Undergraduate Research Symposium May 17, 2019 Mary Gates Hall

Online Proceedings

Poster Session 1

Commons West, Easel 42

11:00 AM to 1:00 PM

Estimating Anthropogenic Influences on Species Occupancy at La Selva Biological Station, Costa Rica

Julie Ramirez, Junior, Biology, Boise State Univ
McNair Scholar
Mentor: Neil Carter, Human-Environment Systems, Boise State University

The global network of nature reserves are intended to be refuges for wildlife species around the world. However, nature reserves are experiencing increasing amounts of human visitation each year, and it is critical to investigate how this influx in disturbance is influencing the space use, abundance, and richness of wildlife species in those reserves. We used camera trap data collected at La Selva Biological Station in Costa Rica, to understand how the presence of humans and other environmental factors are influencing the presence and distribution of various wildlife species. We deployed 9 cameras, in three blocks, on 9 different trails and accumulated 208 active camera nights in 2018. A total of 9,692 photos were obtained of 17 different animal species. We hypothesize that the occupancy rate of species will be primarily influenced by human presence on trails within the reserve. The most commonly detected species were Collared Peccaries (*Pecari tajacu*) with 0.837 average detections per day, Central American Agoutis (*Dasyprocta punctata*) with 0.409 average detections per day, and Great Curassows (*Crax rubra*) with 0.173 average detections per day across all camera sites. Collared Peccaries had a 72% diel activity overlap with humans, Central American Agoutis had a 66% overlap, and Great Curassows had a 78% overlap. I will use the package "unmarked" in the program R to determine the influence of humans on species occupancy and richness. These results will help inform managers at La Selva Biological Station on how to best limit the impacts of human visitation on wildlife species.

Poster Session 2

Balcony, Easel 96

1:00 PM to 2:30 PM

Revolutionizing mRNA Vaccine Platforms with Self-Assembling Nanoparticles

Chelsea Shu, Junior, Biochemistry
UW Honors Program
Mentor: John Wang, Biochemistry
Mentor: Neil King, Biochemistry

As of now, mRNA vaccines have been deemed as a potent replacement for current vaccine models against infectious diseases for their improvements in B-cell and T-cell immune responses. Usually, when soluble, subunit antigens are delivered, they are scattered and randomly bind to B-cell receptors, often loosely. However, with a nanoparticle carrier for antigens, there would be more effective crosslinking with B-cell surface immunoglobins as there is a higher density of structurally ordered antigen arrays presented by the nanoparticle. As a result, the B-cell creates a stronger immune response. Additionally, the multivalent particles also favors the creation of long-lasting immunity against a given virus. My team and I are currently developing a self-assembling protein platform using dn5A and dn5B protein components as a carrier for an mRNA vaccine against the flu. My project mainly focused on optimizing the co-secretion of the two particles by exploring different models and combinations of both. This is important as the translated cage not only has to be able to self-assemble but also be capable of doing so without producing excess protein in order achieve its purpose. To do so, I investigated 12 different constructs of dn5A and dn5B through transfections and analysis with western blots and electron microscopy. We used the data collected to improve the dn5A/dn5b protein platform utilized alongside flu mRNA vaccines, helping them better achieve potency. Overall, if effective, the new vaccination model can be utilized for other infectious diseases, including HIV and meningococcus.

Session 2K

Our Complex Universe: Planets, Stars, Black Holes, and Galaxies

Session Moderator: Jessica Werk, Astronomy

MGH 284

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Observational Astronomy in Tacoma: Analyzing Jupiter's Rotation and the Brightness Profile of Saturn's Rings

Megan Longstaff, Senior, Applied Physics, Pacific Lutheran University
Justin deMattos, Senior, Physics, Pacific Lutheran University
NASA Space Grant Scholar
Mentor: Katrina Hay, Physics, Pacific Lutheran University
Mentor: Sean O'Neill, Physics, Pacific Lutheran University

Jupiter and Saturn are our solar system's largest gas giants with some of the most popular features of any known planet: Jupiter's Great Red Spot (GRS) and Saturn's rings. Over the summer of 2018, we analyzed these characteristics at Pacific Lutheran University's W. M. Keck Observatory. Closer to the Earth, Jupiter's atmosphere is subject to differential rotation in which the atmosphere of the planet rotate at different speeds. We use feature tracking and 2D to 3D mapping techniques to observationally determine the angular rotation of the GRS and compare it to the expected rotation of 11.5 km/s determined by the magnetosphere. Through our analysis we observe the movement of the GRS over multiple nights and determine the average speed to be around 10.97 km/s, a 4.60% difference from the expected value. Further beyond, Saturn's rings are composed of particles of ice and dust that are thought to be remnants of comets, asteroids, or moons that collided in orbit around the planet. Since these rings are not single structures, their particles feature non-uniform spacing. The light intensity of the rings increase as you approach the B ring from either direction (with the exceptions of the Cassini Division, Encke, and Keeler gaps). Our research focused on determining the spatial variation of these intensities as observed from our land-based observatory and comparing this data to Hubble Space Telescope data quantifying atmospheric scattering in Tacoma.

POSTER SESSION 4

Balcony, Easel 91

4:00 PM to 6:00 PM

A Designed Self-Assembling Nanoparticle Vaccine for Parenteral Induction of Mucosal Immune Responses

Rose B Fields, Junior, Biochemistry
Mentor: Neil King, Biochemistry
Mentor: Karla-Luise Herpoldt, Bioengineering

Enteric diseases, or diseases of the Gastrointestinal (GI) tract, remain one of the most prevalent killers of children in sub-Saharan Africa. The most practical way to prevent such diseases is through vaccination, but antigens for enteric diseases need to be delivered directly to the GI tract to be most efficient, making vaccination difficult. Recent studies by the von Adrian group at Harvard University have found that both T and B cells are reprogrammed to home to the GI tract when they encounter retinoic acid, a metabolite of vitamin A. The King Lab at the University of Washington is working to develop a novel vaccine candidate using recently developed self-assembling protein nanoparticles, that can simultaneously package all-trans retinoic acid (ATRA) and multivalently display enteric antigens. Previous work has suggested that two cystine mutations to Cellular Retinoic Acid Binding Protein I (CRABP-I) create a disulfide bond as a result of the conformational change that CRABP-I undergoes when it binds ATRA. This disulfide bond would essentially lock ATRA into CRABP-I, reducing its dissociation constant in vivo and maintaining the gut-homing properties of the nanoparticle post-injection. In order to assess the efficacy of these cysteine mutations, I expressed two versions of CRABP-I, the wildtype protein with no cysteine residues, and a version with no cystine residues except for the two that create the disulfide bond. After establishing that these new CRABP-I mutants folded into the approximate shape of wildtype CRABP-I via circular dichroism, I designed and tested new assays that measured free thiol concentrations of each protein after binding ATRA, as well as free ATRA concentration overtime. This data will help us determine whether these two cystine mutations make a significant difference in the ATRA binding quality of CRABP-I, which could improve the immune response generated by our vaccine candidate.

POSTER SESSION 4

Balcony, Easel 92

4:00 PM to 6:00 PM

Stabilizing Self-Assembling Protein Cage for Use Towards Vaccine Design

Gargi Mukund (Gargi) Kher, Junior, Biochemistry
Mentor: Neil King, Biochemistry
Mentor: Karla-Luise Herpoldt, Bioengineering

Natural proteins often assemble into various complex geometric structures based on their interactions with each other. These structures can hold and transport "cargo" as well as display antigens, making them extremely useful in vaccine design. The King Lab at the University of Washington uses the way these proteins assemble to develop computational models that help them design novel self-assembling protein cages, or nanoparticles. These nanoparticles are then used to develop vaccines or treatments for diseases. Components of the designed protein cage can be modified and expressed individually before being assembled together into the nanoparticle. I am working on stabilizing one of these protein cages known as T33DN2, so it can be used towards creating a vaccine. T33DN2 is a tetrahedral cage comprised of two trimeric proteins known as T33DN2A and T33DN2B. When expressed individually through *E.coli*, DN2A is produced in a soluble form while DN2B is produced in a mostly insoluble form. T33DN2 is currently an unstable cage, as only the A com-

ponent is expressed solubly. Soluble proteins are generally more stable and thus easier to work with than their insoluble counterparts. To increase the solubility of DN2B, I have been making mutations to specific amino acids in the DNA that produces this protein, as well as expressing and purifying this component to determine its stability.

POSTER SESSION 4

MGH 258, Easel 185

4:00 PM to 6:00 PM

Optimization of an FABP5 Ligand Binding Assay and Determination of Xenobiotic Affinities

Wendy Ni, Senior, Biochemistry
UW Honors Program
Mentor: Nina Isoherranen, Pharmaceutics
Mentor: King Yabut

Fatty Acid Binding Proteins (FABPs) are intracellular proteins that facilitate the transport of fatty acids and other lipophilic substances into the cell for various biological functions. For example, FABP5 is important for binding endocannabinoid anandamide (AEA) which helps regulate cognition, learning, and memory. Compounds such as tetrahydrocannabinol (THC), the psychoactive component of cannabis, competitively inhibit FABP5 and prevent catabolism of AEA in the cytosol by fatty acid amide hydrolase (FAAH). Because many drugs (like ibuprofen and progesterone) are also lipophilic and poorly water-soluble, we predict that FABP5 has a role in their metabolism. The goal of this investigation is to better understand how FABP binding may affect drug metabolism by determining the binding affinities of different drugs to FABP5 using a fluorescence displacement assay. We first validated an assay for screening drugs and determining drug-FABP5 binding. Both ANS and NBD-Stearate, molecular probes that generate a fluorescence signal upon binding, were evaluated. FABP5 was titrated with increasing concentrations of each probe and the resulting changes in fluorescence plotted a hyperbolic curve used to calculate Kd (dissociation constant). In these trials, NBD-Stearate was found to have high background fluorescence and low sensitivity to changes in fluorescence upon alternative ligand binding, so ANS was selected for further method development. We found that factors such as mixing and time to equilibrate affected the Kd, possibly from non-specific binding. The binding affinities for ANS were 1.177 ± 1.005 μM (Morrison equation fit average), and 4.744 ± 1.387 μM (One Site Specific average). The preliminary data showed that fluorescence decreased by 48.28% with the addition of arachidonic acid (positive control) which confirmed ANS as a suitable assay. By adding increasing concentrations of various drugs to competitively inhibit the binding of ANS, a decrease in fluorescence will be measured and used to calculate Ki (inhibitor binding affinity).