

Undergraduate Research Symposium May 19, 2017 Mary Gates Hall

Online Proceedings

POSTER SESSION 1

Balcony, Easel 118

11:00 AM to 1:00 PM

Factors Affecting the Geographic Distribution of *Drosera* (Droseraceae) Species in the Cape Floristic Region of South Africa and Implications of Global Climate Change

Alexander Dietrick, *Sophomore, Ecology, Evolution, & Conservation Biology, Seattle Central College*

Mentor: Joshua Whorley, *Science Technology Engineering Math, Seattle Central College*

The Cape Floristic Region of South Africa (CFR) is the smallest of the world's six floristic regions, and is known for both its high biodiversity and high number of endemic species, or species that exist nowhere else. Among such species are sundews in the genus *Drosera*, which are small, herbaceous, and carnivorous flowering plants. Of the 34 species of *Drosera* in Africa and Madagascar, 21 of them are endemic to South Africa. *Drosera* in South Africa can be grouped into two categories: generalist species that are widespread in their distribution, and specialist species with highly restricted ranges, often known from only a few sites. The high diversity and variety of life history strategies of *Drosera* in South Africa make the genus an excellent model system for the study of species distribution through the lens of global change. For this project, occurrence data was sourced from citizen science platforms iNaturalist and iSpot, as well as from publicly accessible herbarium and biodiversity databases. Using MaxEnt niche modeling software, occurrence data for *Drosera* in South Africa were used in combination with geographic and climatic data from WorldClim to create a niche occupancy model, which predicted the distribution of these species. This model was used in combination with future climate estimates from WorldClim to predict changes in the distribution of *Drosera* species in South Africa in response to climate change. Results from this study suggest that generalist species are less susceptible to climate change than specialist species with already highly restricted ranges. Understanding how species respond to global climate change is crucial for the success of long-term conservation initiatives.

SESSION 1C

SENSORY INTEGRATION, LEARNING, AND MOTOR CONTROL IN ANIMAL AND HUMAN MODELS

Session Moderator: Horacio de la Iglesia, *Biology MGH 231*

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Multimodal Integration in the Disease Vector Mosquito, *Aedes aegypti*

Kennedy Keahi Stone (Kennedy) Tobin, *Senior, Neurobiology Mary Gates Scholar, UW Honors Program*

Mentor: Jeffrey Riffell, *Biology*

Mentor: Clement Vinauger, *Biology*

Mentor: Chloe Lahondere, *Biology*

Mosquitoes transmit diseases that affect millions of people each year. As such, there is an urgent need to explore every avenue to develop efficient tools to control them. In this context, my project aims to better understand their host-seeking behavior by exploring how visual and olfactory stimuli affect the mosquito's flight response. In the Zika and yellow fever vector, *Aedes aegypti*, exposure to CO₂ triggers a strong attraction to visual features. However, the temporal and spatial features of this olfactory-gated visual response are still unknown. For my project, I seek to dive deeper into the characterization of this phenomenon. Specifically, I am interested in determining how long the effect of CO₂ lasts, and to what extent this effect is a function of the size and shape of the visual stimulus. To investigate these factors, I utilized a flight LED arena in which a tethered mosquito was presented visual stimuli and CO₂ pulses delivered at different time intervals. I recorded wingbeat frequency and amplitude, torque, head angle, and leg movements while producing 16 distinct sensory scenarios in which the size of the visual stimulus, and the timing between the delivery of pulses of CO₂ and the visual stimulus were manipulated. From this dataset, I will be able to extract the fine scale behavioral flight response to these unique sensory combinations, deepening our understanding of the complex interplay between visual and olfactory stimuli in mosquito host-seeking behavior. These results bear the potential to lead to the improvement of mosquito control strate-

gies that target their behavioral responses to visual and olfactory stimuli.

SESSION 1D

ECOLOGY AND EVOLUTION

Session Moderator: Bonnie Becker, Environmental Science (Tacoma)

MGH 234

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Recent North Atlantic Right Whale Acoustic Presence along the Western North Atlantic Coast

Alyssa Ashley Ann Scott, Senior, Oceanography

Mentor: Genevieve Davis

Mentor: Danielle Cholewiak

Mentor: Sofie VanParijs

The North Atlantic right whale (*Eubalaena glacialis*, NARW) is among the most depleted species of whale existing today, with a current estimated population of only 450. Ship strikes and entanglement issues remain the predominant cause of mortality for this critically endangered species. Thus, understanding NARW distributions, and their overlap with human activities, are a top priority for management and conservation efforts. This study analyzed passive acoustic data collected within the migratory corridor from Cape Hatteras, NC to Brunswick, GA from Oct 2015 - June 2016 as part of a comprehensive seasonal distribution look at NARWs along the Western North Atlantic coast. Four lines of 5-8 Marine Autonomous Recording Units were deployed, stretching across the shelf, in the first deployment of a three year, continuous acoustic monitoring effort. These units were processed using the Low Frequency Detection and Classification System (LFDCS), and detections were screened for daily NARW presence. The results of this study show seasonal movements to and from their calving grounds while passing through Georgia, South Carolina, and North Carolina. Off the coast of Georgia and North Carolina, NARWs are detected primarily on inshore recorders from November to March, suggesting the species take paths closer to shore while migrating. However, in late April, the groups travelling north take a path further away from the Cape Hatteras, NC shore. NARWs were picked up predominantly on inshore recorders throughout all four lines of MARUs, further supporting that critical habitats exist close to the coast in southern US waters. This information provides a better understanding as to where NARWs are spatially and temporally located, which is essential in minimizing human impacts on the species.

POSTER SESSION 2

Balcony, Easel 107

1:00 PM to 2:30 PM

The Alternative Facts of Meditation

Emmanuel Gregory (Emmanuel) Cuevas, Senior, Biology (Physiology)

UW Honors Program

Mentor: Moon Draper, Biology

Enlightenment, transcendence, mystical experience, and spirituality, these are all common descriptors of supernatural experiences that cannot yet be explained scientifically. Recently, the theories of the neural mechanisms behind spirituality have drastically evolved and in the past century, modern advances in science has allowed mankind to describe the natural world more objectively and empirically. Many college-educated individuals no longer believe in the mystic stories given by religious holy scripture. Even with this shifting in perspectives, the human brain cannot always distinguish between external real experiences and internally induced spiritual experiences. Many people use spirituality as a resource in finding meaning and hope in the world yet there is still much to understand about the neural mechanisms encompassing these feelings. Through a literature review, we discuss in detail the neurological mechanisms behind supernatural experiences and spirituality associated with common human emotion pathways. Comparing past research to more recent research we illustrate how the hypotheses behind spirituality have changed through time and note whether spiritual feeling utilizes a known emotional pathway or a completely novel pathway. The objective is to increase the awareness of the physiological mechanism of spiritual experience related to common human emotions and provide a deeper understanding of how this natural phenomenon occurs accessible at a relatively basic level of understanding.

SESSION 2I

McNAIR SESSION - GOING MOLECULAR

Session Moderator: Ray Malfavon-Borja, OMAD

MGH 254

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Homologous Interactions of Meiosis

Michael Ortiz, Junior, Biology, Cleveland State University

McNair Scholar

Mentor: Valentin Boerner, Cleveland State University

Meiosis produces four daughter cells that are genetically dis-

tinct. A crucial step of production is the pairing of homologous chromosomes; however, how these chromosomes align by homologous pairing remains a mystery. One contributing factor to alignment is tension within kinetochores. Experimentation with budding yeast reveals that a lack of tension will influence the spindle checkpoint until all sister chromatids are attached to the fiber. In the same manner, we will use budding yeast to investigate homologous interaction as the yeast provides us with an ideal model of recombination rates and life cycles similar to higher eukaryotes. The question of homologous behavior is also presented in DNA double-strand breaks. During prophase, these breaks (DSBs) create interactions between homologs along with inducing repair of homologous recombination. The strand is able to be repaired by the sister chromatids; however, the DSBs prefer interactions with homologous chromatid. How are the homologous chromatids found and used to repair the strand? These types of questions will be better understood with our research focused on how homologous chromosomes align initially during meiosis.

SESSION 2S

MODULATION OF CELL BEHAVIOR AND ITS COMPONENTS

*Session Moderator: Valerie Daggett, Bioengineering
JHN 175*

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

Immunostaining Histone acetyltransferase p300 (also known as p300) and cAMP response element-binding protein (CBP)

Noah Schlenk, Junior, BBMB (Biochemistry, Biophysics, Molecular Biology), Whitman College

Mentor: Paul Yancey, Biology, Whitman College

Mentor: Samuel LaBarge, Orthopaedic Surgery, University of California, San Diego

Mentor: Simon Schenk, Orthopaedic Surgery, University of California, San Diego

My presentation focuses on research I conducted using immunohistochemistry to identify proteins in insulin stimulated pathways. My research contributed to the lab's ability to analyze p300 and CBP proteins for their use of acetylation. p300 and CBP often are talked about hand in hand as two proteins that function together to induce and carry out acetylation of other proteins. Generally, you can think of them as a messenger, carrying the information from one source to the next in a long line of messengers. Phosphorylation has long been seen as the primary driving force of downstream signaling. Our lab examined the importance and underestimation of acetylation through these two proteins. Initially, the lab

used Western Blotting to look for protein presence, but the results we obtained were faint and difficult to analyze. I was assigned the task of trouble-shooting a protocol for the staining of these two proteins. I sliced tissue, plated it, stained it, and calculated the changes between knockout- and wild-type tissue. I was ultimately successful in identifying p300 but statistically unsuccessful in identifying CBP due to a technical error. My research showed a much more reliable way of identifying at least 1 of the proteins rather than Western Blotting techniques. This has a broader implication that there will possibly be more accurate or reliable research done on these p300 and CBP proteins, and acetylation as a primer for downstream pathway messaging done in the future.

POSTER SESSION 3

MGH 206, Easel 168

2:30 PM to 4:00 PM

Assessing the Taxonomic Utility of Grass Silica Short Cells Using 3-D Morphometrics

Ashly Marie Senske, Senior, Biology (Ecology, Evolution & Conservation)

Brian Connor Desmond, Freshman, Pre-Sciences

Claire Rose Marvet, Senior, Biology (Ecology, Evolution & Conservation)

Sultan Zeb Akbar, Senior, Biology (Physiology)

Mentor: Caroline Stromberg, Biology

Mentor: Timothy Gallaher, Biology

Our research involves microscopic deposits of silica within the leaves of grasses, called phytoliths. Grasses produce distinctive phytoliths which can be diagnostic at various taxonomic levels. Phytoliths are particularly important in paleobotanical work because they can help us reconstruct earth's past vegetation and climate history. Currently, there is a severe lack of quantitative data on phytolith morphotypes and relative abundances within Poaceae, the grass family. We used confocal microscopy to create 3D images of phytoliths in the Bambusoideae, the Bamboo subfamily, and applied geometric morphometrics in order to quantify shape variation. The 3D objects will contribute to a family wide digital reference collection for use by paleobotanists and grass taxonomists worldwide.

POSTER SESSION 4

MGH 206, Easel 178

4:00 PM to 6:00 PM

Tests for Coevolution in a Microbial Mutualism

Navriti Sharma, Senior, Biology (Bothell Campus)

Norhan T. Algetany, Senior, Biology (Bothell Campus)

Doibu Marip, Senior, Chemistry: Biochemistry (Bothell),
Biology (Bothell Campus)

Jagroop Singh Mutti, Senior, Biology (Bothell Campus)

Mentor: Kristina Hillesland, Biological sciences, School of
STEM

Mentor: Colin Feng, STEM

Bees and flowers trade nectar for reproduction. Rhinos provide food to birds in exchange for removal of parasites. Mutually beneficial interactions like these pervade the natural world, but their impact on the process of evolution is not well understood. Here, we test whether each species in a microbial mutualism repeatedly adapts to the changes in their partners, or coevolves. In our model system 22 communities of the *Methanococcus maripaludis* (archaea) and *Desulfovibrio vulgaris* (sulfate reducing bacteria) evolved for over 3000 generations in the laboratory. To test whether coevolution occurred, we separated the *D. vulgaris* and the *M. maripaludis* in the mutualistic community at 1000 generations. We then paired these 1000 generation *D. vulgaris* populations with *M. maripaludis* at different evolutionary time points and measured the growth rate and yield of each population. If *M. maripaludis* coevolved with *D. vulgaris* then we would expect the 1000 generation *D. vulgaris* to perform better with future partners (0-1000 generations) than past partners (1000-2000 generations) because mutualists are expected to have positive effects on each other's fitness. A preliminary experiment with 6 communities indicated the opposite, that *D. vulgaris* grew faster with past generations compared to future generations. The yield of communities was similar across pairings. These results could indicate *D. vulgaris* has coevolved with *M. maripaludis*, and that there is an underlying antagonism between these species that has not been recognized. We present the results of a more extensive experiment, testing more mutualistic communities at more time points, and looking for patterns of coevolution in both species.

POSTER SESSION 4

Balcony, Easel 121

4:00 PM to 6:00 PM

The Effect of Water Variability on Gene Expression in *Arabidopsis thaliana* Mutants Grown in Competition

Kathy Phuong Hao (Kathy) Tran, Senior, Biology (Bothell Campus)

Mary Gates Scholar

Mentor: Thelma Madzima, STEM - Biological Sciences

Mentor: Cynthia Chang, Biology

Plants play a vital role in maintaining a healthy ecosystem such as providing oxygen, food and shelter. Global climate

change can create selective pressures that have the potential to affect plants physiologically, and their genes provide the plants with the ability to potentially adapt to climate change. In regards to water, climate change may not just be about drought but also the increase of variable precipitation, where there are longer periods of drought followed by a large amount of rainfall. This is likely to also affect expression of drought tolerance genes in plants. By studying the gene expression response in genetically different plants grown alone and in competition under variable water treatments, we can gain better insight into the genotype-phenotype relationship of drought tolerance in plants, and the molecular changes that initiate these responses. During harvesting, plant biomass was measured and then shoot tissue was frozen with liquid nitrogen and stored at -80C. To correlate the collected phenotype data to gene expression, five genes known to be involved in drought response in *Arabidopsis thaliana* and expressed in shoots were picked from the Drought Stress Gene Database (DroughtDB) and the Arabidopsis Information Resource (TAIR). RNA will be isolated from the harvested shoot tissue, and reverse transcription and PCR will be used to measure the changes of gene expression of the drought response genes. This research will help us understand how environmental changes affect gene expression, as well as how genetically diverse plants interact with each other under stress conditions and how this affects productivity. In the long term, this understanding can be used to improve plant productivity to maintain a healthy ecosystem especially when the climate is changing drastically.

POSTER SESSION 4

MGH 206, Easel 171

4:00 PM to 6:00 PM

Theropod Dinosaur Diversity Leading Up to the Cretaceous-Paleogene Mass Extinction, Based on Teeth from Uppermost Cretaceous Hell Creek Formation, Montana

Athena Tse, Recent Graduate,

Mentor: David DeMar, Burke Museum

Mentor: Gregory Wilson Mantilla, Biology

The Cretaceous-Paleogene (K-Pg) mass extinction is the most recent of the 'big five' mass extinctions and led to the extinction of all dinosaurs except birds. Theropod dinosaurs, which were mostly carnivorous, were important members of latest Cretaceous terrestrial ecosystems. A popular hypothesis for the K-Pg mass extinction is that a meteor impact caused rapid extinction of many taxa 66 million years ago (Ma). The fossil record of dinosaur skeletons is not sufficient to assess the timing and pattern of the K-Pg mass extinction and its potential cause(s). Here, I documented theropod diversity using a sample of 783 fossil teeth from eight localities that span most of the depositional duration of the Hell Creek Forma-

tion (HCF; ca. 1.9 million years). To test the hypothesis that the bolide-impact was the sole cause of the mass extinction, I wanted to determine if significant changes in theropod diversity occurred before the impact at the K-Pg boundary. New and updated taxonomic identifications were based on the current literature. Raw, range-thru, and rarefied taxonomic richnesses as well as relative abundances and heterogeneity indices (evenness, Simpson's) were calculated for each of the fossil localities. In total, eight theropod taxa were identified from the HCF. Richness shows a slight decrease from eight taxa in the lowermost HCF locality to five to seven taxa higher in section. Rarefied richness was lowest in the uppermost HCF. Although the changes observed in richness are minor, relative abundance and heterogeneity values differed significantly from the middle to upper HCF localities implying that major changes in theropod faunas occurred locally within the last few hundred thousand years of the Cretaceous prior to the bolide impact. Similar patterns have been observed in the amphibian and mammalian faunas suggesting other environmental factors (e.g., volcanism, climate change) contributed to the causes of the mass extinction.

POSTER SESSION 4

Commons East, Easel 58

4:00 PM to 6:00 PM

Aquaculture in Future Oceans: Effects of Food Changes on Mussel Health

Molly K. Payne, Senior, Aquatic & Fishery Sciences

Mary Gates Scholar, UW Honors Program

Mentor: Emily Carrington, Biology

Mentor: Alexander Lowe, Biology

Mussels, Family Mytilidae, are vital to intertidal ecosystems and to a burgeoning aquaculture industry. They act as ecosystem engineers within their environment by controlling resource availability to other organisms and by shaping the structure of their habitat. Unfortunately, with the rise of anthropogenic climate change, mussel populations are seeing growing threats to their ability to survive and reproduce. This includes lower recruitment, increased susceptibility to disease, and weakening of the byssal thread that adheres mussels to their substrate. Understanding the life history of these organisms, in addition to what food sources and conditions are most suitable for their growth, is essential for preserving this economically and ecologically vital species group. *Mytilus trossulus*, a common species of saltwater mussel ubiquitous in the aquaculture industry was used in this study. The mussels were grown at two different depths on aquaculture lines for comparison of the environmental effects at those depths. The first layer at 1 meters depth consisted of a mixed surface layer rich in phytoplankton growth and represented a warmer, more variable ocean environment. The second layer was found below the surface mixed layer at 7 meters depth and represented

a colder, more constant environmental regime. By analyzing the food sources of these mussels through fatty acid extraction, we will draw conclusions not only about what nutrients are most beneficial to mussel growth, but also what effects the environmental differences between the two depth strata has on the mussels. The purpose of this study is to both provide data for the care of mussels in aquaculture farms and to make inferences about what a changing climate will mean for these organisms.

POSTER SESSION 4

MGH 206, Easel 172

4:00 PM to 6:00 PM

Analysis of Nucleotide Sequences to Determine the Placement of *Scalesia* within *Helianthaea*

Valeria Aizen, Sophomore, Pre-Sciences

Mentor: David Tank, Biological Sciences, University of Idaho

The goal of this study was to understand more precisely the placement of the *Scalesia* clade within *Helianthaea*—specifically what taxa are sister to *Scalesia* and what traits diverged between *Scalesia* and its sister clades. Previous research has shown *Scalesia* to be monophyletic and placed *Scalesia* as sister to *Pappabolus* and basal to *Viguiera*, but with low support due to homoplasy. We used extracted ITS, ETS, and psbA sequence DNA from seventeen *Scalesia* samples from the Galapagos and sequence DNA from ninety two species from mainland South America, North America, and Mesoamerica that we obtained from Genbank. Bayesian analyses of concatenated ITS +ETS + psbA sequence data, maximum likelihood analyses of ITS+ETS+psbA/ITS+ETS, and individual gene region data implied that *Scalesia* is sister to *Pappabolus*, *Heiseria pusilla*, *Viguiersimsioides*, and *Syncretocarpus sericeus* with high likelihood support and is monophyletic consistently throughout all trees. Our data also implied that all *Scalesia* taxa is very closely related and very recently diverged. An interesting split between a woody ancestor (*Zaluzania grayana*) and an herbaceous, derived species (*Scalesia baurii*) was observed. Further taxonomic work, especially on the reclassification of *Aldama* and *Viguiera* is still necessary.