypothesize that this mutation is responsible for changing how *FLO1* is expressed and have now identified this mutation in 13 of the clones, some of which exhibit varying phenotypes. We believe that additional mutations may be responsible for this phenotypic variation and are using microscopy to target our sequencing for the gene(s) of interest. We also used these findings to engineer a new strain with *FLO1* deleted, which we hypothesized would take longer to flocculate. We report the results of a new evolution experiment comparing flocculation time between the deletion strain and the wild-type strain and demonstrate that our engineering effectively decreases flocculation ability. This is a promising result for both medical and industrial applications.