Online Proceedings

POSTER SESSION 1

MGH 241, Easel 163

11:00 AM to 1:00 PM

Identifying Genetic Modifiers of Abeta and Tau Expressed in the *Drosophila* Nervous System

Irene Cruz Talavera, Senior, Anthropology: Medical Anth & Global Hlth, Microbiology

Mary Gates Scholar

Mentor: Daniel Promislow, Department of Lab Medicine & Pathology, University of Washington School of Medicine

Alzheimer's Disease (AD) is a progressive brain disorder that results in middle to late life dementia. AD, the most common form of dementia, is the sixth leading cause of death in the United States, and the third leading cause of death for older people over 65 years of age. AD is pathologically characterized by the accumulation and aggregation of an alternatively spliced amyloid-beta (Aβ) and hyperphosphorylated tau, which lead to the formation of neuritic plaques and neurofibrillary tangles (NFT's) in the brain and ultimately to decreased neural function and cell death. Previous studies indicate that the extent to which an individual is affected by the interaction of these proteins and the severity of AD is largely influenced by genetic variation. However, the specific genes involved, their regulation and expression remain largely unknown. Our ongoing project explores the genetic variation underlying Drosophila susceptibility to severe eye cell degeneration caused by human Aβ and tau. We express Aβ and tau in the fly eye through the UAS-GAL4 system to create our AD model Drosophila, and cross them with a panel of flies (the Drosophila Genome Reference Panel, DGRP) that allows us to map natural genetic variation for resistance to Aβ and tau. Our preliminary results show significant variation in neuronal eye cell degeneration among DGRP lines, implying that neurodegeneration would also differ between DGRP lines if Aβ and tau were expressed in the nervous system. Based on current progress, this new project will continue exploring variation in DGRP lines, but this time we will express them in the fly brain. I will measure how different genotypes shape the effect of brain-specific Aβ and tau on lifespan and protein aggregation, and will use Genome Wide Association Studies to identify single nucleotide polymorphisms associated with variation in expression of Aβ and tau.

POSTER SESSION 1

MGH 241, Easel 164

11:00 AM to 1:00 PM

Breaking Down the Doors of Perception: Identifying Genetic Modifiers of Alzheimer's Disease Proteins Expressed in *Drosophila melanogaster* Eyes

Alexander Weihua (Alex) Zhu, Senior, Neurobiology

Valeria Aizen, Junior, Biology (Molecular, Cellular & Developmental)

Mentor: Daniel Promislow, Department of Lab Medicine & Pathology, University of Washington School of Medicine

Alzheimer's Disease (AD) is one of the leading causes of death in the United States. Studies suggest that the root cause of AD is due to two proteins, Aβ1-42 and tau, which accumulate and aggregate into amyloid plaques and neurofibrillary tangles, respectively. Current studies on the heritability and genetic foundation for AD are not well resolved. In order to understand which genes are best able to resist the effects of Aβ1-42 and tau, we utilized an AD fruit fly model. More specifically, we used a mutant line of *Drosophila melanogaster*, which we call R32, in which human transgenes of Aβ1-42 and tau are expressed in the fly eye. We used this reagent to express AD proteins in the Drosophila Genome Reference Panel (DGRP), a set of 200 fully sequenced, inbred lines derived from a wild population, in order to simulate a model of natural genetic variation. Aβ1-42 and tau proteins lead to degradation in the eyes causing fusions and irregular shaping of ommatidia. Accordingly, we imaged fly eyes at 28 days of age. We found significant genetic variation in ommatidial circularity and area, two measures of eye quality. We performed a genome-wide association study to identify specific single nucleotide polymorphisms (SNPs) that act as markers signaling degradation in the ommatidia. Significant SNPs were found linked to genes associated with neurotransmitter receptors, neural signalling, and photoreceptor differentiation. Further studies will try to validate the effect of the identified genes and quantify the effects of the SNPs on the degenerative eye phenotype. Additionally, metabolomic studies as well as a model that expresses the AD-related proteins in the brain would be utilized to study the effects on lifespan, memory, and locomotion.

SESSION 1E

FROM VIRAL PATHOGENESIS TO GENETIC DISEASES TO BUILDING A BETTER KIDNEY

Session Moderator: Michael Lagunoff, Microbiology
MGH 231
12:30 PM to 2:15 PM
* Note: Titles in order of presentation.

Hypoxia-Induced Factors in Latent KSHV Infection of Endothelial Cells
Jie Yin, Senior, Biochemistry, Microbiology
Levinson Emerging Scholar, Mary Gates Scholar, UW Honors Program
Mentor: Michael Lagunoff, Microbiology
Mentor: Daniel Holmes, Microbiology

Kaposi's sarcoma-associated herpesvirus (KSHV) is the etiological agent of Kaposi's Sarcoma (KS), a highly vascularized tumor made up of cells of endothelial origin. KSHV establishes a predominantly latent infection in endothelial cells in culture and in the KS tumor. A previous study has shown that KSHV induction of the Warburg effect is required for the survival of latently infected endothelial cells. The Warburg effect, a common metabolic alteration in cancer cells, refers to an increase in glycolysis and a decrease in oxidative phosphorylation. The mechanism of Warburg induction by KSHV is currently unknown. I proposed to evaluate the role of endothelial cell specific hypoxia-induced factors (HIFs) on KSHV Warburg induction since HIFs have been implicated in Warburg induction in other types of cancer. I hypothesized that HIF2α mediates KSHV Warburg induction through expression of glycolytic genes. To test this, I constructed HIF2α knock-out cells using CRISPR/Cas9 gene editing. I then used RT-qPCR to measure glycolytic gene expression during KSHV infection of wild-type and HIF2α knock-out cells. I found that the transcript levels of certain glycolytic genes remained constant in KSHV-infected HIF2α knock-out cells as compared to KSHV-infected wild-type cells, showing that HIF2α is not responsible for glycolytic gene expression during KSHV infection. I am following up on the role of the KSHV latent gene KapA on the induction of glycolytic gene expression. KapA was previously found to interact with components of the Ras pathway. As the Ras pathway activates glycolytic genes through HIF1α, I hypothesize that exogenous expression of KapA will lead to increased glycolytic gene expression through increased expression of HIF1α. I will construct an endothelial cell line that overexpresses KapA using CRISPR/Cas9 system and then use RT-qPCR to evaluate glycolytic gene expression. These results will aid in the future efforts to develop antiviral drugs by targeting cellular metabolism.

POSTER SESSION 2

MGH 241, Easel 128
1:00 PM to 2:30 PM

Effects of Glycogen Metabolism on *Drosophila melanogaster* Lifespan Under Stress
Elise Hoffman, Senior, Public Health-Global Health
Julie Ann (JulieAnn) Uh, Junior, Pre-Sciences
Mentor: Daniel Promislow, Department of Lab Medicine & Pathology, University of Washington School of Medicine
Mentor: Ben Harrison, Pathology

Multiple factors interact to determine the lifespan of an organism. The Promislow lab uses the fruit fly *Drosophila melanogaster* to study the interaction between the metabolome (the profile of all small molecules within an organism), and the lifespan of a fly under stress. In a study of metabolome and lifespan data for many genotypes of *Drosophila,* our lab found that fly strains with relatively long lifespans when exposed to oxidative stress (peroxide food), had high levels of maltose, a disaccharide of glucose. We hypothesized that maltose was beneficial to flies on peroxide food, and tested this by supplementing the diet with maltose to see if this would extend lifespan. Flies fed supplemental maltose prior to exposure to peroxide food lived longer than flies fed unsupplemented food, supporting our hypothesis. Maltose could extend lifespan by providing energy to the fly via metabolism into glucose, or through another function as a disaccharide. To distinguish between these possibilities, we tested lactose, a disaccharide, to determine if any disaccharide could extend lifespan. Lactose did not extend lifespan, suggesting that disaccharides in general do not extend lifespan under stress. We found that glucose extended lifespan, supporting the hypothesis that maltose extends lifespan via conversion to glucose. Maltose can be stored as glycogen, a polysaccharide, and glucose is derived from glycogen by glycogen phosphorylase, encoded by the gene GlyP. To test the role of glycogen metabolism on lifespan under stress, we manipulated the expression of GlyP. Several transgenes were used to reduce the expression of GlyP by RNA interference (RNAi). RNAi of GlyP decreased lifespan, which supports our hypothesis that glucose derived from glycogen promotes survival. Our work suggests that glucose derived from glycogen or maltose is an important determinant of lifespan under stress, furthering our understanding of links between metabolism and complex phenotypes, like lifespan.

POSTER SESSION 2

Commons West, Easel 11
1:00 PM to 2:30 PM

Comparison of Ecosystem Service Valuation Methods: Wetland Restoration and Carbon Sequestration in Úlfarsárdalur, Reykjavik

Emily Paige Menz, Senior, Economics, Environmental Studies
UW Honors Program
Mentor: Brynhildur Davidsdottir
Mentor: Daniel Govoni, Climate Change and the Arctic

Icelandic wetlands have ecological, climatological, and historical significance. The Millennium Ecosystem Assessment defines ecosystem services as the benefits humans receive from nature. Many of these benefits are not included in the economic market which leaves them out of cost-benefit analysis in decision making. Although the Kyoto Protocol approved wetland restoration as an official climate mitigation activity, wetland restoration activities in Iceland have yet to catch up. Valuing the ecosystem service of carbon sequestration can help clarify for Icelandic policy-makers that the benefits outweigh the costs of restoration. This study conducts an economic valuation of the carbon sequestration service in Úlfarsárdalur to provide the city of Reykjavik with new information to include in a cost-benefit analysis of restoration. Three methods are used to quantify the monetary benefit provided by potential carbon sequestration in Úlfarsárdalur – direct market pricing, damage avoidance cost, and replacement cost. The results relied on physical data provided by the Verkís report of restoration potential in Úlfarsárdalur as well as data collected by Hlynur Óskarsson, a wetland ecology expert. In accordance with claims from the Millennium Ecosystem Assessment, all three methods reflected that the economic benefits of carbon sequestration exceed the costs of restoration by a significant amount. The direct market pricing and replacement cost methods yielded similar values, while the damage avoidance cost came out much lower. These findings suggest that wetland restoration to promote carbon sequestration could serve as a cost-effective climate mitigation measure. Researchers must continue to investigate the accuracy of such valuation techniques as well as their transferability and scalability to larger ecosystems.

POSTER SESSION 2

MGH 241, Easel 148

1:00 PM to 2:30 PM

Molecular Characterization of Human Blood Antigens using Mass Spectrometry Techniques

Vaishnavi (Vaish) Dhawan, Senior, Bioengineering
Mary Gates Scholar
Mentor: Daniel Ratner, Bioengineering

In the US, someone needs blood every two seconds, making blood transfusion a frequently performed procedure in hospitals. Transfusion of incompatible blood due to clerical error in clinical blood typing procedures can induce a multitude of life-threatening immune responses in the recipient's body. The most prevalent typing procedures are based on the overly simplified characterization of surface antigens on an individual's red blood cells (RBCs) into the commonly known ABO blood type system. However, studies have shown that the antigens embedded in the RBC membrane, comprising of glycolipids and glycoproteins, are structural determinants of variations in the blood type outside of the ABO system, elucidating the limitations of current typing methods. This project follows the hypothesis that gas-phase hydrogen/deuterium exchange (HDX) and ion mobility mass spectrometry (MS) techniques can be employed to characterize and further elaborate the structure of these RBC antigen constituents. To test this hypothesis, genotypically defined donor blood samples undergo an osmotic lysis procedure to obtain RBCs ghosts, which are RBC membranes without the cellular components. Glycoprotein and lipid fractionation, and digestion is employed to isolate carbohydrate components in preparation for MS analysis which provides insight into structural composition of the carbohydrate antigens. Preliminary analysis on the donor samples has suggested the presence of clinically relevant carbohydrate antigens.This knowledge will be crucial in further developing glycobiological sensors that can be functionalized onto silicon chips used by Ratner Lab, facilitating novel blood typing techniques. Through this study, we expect to develop a deeper understanding of the heterogeneity encoded into the carbohydrate RBC antigens which play a critical role in transfusion medicine.

SESSION 2E

MODELS OF BRAIN AND BEHAVIOR

Session Moderator: Tara Madhyastha, Radiology

MGH 238

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Moths Regulate Body Attitude and Gaze to Stabilize Small- and Wide-Field Visual Cues

Monica Dee (Monica) Harris, Senior, Neurobiology
Mary Gates Scholar, Washington Research Foundation Fellow
Mentor: Tom Daniel, Biology

Insect flight relies heavily on visual sensing. In many flight behaviors (e.g. navigating over long distances or through cluttered environments, finding food sources, or evading predators), insects must parse the visual scene to extract an estimate of their own motion and identify external objects or agents moving in their environment. Across numerous taxa and behaviors, there is a rich literature exploring behavioral responses to wide-field optic flow (visual stimuli aris-

ing from egomotion) and small-field target motion (cues corresponding to exogenous motion), primarily in the yaw dynamics involved in navigation. In contrast to yaw which is marginally stable, the equilibrium about pitch angle is inherently unstable, hence there are significant consequences to adjusting the flight attitude. To stabilize the visual scene under this constraint, insects can either reorient their body or move their head to redirect gaze. In this work, we investigate how the hawkmoth, *Manduca sexta*, modulates body pitch and gaze angle in response to wide- and small-field visual motion. Moths are tethered to a freely rotating armature at the center of a cylindrical arena and presented an image of a circular flower against a background grating. Figure and ground are oscillated both individually as well as simultaneously (both synchronously and incongruously). A multi-input–multi-output analysis reveals correlations that suggest moths employ parallel strategies for stabilizing posture and gaze dependent on the spatio-temporal content of the visual scene. The inherent instability in pitch dynamics necessitates these dual strategies. Distinguishing between and reacting to wide- and small-field visual stimuli are necessary parts of many animal behaviors; through this research we hope to better understand how biological systems assimilate motion and mechanical cues to coordinate effective movements.

SESSION 2L

MCNAIR SESSION - ISSUES IN CONTEMPORARY AMERICA: ENVIRONMENT, GOVERNMENT, SEX, GENDER AND RACE

Session Moderator: Stephanie Selover, Near Eastern Languages and Civilization

MGH 287

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Argentina - The U.S.' Struggle Against Communism

Erika Arias, Senior, International Studies, Law, Societies, & Justice

McNair Scholar

Mentor: Daniel Bessner

Beginning in the 1960s, civil unrest in Latin America engendered worldwide concerns. The uprisings were fundamental to the Cold War as tensions were heightened between the capitalist U.S. and the communist U.S.S.R. The U.S. worked to prevent communism from spreading to the Americas. My research explores the degree to which the United States' economic policies played a vital role in the outcome of Argentina's Dirty War and how they impacted U.S. relations with Latin America today. Throughout the 1960s and 1970s, U.S. foreign policy elites viewed Argentina as an essential puzzle piece whose loyalty was critical to maintaining order in Latin America while preventing other countries from turning to socialism. I hypothesize that by issuing economic policies that funded a capitalist and U.S.-friendly Argentine government, the U.S. hoped to prevent socialist ideas from developing in the Americas. In turn, the economic policies would create a domino effect of capitalism across Latin America that would ultimately help win the Cold War. Drawing on several scholarly articles, declassified documents, and secondary sources, I argue that the configuration and development of U.S. policies were done primarily for American gain, to continue being a superpower and prove that capitalism was the most superior social system. By taking a look at hidden involvement of the U.S., one can begin to understand the reasoning behind the implementation of policies. In my research, I analyze the consequences, both good and bad, of the U.S. economic policies throughout the Dirty War, as well as how attitudes changed and shaped current relations not only with Argentina but with other Latin American countries as well. Ultimately, I hope that the findings of my research will give more emphasis on the financial role the U.S. had and its core responsibility in atrocities committed by its economic policies.

POSTER SESSION 3

MGH 206, Easel 166

2:30 PM to 4:00 PM

Comparative Analysis of Smoking-Induced DNA Methylation in Blood Versus Lung

Joshua Michael (Josh) Dawson, Senior, Biology (Molecular, Cellular & Developmental)

Mentor: Ite Offringa, Surgery, Biochemistry and Molecular Medicine, Norris Comprehensive Cancer Center, Keck School of Medicine, University of Southern California

Mentor: Daniel Mullen, Surgery, Biochemistry and Molecular Medicine, University of Southern California

Lung cancer is the leading cause of cancer-related death in both men and women in the United States. Smoking is the major cause of lung cancer. While tobacco smoke is well-known to cause mutations in DNA that drive the cancerous phenotype, it also induces epigenetic changes - changes in the regulatory information overlaid on the genome. Smoking has been shown in numerous epidemiological studies of subjects' whole blood to affect an epigenetic mark called DNA methylation. DNA methylation commonly refers to the addition of a methyl group to cytosine in the context of a Cytosine-Guanine (CpG) dinucleotide. Hypomethylation at several CpGs in the blood has been shown to predict lung cancer risk, but the mechanisms by which DNA methylation changes in blood are linked to cancer in the lung are poorly understood. To investigate this, I used R to analyze 18

published peer-reviewed articles and collected 20,946 unique CpGs that have been found to be statistically significantly differentially methylated in the blood of smokers compared to non-smokers. I then utilized the UCSC Genome Browser and The Cancer Genome Atlas (TCGA) data to compare smoking-induced methylation changes in whole blood with those of non-tumor lung tissue and lung adenocarcinoma. Understanding the relationship between whole blood methylation and lung methylation can reveal if blood DNA methylation patterns are good surrogate markers for DNA methylation that occurs in the lung. Further studies of select differentially methylated lung CpGs can help unravel the mechanism by which smoking-induced epigenetic changes contribute to lung cancer development.

POSTER SESSION 3

Balcony, Easel 86

2:30 PM to 4:00 PM

UW Solar Power Monitor

Kamil Jiwa, Senior, Electrical Engineering
Yuxuan Chen, Senior, Electrical Engineering
Nathan Hills, Junior, Electrical Engineering
Jerome Paliakkara, Freshman, Pre Engineering
Mentor: Daniel Kirschen, Electrical Engineering

UW's electricity bill is around $1MM per month, making it Seattle City Light's second-largest customer. Solar power represents one way that UW can reduce load on the city's power grid. In 2017, UW Housing and Food Services completed installation of four solar panel arrays to its buildings on campus. How have those panels performed, and has UW benefited from their presence? To gain insights into the effect of these installations, we developed the UW Solar Power Monitor to collect and present data about solar power usage within these buildings. The data was analyzed, interpreted, and integrated into the dashboard. Our hope is that the tools we have developed will enable UW administrators to make informed decisions about power infrastructure on campus, educate the public and promote awareness about solar projects on campus, facilitate the study and analysis of solar power, and encourage increased investment in solar infrastructure at the University of Washington.

POSTER SESSION 3

Balcony, Easel 102

2:30 PM to 4:00 PM

Emergency Clinicians Mitigate the Uncertainty Surrounding Identifying Infection with Antibiotics: A Target for Antibiotic Stewardship

Osman S Salahuddin, Senior, Neurobiology
Mentor: Daniel Henning, Emergency Medicine

Early antibiotic administration is a critical intervention in sepsis; however, identifying infection in the emergency department can be challenging. We hypothesize that emergency clinicians over-treat for infection overall, even when non-infectious etiologies are felt most likely. In two academic Emergency Departments (EDs), we prospectively investigated clinician gestalt – the use of historical facts and physical examination findings to recognize disease patterns and make a clinical decision – for infection and antibiotic administration to assess 1) the frequency in which clinicians administer antibiotics to patients felt most likely to not have infection, and 2) the number of patients felt to have infection and received antibiotics, who ultimately did not have infection. We enrolled subjects at both the University of Washington and Harborview Medical Centers. We included patients with signs of critical illness, defined as 1) two or more systemic inflammatory response syndrome criteria and organ dysfunction, 2) systolic blood pressure < 90 mmHg, and/or serum lactate levels greater than 4.0 mmol/L. At the time of admission, attending physicians were surveyed regarding the etiology of illness (infectious or non-infectious). Patient demographics, medical history, and ED interventions, including antibiotics, were abstracted by chart review. Ultimate determination of diagnosis was adjudicated by chart review by an attending emergency physician. We enrolled 405 patients, 191 (47.2%) with infection by final adjudication. Physicians identified 199 (49.1%) as most likely non-infectious, of whom 79/199 (39.7%) received antibiotics. Of these, 53/79 (67.1%) did not have the infectious etiologies. Of the 206 patients whom physicians suspected to most likely have infection, 185/206 (89.9%) received antibiotics, and 37/185 (20%) were adjudicated to non-infectious etiologies. Emergency clinicians mitigate diagnostic uncertainty by administering antibiotics. Improving the identification of infection among critically ill emergency patients may be a meaningful target for antibiotic stewardship efforts.

POSTER SESSION 4

Commons West, Easel 14

4:00 PM to 6:00 PM

Synthesis of Lead-Free Double-Perovskite (Elpasolite) Colloidal Nanocrystal Semiconductors

Evan Crites, Senior, Physics: Comprehensive Physics, Chemistry
Mentor: Daniel Gamelin, Chemistry
Mentor: Sid Creutz, Chemistry

Perovskites are a class of material with the formula ABX_3 with lead-halide perovskites having promising photovoltaic properties. Over the past few years syntheses of colloidal inorganic lead-halide perovskites have been reported. Recently concerns over the toxicity and instability of lead-halide perovskites have driven research toward lead-free alterna-

tives, including double perovskites with the elpasolite structure. Elpasolites are double perovskites where the divalent cation is replaced with a trivalent and a monovalent cation to get the formula A_2BCX_6. Despite this motivation towards less toxic alternatives, synthetic approaches remain limited with no examples of heterometallic elpasolite nanocrystals being reported. We report colloidal synthesis and characterization of nanocrystals of Cs_2AgBiX_6 (X = Cl, Br) elpasolites via hot-injection of TMS-halide under inert atmosphere and rapid quenching with an ice bath. We further show that through postsynthetic anion exchange or cation extraction the nanocrystals can be converted to new materials, such as the previously experimentally unknown Cs_2AgBiI_6. Nanocrystals of Cs_2AgBiI_6 were made via anion-exchange using trimethylsilyl iodide and have strong absorption throughout the visible region which confirms predictions that this material could be a good photovoltaic absorber. The synthetic methodologies presented are expected to be generalizable, with work already under way to optimize this for more well-known nanocrystals. This work also shows how ion-exchange reactivity of nanocrystals can lead to the discovery and development of lead-free halide perovskite materials which would be difficult, if not impossible, to make via direct synthesis.

POSTER SESSION 4

MGH 241, Easel 139

4:00 PM to 6:00 PM

The Role of the Pentose Phosphate Pathway in the Survival of Endothelial Cells Latently Infected with KSHV

Madeleine Hart, Recent Graduate, Biochemistry, Public Health, University of Washington

UW Post-Baccalaureate Research Education Program

Mentor: Michael Lagunoff, Microbiology

Mentor: Daniel Holmes, Microbiology

Viruses are nonliving entities and therefore lack their own metabolism, but they do have the ability to alter the host cell's metabolic pathways for their own gain. Kaposi's Sarcoma-associated herpesvirus (KSHV), a human herpesvirus, is the etiological agent of Kaposi's Sarcoma (KS), the most common tumor in AIDS patients worldwide. In KS tumors and cultured endothelial cells, KSHV is predominantly in the latent state, with only a small portion of viral genes and a microRNA cluster expressed, and no virion assembly. Our lab has shown that KSHV dramatically activates many host cell metabolic pathways during latent infection, including glycolysis. A global metabolomics screen suggested that glycolytic intermediates might be shuttled through the pentose phosphate pathway, (PPP) during KSHV infection. Our hypothesis is that the PPP is important for viral perseverance and the survival of human endothelial cells latently infected with KSHV. Infected endothelial cells were treated with the glucose-6-phosphate dehydrogenase (G6PD) inhibitor 6-aminonictotinamide (6-AN) at different concentrations and the amount of cell death was quantified. The inhibition of the PPP by 6-AN significantly increases cell death in KSHV infected TIME cells, but not in matched uninfected cells. KSHV microRNAs are expressed during latent infection and have been shown to be sufficient to induce glycolysis. Interestingly, a KSHV mutant, ???miR, which lacks the microRNA cluster is less sensitive to inhibition of the PPP. This suggests that the microRNA cluster may be responsible for the reliance of KSHV infected endothelial cells on the PPP. The data suggest that inhibitors of the PPP provide novel therapeutic agents for KS tumors.

POSTER SESSION 4

Commons West, Easel 33

4:00 PM to 6:00 PM

Developing an Effective Microfluidic Instrument for Medical Diagnostics of HIV and HPV

Bob Weng, Junior, Pre-Health Sciences

Mentor: Daniel T. Chiu, Chemistry

Mentor: Thomas Schneider, Chemistry

Over 70 million people are infected by HIV and 79 million of Americans by HPV every year. Even in developed countries, these particular sexually transmitted diseases (STDs) grow at an unyieldingly steady rate. In the Chiu Group, we address this increase in infection by working on the development of a fully automated microfluidic instrument to help improve early diagnosis of HIV and HPV. While many diagnostic techniques already exist, our goal is to advance state-of-the art approaches in novel microfluidic technologies, primarily concerning the reduction of cost to run clinical samples, shortening the time required to analyze samples, and enhancing the reliability of results. We are developing our automated microfluidic instrument in two phases. The first is a preparative step in which we create high-quality microfluidic chips that help digitize thousands of nanoliter droplets in a static array of wells. In the following experimental step, we amplify target HIV/HPV sequences in these nanodroplets from patient samples through polymerase chain reaction (dPCR) and the static array format provides a direct readout through changes in fluorescence of the sample droplets.The successful implementation of the instrument together with the microfluidic chip will maintain a high level of accuracy and sensitivity as well as observe a large decrease in cost and time for diagnostics. Among the conventional diagnostic instruments available today, our development will offer a faster, cheaper, and more accessible way to diagnose HIV and HPV, and ultimately slow the rate of STD cases throughout the world.

POSTER SESSION 4

Commons West, Easel 13

4:00 PM to 6:00 PM

Quantitative Analysis of Negative-Trion Auger Recombination in Colloidal Semiconductor Quantum Dots

Skylar Javin Sherman, Senior, Chemistry
Mary Gates Scholar, UW Honors Program
Mentor: Daniel Gamelin, Chemistry

Colloidal semiconductor quantum dots (QDs) have recently garnered attention for applications in nanoscale technologies including photovoltaics, displays, sensing, and energy storage. Radiative luminescence originating from recombination between one electron and one hole in the excited state is vital to the performance of these materials for these applications. One prominent relaxation pathway that competes with radiative luminescence in QDs is non-radiative Auger recombination, a process that can either be detrimental to device performance or in some cases harnessed to enhance various technologies. For this project, we use redox chemistry to controllably engineer negative trions (two electrons and one hole) in colloidal QDs, purposely introducing a negative-trion Auger recombination pathway. Previous results have demonstrated a size dependence of negative-trion Auger recombination rates in various QDs. This work uses time-resolved photoluminescence spectroscopy to explore the difference in size dependence for QDs with and without trap states. Preliminary findings indicate that negative-trion Auger recombination generally occurs more efficiently and exhibits a shallower size dependence when one of the carriers is trapped than when all carriers are delocalized. This work will allow for future scientists and engineers to design QDs that either suppress or make use of Auger recombination to optimize device performance.