UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

Online Proceedings

Session 1P

McNair Session - Divides of Power: Ecology, Identity, Media, and (Re)presentations

Session Moderator: Devon Pena, Anthropology
295 MGH
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Bacchabazi in Afghanistan
Danielle Huxley, Senior, Women's Studies, Sociology, Portland State University
McNair Scholar
Mentor: Danielle Huxley

Between 2001- 2003 there has been a surge in an ancient yet taboo tradition of bacchabazi in Afghanistan; baccha meaning "child "and bazi meaning "gaming" with a connotative meaning of "boys for play". This is a significant concern because the act of bacchabazi is one that focuses on the sexual exploitation of young poverty-stricken Afghan boys for the sole purpose of elevating the statuses of their owners, mainly high ranking ex-military officers. By engaging in research of bacchabazi I intend to find answers surrounding why the act of bacchabazi has increased and what the triggers are, that permit it to flourish? The objective of my research is to look at the factors involved in this practice, including aspects of class, socioeconomic status, and conflict areas. The method I am going to use is a feminist discourse analysis of media artifacts current and historical ones. This will include newspapers foreign and domestic, blogs, academic texts, and documentaries reported by researchers within the field of child exploitation in Afghanistan, specifically focused around bacchabazi. This analysis will be done through a lens of transnational feminism while supplementing theories of colonization and post-colonization. Since the theoretical context is colonization and post-colonization, my research will fit into existing related scholarship and contribute to the field because there is not a substantial amount of research currently being published. Since my data is still accumulating I do not have solidified results but rather, informed opinions that would infer recommendations for the young men affected. Some proposed findings/recommendations include: education for the young men with the purpose of identifying the ramifications of being selected/recruited as a bacchabazi, support in way of agency for the young men, and an increased awareness among local jurisdiction in regards to not criminalizing the actions forced upon the young men.

Session 1T

Molecular and Cellular Biology

Session Moderator: Hannele Ruohola-Baker, Biochemistry
111 JHN
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

An Analysis of the Conservation of Phosphorylation Patterns across Yeast Species using Comparative Phosphoproteomics
Joanne Ino (Joanne) Hsu, Senior, Neurobiology
Howard Hughes Scholar, Levinson Emerging Scholar, Mary Gates Scholar
Mentor: Judit Villen, Genome Sciences
Mentor: Danielle Swaney, Genome Sciences

The reversible phosphorylation of proteins mediates a wide range of biological processes that range from signal transduction cascades to regulation of protein abundance. However, little is known about the mechanisms and evolution of phosphorylation networks. Despite the extraordinary advances in genome sequencing of many yeast species, evolutionary studies on the phosphoproteome of yeast species have been limited to the experimental analysis of phosphorylation in one species and theoretical analysis of the conservation of phospho-acceptor residues with other species. To properly study the evolutionary conservation phosphorylation in yeast, we are utilizing mass spectrometry to study and compare the phosphoproteome of 21 species of yeast, including representative species from each clade of the yeast phylogenetic tree. Most of these species have not been studied before by proteomics. This high-throughput phosphoproteomic study on the yeast species will contribute to the construction of phosphoproteome datasets, which can be exploited for comparative analysis of phosphorylation between the species. One of main aims is to identify phosphorylation sites that show a high degree of conservation across the 21 species of yeast.

These highly conserved phosphorylation sites likely regulate the same functions across the different species, and these functions can be further studied and correlated to our understanding of the mechanistics of phosphorylation in key biological processes, as well as the diseases that occur when the signaling pathways that involve these sites are defective. The second aim of this project is to study the correlation between the conservation of the phosphoproteome with the conservation of the genome and transcriptome, which will expand our understanding of the evolution of phenotypic diversity. Finally, the large-scale dataset of the proteomes and phosphoproteomes holds a great potential for other types of computational analysis, and also serves as a foundational reference for future experiments.

POSTER SESSION 2

MGH 241, Easel 172

12:45 PM to 2:15 PM

Characterizing Yeast and Breast Cancer Cell Line Phosphoproteomes via Mass Spectrometry

Kelsey Marie (Kelsey) Haas, Senior, Biology (Molecular, Cellular & Developmental)

Amgen Scholar, Mary Gates Scholar

Mentor: Judit Villen, Genome Sciences

Mentor: Danielle Swaney, Genome Sciences

Protein phosphorylation is a common regulatory mechanism carried out by the cell, as adding a phosphate group to a particular protein can switch its activity on or off. Signaling pathways employ this control method to instigate series of phosphorylation events that elicit a particular cell response. Our research involves extracting and characterizing the phosphoproteome, or the cell's entire set of expressed phosphorylated proteins, in both yeast and mammalian cell models. To generate lists of phosphoproteins present in these cell models, we use mass spectrometry, an analytic technique that produces characteristic spectra for individual phosphopeptides that are then matched to a library of known protein spectra through the use of computer algorithms. In our preliminary results, we have generated large-scale data sets identifying thousands of phosphorylated proteins present in each species and cell type. The goal of the first project, the yeast study, is to determine the degree of evolutionary conservation in phosphorylation events across 19 yeast species to learn about the basic principles of phosphoregulation. The conservation of phosphorylation can also give insight into phosphorylation events in other species evolutionarily related to yeast, such as humans. The second project, the mammalian cell study, examines the phosphoproteome of different breast cancer cell types in order to identify common phosphorylated proteins, from which we can deduce a molecular signature for breast cancer. This signature can be used in future studies to design a universal protein inhibitor drug as an alternative anti-cancer therapy. Additionally, by identifying the phosphoproteins exclusive to each cell type, we can uniquely characterize specific types of breast cancer. Knowledge of the proteins active in one type of breast cancer may facilitate development of inhibitor drugs as a form of personalized medicine.