UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

Online Proceedings

POSTER SESSION 1

Commons West, Easel 13

11:00 AM to 12:30 PM

Exploring the Genetic Basis of Thermostability in the RNA Virus phi-6

Kimber Clementine (Clementine) Dunnell, Senior, Biology (Ecology, Evolution & Conservation)
Emily Hsieh, Senior, Biochemistry, Biology (Molecular, Cellular & Developmental)
Levinson Emerging Scholar, Mary Gates Scholar, Undergraduate Research Conference Travel Awardee
Mentor: Benjamin Kerr, Biology
Mentor: Sonia Singhal, Biology

Thermostability is the capacity of an organism to survive and thrive at high temperatures and is a characteristic with many biotechnological applications, such as food processing. We are seeking to understand the mechanisms of thermostability in viruses by using an RNA virus, phi-6 Cystovirus. We are evolving the phi-6 virus to become thermostable by exposing it to a target temperature of 61C over many generations (wild type viruses grow at 25C). In order to see if exposure to different intermediate temperatures affects the genetic pathway to thermostability, we will expose the phi-6 virus to different temperature regimes prior to reaching the target temperature. The temperature treatments are sudden, where the virus is exposed to the target temperature throughout the entire course of the experiment, moderate, where the virus is exposed to the target temperature halfway through the experiment, and gradual, where the virus is exposed to the target temperature on the final day of the experiment. The genome of phi-6 has already been characterized, which enables us to compare the genome of the evolved, thermostable phi-6 viruses to the ancestor and allows us to study the genetic basis of thermostability. In future studies, we hope to use these thermostable viruses to learn about costs and benefits of maintaining thermostability.

POSTER SESSION 1

Commons West, Easel 24

11:00 AM to 12:30 PM

Local Processes of Genetic Recombination in Populations of *Rhododendron macrophyllum*

Shayna R. (Shayna) Waldbaum, Junior, International Studies: Jewish Studies
Mentor: Michelle Stitzer, Biology
Mentor: Benjamin Hall, Biology

Rhododendrons are plants native to the Northern hemisphere, comprising over 1000 species, most of which have eye-catching flowers. The native Rhododendron of the Pacific NW, R. macrophyllum, harbors a degree of DNA sequence variation exceptional for a single species. Our study focuses on RPB2d, the gene encoding the second largest subunit of RNA polymerase II. Within intron 4 of R. macrophyllum RPB2d, there exist four conserved haplotypes, which have a structured geographical distribution. (Puget Sound differs from Oregon Cascades differs from Oregon Coast.) This surprising pattern of intraspecies variation inspired my project of looking into the degree and pattern of genetic homogenization in these populations by recombination events within and near the RPB2d gene. Thus far, I have sequenced most introns throughout RPB2d and some of the non-coding region upstream. The results have shown that the intron 4 haplotypes are linked to specific variants in intron 1. However, the later introns (6-13, 13-15, and 23-24) are uncoupled from the intron 4 haplotypes and show increasing recombination. About 1 kb upstream, there is a 341 bp DNA sequence inversion in certain plants. An inversion is a segment of a chromosome that has been reattached on the same chromosome in the same location, but in the opposite direction. The inversion found in most RPB2d genes of R. macrophyllum is not found in other species or in haplotypes 1 and 4, the ones most similar to other species. The data continues to show that fewer recombination events occur in introns closer to the inversion. My research is now focused on how the inversion limits the rate of recombination. The next step will be to sample heavily from homozygous populations to see if there is a normal rate of recombination. This regulation could help explain the persistence of varied haplotypes in intron 4.

SESSION 1D

MEDICAL THERAPEUTICS AND ENDOCRINOLOGY

Session Moderator: Ian Sweet, Medicine
231 MGH
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Pathologic Onset of Megaesophagus in the Aging Mouse Model of Duchenne Muscular Dystrophy
Ladan Laurel (Ladan) Mukherjee, Senior, Biochemistry
Mentor: Jeffrey S Chamberlain, Neurology
Mentor: John Hall, Neurology

Pathologic enlargement of the esophagus, termed megaesophagus, results in a failure to complete peristalsis leading to vomiting, severe weight loss and potential death. Megaesophagus is characterized in a number of disease states including parasitic (Chaga's disease), autoimmune (myasthenia gravis), and neuromuscular (muscular dystrophies), however, a detailed cellular and mechanistic understanding is lacking. To address this deficit, we performed a comprehensive examination of the onset, pathology and cellular composition of megaesophagus in the mouse model of Duchenne muscular dystrophy (DMD). DMD affects ˜1/3500 male births and is a catastrophic and ultimately fatal muscle wasting disease resulting from a mutation in the gene encoding the integral skeletal muscle protein dystrophin. Although poorly defined in human DMD patients, megaesophagus is documented in canine and mouse models of DMD. Advancements in DMD therapies has increased patient lifespan and underscored a need to assess the impact of the disease in a range of organ systems, including the esophagus. We find that older dystrophic mice can develop severe megaesophagus, but that the timing of onset depends on the nature of dystrophin expression in muscle and non-muscle tissues and the genetic background of the mice. Further studies are in progress to delineate the precise dystrophin expression pattern in different cell types of the esophagus that contribute to pathology. Work presented here will be essential for future work aimed at identifying new therapeutic targets for DMD.

SESSION 1K

PHILOSOPHY AND ETHICS

Session Moderator: Benjamin Hole, Philosophy
258 MGH
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Contemplating Kant's Ethical Conundrum: An Intersectional Approach to Autonomous Moral Decision-Making
Allison Renee Greer (Allison) Ross, Senior, Comparative Literature (Cinema Studies), Latin
Mary Gates Scholar, Mary Gates Scholar
Mentor: Benjamin Hole, Philosophy

This paper challenges the Kantian account of autonomous moral decision-making. Kant's definition of autonomy, I argue, is excessively narrow and does not place sufficient importance on the contextual factors which one encounters when attempting to act as an ethical agent in the empirical realm. An intersectional view of autonomous moral decision-making such as that put forth by Meyers takes these considerations more fully into account. By way of an exemplification illustrating a "real-world" scenario, I show how an application of Kant's definition generates seemingly irresolvable conflicts. Then, through utilization of an intersectional definition of autonomy, I demonstrate how this alternative moral reasoning system allows for a more holistic understanding of individuals and the multiplicity of factors which shape and influence their situations and choices.

SESSION 1R

SYNTHETIC BIOLOGY AND MOLECULAR BIOTECHNOLOGY

Session Moderator: Daniel Ratner, Bioengineering
022 JHN
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Social Dynamics of a Synthetic Cooperative *E. coli* System
Melissa Delaine (Melissa) Arnold, Senior, Biology (General)
Mentor: Benjamin Kerr, Biology
Mentor: Sonia Singhal, Biology

In this project, we explore conditions that are critical for *de novo* evolution of cooperation and altruism in a bacterial system. Previous theoretical work has shown that there is a competitive advantage to defection and selfishness, but the ubiquity of cooperation in nature suggests that cooperation may be adaptive. Here, we aim to uncover environments and genetic conditions that actually promote greater cooperation. We use an engineered cooperative strain of *Escherichia coli*. Through a bistable genetic switch, single cells have the capability to be either a producer cell that makes the cellulase enzyme to break down cellulose, or a consumer cell that eats the byproducts of cellulose breakdown. Our first aim is to characterize the social dynamics of this synthetic system and determine if a social dilemma is in fact occurring—i.e., is there a cost

to producing cellulase, and can cheaters that do not produce cellulase displace the cooperators that do? Our second aim is to evolve the system over many generations and analyze how it changes. Uncovering the conditions favoring higher cooperation (e.g., greater production of cellulase) provides insight into how cooperation can evolve and how populations circumvent social dilemmas. We hope to use evolution as a tool to tune the synthetic genetic circuit for maximal cellulose breakdown. On a broader scale, these conditions that favor cooperation may have practical applications in waste degradation and biofuel production.

POSTER SESSION 2

MGH 241, Easel 167

12:45 PM to 2:15 PM

Modeling the Evolution of Multicellularity

Joseph Henry (Joe) Marcus, Senior, Biology (General)
Mary Gates Scholar
Samuel Evans (Sam) Reed, Senior, Biology (Ecology, Evolution & Conservation)
Mary Gates Scholar
Mentor: Benjamin Kerr, Biology
Mentor: Peter Conlin, Biology

The evolution of multicellularity is one of the most important yet least understood biological phenomena. What selective pressures drive this major evolutionary transition? To address this question, we use a theoretical approach to model the spatial properties of cell groups in a simulation entitled TreeMulticellularity (TreeMu). In TreeMu a simple multicellular organism is represented as a graph, with nodes representing cells, and edges representing physical connections between cells. Like cells, nodes carry intrinsic attributes, such as reproduction, mutation and death rates; these dictate life processes and define an individual's fitness. Like multicellular groups, graphs have similar properties that emerge from individual contributions. When a node dies it splits the graph in two, analogous to group level reproduction. We explore how the evolution of a node's death rate affects multicellular growth. In the simulation we implement an evolutionary algorithm that selects for 'multicellular' graphs of large sizes by removing small groups from the population. Preliminary data supports a tradeoff between group size and reproduction. TreeMu provides a computational framework to explore the dynamics of multicellular evolution.

SESSION 2R

EVOLVING SYSTEMS IN BIOLOGY: FROM MOLECULES TO MARSUPIALS

Session Moderator: Billie J. Swalla, Biology

022 JHN

3:45 PM to 5:15 PM

* Note: Titles in order of presentation.

Experimental Evolution of Phenotypic Plasticity

Samuel Evans (Sam) Reed, Senior, Biology (Ecology, Evolution & Conservation)
Mary Gates Scholar
Joseph Henry (Joe) Marcus, Senior, Biology (General)
Mary Gates Scholar
Mentor: Benjamin Kerr, Biology
Mentor: Peter Conlin, Biology

Darwinian natural selection produces an organism that is adapted to its environment, an organism whose traits (phenotype) are tuned in critical ways to its habitat. If organisms and their phenotypes are so finely tuned to their environment, how can they deal with changes to that environment? One strategy is to evolve the ability to change phenotype in response to a change in the environment, or phenotypic plasticity. Theory predicts phenotypic plasticity to be adaptive when (1) organisms experience different environments either spatially or temporally and (2) different environments favor different phenotypes. In some cases, changes may be accompanied by cues that provide reliable information about future selection. Previous studies modeling adaptive plasticity suggest plasticity to be favored when the environmental cue always predicts the correct selection and not when the environmental cue is unreliable. We experimentally tested theoretical predictions about the de novo evolution of adaptive phenotypic plasticity with a clustering phenotype of baker's yeast by selecting alternately for large or small clusters. Selection for size was cued by alternate forms of growth media and this cue was either a reliable predictor of future selection or an unreliable predictor. After a preliminary run of the experiment, we have found indications of an emergent plastic response in one of our replicates from the reliable cue treatment. This provides a biological example that is consistent with accepted theoretical predictions.

SESSION 2S

ASTRONOMY AND PHYSICS

Session Moderator: Suzanne Hawley, Astronomy

026 JHN

3:45 PM to 5:15 PM

* Note: Titles in order of presentation.

Detection of Transiting Exoplanets using Kepler Lightcurves
John Mark (John) Mehlhaff, Junior, Computer Science, Physics: Comprehensive Physics
NASA Space Grant Scholar
Nancy Helen (Nancy) Thomas, Senior, Astronomy, Physics
Mary Gates Scholar, NASA Space Grant Scholar, Undergraduate Research Conference Travel Awardee, UW Honors Program
Christopher James Martin, Senior, Astronomy, Physics
Mentor: Eric Agol, Astronomy
Mentor: Andrew Becker, Astronomy
Mentor: Benjamin Vega-Westhoff, Astronomy

Exoplanets are planets outside our solar system, and the current explosion in exoplanet discoveries is revolutionizing our understanding of the potential for extraterrestrial life. This prolific era of detections has stemmed largely from the unprecedented observing capabilities of NASA's Kepler Space Telescope. The Kepler Spacecraft collects high precision time-series photometric data on a fixed group of approximately 160,000 stars. The data are represented by temporal lightcurves (i.e. brightness vs. time) that can be used to detect transiting exoplanets, the topic of our research. Transits are events where an orbiting planet partially eclipses its host star, casting a small shadow on the telescope. To detect transit signals, we rely on the Quasi-Periodic Automated Transit Search Algorithm (QATS). As an automated tool, QATS provides a crucial means to reduce the Kepler dataset to a manageable size. However, since the algorithm is sensitive to stellar variability, eclipsing binary stars, and systematic artifacts of the spacecraft, additional analysis is required to separate true detections from false positives. Determining the best way to do this is the present focus of our work. Concurrently, we are exploring the potential for QATS not only to determine orbital period, but also to constrain transit depth and duration (properties related to the size of the exoplanet and to the density of the stellar host). While this increases the complexity of the QATS algorithm and the amount of output to manage, it provides greater potential for a fully automated transit search process with results that are more descriptive of the exoplanet systems detected.

SESSION 2T

EVOLUTION, GENETICS, AND BIOCHEMISTRY OF PLANTS, ALGAE, AND FUNGI

Session Moderator: Richard Olmstead, Biology, Burke Museum
111 JHN
3:45 PM to 5:15 PM

* Note: Titles in order of presentation.

Fungal Symbionts in Genus *Rhododendron*: Evaluation of Ericaceous Mycorrhizal Relationships
Katie L. (Kate) Jenks, Senior, Biology (Plant)
Mentor: Michelle Stitzer, Biology
Mentor: Benjamin Hall, Biology
Mentor: Joe Ammirati, Biology

The presence of fungal symbionts residing in the root tissue of plants is a well-documented occurrence, yet questions regarding the identification and comparison of fungal partners in mycorrhizal relationships have been largely unanswered. Ericoid mycorrhizae, an example of a mycorrhizal relationship, are found in host plants within the order Ericales. Ericales, which contains such familiar species as persimmon, blueberry and Rhododendron, are able to persist in edaphic conditions due to their fungal symbionts. These symbionts form hyphal coils inside plant cell membranes, and thereby exchange crucial nutrients with the host plant. This project aims to evaluate the specificity between fungal communities and their host Rhododendron species, with the expectation that differing communities may exist, even in closely related hosts. Using known techniques to extract fungal DNA from the root systems of Rhododendron species in varying conditions and proximity, this DNA is then used to generate species based communities within specific Rhododendron hosts. By using type-cultures and genomic sequencing, comparisons of the presence or absence of fungal species within host roots can be made. This will shed light on infection intensity, and specificity between roots and fungal symbionts. Anticipated results of high levels of specificity between host plant and fungus could prompt questions regarding the importance of fungal symbionts in genus Rhododendron, especially with regards to the speciation between individual host plants.

POSTER SESSION 3

Balcony, Easel 88
2:30 PM to 4:00 PM

The Multi Dimensions of Blackness: Cultural Hegemony in the U.S. and Hispaniola

Marcus Johnson, Senior, Global Studies (Bothell)
Mary Gates Scholar
Mentor: Benjamin Gardner, Interdisciplinary Arts & Sciences

Since the French and Spanish occupation of Hispaniola and specifically the US occupation from 1915-1934, Dominicans and Haitians have lived in a borderlands of blackness. However, these imaginary boundaries have been entwined with the African American response to the US occupation in Haiti. There have been many studies on the relationship between Dominicans and Haitians, but few have complicated how the relationship of African Americans living in Hispaniola played a fundamental role in shaping the multiple dimensions of blackness. By drawing upon Antonio Gramsci's theory of cultural hegemony, Stuart Hall's concept of cultural identity and diasporas in the Caribbean, in conjunction with Michael Omi and Howard Winant's work on racial formation in the United States, my research aims to draw the connections between these three groups and determine how these understandings have transformed preexisting definitions of blackness on the island. This paper is significant for comprehending the complexity of Dominican and Haitian identity, as well as locating the mechanisms of Western power, privilege and discourse. My research contributes to scholarship on the cultural production of blackness and race in the Caribbean and the United States.

POSTER SESSION 4

Commons West, Easel 41

4:15 PM to 5:45 PM

Unexpected Stories: Nikkei Concerns Oral History Project

Crystal (Crys) Donovan, Sophomore, Anthropology, Edmonds Community College
Mentor: Thomas Murphy, Anthropology, Edmonds Community College
Mentor: Marshall Kramer

The Learn and Serve Environmental Anthropology Field (LEAF) School at Edmonds Community College has partnered with Nikkei Manor and the Wing Luke Museum to develop the Nikkei Concerns Oral History Project. Through this project, students have the opportunity to serve as both mentors and mentees. Eight students have undergone training, interviewed and recorded the experiences of Japanese Americans who were interned during World War II. From these survivors we are learning more than the easy to record factual history, we are learning about experience, about the diversity of coping strategies, adaptive solutions, and emotional struggles these Americans lived. We found unexpected stories relating to aspects of control and freedom within the camps, as well as humor, acceptance, bitterness and forgiveness. The hope in a project such as this is to develop a greater understanding of the experience of these people, to record their stories and create awareness of what they faced. This is a unique opportunity for students to hear firsthand accounts from internment survivors and participating students will continue to learn about the internment era while transcribing the stories shared by Nikkei residents, and mentoring their classmates in the transcription process. While there has been much research elsewhere, the story of internment in the Northwest has received less attention. This project has allowed for student engagement and development as well meeting the needs of the Nikkei residents who wished to share their stories. Recordings will be kept both by the Wing Luke museum and Edmonds community college.

POSTER SESSION 4

Commons East, Easel 44

4:15 PM to 5:45 PM

Low Drug Concentrations Prime Bacteria for High Levels of Antibiotic Resistance

Caroline Elizabeth (Carrie) Miller, Senior, Biology (General)
Mentor: Benjamin Kerr, Biology
Mentor: Peter Conlin, Biology

It is well documented that low levels of antibiotics are present in both surface water sources and in soil near industrial, large-scale farms. However, very little work has been done exploring the selective pressure for the evolution of resistance at these sub-inhibitory antibiotic concentrations. It is our concern that mutations acquired in a low antibiotic environment may be "potentiating:" that is, the presence of these first mutations opens more mutational paths after a shift to a high antibiotic environment. The converse may also be true in terms of "dooming" mutations that close off evolutionary paths in the new environment. Here we aim to investigate the prevalence of potentiating and dooming mutations and to understand their role in adaptive evolution. We study these phenomena by performing evolution experiments with *Escherichia coli* grown in a permissive environment (low drug concentration) followed later by a sudden shift to a new environment that imposes a strong selective pressure (high drug concentration). Here the permissive environment serves to generate mutational diversity and the harsh selective environment serves to assess the evolutionary potential of mutant isolates relative to their wild type ancestor. This will increase our knowledge of the evolution of antibiotic resistance and as well as the unintended but potentially dangerous effects of long term selection in the presence of low levels of antibiotics.