UNIVERSITY of WASHINGTON

# Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

# Online Proceedings

## 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.

## POSTER SESSION 2

**Commons East, Easel 45**

*12:45 PM to 2:15 PM*

**Engineering a Survival-Based Protein-Fragment Complementation Assay to Detect Ubiquitination in *Escherichia coli***

*Anupam Kumar (Anupam) Garg, Senior, Bioen: Nanoscience & Molecular Engr*
*Mary Gates Scholar*
*Mentor: Richard Gardner, Pharmacology*
*Mentor: Michelle Oeser, Pharmacology/Molecular & Cellular Biology*

Ubiquitin is a protein modifier that is essential for many eukaryotic cellular processes. Attachment of ubiquitin to substrate proteins (ubiquitination) occurs in a three-step cascade that involves a ubiquitin activase, ubiquitin conjugase, and ubiquitin ligase; it is the ligase that targets substrate proteins. One challenge for the ubiquitin field is identification of substrate cohorts for ubiquitin ligases. Although ubiquitination only occurs naturally in eukaryotic organisms, we previously demonstrated that it is possible to reconstitute the ubiquitination cascade in *E. coli*, allowing for analysis of ubiquitination outside of its natural environment. Our project consists of the construction of a protein complementation assay, using two fragments of dihydrofolate reductase (DHFR) to detect the ubiquitination of proteins in *E. coli*, outside of the natural eukaryotic environment of ubiquitin. To perform the assay, I transformed all of the essential components of the ubiquitination pathway, including individual fragments of DHFR fused to ubiquitin and a substrate protein of interest, into *E. coli* cells. The assay tests for the covalent attachment of ubiquitin to the substrate protein through growth on selective medium, which is possible only through the combination of the separated fragments of DHFR. After construction and transformation of vectors using a known yeast ubiquitin ligase and substrate partner, I have found that ubiquitin fused to a fragment of DHFR functionally attaches to other proteins via a known ubiquitin ligase. Transformation of entire cDNA libraries into the bacterial cell in place of a ubiquitin ligase will allow for high throughput screening of ligases with homologous function as well as discovery of new ubiquitin ligase substrates. As no functional screening mechanisms presently exist, our system to efficiently screen for ubiquitin ligases and substrates provides a novel tool to address a significant chal-

lenge faced by the ubiquitin field.

## SESSION 2P

## MCNAIR SESSION - ECONOMIES OF EXPLOITATION, CULTURES OF RESISTANCE

*Session Moderator: Sonnet Retman, American Ethnic Studies*
**295 MGH**
*3:45 PM to 5:15 PM*

* Note: Titles in order of presentation.

**Behind the Veils of Industry: The Filipina Mail-Order Bride as the Ultimate Western Male Fantasy**
*Merzamie Sison (Mimi) Cagaitan, Senior, English, Comparative History of Ideas*
*EIP Scholar, Mary Gates Scholar, Presidential Scholar, McNair Scholar*
*Mentor: Michelle Liu, English*

Despite its negative associations with criminalized activities such as human trafficking, sex tourism, and prostitution, the modern mail-order bride industry continues to flourish – facilitating thousands of international marriages between "American men" (a category that includes all "Caucasian" or "Western" men) and foreign women (the majority of whom originate from Latin America, Eastern Europe and Southeast Asia). While there are legitimate factors tying the industry to the aforementioned criminal activities, my research will not dwell upon (nor will it altogether dismiss) a victim discourse in considering the life experiences of marriage migrants. Instead, my research will seek to recast women's role in this international marriage-scape as agents who, despite institutional and structural limitations on their mobility and quality of life, manage to achieve forms of women empowerment through strategic participation in the international marriage market. In particular, I focus on women marriage migrants from the Philippines, a country of origin which, in being "formerly colonized by the United States, and currently neocolonized by U.S. corporate capital, best illustrates how colonial and military dominations are interwoven with sexual domination to provide the "ultimate Western male fantasy." Part of an orientalist discourse, this "fantasy" posits Filipino women as politically passive, sexually exotic, and domestically compliant. My research utilizes the theoretical frameworks of Intersectionality and of Social Construction to examine how this "fantasy" combines sexualized racial stereotypes with racialized gender stereotypes to the harm of particularly Asian (and Asian Pacific American) women. Despite the various harm this colonial sexual mythology engenders, case studies, a literature review, and content analysis reveal Filipino marriage migrants to be empowered women who are strategically, creatively, and, oftentimes, successfully, utilizing the same colonial fantasy to their economic, social, and national advantage – a counter-narrative marked by processes of self-construction, participation in hypergamy, and the production of a corollary female fantasy.

## 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.