UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 18, 2018 Mary Gates Hall

Online Proceedings

Poster Session 1

Commons East, Easel 47

11:00 AM to 1:00 PM

Bubble Stripping to Mitigate High CO2 in Coastal Ecosystems

Signe Marie Bergman, Senior, Oceanography
NASA Space Grant Scholar
Mentor: Alexander Gagnon, School of Oceanography
Mentor: Nick Roden, College of the Environment

Ocean acidification is projected to put coral reefs in a state of net dissolution by the end of the century. Coral reef ecosystems are important habitats, supporting 25% of marine biodiversity in less than 0.1% of its surface area. As humans continue to burn fossil fuels, adding CO2 to the atmosphere and oceans, local mitigation approaches become increasingly important to consider for preserving these vital ecosystems. Bubble stripping is a geoengineering approach to ocean acidification that has been modeled and tested in the laboratory as an effective means of enhancing air-sea gas exchange in coastal ecosystems. Bubbling of CO2-deplete air through the water column allows dissolved CO2 to diffuse into the bubbles and, ultimately, the atmosphere. Bubbling is strategically timed to occur at night, when organisms are respiring and CO2 is not removed by photosynthesis. By increasing the rate of air-sea gas exchange, the ocean and atmosphere equilibrate such that concentrations of CO2 do not reach the extremes that would otherwise occur in the water column. In this study, we used airstones (bubble diffusers) and a test tank to confirm the results of an earlier bubble stripping experiment. Bubbling increased pH and decreased dissolved inorganic carbon (DIC). Its effectiveness could be optimized by testing parameters like bubble size, air flow rate, and water column height. However, obtaining and expelling compressed air is an energetically expensive process, so bubble stripping would likely be useful only for stabilizing seawater chemistry in specific, small sections of reef.

Session 1M

Life and Death in the Ocean

Session Moderator: Virginia Armbrust, Oceanography

MGH 284

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Fatty Acids Show Variability in Food Sources for Aquaculture Mussels (*Mytilus spp.*) across Spatial and Temporal Scales

Molly K. Payne, Senior, Aquatic & Fishery Sciences
Mary Gates Scholar, UW Honors Program
Mentor: Alexander Lowe, Biology
Mentor: Emily Carrington, Biology

Seasonal stratification of the water column likely influences food availability to mussels grown at certain depths on aquaculture lines, as well as the environmental conditions experienced by the mussels. Fatty acids are important structural molecules that reflect the diet of the organism, such that fatty acid composition provides information on how the condition of mussels grown in different environments responds to food changes. Food sources vary based on a number of environmental conditions, including water temperature and turbulence, which differ between stratified water layers. Fatty acids in aquaculture mussels grown at 1m depth were compared to those at 7m in depth in the summer and fall of 2016 to test effects of varying environmental conditions between the depth layers. The results showed significant variability in the fatty acid composition of mussels grown at different depths in the summer months, but none in the fall. The difference between depths was contingent on the season. The variability in the summer months is likely due to stratification from increased surface temperatures, which decreases mixing and nutrient supply to mussels at lower depths. Stratification is then reduced in the fall and may explain homogenization of mussel fatty acid signatures from that period. In 2017, monthly sampling at the two depths was repeated and another experiment analyzing mussel plasticity was conducted in which mussels growing at 1m and 7m depth were switched during the summer and monitored at the new depth. Fatty acid signatures of switched mussels are predicted to adjust to become consistent with signatures of mussels established at the new depth by the end of the five-month sampling period. The results of this study will demonstrate the adaptability of mussels to new feeding environments and the effects of environmental changes on mussels as variable water conditions impact their algal food sources and overall health.

POSTER SESSION 2

Balcony, Easel 98

1:00 PM to 2:30 PM

Design of a High Reliability Micropump for Liquid Cooling High Heat Semiconductors

Molly Veronica Foley, Junior, Mechanical Engineering
Undergraduate Research Conference Travel Awardee
Karl Edward Kintner Meyer, Senior, Mechanical Engineering: Mechatronics
Phillip Dwight Rudolph, Senior, Mechanical Engineering: Mechatronics
Mentor: Elizabeth Rasmussen, Electrical Engineering
Mentor: Alexander Mamishev, Electrical Engineering

Large data centers, such as those built by Google, Amazon, and other information technology leaders consume about 1.3% of the world's energy, of which about 40% is used on electronics cooling [1, 2]. This amounts to 245 TWh per year, which, with the average US price of 12 cents per kWh, amounts to about $29.4 billion dollars spent per year on cooling high heat semiconductors [3, 4]. The work presented here proposes an innovative way to improve this cooling process. The proposed concept features a levitating inner rotor using fluid bearings that result in no physical contact between solid parts, eliminating friction. For the first time, precision-manufactured plastic parts are utilized to achieve both a low cost and a high reliability. The micropump is expected to last in operation for over one million hours Mean Time to Failure. This work emphasizes model-based design verification and optimization to ensure adequate performance for different form factors – so that a drop-in replacement of an air fan passive heat sink can be quickly developed for every microelectronics product. Twenty-four designs and prototypes were used in evaluation of two key criteria in order to optimize the pump's design. Three separate herringbone geometries, square, beveled-step, and circular, of herringbone grooves were prototyped based on experimentation of optimum groove parameters. These findings helped determine the optimal layer height of 100 micron for use in the micropump design. Finally, the application of a sensorless, brushless DC motor reduces overall cost of the pump and increases efficiency due to the removal of friction.

POSTER SESSION 2

MGH 241, Easel 149

1:00 PM to 2:30 PM

Application of Rationally Modified Self-Assembled Two-Dimensional Protein Array

Karl Benjamin Gilmore, Sophomore, Chemical Engineering
Mentor: Fran??ois Baneyx, Chemical Engineering
Mentor: Alexander Thomas

Although crystalline two-dimensional (2D) protein arrays are often found on the surface of archaea and bacteria where they form a protective S-layer, their potential in bionanotechnology applications remains unfulfilled. Progress in computation has recently allowed the (re)design of proteins for self-assembly into arbitrary structures. We are working with a rationally modified protein from S. typhimurium that can self-assemble into large ($> 100\ \mu$m) and thin (˜5 nm) hexagonal 2D arrays pierced by ˜3 nm pores upon addition of divalent cations (e.g., Ca^2+). The goal of our research is to test the ability of these arrays to organize gold nanoparticles (AuNPs) with desirable plasmonic characteristics. To this end, we stain protein arrays with the lipophilic fluorescent dye Nile Red, and analyze fluorescence microscopy images to quantify how the decoration of arrays with various concentrations of AuNPs affects the rate of photobleaching of the Nile Red fluorophore. Understanding how AuNPs bind to protein arrays could lead to further applications, such as templated growth of inorganic materials or co-assembly of enzymes and inorganic catalysts.

SESSION 2F

PLANT FORM AND FUNCTION: FROM MOLECULES TO FOSSILS

Session Moderator: Caroline Stromberg, Biology

MGH 242

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Mapping Repressive Function of the *Arabidopsis* Corepressor Protein TOPLESS (TPL)

Mollye Lucile Zahler, Senior, Biology (General)
Mary Gates Scholar
Mentor: Alexander Leydon, Biology
Mentor: Jennifer Nemhauser, Biology

TOPLESS (TPL) is a transcriptional co-repressor protein that plays a central role in the regulation of plant growth and development. In the model plant *Arabidopsis thaliana*, TPL acts in essential hormone response pathways, including that of auxin, a small signaling molecule. TPL acts in the auxin response pathway by binding another co-repressor from the Aux/IAA family (henceforth referred to as IAAs). In the presence of auxin, IAAs are degraded, relieving TPL repression and allowing for transcription of auxin responsive genes. Despite its central role, the molecular mechanism by which TPL confers repression is not well understood. Recent structural analyses indicate that TPL has interfaces for both homodimerization and homotetramerization. Synthetic assays have shown that TPL truncations in which the tetramerization interface has been deleted have a significant decrease in repressive function. To determine the repressive mechanisms

of TPL, we created a structure-function map. We have created full-length TPL variants with point mutations at the dimerization and tetramerization interfaces, as well as serial domain deletions. We tested the repressive function of these variants in a yeast synthetic assay in which TPL represses expression of a fluorescent protein. Repressive function was then quantified from fluorescent reporter output with stronger repression corresponding to decreased fluorescence. We then validated the results of our synthetic assays *in planta* by expressing TPL-IAA14 variants that negatively regulate lateral root development. The repressive strength of each TPL variant will be quantified by measuring the number of lateral roots, with fewer lateral roots corresponding to increased TPL repressive strength. TPL homologs exist in many species. Defects in TPL homologues have been implicated in the causes of many cancers and developmental diseases, therefore a better understanding of the functional mechanisms of TPL will have broad implications across organisms, including humans.

POSTER SESSION 3

Commons West, Easel 19

2:30 PM to 4:00 PM

The Role of the Auxin Insensitive IAAs in the Auxin Signaling Network

Mega Okoloko, Senior, Political Science, Biology (Molecular, Cellular & Developmental)
Mentor: Alexander Leydon, Biology

In plants, the hormone auxin plays a crucial role in the regulation of many different genes during growth, embryogenesis, differentiation, and many more developmental processes. The promoters of auxin responsive genes are bound by a transcription factor called an Auxin Response Factor (ARF), which is repressed by a protein complex consisting of a linker protein called an IAA and a corepressor known as TOPLESS (TPL). In the presence of auxin, the IAA is degraded resulting in the dissociation of TPL and subsequent activation of transcription of these auxin responsive genes. IAA20, IAA30 and IAA31 are members of a closely related sub-clade of IAAs that are known to be auxin insensitive. These genes are transcribed at low levels in nearly every cell type, yet their role in the auxin signaling network is completely unknown. I hypothesize that the auxin insensitive IAAs create an auxin concentration threshold to reduce the noise of auxin signaling output. In this model, auxin insensitive IAAs interact with all ARFs to generally increase the concentration of auxin required to elicit a transcriptional response. To test my hypothesis, I examined phenotypic changes in single, double and triple-mutants for the auxin insensitive IAAs, which I have generated via CRISPR/Cas9 mutagenesis combined with existing mutations. I am currently testing whether these mutants have quantifiable auxin-related defects in the highly stereotyped root development and arrangement of organs along the stem, or phyllotaxy. If I observe that mutants in the auxin insensitive IAAs have defects with these processes, it will suggest that these IAAs buffer noise present within the auxin signaling network. This work will enhance our understanding of how auxin coordinates transcriptional repression and how signaling noise is reduced in a multi-component molecular system.

POSTER SESSION 3

MGH 206, Easel 172

2:30 PM to 4:00 PM

Healthspan Metrics for Uncovering the Physiological Impacts of Alzheimer's Disease in *C. elegans*

Franklin Xavier Faust, Senior, Neurobiology
UW Honors Program
Tyler J Schmitz, Senior, Biology (Physiology)
Rahul Kishore Chaliparambil, Senior,
Mentor: Josh Russell, Pathology
Mentor: Matt Kaeberlein, Pathology
Mentor: Alexander Mendenhall, Laboratory Medicine and Pathology

C. elegans is a prolific model organism that is well established in the field of aging research and age-related diseases. *C. elegans* can be genetically manipulated to express human toxic proteins associated with neurodegenerative diseases. Its amenability to genetic screening and short lifespan make it an ideal animal model for studying the genetic basis for the neurological health-declines associated with Alzheimer's disease (AD). Here we introduce new experimental approaches for quantifying the organism-wide impacts of nervous system specific expression of human AD-associated toxic proteins.. The pharynx in *C. elegans* is an oral pumping structure used in feeding. The pharyngeal nervous system, comprised of only twenty neurons, dictates the rate of pharynx pumping in the animal. Pharyngeal pumping rates have been shown to change and decay with the age of the animal, making it an ideal metric in aging research. The frequency of pharynx pumping can be measured via an electrophysiological recording of the pharynx's contractions. We plan to use this electropharyngeogram (EPG) as a measure of neurodegeneration to compare wildtype animals with our AD-model mutants. Furthermore, the proper function of extracellular vesicles (ECVs) are thought to be important in the clearance of toxic peptides associated with AD. The only reported phenotype for ECV signaling is the differential development of the cuticle, the animal's outer-most layer of epidermis. The cuticle's formation can be assessed through the appearance of the worm's alae, a set of three lateral stripes running across the animal from head to tail. The appearance of alae has been observed to be different in our AD model mutants, indicating that ECV signaling has been disrupted. Using these AD-model mutants, we aim to establish these novel phenotypes as

a means to further investigate the physiological consequences of AD-associated toxic peptide expression.

POSTER SESSION 3

MGH 258, Easel 188

2:30 PM to 4:00 PM

Impact of Interactions with Eelgrass on Native and Aquaculture Oyster Essential Fatty Acid Composition

Kristine Avygail Estrada (Kristine) Leano, Junior, Biochemistry
Mentor: Michael Brett, Civil & Environmental Engineering
Mentor: Alexander Lowe, Biology

Oysters support a multi-million-dollar aquaculture industry in Washington State and provide important ecosystem services in estuarine habitats. Sustaining aquaculture and restoring native oysters depends on oyster health. Food availability is a driver of oyster health that interacts with environmental effects of global climate change. These global changes may be altered by the effects of local species interactions like association with eelgrass. Measuring essential fatty acids, which are necessary for survival and physiological processes of oysters, can show the level of food availability to oysters in environments with and without eelgrass. We tested the hypothesis that eelgrass alters oyster health by growing oysters inside and outside of eelgrass at 5 sites in Washington state. We used fatty acid composition of tissue from Pacific and Olympia oysters to look at changes of assimilated food in relation to habitat and environment. We predict that eelgrass will slow water flow, resulting in a decrease in food availability and thus essential fatty acid concentration in oysters grown in eelgrass. Looking at essential fatty acids of oysters from different environments, specifically with or without eelgrass, provides a better understanding of environmental impacts on oyster health and contributes to a collaborative effort in Washington state focused on sustaining the valuable food production and ecosystem services of oysters in our ever-changing climate.

VISUAL ARTS & DESIGN SHOWCASE

Odegaard Undergraduate Library

3:00 PM to 4:30 PM

* Note: Titles in order of presentation.

Hue

Erika Jeneve Morales, Senior, Interdisciplinary Visual Arts
Mentor: Alexander James, Computer Science and Engineering

Color is often a very intentional and comprehensive choice as a visual element; artists, filmmakers, designers, and animators recognize color as a tool that signficantly shifts a viewer's perception of their work. While there are universal associations of solid colors- blue for sadness, and red for love, for example, the vastness and complexity of the color wheel leaves much room for nuance between the relationship of humans and color. Color in animation makes use of this nuance, but with a more varied stylistic choice and a greater control over very specific palettes. Through the conceptualization and production of a series of short animation clips, I aim to use color as a deliberate element to evoke subtle shifts in mood, as well as further explore the relationship between animation and color psychology. I've taken inspiration from color scripting in films through the use of a specific color palette to achieve visual balance and strong story support. My work, through tradittional and digital animation methods, aims to bring color in harmony with motion and composition to create a unique visual experience. I hope for my project to contribute to the growing understanding of color as an artistic, technical, and psychological asset in the viewer's engagement in animated films.