



Undergraduate Research Symposium May 17, 2019 Mary Gates Hall

Online Proceedings

SESSION 1C

MOLECULAR CONTROL OF THE CELL

Session Moderator: *Hannele Ruohola-Baker, Biochemistry*
MGH 171

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Identifying Genes that Influence Hybrid Fitness

Angela Shang Mei Hickey, Senior, Biology (Molecular, Cellular & Developmental)

Mentor: Maitreya Dunham, Genome Sciences

Hybrid vigor or heterosis describes superiority of a hybrid compared to its parents; however, the genetic mechanisms underlying this phenotype remain largely unresolved. One potential mechanism is loss of heterozygosity (LOH), a process where there is loss of one copy of a gene or surrounding chromosomal region. In our previous work, we evolved hybrids between two species of yeast, *Saccharomyces cerevisiae* and *Saccharomyces uvarum* - which differ in their temperature preference - by growing them in a chemostat at different temperatures in phosphate limited media for several hundred generations. We repeatedly observed LOH events in these hybrids in response to changes in temperature. Each LOH event incorporated the gene region encoding the Pho84 membrane bound inorganic phosphate transporter protein on chromosome 13, which is important when phosphate is limited in the environment. These repeated LOH events all affect fitness based on environmental temperature; however the events span various lengths with some as short as a few kilobases and others as large as 200 kilobases. Because they are different in length we also know that they include different numbers of genes. To investigate whether these varying LOH lengths may include other genes that affect hybrid fitness, we have used CRISPR/Cas9 to create double strand breaks at specific sites along the *S. cerevisiae* chromosome 13, resulting in DNA repair using the *S. uvarum* chromosome as a template and formation of LOH events of different lengths. Our aim is to create a pool of hybrids with varying LOH tracts and let them compete in a phosphate limited environment to assess the relationship between the different LOH regions and fitness. This will allow us to narrow down genes that may be responsible for temperature sensitivity or that contribute

to higher hybrid fitness in organisms that are heterozygous or homozygous.

SESSION 2J

MEASURING CELL GROWTH AND EVOLUTION

Session Moderator: *Kristin Anderson, Immunology*
MGH 271

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Creating a Continuous Culture Monitoring Device to Determine Relative Strain Frequency in Solution

Nick Righi, Junior, Bioengineering

Mentor: Maitreya Dunham, Genome Sciences

Mentor: Anja Ollodart, Molecular Cellular Biology

One method of comparing strain fitness is to compete strains head to head; over time, the competitor with a fitness advantage will increase in frequency in the population. To track the frequency of each strain, they must be differentially marked such that their frequencies can be measured by plating the culture and counting colonies of each type - a time and labor-intensive process. One common marker used by our lab and others is using pigment production to produce colonies of different colors. My project is to create a continuous culture monitoring device named a chromostat that uses a color sensor to measure the relative abundance of different colored strains in solution, removing the need for plating and increasing the automation of competition experiments. By comparing the color of the individual yeast strains to the color of them mixed together, the chromostat can calculate, in real time, the relative abundance of each strain in solution and determine which strain is more fit and by how much. I built the chromostat on a raspberry pi minicomputer using an open source Java library, pi4j, to control the attached color sensor. This sensor converts light waves to red, green, and blue color values, which are then converted to frequency values for each strain and displayed to the user. The chromostat is controlled through a text-based interface that operates on the command line and has a variety of functions to modify data acquisition to increase overall accuracy and allow for data analysis. It will be used as part of a high school teaching laboratory in which students conduct evolution experiments and later com-

pete different yeast strains against each other to generate fitness data.