Online Proceedings

Poster Session 2

Balcony, Easel 107

1:00 PM to 2:30 PM

Analysis of Epithelial-Mesenchymal Transition in HEK 293 Cells

Kevin Ngoc Nguyen, Senior, Anthropology: Medical Anth & Global Hlth
Mentor: Chris Hague, Pharmacology, University of Washington School of Medicine
Mentor: Dorathy-Ann Harris, Pharmacology

Epithelial-mesenchymal transition (EMT) refers to a biologic process that allows a polarized epithelial cell, which normally functions in the basement membrane of a cell, to undergo biochemical changes that makes it express as a mesenchymal cell phenotype. This mesenchymal phenotype allows the cell to have enhanced migratory capacity, invasiveness, elevated resistance to apoptosis, and increased production of extracellular matrix (ECM) elements. The process of EMT is considered completed once the underlying basement membrane breaks down, and the mesenchymal cell becomes migratory. Another component that proves EMT is the loss of e-cadherin. E-cadherin refers to cell-to-cell adhesion and the degradation of e-cadherin levels are a hallmark of EMT happening. There are three distinct types of EMTs; I will be focusing on type II EMT. Type II EMTs are associated with inflammation/wound repair but usually stops once inflammation subsides. However, in the context of organ fibrosis, type II EMTs can continue to over-respond to a persisting inflammation and can lead to organ death. In my experiment, I hypothesize that in HEK 293 human cells, SNAP -Δ1-91 alpha-1D adrenergic receptors undergo type II EMT. SNAP -Δ1-91 alpha-1D adrenergic receptors are a truncation of the extracellular portion of the receptor. Certain receptors undergo this truncation to increase its expression. It is shown that in SNAP – Full Length alpha-1D adrenergic receptors (wild type receptors) do not undergo EMT. I will be able to observe the process of type II EMT through imaging the breakdown of the cell membrane in SNAP- Δ1-91 alpha-1D adrenergic receptors and the measuring of e-cadherin levels. The purpose of this research would be to potentially influence future therapeutic interventions that target wild type receptors to induce would repair.

Session 2O

Economic Issues

Session Moderator: Michelle Turnovsky, Economics

MGH 389

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

When Lower Taxes Are Not Actually Lower Taxes: A State-Level Study of Legal Financial Obligations

Konan Mauritz Kile, Senior, Sociology, Economics
UW Honors Program
Mentor: Alexes Harris, Sociology

Court fines and fees, previously an overlooked part of the justice system, are much more impactful than once thought. Recent research has traced the rise of court mandated fines and fees, or legal financial obligations (LFOs), and detailed their various effects. LFOs have been shown to have significant, detrimental effects on poor and minority groups in relation to other parts of the population. The disparity of effects from LFOs exacerbates the already prevalent issue of wealth inequality within the United States. This study evaluates whether LFOs are higher in low tax counties than in high tax counties. This is accomplished by gathering county level tax and LFO data for four states: Florida, Pennsylvania, Washington and Wisconsin. I perform linear regression analysis of the data and performed t-tests on all variables included in the equation. Regression shows whether lower taxes are correlated with an increase of LFO severity. I anticipate that LFOs will be more severe in areas with lower taxes due to the increased financial strain on the county government. A correlation between revenues and LFOs could indicate that counties are essentially using LFOs as secondary to make up for lower tax revenues, rather than their intended purpose of disincentivizing criminal activity. With better information on potential consequences of lowering taxes, we will be able to draft smarter fiscal policies rather than arbitrarily increasing the financial burden on the poor.

Poster Session 3

Balcony, Easel 104

2:30 PM to 4:00 PM

Differences Between 2D and 3D Cell Modeling
Jessica Han Giang, Senior, Public Health-Global Health, Linguistics
Mentor: Dorathy-Ann Harris, Pharmacology
Mentor: Chris Hague, Pharmacology, University of Washington School of Medicine
Mentor: Eric Janezic, Pharmacology

2D cell models have traditionally been used in labs to test the effects of new drugs on certain cell types due to the ease and convenience of use. While 2D methods are great, they often simplify the cell-to-cell interactions and may not accurately represent cell systems in humans. 3D methods show the complex cell communication systems and better simulate actual organ systems. Research comparing these two methods can inform scientists on the benefits of 3D models which can help efficiency in creating new drugs. Our lab looked into various 3D models to determine their effectiveness and reliability and looked into the differences in perceived cell mechanics and functionality between 2D and 3D methods. We tried Corning Matrigel and Corning 3D Spheroid microplates for 3D cell modeling using HEK293 cells, which are human embryonic kidney cells that were grown in lab. They are known for being easy to grow and transfect. We used SNAP-Gels, which are protein assays that show the protein levels in the cells, to ensure that the protein levels were similar between the 2D and 3D systems. We then did florescent imaging to determine cell localization and EPIC dynamic mass redistribution (DMR) to determine cell functionality. We found Matrigel to have inconsistent results, so we focused on using the spheroid microplates. Based on our initial results, we saw increased functionality and expression levels for full-length protein cells compared to cells with a truncated N-terminal protein in the 3D method. This increase in functionality and expression levels was not seen in the 2D method. Our results show that 3D modeling methods can be reliable, and do show results that differ from 2D models. This is important for future studies that require cell modeling because 3D models can provide a more accurate and reliable modeling system to create novel therapeutics.

POSTER SESSION 3

MGH 241, Easel 152

2:30 PM to 4:00 PM

A Metabolomic Study of Sex Variation in *Drosophila melanogaster*
Rene Coig, Fifth Year, Biology (Molecular, Cellular & Developmental)
Mary Gates Scholar
Mentor: Daniel Promislow, Department of Lab Medicine & Pathology, University of Washington School of Medicine
Mentor: Ben Harrison, Pathology

Sexual dimorphism is a characteristic of many organisms that is genetically encoded and typically studied as a binary trait. Biomedical research routinely categorizes subjects into "male" and "female", and the resulting data are used to establish sex-specific measures of good health and disease. However, this practice overlooks the existence of intersexual phenotypes and oversimplifies the overlapping variation between sex-specific groups. The phenotypic expression of sex is directed by a complex orchestration of many genes. As such, it is reasonable to consider that there are more than just two discrete expressions of sex, and furthermore that the dimorphism of so-called sex-specific traits resides along a continuum. Metabolomics studies the small molecules that make up all the molecular building blocks in the body, and offers a unique opportunity to quantify sex variation that is morphologically invisible. Doublesex (*dsx*) is a gene that plays a pivotal role in the sex development of *Drosophila melanogaster*, and its absence results in an intersexual morphological phenotype. This study models sex in *Drosophila melanogaster* as a continuous trait by comparing metabolomic profiles for wildtype females, males and *dsx* null mutants using statistical analysis of metabolome data. While many studies have been conducted to understand the role of *dsx* in sex determination, to our knowledge no one has attempted to use this novel approach to quantify sex variation as a complex trait. Here we measure over 1000 metabolites in fly samples and test a hypothesis that some metabolites exhibit continuity between male, intersex and female phenotypes. Future work could explore the degree to which these metabolic sexual continuities exist in natural fly populations, and provide a powerful model to study factors that are influenced by sex differences more comprehensively.

POSTER SESSION 3

Balcony, Easel 116

2:30 PM to 4:00 PM

Connecting the Effects of Rapamycin on Lifespan and Development in *Drosophila melanogaster*
Shufan Zhang, Senior, Biology (Physiology)
Jjay Sukomol, Sophomore, Pre-Health Sciences
Kenneth Daniel (Kenneth) Han, Junior, Pre-Sciences
Vanessa L. Paus, Sophomore, Biochemistry
Mentor: Mitchell Lee, Pathology
Mentor: Ben Harrison, Pathology
Mentor: Daniel Promislow, Department of Lab Medicine & Pathology, University of Washington School of Medicine

Understanding how genetic variation shapes phenotypic variation for complex quantitative traits is fundamental to developing more accurate disease prognoses and therapeutic interventions. Genes that are important in early development contribute to adult quantitative traits, such as height, vision, and health. The fruit fly *Drosophila melanogaster* is

a model organism for studying complex traits, such as aging. *Drosophila* possesses many well-developed genetic tools and shares evolutionarily conserved age-regulating pathways with our species. One such conserved pathway is the mechanistic Target Of Rapamycin (mTOR) nutrient signaling pathway. Rapamycin is a specific allosteric inhibitor of mTOR signaling that extends lifespan in adult *Drosophila melanogaster* and delays development in larvae. However, the functional explanation for these effects is incomplete and a genetic association between development and lifespan is unknown. We used the Drosophila Genetic Reference Panel (DGRP), a highly inbred fruit fly population representing natural genetic variation, to measure rapamycin-mediated developmental delay. We used these data to carry out a Genome Wide Association Study (GWAS), and combined our data with data from a screen for the effects of rapamycin on lifespan in the DGRP, also carried out in our lab. GWAS analysis will help us to identify genetic variants associated with rapamycin efficacy and to discover novel variants associated with developmental timing. By connecting lifespan and development genetically, we identified shared candidate genes that modify these two very different molecular genetic programs. Accomplishing this is the first step towards identifying early life biomarkers that are predictive of rapamycin success as a longevity intervention in later years. These pharmacogenomic analyses advance a precision medicine approach where interventions are tailored towards genetic background to maximize human health.

POSTER SESSION 4

MGH 206, Easel 178

4:00 PM to 6:00 PM

Do Marine Microplastic Publications Influence Popular Awareness? A Comparison of Publication Metrics, News Media Coverage, and Social Media Impact

Anthony Krishtan Abruzzini, Senior, Neurobiology
Mentor: Lyda Harris, Biology
Mentor: Emily Carrington, Biology

Publication metrics have often played a major role in understanding the interaction between research, popular opinion, and public policy. The field of scientometrics has been especially successful in bridging this gap for hot-button environmental issues, such as global climate change. Here, we used publication metrics to look at another burgeoning environmental topic: marine microplastic pollution. Research into marine microplastics has risen explosively in recent years, and some governments have already introduced anti-plastics policies in response. Here, we looked into the influence of microplastics research in news outlets and public opinion. First, we searched *ISI's Web of Science* for articles containing the search terms "MARINE" and "MICROPLASTIC," and recorded the number of publications over time. Second, we used a web scraper to gather similar publication counts for popular news outlets. Finally, we gathered data on social media interest in microplastic pollution by looking at the frequency of Twitter posts containing relevant keywords over time. Differences in article and tweet lexicons were analyzed using *WordSmith Tools*. We hypothesized that increased published research on microplastics correlates with stronger media coverage and more social media presence. Overall, the project found a unique interplay between microplastics research and popular sources, and we discuss how this interaction might impact public policy changes.

POSTER SESSION 4

Commons West, Easel 10

4:00 PM to 6:00 PM

Differential N-Glycosylation Controls Function and Expression of α1D-Adrenergic Receptors

George Williams, Senior, Neurobiology
UW Honors Program
Mentor: Eric Janezic, Pharmacology
Mentor: Chris Hague, Pharmacology, University of Washington School of Medicine
Mentor: Dorathy-Ann Harris, Pharmacology

G-protein coupled receptors (GPCRs) - characterized by seven transmembrane alpha helical domains - are the largest family of membrane proteins, constituting ˜1% of the human genome. The α1D-adrenergic receptor (A1DAR) is a GPCR that regulates function of the cardiovascular, urinary, and central nervous systems. Dysfunction of this receptor can lead to various diseases including schizophrenia, benign prostate hypertrophy, hypertension, and PTSD. Prazosin, a non-specific α1-antagonist is the first line treatment for PTSD, however, chronic use has deleterious side effects including orthostatic hypotension and potentially fatal reflex tachycardia due to interactions with off-target related receptors. Thus, understanding how A1DARs are regulated will allow for the development of targeted therapeutics. To this end, the Hague Lab has previously discovered that A1DAR undergoes an endogenous cleavage of its extracellular N-terminal domain, affecting its membrane localization and response to agonist stimulation. Located within the N-terminal domain of A1DAR are two glycosylation sites at amino acids 65 and 82. Currently, how glycosylation of these sites regulates the cleavage event remains unknown. To characterize this phenomena, I used molecular cloning to mutate the glycosylation sites of A1DAR in the pSNAP vector for expression in Human Embryonic Kidney 293 (HEK293) cells. Near Infrared PAGE analysis revealed that glycosylation of both amino acids is required for cleavage and proper expression of A1DAR. Sucrose density gradient and dynamic mass redistribution further showed that glycosylation controls function and trafficking of A1DAR to the membrane. These results allow for

the development of targeted medications specific to the N-terminal glycosylation sites of A1DAR, further reducing the potential side effects experienced by patients.

POSTER SESSION 4

MGH 206, Easel 170

4:00 PM to 6:00 PM

Determining the Distribution of Microplastics in the Salish Sea

Louise Miranda Sutters, Senior, Biology (General)
Mentor: Emily Carrington, Biology
Mentor: Lyda Harris, Biology

Microplastics are fragments of plastic smaller than five millimeters in length, often created by the breakdown of larger plastic materials. The ubiquitous presence of this form of debris in marine environments has led to detrimental effects when ingested by marine organisms including false sense of fullness, impaired reproduction, and stunted growth. Microplastics are heterogeneously distributed in water, animals, and sediment, making it necessary to compare and contrast conditions when considering any biological effects. Due to the variability of microplastics across space and time, different locations may have varying types and sizes of microplastics. This study examines the relationship between anthropogenic activity and microplastics in areas ranging from low to high population density in the Salish Sea. In July and August of 2018, samples of mussels, water, and sediment were collected from ten sites around the Salish Sea. The samples were chemically digested with hydrogen peroxide over a five-micrometer filter. Debris collected by the filters was photographed through a microscope and subsequently characterized. The images were processed using ImageJ for length, width, shape (fiber, fragment, film, or sphere), and color. We hypothesized sites have different microplastic compositions and there is a correlation between anthropogenic activity and microplastic abundance. The results of this study could aid in efforts to locate point sources of specific types of microplastics in the Salish Sea and determine priority locations for marine debris management.