INTRODUCTION

"The sciences at Smith will provide transformative opportunities for all students to engage with real problems while empowering them to generate innovative solutions that benefit our world."
Our vision for the future is grounded in a shared aim to "cultivate the scientist in the next generation of women leaders." Our strategic plan for the sciences (*Vision for the Future, 2015*) builds on Smith College's strength as a national leader in science research and education among liberal arts colleges. An increasing number of Smith students study sciences. In 2015, forty percent of our current students declared a science major, a rate at least double the national average for women. In disciplines in which women are most under-represented (e.g., computer science), our students major at rates up to three times the national average. At Smith, our approach to education in the sciences also represents a response to societal matters – lower female participation in STEM higher education and later in work, as well as academic, economic, and political leaders' advocacy of full representation of women in all STEM fields as a matter of equity and good policy based on the benefits that flow from diversity.

Ensuring access for all. As its first principle of excellence, the Association of American Colleges and Universities' Liberal Education and America's Promise (LEAP; 2011) initiative tells us to "aim high—and make excellence inclusive" (p6). For the sciences at Smith, we are guided by understanding that persistence and the best scientific thinking emerge from healthy climates that promote and value a diversity of perspectives. As our strategic direction, we work to address disparities in gender, racial, and socioeconomic representation in the sciences by pairing rigorous learning expectations with robust support and community-building for our students.

Engaging with the world. Another essential principle of excellence in undergraduate education is to provide opportunities for students to engage with big questions and tackle real-world problems that connect their knowledge to solutions and action (AAC&U, 2011). At Smith, we are guided by the belief that interactions with bona fide scientific problems connecting our students to the larger world facilitate the best learning. As our strategic direction, the sciences at Smith will strive to engage our students with complex, real-world problems, ranging from local to global, that are often best understood through the multiple disciplinary lenses of the liberal arts.

Strategic Directions

	Ensuring access for all
	Engaging with the world
	Developing knowledge and skills
	Fortifying agency and identity

Developing knowledge and skills. Research is a core practice of scientific education at Smith College. We are guided by a shared understanding that best-practices pedagogies and faculty-student research collaborations will result in optimal learning and future success for our students. As we move forward, we build on evidence that through rigorous coursework and undergraduate research opportunities that connect the work of students with cutting-edge faculty scholarship, we develop student mastery of the key concepts and competencies of our disciplines.

Fortifying agency and identify. Persistence and success in STEM rest not only on access, opportunity, and knowledge, but also on the actions taken by individual women in particular environments using specific social understandings. Smith faculty adopt a guiding principle that students' mind sets, metacognition, and identity development are essential to learning as well as professional and personal fulfillment. We understand that through our cultivation of students' agency, confidence, and resourcefulness in learning, we will foster their sense of identity as scientists.

Undergraduate research is a high-impact educational practice in which the sciences at Smith have considerable expertise. Research experiences and collaborative projects that occur in research labs, the Science Center's five multidisciplinary research centers, and our field research sites demand the applied and integrative learning that deepens student engagement and learning (AAC&U, 2011). The sciences at Smith have a strong history of providing meaningful research opportunities to students, with a thriving honors program, active faculty research labs in which students participate as collaborators, and almost 50 years of a vibrant Summer Research Fellowship (SURF) Program. Our students present their research in many venues, including at the annual campus-wide *Celebrating Collaborations* exhibition and *Smith in the World Conference*, in public honors thesis presentations, and at regional and national professional meetings in their disciplines. With at least one undergraduate student co-author on a third of science faculty members' peer-reviewed scholarship and SURF participation doubling the likelihood of our students pursuing a graduate degree (data provided, Smith College Institutional Research, 2015), we believe that challenging our students to work at the cutting edge of knowledge helps prepare them for their lives beyond Smith.

Women in Science 2015 **summarizes research done by Smith College's Summer Research Fellowship (SURF) Program participants.** Ever since its 1967 start, SURF has been a cornerstone of Smith's science education. In 2015, 162 students participated in SURF (153 hosted on campus and nearby field sites), supervised by 60 faculty mentor-advisors drawn from the Clark Science Center and connected to its eighteen science, mathematics, and engineering departments and programs and associated centers and units. At summer's end, SURF participants were asked to summarize their research experiences for this publication.

We have many reasons to be proud of our 2015 SURF researchers.

- SURF researchers worked on some of the biggest research challenges of our times, including eradicating human disease, reexamining human life and the earth around us at the nano-scale, documenting climate change and its impact on the living world, testing and improving sustainable energy technologies, and developing materials and testing methods not just for earth but also for use in space.

- SURF research took place not just on the Smith campus, but in a wide variety of research settings in the wider world: including, locally (study of local forests, wild life, and water courses at the Ada and Archibald MacLeish Field Station in West Whately, MA and the study of building stones and waterfront plants on campus), nationally (projects on the Atlantic and Pacific coasts with NOAA scientists), and internationally (examination of coral reefs in Belize and Newfoundland, geological features in Australia and Scotland).

- Technical know-how, quantitative literacy, and presentation skills grew as students used state-of-the-art instrumentation, analyzed data with specialized software, and presented their results in lab meetings, posters, and conference presentations. In lunchtime workshops, students developed personal narratives and made presentations to peers and visitors.

- SURF students learned how to work with mentors and peers and, for some, across the boundaries of academic disciplines with other research teams. More experienced undergraduate researchers learned how to mentor others and take on research leadership roles.

We are excited about what SURF participants say they learned from SURF.[1]

- SURF research deepens students' understanding of research. They discover that scientific research requires flexibility and creative problem-solving, patience, and persistence.
  - *"It is clearer and clearer that being a scientist does not mean knowing everything, but means having the courage to face the unknown and the determination to reveal it."*
  - *"I learned to think of as many angles as possible from which to examine something, and then think of even more that I hadn't considered the first time around. I learned to identify and ignore my assumptions, as they would affect what patterns I noticed."*
  - *"I learned to add to and tailor [published experimental methods] to best suit my experiments."*
  - *"A Smith professor once told me that learning is first confronting the difficult parts, struggling and then having that 'ah-ha' moment [and] the sweet relief of finally figuring out the puzzle ..."*
  - *"This summer taught me about how much patience science can require, but also how exciting and rewarding it can be to make new discoveries."*

- *"I learned that it is important to pay attention to small details, because when people ignore subtle details they can miss things that are very important"*
- *"I learned how to bounce back when experiments fail or they don't go the way you want them to."*

- Each student commits substantial time to SURF research: typically, 30-40 hours per week for 8-10 weeks of the summer.
  - *"Summer research is more intense than during the academic year. I enjoyed putting my whole day into doing research."*
  - *"I was able to learn more during summer research because I was able to be more fully immersed in my project with more time and [fewer] distractions."*
  - *"[I] spend A LOT more time in lab in the summer when I'm not juggling classes, TA-ing, and [going] to extra jobs."*
  - *"I learned that hard work does pay off and even when it seems as though you have not accomplished anything on your project, you have done more than you think."*
  - *"[F]ield work takes a lot more time and effort than I originally perceived."*
  - *"[T]he sheer amount of time we spent immersed in lab was very valuable to my understanding of what research really entails."*

- Many students make a distinct contribution to a collaborative research project with a faculty member and often a joint publication is prepared.
  - *"I will be presenting my SURF research in a talk at Smith, a poster session (or talk) at a national conference as well as submitting a peer-reviewed article for publication."*
  - *"With the upcoming submission of a manuscript derived from my undergraduate thesis, including additional data I collected this summer ..., I will have ... executed what I intended to do with my SURF project."*
  - *"The paper that [my professors] and I hope to write is intended to serve as a guide for anyone interested in constructing a system similar to what we have made."*

- In many cases, SURF research contributes to the particular student's honors thesis or continues as a special studies project.
  - *"Because of my SURF experience, I feel more prepared about my senior year thesis."*
  - *"SURF enabled me to learn a totally new technique that ... will be the foundation for my thesis investigation."*

- Students discover the social aspects and interpersonal skills involved in research teamwork, as well as the value of communication.
  - *"[T]his summer, I really came to understand the true value of teamwork in a research setting. ... [W]e are strongest and most productive, and have the most fun, when we are working together with open minds."*
  - *"I ... learned that when working with a research team ... communication is of the utmost importance."*
  - *"Working in the same room as my coworkers not only let me practice communication and acclimate to a full-time working environment, but also built great relationships."*
  - *"I learned how to present the same information in multiple ways, so that my project would be comprehensible to my advisor, to my classmates, and even to friends with very little science background."*
  - *"The nature of my work pushed me to articulate my ideas and understanding in a succinct manner."*

- SURF is where students find direction for graduate school and future careers.
  - *"[SURF research] definitely inspired me to continue to pursue research as a career."*
  - *"My SURF research experience was exactly what I had hoped for. I was able to discover my interest in research and my desire to go to graduate school is stronger now."*
  - *"This summer I was able to work independently on my project in [a research] lab; this was a great introduction to what life as a graduate student will be."*

[1]The comments are drawn from two surveys SURF participants completed in August 2015. First was a Smith survey (unpublished) in which students were asked what they had learned and how they expected to build on their SURF experience. Second was the SURF III national survey administered by Grinnell College (Smith student comments extracted from an anonymous summary provided by the survey administrators). See the following reports of the SURF survey data across a large number of colleges and universities: Lopatto, D. (2004). Survey of Undergraduate Research Experiences (SURF): First Findings. *Cell Biology Education*, 3, 270-277 and Lopatto, D. (2007). Undergraduate research experiences support science career decisions and active learning. *CBE - Life Sciences Education,* 6, 297-306.

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We wish to recognize and express gratitude to the faculty members and staff who provided supervision, guidance, encouragement and support to SURF participants in the lab, doing field research, on-campus, and away from campus. SURF would not be possible without your devoted and generous contributions.

Thank you, Smith College students, faculty, staff, friends, and benefactors. It truly takes a diverse and dedicated community to sustain a program like SURF.

Margaret Lamb, Ph.D,
Administrative Director, Clark Science Center

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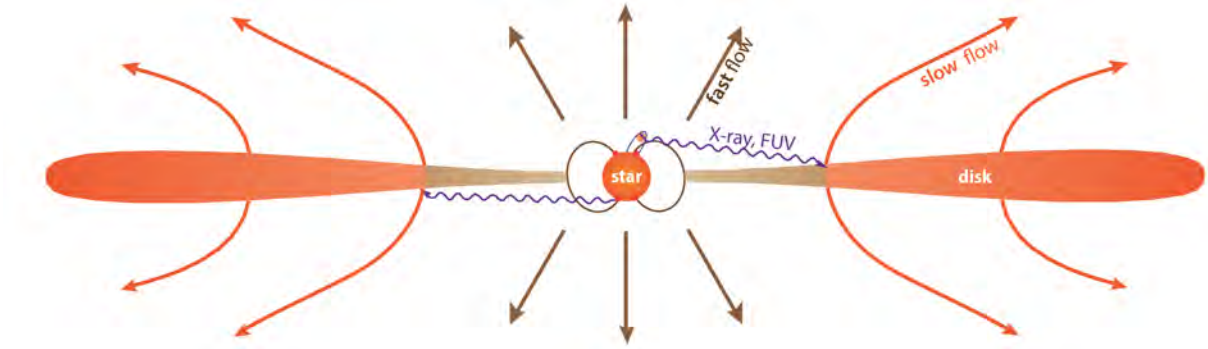
Mass Accretion and Ejection of T Tauri Stars

Wanda Feng/2015



The major questions in star formation involve understanding how stars form from interstellar matter, how young stars evolve and interact with their surrounding medium, and how they reach the main sequence stage of stellar evolution. A star that is of particular interest is the Sun, which is a low-mass star that is about 5 billion years old. Investigating how the Sun formed and how the solar system developed relies heavily on the study of young, low-mass stars. The study of T Tauri stars is crucial to answering these questions. This project, an extension of my senior thesis, addressed determining mass accretion and ejection rates.

This study involves 20 T Tauri stars, which were observed with the High-Resolution Echelle Spectrometer (HIRES) on the W. M. Keck I telescope at Mauna Kea Observatories, Hawaii. The majority of the stars were observed in 2006. To obtain an accurate profiles for each emission line, "contaminants" in the form of absorption lines due to the Earth's atmosphere and the stellar photosphere - the outer layers of the stellar atmosphere - were removed.

T Tauri stars undergo accretion of material from their surrounding disks. Several hydrogen emission lines were used to calculate mass accretion rates: H α (λ = 6563 Å); Paschen ϒ(λ = 10938 Å); and, Paschen β (λ = 12822 Å). The observed strength of emission for these lines was used to calculate line luminosities. Published calibrations were used to determine accretion luminosities, the excess emission attributed to accretion shocks, from the line luminosities. The mass accretion rates were determined from the accretion luminosity and stellar parameters. The 20 stars in this sample accrete material at rates between log -9.12 M_{sun} yr^{-1} and log -5.09 M_{sun} yr^{-1}.

As the stars accrete material, matter is simultaneously ejected from bipolar jets and disk winds. Forbidden lines, particularly that of oxygen [O I] λ 6300 Å, have long been recognized as mass outflow tracers due to their blueshifted emission. By fitting these line profiles with Gaussian functions, it is possible to distinguish high and low velocity components. The high velocity components originate in bipolar jets and are used to determine mass ejection rates. The 20 stars in this sample eject material from bipolar jets at rates between log -7.69 M_{sun} yr^{-1} and log -6.44 M_{sun} yr^{-1}.

(Supported by the Schultz Foundation)

Advisor: Suzan Edwards, Astronomy

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Base Pair Opening Rates in Cisplatin-DNA Adduct

Emily Boerger/2016

Since receiving FDA approval in 1978, the anti-cancer drug cisplatin, has been used to treat testicular, ovarian, bladder and lung cancers successfully.[1] Although the mechanism by which cisplatin kills cancer cells is not completely understood, many labs have been trying to elucidate this mechanism since its discovery. Cisplatin, a platinum based drug, enters cells through passive diffusion where it is hydrolyzed to form a more active compound.[1] The platinum component binds and cross-links with DNA at a GG base pair site, creating a lesion, which is then recognized by nucleotide excision repair (NER) enzymes.[1] NER uses proteins to remove 24-32-mer fragments from the damaged DNA. It has been shown that NER proteins bind with higher affinity to platinum damaged DNA, however, how the proteins recognize the platinum damaged DNA is unclear.[1] This summer I began focusing on the base pair opening rates in cisplatin damaged DNA through NMR analysis using a 9-mer DNA oligonucleotide.

DNA, whether damaged or not, is in a constant equilibrium of an open and closed state. It is known that the base pair opening rates vary in damaged and non-damaged DNA, and hypothesized that this is a contributing factor to protein recognition of the damaged DNA in repair pathways.[2] Using NMR analysis, quantitative data will be gathered on the base pair opening rates in a control DNA 9-mer and a cisplatin damaged DNA 9-mer, helping to form a conclusion about repair proteins recognition of the cisplatin-DNA adduct.

HPLC Preparation and purification of a cisplatin damaged 9-mer began as the 9-mer control was analyzed. This time consuming preparatory step produced about half of the mM concentration of lesioned DNA necessary to perform NMR experiments. Data from the literature used NMR of the imino region to suggest that DNA with a lesion, such as platinum, is less stable at higher temperatures than its control.[3] A temperature study was completed on the 9-mer control (Figure 1) and will be compared to the cisplatin 9-mer once it is made.

The temperature and base pair opening rate studies of the DNA 9-mer will continue into the fall, hopefully leading to an honors thesis.

(Supported by the Howard Hughes Medical Institute)

Advisor: Elizabeth Jamieson, Biochemistry

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2. Wenke B, Huiting L, Frankel E, Lane B, Núñez M. Base Pair Opening in a Deoxynucleotide Duplex Containing a cis-sy Thymine Cyclobutane Dimer Lesion. *Biochemistry* [serial online]. December 24, 2013;52(51):9275-9285

3. Julien, O., Beadle, J., Magee, W., Chatterjee, S., Hostetler, K., Evans, D., & Sykes, B. (n.d). Solution Structure of a DNA Duplex Containing the Potent Anti-Poxvirus Agent Cidofovir. *Journal Of The American Chemical Society*, *133*(7), 2264-2274

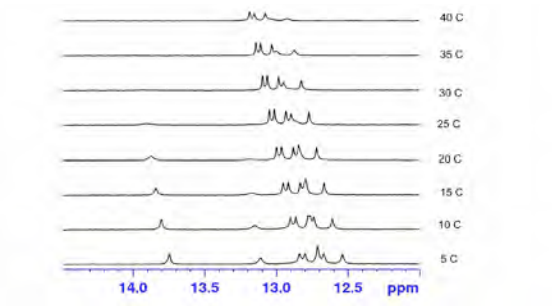

Figure 1: Temperature studies of the 9-mer control guanine and thymine imino protons from 5-40^{0}C.

Assessing Cell Growth on an Airbrushed Chitosan Wound Dressing

Emmie Knobloch/2017

Chitosan is a polysaccharide derived from chitin, a component of crustacean shells. It is known to have hemostatic and antibacterial properties, and is a common component in wound dressings. When combined with polymers such as poly(lactic-co-glycolic acid) (PLGA) and polyethylene glycol (PEG) in solvent, it forms a solution that can be easily airbrushed directly onto a number of surfaces and has potential for a self-adhering, easily administered wound dressing with healing properties. The purpose of my project was to assess the in vitro growth and activity of keratinocytes grown on airbrushed nanofiber scaffolds containing chitosan and to quantify their antimicrobial properties.

The effects of these scaffolds on cell growth and healing were assessed by growing cells, specifically rat keratinocytes, on samples of this material containing a range of 0-10% dry weight of chitosan, and either 0% or 15% PEG. Their growth and metabolic activity over a period of nine days were measured using a number of methods, including WST cell proliferation assays, PicoGreen assays, and RT-PCR. The antimicrobial properties of the scaffolds were assessed by inoculating samples of chitosan-polymer scaffolds with a culture of Streptococcus mutans and incubating for two hours. The number of living bacteria was then determined via a count of colony-forming units (CFU) from cultures of these samples grown on agar (Figure 1). Hemcon, a commercially available chitosan wound dressing, was included for comparison as a positive control.

This range of analyses provides a comprehensive view of the cells' behavior and enables predictions about how a wound in vivo would likely react to such a wound dressing. Initial results indicate that those sample groups containing chitosan or PEG do not exhibit increased cellular toxicity when compared to those without. Groups containing PEG do have visibly increased antibacterial properties compared to those without, however. Further investigation and analysis is necessary, but these results show promise for the development of a novel wound dressing with low cytotoxicity and significant antibacterial properties.

(Supported by the National Institute of Standards and Technology)

Advisor: Diane Bienek, Material Measurement Laboratory, NIST

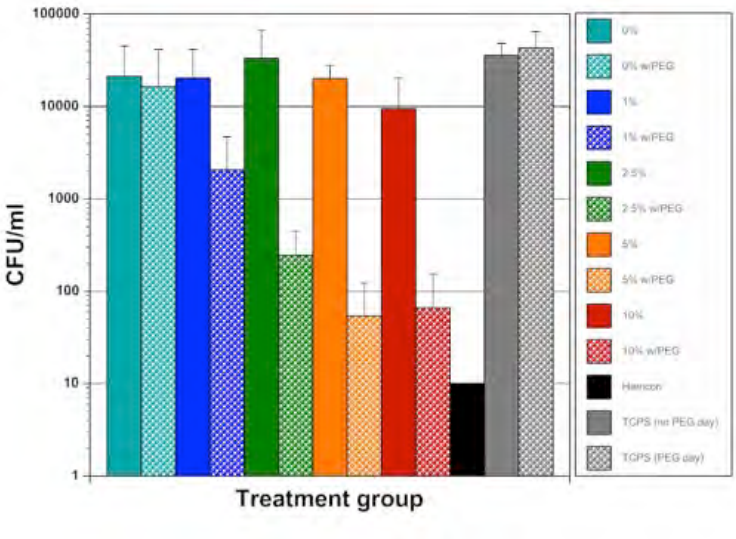

Figure 1: Fewer colony-forming units were found on nanofibers containing PEG and chitosan.

Investigating the Molecular Interactions of Heat Shock Protein 25

Natalie Kolber/2017

Heat shock proteins (HSPs) are a family of stress-response proteins that prevent the aggregation of misfolded proteins in the cell.[1] They are therefore tantalizing therapeutic targets for the treatment of a variety of diseases caused by the accumulation of misfolded protein aggregates. Murine HSP25 and its human analog HSP27 in particular have been shown to reduce the accumulation of protein aggregates in models of Huntington's and Alzheimer's disease.[2] Furthermore, the anti-apoptotic effects of HSP25/27 have been shown to reduce cell death in the face of a wide variety of insults, from oxidative stress, to cytotoxic drugs, to hyperthermia.[2]

Protein was extracted from the biceps brachii muscles of mice and probed for HSP25 via Western blot (Fig 1). While this indicated that the protein was present and could be detected by our antibody, Western blotting requires that proteins be denatured and hence rendered inactive. It therefore cannot determine interacting proteins. To determine which other molecules interact with HSP25 in vivo, a protocol for magnetic co-immunoprecipitation is under development. In a co-immunoprecipitation assay, beads are coupled to an antibody against the target protein, generally via protein A or G. Cell lysate is then applied to the coupled bead, and the target protein (along with its various binding partners) binds to the bead.[3] Our protocol uses magnetic beads, allowing the bead-antigen complex to be separated out from the cell lysate using a magnet rather than chemical precipitation.

Developing a co-immunoprecipitation protocol for HSP25 is particularly difficult due to the fact that the molecule is of the same size (25 kilodaltons) as the light chain of the IgG antibody. Hence, when proteins are eluted off the surface of the magnetic bead, special precautions must be taken to ensure that the antibody is not eluted along with the antigen, as the two are indistinguishable on a protein gel. Initially, dimethyl pimelimidate dihydrochloride was tried as a coupling agent to covalently link the antibody molecule to the protein G on the bead surface. As this proved unsuccessful, the protocol currently under development involves biotinylating the antibody and covalently coupling it to streptavidin-coupled beads.

The development of a successful co-immunoprecipitation protocol involves continuous adjustments, multiple checks of quality control, and the acquisition of additional antigen in the form of mouse muscle extract. This process will continue in the fall semester as a special studies in the biochemistry department.

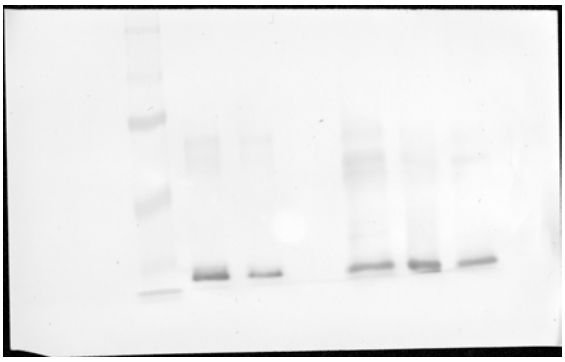

Figure 1. Western blot of mouse biceps brachii probed with anti-HSP25 antibody. From left to right: molecular weight standard, 5 ng recombinant HSP25, 2.5 ng recombinant HSP25, 20 ng whole extract, 20 ng pellet, 20 ng supernate.

(Supported by the Howard Hughes Medical Institute)

Advisor: Stylianos Scordilis, Biochemistry

1. Smith, H. L., Li, W., and Cheetham, M. E. (2015) Molecular chaperones and neuronal proteostasis. *Semin. Cell Dev. Biol.* **40**, 142–152

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Development of Immunoprecipitation Protocol for Determination of Phosphorylation States of Creatine Kinase Isoforms Throughout C2C12 Myogenesis

Arcadia Kratkiewicz/2016

I am developing an immunoprecipitation (IP) protocol, to elucidate the phosphorylation states of three of the creatine kinase (CK) isoforms during C2C12 myogenesis to understand CK regulation. The C2C12 murine myoblast cell line[1] serves as an *in vitro* model of muscle repair after injury, as well as skeletal muscle development. Undifferentiated myoblasts fuse, become multinucleate early myotubes (EM), and develop into spontaneously contracting late myotubes (LM). CK is an important ADP phosphorylating enzyme in cellular energy homeostasis, and exists in multiple isoforms, including the muscle isoform CK-M, the non-muscle isoform CK-B, and the sarcomeric mitochondrial isoform CK-MT2.[2]

Three methods of IP using magnetic nanoparticles (Nvigen MagVigen Protein-G Nanoparticles) were tested with anti-CK-B IgG (DSHB). First, the antibody was bound and cross-linked to the nanoparticles with dimethyl pimelimidate dihydrochloride. Mouse skeletal muscle extracted in RIPA buffer was pre-cleared with fresh nanoparticles. This extract was incubated with the antibody-cross-linked-nanoparticles, the nanoparticles were separated from the supernatant with a magnet, and the bound protein was eluted. The eluate, as well as the supernatant and washes, was analyzed for protein using SDS-PAGE (Figure 1a). The presence of CK-B was expected, but no protein was visible. The IP was repeated without cross-linking the antibody. Pre-cleared muscle extract was incubated with the antibody, and then with the nanoparticles. The nanoparticles were separated from the supernatant and bound protein was eluted and analyzed with SDS-PAGE. Antibody and CK-B were expected, but no protein was seen in the eluate, indicating that either the protein was not binding to the nanoparticles or that it was binding but not eluting (Figure 1b). To test this, the protocol was repeated with only the antibody and no muscle extract. After incubation with the nanoparticles, IgG was still present in the supernatant and none in the eluate, indicating that it was not binding to the protein G on the nanoparticles (Figure 1c). A third IP protocol was tested, with the antibody and nanoparticles incubated together first and then with the muscle extract. The antibody was seen in the eluate (Figure 1d).

I will continue this project with a senior honors thesis. Once optimized, IP will be used to isolate the three isoforms of CK from each stage of C2C12 myogenesis for analysis by LCMS to determine their phosphorylation state. The results will be verified using 2-dimensional gel electrophoresis.

(Supported by the Howard Hughes Medical Institute)

Advisor: Stylianos Scordilis, Biochemistry

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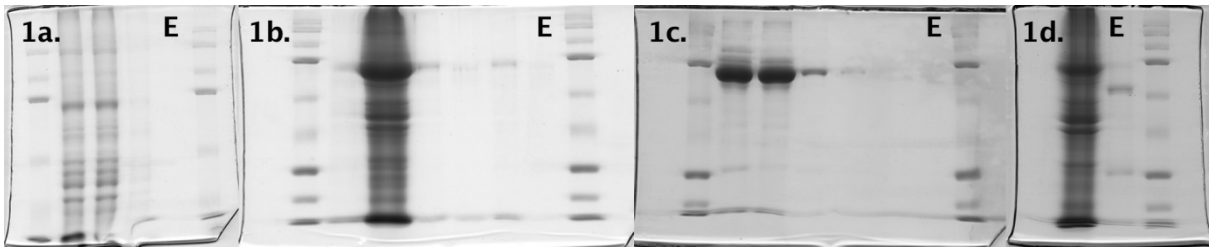

Figure 1. SDS PAGE analysis of IP protocols. E=eluate. 1a. No proteins seen in the eluate of the protocol cross-linking the antibody to the nanoparticles. 1b. No protein seen in the eluate of the protocol without cross-linking. 1c. No antibody eluted when testing the IP with only the antibody. 1d. IgG eluted when nanoparticles first incubated with antibody.

Size Matters Not: sRNA's in Thermoregulatory Pathways in *Escherichia coli*

Madeleine Sutherland/2016

Temperature is a major cue *Escherichia coli* uses to modulate gene expression and adapt to new environments.[1] Small regulatory RNAs offer another level of regulation by altering mRNA stability or translation. The commensal *E. coli* K-12 genome contains 80 small non-coding RNAs (sRNAs),[2] around forty of which have been confirmed in uropathogenic *E. coli* (UPEC).[3] My project explored if sRNAs that control thermoregulated genes are temperature regulated.

Using qRT-PCR, I measured relative expression of sRNAs in both commensal and uropathogenic bacteria shifted from 23˚C to 37˚C (human body temperature). In UPEC, I found that the sRNAs GadY, MicC, OmrA and RprA all show ≥ 2-fold change in gene expression by four hours after upshift to 37˚C. In K-12 I found that MicC and MicF are inversely thermoregulated (Fig. 1) and confirmed the regulatory pattern of the GAD genes (Fig. 2).

In a time course, the sRNAs MicC and MicF, which downregulate the outer membrane proteins OmpC and OmpF respectively, show opposing thermoregulatory patterns (Fig. 1). The downregulation of MicC matches with known upregulation of OmpC – this is important because OmpC is implicated in antibiotic resistance.[4] Second, the glutamate-dependent acid resistance pathway is slightly up and then downregulated at 37˚C, suggesting a role for the sRNA GadY in this thermoregulatory response (Fig. 2).

The confirmed thermoregulated sRNAs all regulate pathways where the protein-coding genes are thermoregulated, as shown by previous RNA-Seq data; thus, my research shows that sRNAs may play an important regulatory mechanism for gene regulation in response to temperature.

This work will be continued into 2015-16 with my honors thesis, which will involve sRNA knockouts. I hope to present my findings at the American Society of Microbiology conference.

(Supported by the Howard Hughes Medical Institute)

Advisor: Christine White-Ziegler, Biochemistry

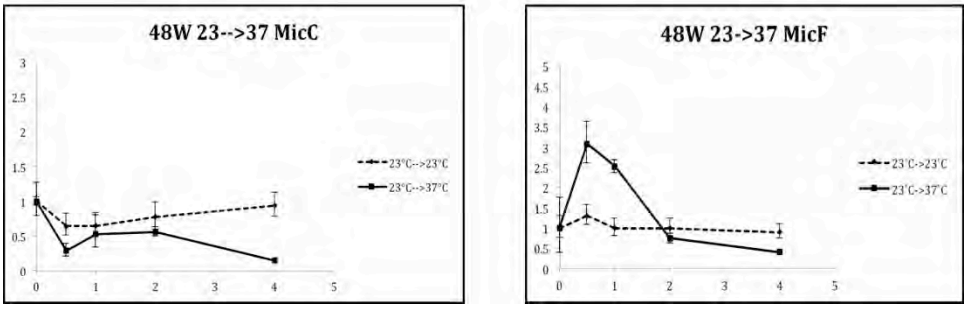

Figure 1: Initially opposing expression patterns of MicC and MicF, as shown by time course qRT-PCR studies (relative expression vs. time in hours). This should lead to increase in OmpC and initial decrease in OmpF.

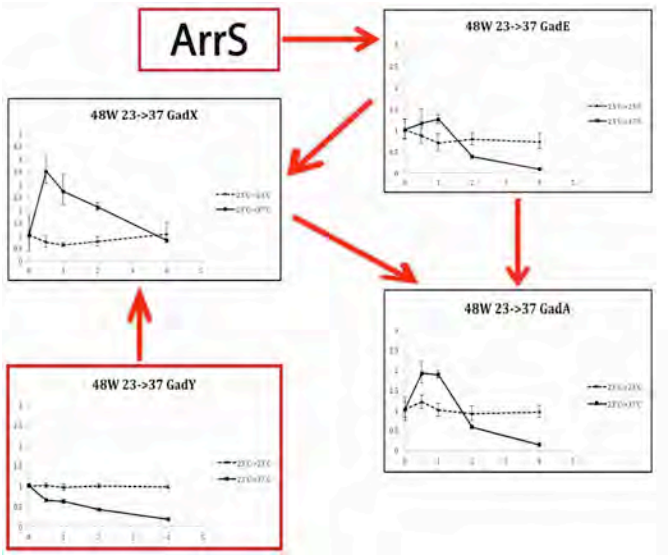

Figure 2: Thermoregulation of the glutamate-dependent acid resistance (GAD) pathway shown by time-course qRT-PCR studies (relative expression vs. time in hours). Red arrows connect genes to the genes they up-regulate; bold red borders denote sRNA's. GadA is catalytic; the up and then downregulation of GadA could be a synthesis of the effects of GadX and GadE. Downregulation of GadY contributes to decreasing expression of GadX. Later, the role of ArrS in this pathway will be clarified by qRT-PCR and/or knockout studies.

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Ecological Consequences of Invasive Pests on Eastern Hemlock Population

Youngjoo Ahn/2018

The Eastern hemlock, *Tsuga Canadensis* is a foundational species in many forest communities throughout the United States and Canada because they provide optimal conditions for rich diversity. Hemlocks, a coniferous species, have needle-like leaves which take a long time to decompose, resulting in a deep organic layer. This organic layer, coupled with dense canopies, create an acidic, shady understory for other plants and animals to thrive in.

However, in recent years, exotic pests, Hemlock Woolly Adelgid [HWA], *Delges tsugae annand*, and Elongate Hemlock Scale [EHS], *Florinia externa*, threaten the existence of Hemlock trees. HWA is an invasive insect that feeds off essential cells by burrowing a needle- like tube through the branch and often kills the tree in 4-10 years. While EHS doesn't kill the hemlock completely, it infests the underside of leaves, reducing the overall health dramatically. Interestingly enough, deciduous species, the *Betula lenta* (Black Birch) in particular, have mainly repopulated the hemlock's place. Deciduous species shed their leaves with the seasonal changes and do not provide a constantly shady understory. Fortunately due to an accidental clearing in the MacLeish forest, we were able to study paired plots of hemlock and birch forests. This specific research project aimed to study the many different factors that contributed to overall ecosystem changes.

One main part of the project was measuring efflux levels, volumetric water content, and soil temperature of hemlock and birch forests using the Li-Cor 6400. From May-August, each forest was measured approximately every two weeks in order to track the long-term patterns. In May, birch forests were more productive than hemlock forests but as time progressed, hemlocks efflux levels surpassed those of the birch forests. However, the volumetric water content of birch forests are almost always higher. This data will be compared to overall weather patterns and continued throughout the academic year.

Another main part of the project was comparing bacterial counts for hemlock and birch soils. Using agar plates and soil dilution techniques, colony forming units (CFU) were counted for both soils and this experiment was repeated twice. Hemlock forests have shown both times to have ten fold more bacteria than birch forests.

These preliminary experiments have shown that there are significant differences in the forest ecology under hemlock domination compared to birch. In the future, more data will be collected to observe seasonal changes on these two forests as well as an older, more established birch forest.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences)

Adviser: Danielle Ignace, Biological Sciences

Radial Glia in the Central Nervous System

Katrina Anderson/2018

Radial glia are an essential group of progenitor cells that are crucial for the proper development of the central nervous system. Through two separate projects, one studying the health of radial glia daughter cells following ablation and one looking at *glial fibrillary acidic protein* (*gfap*), the role of radial glia and their daughter populations in the developing spinal cord was explored.

To obtain further information regarding the effects of radial glia cell ablation on two daughter populations, the oligodendrocytes and secondary motor neurons, a local cell ablation technique was utilized (Curado, Stainier and Anderson, 2008). The aim of this technique was to obtain a mosaic pattern of *nsfb* gene incorporation into radial glia, which allows for the destruction of only certain cells that can then be characterized alongside healthy cells. To obtain this, an *nsfb* gene construct driving the production of the nitroreductase enzyme (NTR) was microinjected into the zebrafish embryo at the one cell stage. When NTR is exposed to a prodrug, metranitozol, it produces toxic metabolites which induce cell death. Following ablation, the oligodendrocytes and secondary motor neurons were assayed using two transgenic lines, *tg*(*olig2:gfp*) and *tg*(*gata2:gfp*) respectively, between 24-72hpf. After analysis, it did not appear as though the two cells types were negatively affected by the ablation, indicating that there may have been a recovery process and therefore this work was not published.

Gfap is an intermediate filament which provides vital mechanical support to radial glia. The removal of the entire glial protein, or the creation of an ineffective one in zebrafish, would allow a better understanding of its function and vitalness. This is accomplished using the CRISPR/CAS9 system which utilizes properties of the bacterial immune system in order to remove a certain part of the genome. Two sequences in the coding region for the *gfap* gene were chosen, in exon 5 and 6 of chromosome 3. The system works by inducing double stranded breaks in a targeted location of the DNA, which leads to a relatively ineffective repair process known as non homologous end joining. Due to the damage caused by the break in the DNA, mutations are produced which can then be characterized in vivo and used as research tools for future experiments. Due to difficulties with the purification of both the *gfap* guide RNA and the CAS9 protein, an established mutant was not able to created before the termination of the fellowship, although another lab member has now completed that work.

Although the results obtained did not allow for extensive knowledge of radial glia to be acquired, steps have been made that will permit future experiments and projects.

(Supported by the Schultz Foundation)

Advisor: Michael Barresi, Biological Sciences

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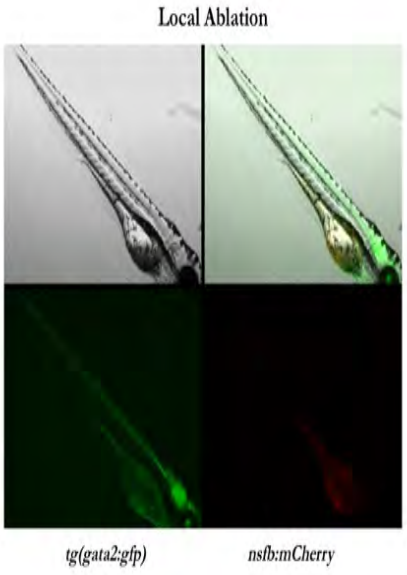

Characterizing Cell Types That Express PAX3.2

Margarita Arellano-Murgo/2016

My project goal is to characterize cell types that express Pax3.2. Pax is a gene and its importance lies on the fact that most pax genes are transcription factors, which transcribe DNA into RNA. Transcription is a process that occurs in all organisms and is essential to the development of the organism. When DNA is being replicated in an organism, transcription is part of the process that allows for the organism's growth. If transcription fails or an error occurs, the organism could be at risk of not developing properly. Within transcription there are transcription factors that aid and regulate the process. Essentially, transcription factors are an important subject of study, because without them transcription would not be able to occur and DNA replication would be interrupted as well. The pax genes have been found to be transcription factors. The Pax3.2 is specific pax gene, therefore is also likely to be a transcription factor. It can only be assumed that Pax3.2 is also a transcription factor, because really nothing is known about it. This summer was dedicated to studying Pax3.2, a gene which has no previous literature nor any known data. The main goal was to characterize the cell types in which Pax3.2 exists. This way this specific pax gene and its function can be fully described. The Barresi Lab, which is where I conducted my research, has retrieved the DNA construct from another lab and has created its own transgenic reporter line of Pax3.2. The transgenic reporter line should have enabled me to visualize the cells of interest. However, since this is a newer project the methods have not been figured out yet. So most of the time and research was put in finding a method that would give us reliable results. The future goal is to establish a protocol that will produce strong and reliable findings.

(Supported by the Howard Hughes Medical Institute)

Adviser: Michael Barresi, Biological Sciences

Investigating Marine Ciliate Tide Pool Communities

Mary Badger/2016

There is a high diversity and abundance of ciliate communities in our oceans, especially in coastal and near-shore areas.[1] These ciliates provide major links in the food chain serving as important links between micro ages in the ocean to large marine animals.[2] Marine ciliates can also play a large role in nutrient cycling and can negate the negative effects of harmful algal blooms.[3] Despite the important roles they play in their ecosystems, little is known about the phylogeny of marine ciliates and and even less is known about the spatial and temporal dispersion patterns of these important organisms in the natural world. One environment in particular that has been found to have a high diversity of Oligotricha Ciliates is the coastal tide pool environment.[4] The tide pool environment is a particularly advantageous one for some marine organisms it is an area of high primary productivity due to the high levels of sunlight and water movement that support alga growth.[5,6] However, the dynamic nature of the abiotic factors within this environment means that organisms must possess special adaptations that allow them to survive in tide pools. Tide pool ciliates in particular have been observed to have a life cycle that allows them to synchronize their periods of activity with the daily tidal cycle. This life cycle includes becoming active, feeding and reproducing during low tide when their pool is isolated from the open ocean, and becoming inactive and taking refuge in the sediment when their tide pool is connected to the rest of the ocean.[7] Understanding how ciliates are dispersed over this environment will provide greater insight in to how these organisms are influenced by, and interact with, species on other tropic levels within the rocky intertidal zone. This in turn will inform efforts that help to conserve and protect this unique and important ecosystem, which provides many benefits such as acting as a buffer between land development and the ocean, as well as being home to many important commercially important species such as muscles and algae.[8,9] During my month researching this summer, I collected samples from tide pools at two different locations: Portland, ME and Avery Point, CT (Figure 1). Where I sampled from a variety of tide pools over the time span that various tide pools became isolated from the open ocean. I have started to use molecular techniques such as PCR and DGGE, which will allow me to get a snap shot of the molecular diversity present in the different tide pools from which I took samples. In addition to getting greater insight to these organisms ecologically, my research will also help elucidate the genetic diversity patterns of marine microbes, which has been a topic of hot debate in recent years. It still remains unclear whether eukaryotic microbes, such as ciliates, are widely cosmopolitan and have high rates of gene flow as some studies suggest, or if in certain environments, such as tide pools, there is a level of endemism within this groups species. [10,4] As I am using molecular, culture independent methods, I hope my study will contribute to a greater understanding of this matter as I move forward with the samples I took this summer and continue on working on them this year.

(Supported by the National Science Foundation)

Advisor: Laura Katz, Biological Sciences

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Figure 1: Example of tide pools sampled from in Portland Maine:

The Role of Canonical Wnt Signaling in the Zebrafish Pharyngeal System Development and its Implications in Regards to Naphthalene-Induced Teratogenesis

Kathryn Berg/2016 and Gina Cho/2017

Considered the largest oil spill in U.S. history and greatly impacting a diversity of ecosystems, the Deepwater Horizon oil rig explosion released 200 million gallons of crude oil into the Gulf of Mexico from its occurrence on April 22nd 2010.[1] Crude oil components, specifically polycylic aromatic hydrocarbons (PAH's), are in products that increasingly contaminate the environment. By using zebrafish as a model organism in a controlled laboratory setting, our ongoing project has entailed studying the mechanisms via which PAH's induce teratogenic defects in vertebrate systems. In particular, we have focused on the loss of jaw cartilage and heart edema stemming from naphthalene-induced pharyngeal arch deformations.[2] As canonical Wnt signaling is known to regulate arch formation, we attempted to expand upon this research by performing in-situ hybridization of Frizzled proteins to understand how naphthalene affects Wnt.[3]

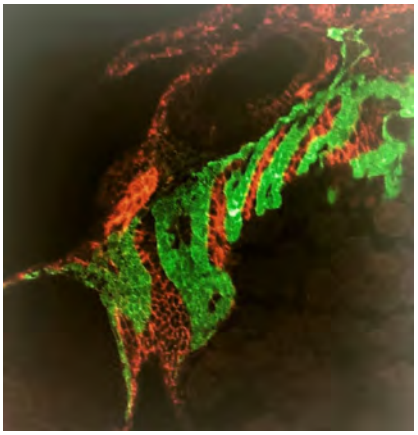
We first created and tested in-situ probes for Frizzled 7A, 7B, and 8A from DNA constructs sent by the Topczewski Lab. Each probe was confirmed on a gel to verify plasmid size and orientation. Cryostat slices were used to measure probe penetration. Additionally, trials with Alcama (Zn-8) antibody, a fluorescent marker of pharyngeal pouches, via immunohistochemistry were used. All experiments were performed on AB (WT, as a control), Sox10:eGFP, and Fli1A:eGFP lines. Embryos were treated with 200 uM naphthalene solution at 4, 10, and 20 hpf (DMSO-treated embryos were used as a control). Imaging was performed on LUMAR, Axio, dissection, and confocal microscopes.

Probe expression was found to become more prominent with age, peaking at about 24 hpf. The pouch/arch relationship was seen to be affected by naphthalene, with a stunted arch correlating to a wider, but also stunted pouch. The time of treatment (4, 10, or 20 hpf) and the age of the embryo did not seem to significantly impact this relationship, though less teratological effects were overall found in older embryos.

The in-situs showed that peak Frizzled protein expression is correlated to peak arch formation, confirming Frizzled proteins' role in overall development. Additionally, immunohistochemistry data showed that pouches were affected by naphthalene similarly to how arches were, albeit by taking up the space of missing arches following treatment. Naphthalene was thus implicated to affect cell differentiation (from pouch to arch mesoderm) and migration. In future trials (for Kathryn Berg's thesis and Gina Cho's special studies), we will aim for a better visualization of the mechanism behind Frizzled proteins' response to naphthalene via in-situs. We also plan to expand our research to other lines, such as AHR (-/-), for a better understanding of other signal pathways.

(Supported by the Schultz Foundation)

Advisor: Michael Barresi, Biological Sciences



Pouches (red) and arches (green) in control embryo.

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2, Chen, D. (2014). PAH-induced activation of aryl hydrocarbon receptor signaling and its effects on neural crest development in zebrafish. Smith College Archives.

3, Choe, Chong Pyo, Andres Collazo, Le A. Trinh, Luyuan Pan, Cecilia B. Moens, and J. Gage Crump. "Wnt-Dependent Epithelial Transitions Drive Pharyngeal Pouch Formation." Developmental Cell (2013). ScienceDirect. Elsevier. Web.

Testing a PCR-Based Diagnostic Test for Dengue Virus

Kate Brien/2015

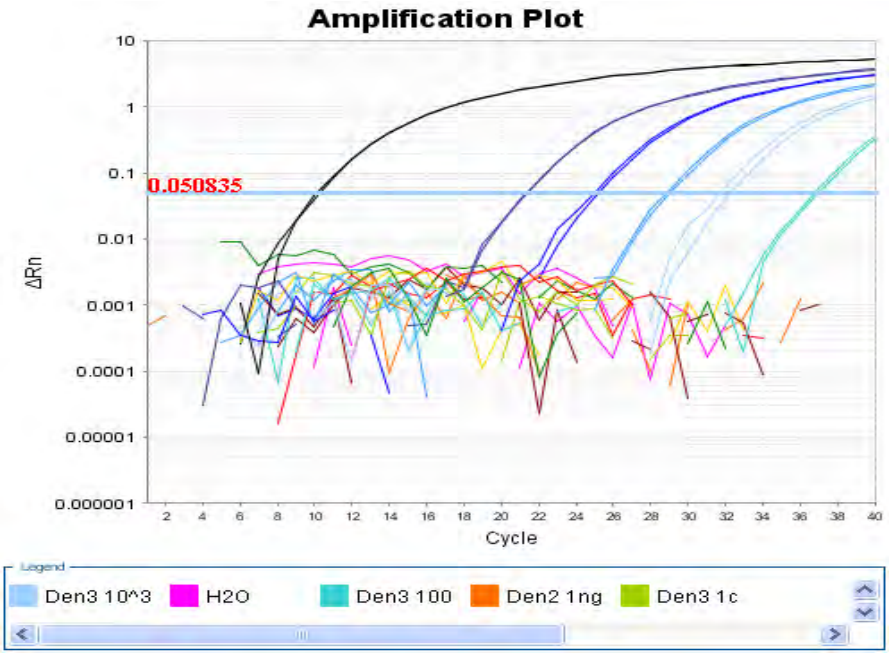
Over half of the world's population lives in areas at risk for Dengue Fever, a disease that has been rapidly increasing over the past twenty years. Without any specific vaccines or treatment, public health measures against dengue virus have focused on developing effective diagnostic tests. In the Williams lab this summer I have been working on using a PCR-based diagnostic test that our lab is developing to identify samples of heat-killed dengue viral RNA sent from the Centers of Disease Control and Prevention (CDC).

As part of this project, I used bioinformatics techniques for designing consensus sequences for each of the four serovars of dengue virus, and identified highly conserved, serovar-specific regions of the genome. I designed and assessed primers and probes to target amplification of those specific regions of the dengue genome. Using bioinformatics and qPCR, I demonstrated that our targeted regions represented distinct serovars and would deliver consistent identification without cross-amplification of the other serovars or of host human genetic material. I optimized the test for use on a synthetic DNA target, based on serovar-specific sequences of the Dengue genome, and used Taqman probes to increase the sensitivity of the test. The goal was to optimize the test for use with the RNA panel from the CDC by the end of the summer.

Unfortunately, the samples from the CDC diagnostic panel did not amplify using a series of real-time reverse transcription PCRs (qRT-PCR) with various volumes of template, three different master-mixes, or with one-step and two-step reverse transcription PCRs. When these changes did not yield results, I performed a phenol chloroform extraction and dialysis purification of the RNA samples. We were finally able to demonstrate that the samples themselves were degraded, and that acquiring fresh samples would likely solve the amplification problem. Further development of this PCR test will be required for it to be used around the world as an effective public health measure against dengue virus.

(Supported by the Schultz Foundation)

Advisor: Steven Williams, Biological Sciences



qPCR amplification plot of a 10-fold copy number dilution series of synthetic DNA template for dengue-3 serotype. Visible DNA concentrations ranged from 1ng to 100 copies/reaction

Assessing Seasonal Photosynthetic Function of Dominant Species Post-Clearcut

Kyle Boyd/2015

The Li-Cor 6400xt

New England forests have a long history of disturbance and recovery. Forests have been clearcut for farmland and then regrown following farm abandonment over the past centuries. Global shifts in land use has led to changes in the environment. The rise of atmospheric CO_2 has led to increased study on the effect of disturbances on the carbon cycle. The photosynthetic capacity of plants plays a vital, but often unstudied role in the carbon cycle of forest ecosystems. This study focused on the effect of environmental factors including water and nitrogen availability on the photosynthetic capacity of species after a large scale clear-cut disturbance. To test for the role of dominant species within a rebounding ecosystem I measured their photosynthetic capacity suing the Li-Cor 6400xt. Results showed that each species was limited by different environmental factors. Overall species appear to be improving their photosynthetic capacity from year to year after the clearcut. These results are import to better understand how forest ecosystems recover from large scale disturbances. This summer's research was an extension of an honors thesis conducted last year.

(Supported by the Nancy Kay Holmes Fund)

Advisor: Danielle Ignace, Biological Sciences

Khomik, M. W. (2014). On the causes of rising gross ecosystem productivity in a regenerating clearcut environment: leaf area vs. species composition. *Tree Physiology, 34*, 686-700.

Williams, C. A. (2014). Post-clearcut dynamics of carbon, water and energy exchanges in a midlatitude temperate, deciduous broadleaf forest environment. *Global Change Biology, 20*, 992-1007.

Intertidal Bully: Introduced *Littorina littorea* Interferes with Native *L. obtusata*

Noemi Collazo/2016, Alysha Putnam/G'2016

Direct and indirect interactions between grazers in temperate intertidal habitats are poorly understood. While the gastropod *Littorina obtusata* is usually found among fucoid algae (*Fucus vesiculosus* and *Ascophyllum nodosum*) in the upper intertidal region, *L. littorea* (an introduced species) shows widespread distribution on rocky substrata and algae throughout the intertidal zone. Because there are areas of species overlap, we hypothesized that competition for food or habitat may be occurring. Through a variety of laboratory and field experiments, we explored species interactions between these important grazers.

We conducted a 30-day laboratory growth experiment to investigate interspecific and intraspecific competition between these species under high and low food (*F. vesiculosus*) availability. Growth rates of *L. obtusata* were significantly lower in the presence of *L. littorea* under both high and low food availability, demonstrating interference competition (Fig. 1). Growth of *L. obtusata* was not reduced in high densities of its conspecific. In contrast, presence of *L. obtusata* did not depress growth rates of *L. littorea*; instead, intraspecific competition was revealed for the latter species. To address the mechanism of interference competition by *L. littorea* on *L. obtusata*, we investigated induction of chemical defense (phlorotannins) in *F. vesciulosus* and *A. nodosum*. After each snail species grazed (induced) algal fronds for one week, we conducted grazer preference experiments. *L. littorea* grazing rates were not affected by conspecific or congeneric induction, while *L. obtusata* demonstrated a significant preference for control *Fucus* and *Ascophyllum* over fronds previously grazed by *L. littorea*. We will determine phlorotannin levels of induced and control algal tissues to understand the role chemistry plays in interference competition.

Field manipulations were designed to assess the impact of *L. littorea* abundance on *L. obtusata* distribution. Our treatments included maintaining control, removal, and 2X higher densities of *L. littorea* through several tidal cycles. We found a significant increase in *L. obtusata* densities in areas of *L. littorea* removal, suggesting that the latter species regulates *L. obtusata* distribution in nature.

Taken together, our laboratory and field experiments revealed interference competition by introduced *L. littorea* on *L. obtusata*. Further, grazing preference experiments indicated that *L. obtusata* showed a significant preference for *Fucus vesiculosus* over other common intertidal algae, while *L. littorea* strongly preferred *Ulva lactuca* and *Chondrus crispus* over *F. vesiculosus*. Thus, these snail species may demonstrate resource partitioning of both food and habitat, allowing coexistence in nature.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences, Collazo; Margaret A. Walsh Grantham Fund, Putnam)

Advisor: Paulette Peckol, Biological Sciences

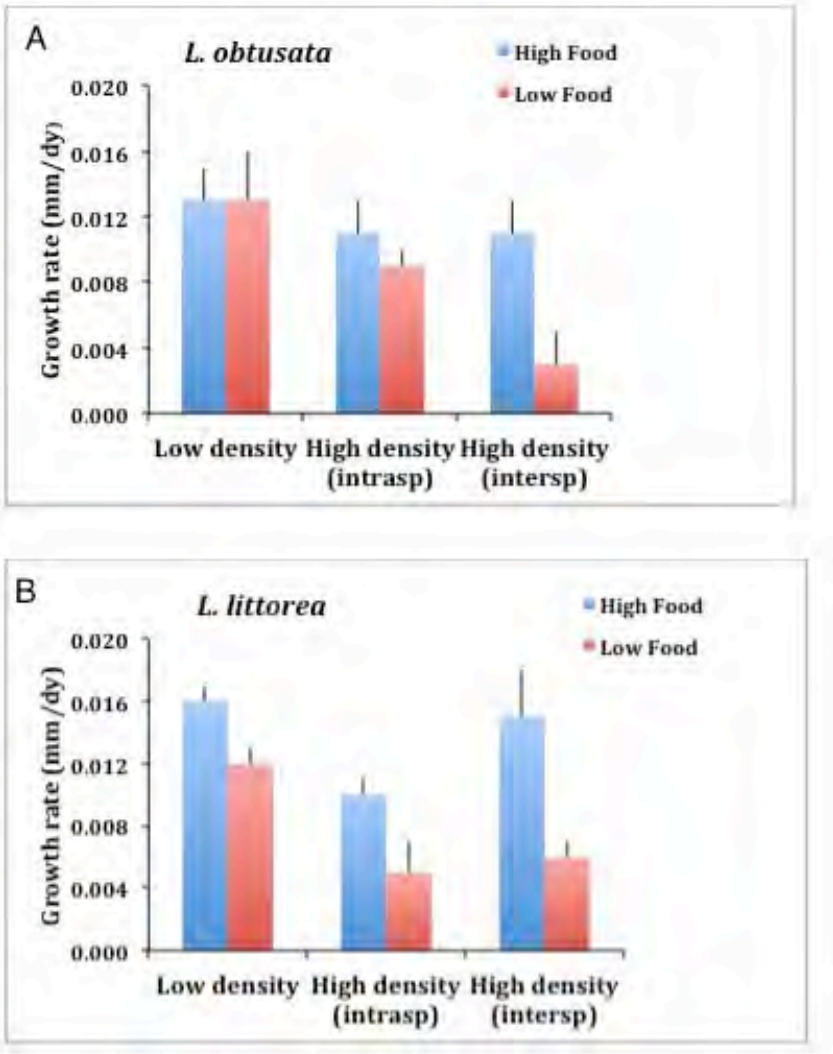


Fig. 1 Mean (+ SE) growth rate (mm/dy) of Littorina obtusata (A) and L. littorea B) under low (and high (intraspecific and interspecfic) snail densities and low and high food availability.

Biofilm Formation in Uropathogenic Escherichia coli at Various Temperatures

Daniela Deny/2018

Uropathogenic Escherichia coli (UPEC) receives a lot of attention because of the huge impact it has on many lives every year. It is the main culprit of community acquired UTIs, accounts for about half of nosocomial infections, and can be fatal if left untreated[1]. UPEC is able to persist by collaborating with other nearby UPEC in the form of a biofilm. Our laboratory has shown that temperature regulates many genes required for virulence and biofilm formation, but it is unknown what temperature thresholds program a pathogenesis gene expression profile. My project used quantitative reverse transcriptase polymerase chain reaction (QRT-PCR) to measure the mRNA levels of genes associated with biofilm formation at various temperatures.

Using RNA samples isolated from previous growth experiments done by the lab, six different temperatures (23˚C, 28˚C, 30˚C, 34˚C, 37˚C, and 40˚C), ranging from room temperature to fever temperature were tested. In previous experiments, results indicated that in UPEC, biofilm formation was increased at 37˚C in comparison to 23˚C. Taking this into account, I expected a gradual increase in the expression of these biofilm genes as the temperature increased. I also hypothesized that the expression of motility genes (e.g. fliC) would decrease as the temperature increased because of biofilm formation.

QRT-PCR was used to quantify focA, csgA, and fliC mRNA levels in our UPEC strain at the various temperatures. focA and csgA genes encode adhesins while fliC encodes the major subunit of the flagella. Recent literature suggests that motility is needed when the biofilm is initially being established. In that study, it was found that strains that had a mutation affecting the flagella had weaker biofilms[2].

In regards to fliC, the qRT-PCR results indicated that there is a slight increase of expression starting at 28˚C that decreases as it reaches 34˚C. In line with the hypothesis, the results showed a slight decrease in fliC expression at 37˚C and 40˚C. The focA and csgA results were significantly different from each other even though both of these genes contribute towards the formation of biofilms. The focA results indicated high fold changes, while the csgA fold change remained low throughout the temperature shifts. While these results are inconclusive, previous experiment have shown that temperature affects such genes at 23˚C and 37˚C. I will continue this research in the fall through Special Studies and investigate more genes involved in the formation of biofilms.

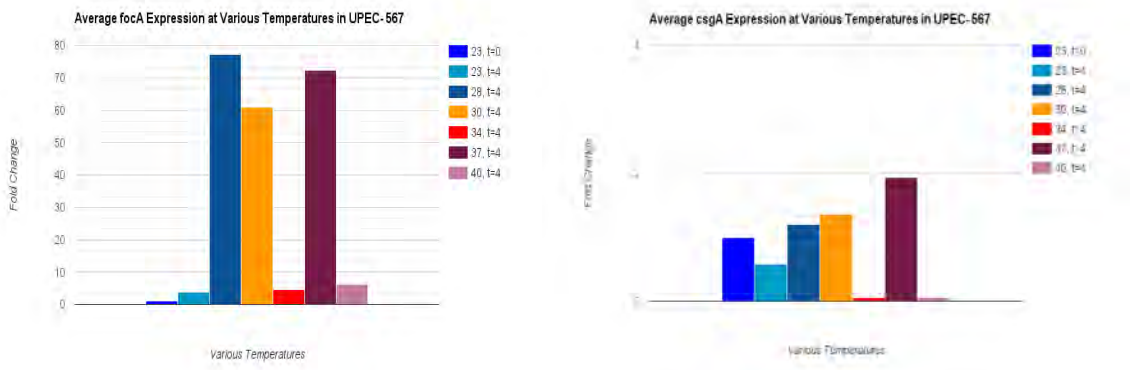


Figure 1: Average fold change from qRT-PCR data analysis of focA and csgA at 23˚C, 28˚C, 30˚C, 34˚C, 37˚C, and 40˚C

(Supported by Howard Hughes Medical Institute)

Advisor: Christine White-Ziegler, Biological Sciences

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Comparing the Yeast and Human Microtubule Binding Domains

Ria Deshpande/2016

Dynein is a minus-end directed microtubule associated molecular motor. In Eukaryotic organisms, dynein helps with the segregation of chromosomes, nuclear positioning, cell division and the transport of organelles with the cell or along the axon. Dynein is a large homodimer consisting of to identical heavy chains, a coiled stalk with a microtubule binding domain and a slender tail for dimerization. The process of walking for microtubules involves a dimer of two motor proteins. Dynein has the ability to step in increments of 8nm by alternating movement of its two motor domains and multiple dynein molecules may contribute to movement inside the cell.

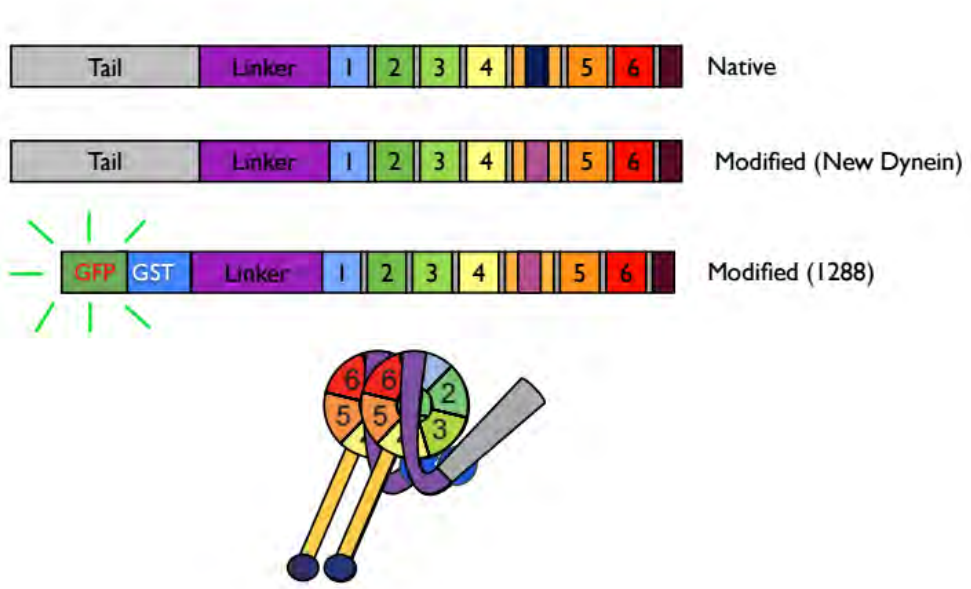
The main difference in function between yeast and human dynein is during cell division. During division, the yeast dynein is able to embed its tail into the cell membrane while the microtubule binding domain acts as a pulley to pull the microtubule towards itself and thus allow nuclear positioning. In mammalian or human dynein, position of the nucleus is not determined by this process. It has been observed that yeast and mammalian domains exhibit a high degree of sequence and structural conservation. A recent study hypothesized that a C terminal cap that exists in yeast dynein but not in mammalian dynein could be a possible explanation for the differences in processivity between the two dyneins. However, this has not been proved to be the only explanation.

My project works with the microtubule binding domain, and discusses the similarities and differences between the yeast and mammalian dynein. The in vitro part of this research involves replacing the yeast microtubule binding domain with the human microtubule binding domain. This will allow me to look at single molecules and study the processivity of the modified molecule with respect to the unmodified one. The in vivo part of my project involves figuring out if the human microtubule binding domain helps in nuclear segregation and works like the yeast microtubule binding domain. A nuclear segregation assay will be done to confirm the hypothesis that the microtubule binding domain is the part that differs and explains the structural and functional differences in the two different species of dynein. This summer I was able to work on creating the chimeric yeast and analyzing preliminary data on the TIRF Microscope. I was also able to learn other useful laboratory techniques which will help me conduct the rest of my research at Smith College over the year.

(Supported by the Blakeslee Fund in the Biological Sciences)

Advisor: Nathan Derr, Biological Sciences

Image 1: Diagram showing the experimental scheme of the project showing the native dynein (containing the yeast microtubule binding domain) , the modified dynein for in vivo (nuclear segregation assays) and the modified dynein for in vitro studies with the yeast microtubule binding domain replaced by the human microtubule binding domain.



The Biophysics of Motor Protein Ensemble Motility

Amalia Driller-Colangelo/2018

Dynein is a motor protein that organizes the interior space of cells by transporting and distributing various intracellular components. Termed "cargo transport" this process is achieved by groups, or "ensembles" of dyneins working together to move various cargos. While the implications for understanding disease at this level would be monumental, the actual biophysical mechanisms that move this cargo-transport process along are currently unknown.

Using TIRF microscopy and dynein motors purified from yeast, we determined the motile properties of individual and ensemble dynein. Until recently, studying ensembles with known numbers of motor proteins was challenging. Now, using a ground-breaking new technique based upon DNA origami, we were able to create ensembles of motors that allowed us to determine the motility of ensembles with defined numbers of motors.[1] In this work, we used DNA origami structures that can be tuned for varying levels of flexibility and can accommodate one to seven motors. Under tightly controlled laboratory conditions, we were able to observe the motile properties of dynein while carrying this flexible cargo structure. We observed that the ensembles moved faster as the number of motors increased.

Following early adjustments to fine-tune our experimental system, we observed results that advance our understanding of how cellular cargo transport is achieved. Previous work found that ensembles on a non-flexible rigid cargo slowed as the number of motors increased. Our discovery that the velocity of the flexible synthetic cargo structure increased as more motors were added suggests that ensemble velocity is dependent on cargo rigidity. We also noted differences in the motile properties of ensembles while carrying a less flexible cargo structure. When comparing the two different structures, one flexible and the other less so, we found the less flexible structure to move slower, which suggests our system will enable us to more closely examine the role of cargo rigidity in ensemble motility.

Future work will involve testing the experimental system to determine the mechanism by which cargo rigidity affects ensemble velocity. Those discoveries remain for a Special Studies project in the fall semester. This data will be submitted soon for publication.

(Supported by the Howard Hughes Medical Institute)

Advisor: Nathan Derr, Biological Sciences

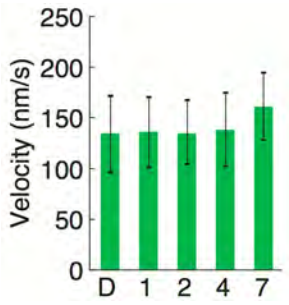


Figure 1: Quantification of average velocities of dynein ensembles. The 7D ensemble moved significantly faster than dynein alone or the 1D or 2D ensembles.

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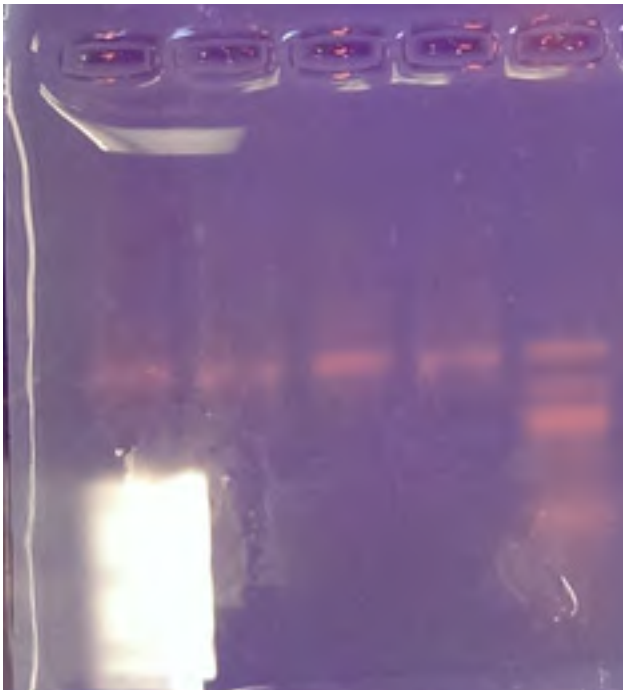
Natural Acquisition and Identification of Microbiota in Foals

Ashanta Ester/2015



Gel Photo of one of my PCRs

Mecomiun is a viscous caramelized feces composed of intestinal secretions, swallowed amniotic fluid and cellular debris usually evacuated within the first two hours of birth.[1] Meconium has been used to describe the composition of the human infant gut. Our Lab has decided to use meconium from foals in effort to categorize the bacterial composition of the equine gut. By understanding the gut bacterial composition from an early stage we will be able to determine the acquisition of bacteria by DNA extraction and amplification of the 16S ssu from these fecal samples by isolating DNA from fresh samples until the foal is a month old. By identifying the bacteria seeding the gut future work would allow us to correlate these findings to gut flora change induced by helminthes and the treatment with antihelmintic, which we study in our lab.

The project itself is more than a summers worth of work and my main focus is DNA isolation for the meconium as this is a challenge and Quality control of these DNA samples. My research consisted of finding and optimizing stool DNA extraction protocol that would be the standard for meconium. By the end of the summer I have mastered the Phenol-Chloroform extraction, Overnight dialysis of DNA from meconium and PCR. In addition to these techniques I learned to use a host of other molecular techniques. I am able to pass this work on to an undergrad to continue the work of answering our main question about acquisition of microbiota in foals.

The research experience this summer helped me gain more insight to the many approaches to answer bigger questions. The ability to get the answers that I was looking for by following my own path and new molecular techniques and analysis software, which will help me as I continue my education and research career making this experience very helpful.

(Supported by the Schultz Foundation)

Advisor: Steven Williams, Biological Sciences

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Macrofungi Richness and Forest Floor Characteristics in Hemlock vs. Black Birch Forest Plots

Aliza Boles Fassler/2017

In New England two exotic insect pests are threatening the Eastern Hemlock (Tsuga canadensis); the Hemlock Woolly Adelgid (Deluges tsugae, HWA) and the Elongate Hemlock Scale (Fiorinia externa, EHS). In southern New England, hemlock decline typically leads to its replacement by Black Birch (Betula lenta), a deciduous tree species with substantially different effects on forest ecosystems than hemlock.[1,2] The goals of this research were to look at how carbon cycling and fungal communities will change with the elimination of eastern hemlock. Hemlock plots have been shown to have a higher forest floor C:N compared to plots of other northern hardwood tree species and a greater organic layer depth then black birch plots.[3,2] Systems where fungi dominate the soil microbial community are characterized by high C:N.[4] Similar forest declines have decreased macrofungal diversity and abundance in other forest types, such as Jarrah forests affected by Phytophthora cinnamomi.[5]

This research was conducted Smith College's MacLeish Field Station in Whately, MA and a site in Chesterfield, MA. Organic layer samples were collected in 10x15m forest plots. Eight 0.25 x 0.25 subplots were randomly established in each plot, from which a sample of the soil organic layer was collected. This material was air-dried and then oven-dried to determine dry mass of the organic layer (OM). Four surveys of macrofungi fruiting bodies were conducted in the same plots at MacLeish and Chesterfield. All mature fruiting bodies within plots were collected.

As expected hemlock plots had the highest OM at both MacLeish and Chesterfield. The OM of mature hemlock plots was consistently, significantly higher then both young and mature birch plots (Figure 1.). Data on fungi morphospecies richness from spatially paired hemlock and birch plots was analyzed with paired T-tests for 3 of the survey dates. The survey at Chesterfield yielded significantly different numbers of morphospecies in mature hemlock vs. birch plots ($p= 0.0234$). The two MacLeish surveys showed no significant difference between plot types ($p= 0.774$ and $p= 1$). New plots established in mature birch stands had similar numbers of morphospecies as mature hemlock and young birch plots.

Given that hemlock plots regardless of stand age generally have a greater organic layer mass then birch, hemlock decline may have a significant effect on carbon storage in regional forest ecosystems. Despite the lack of a strong significant difference in macrofungi species richness between hemlock and birch plots, future work could continue to look at abundant fungi species in order to determine which species may be affected by the shift in dominant tree type.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences)

Advisor: Jesse Bellemare, Biological Sciences

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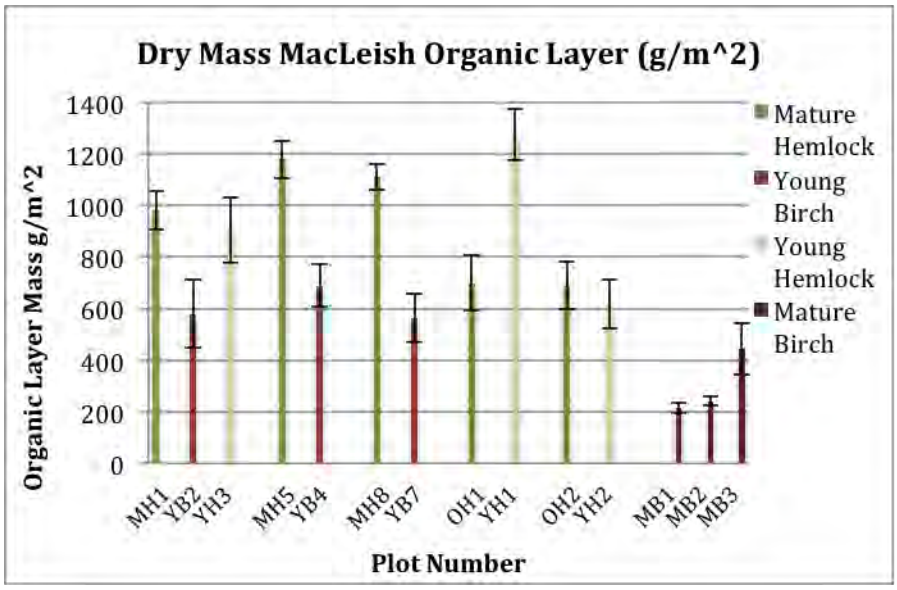


Figure 1. Organic layer dry mass of 14 forest plots at MacLeish. MacLeish plots included 4 different forest types of varying stand ages in order to rule out the effects of stand age on OM.

Using Horticultural Escape and Naturalization to Better Define Plant Species Fundamental Niches

Anna George/2017

At present, a significant area of study in conservation biology is how species distributions will change over the next decades in response to the effects of global climate change, including changes in temperature and weather patterns.[1] In order to predict this, we need to know several pieces of information about a species: the realized range, where the species currently lives, the fundamental range, where the species could or does have a self-sustaining naturalized population, and the tolerance range, where individuals can live, but there are no self-sustaining populations. By figuring out the extent and shape of these ranges for a species, we can better predict how changes in temperature and weather patterns will affect the species.[1] My project this summer was nested within this framework of trying to define species' fundamental and tolerance distributions. I did this by taking part in a larger project looking at plant naturalizations, which allow us to see if a plant can grow and establish a self-sustaining population at various locations outside of their realized distribution by looking at accidental introduction due to horticulture.

This summer, I worked on the initial data-gathering portion of this project. I learned ArcGIS programming and, in collaboration with others in the lab built a list of focal species that are adventive, or native to the US, but non-native in New England and New York, and used online herbarium queries gathered information about adventive populations of the focal species that were located in those states. In preparation for fieldwork, I mapped the population information on GIS maps. I then worked with others in the lab to track down the physical specimens, documenting places where the focal species have escaped in both Connecticut and Massacusetts. At each site, we determined whether the population was adventive, filled out a detailed questionnaire about the population, and took voucher specimens for both Brown University and Smith College.

This fieldwork will continue for the next eighteen months all over the continental United States until all of the populations have been visited. Then, using the data we gather, conclusions will be made about the realized, fundamental, and tolerance ranges for different types of plants and how these plants will react to climate change. My work with this project will continue through assisting in the lab during the year, and likely a senior thesis. (Supported by DoD/Brown~Bellemare, J. "Plants")

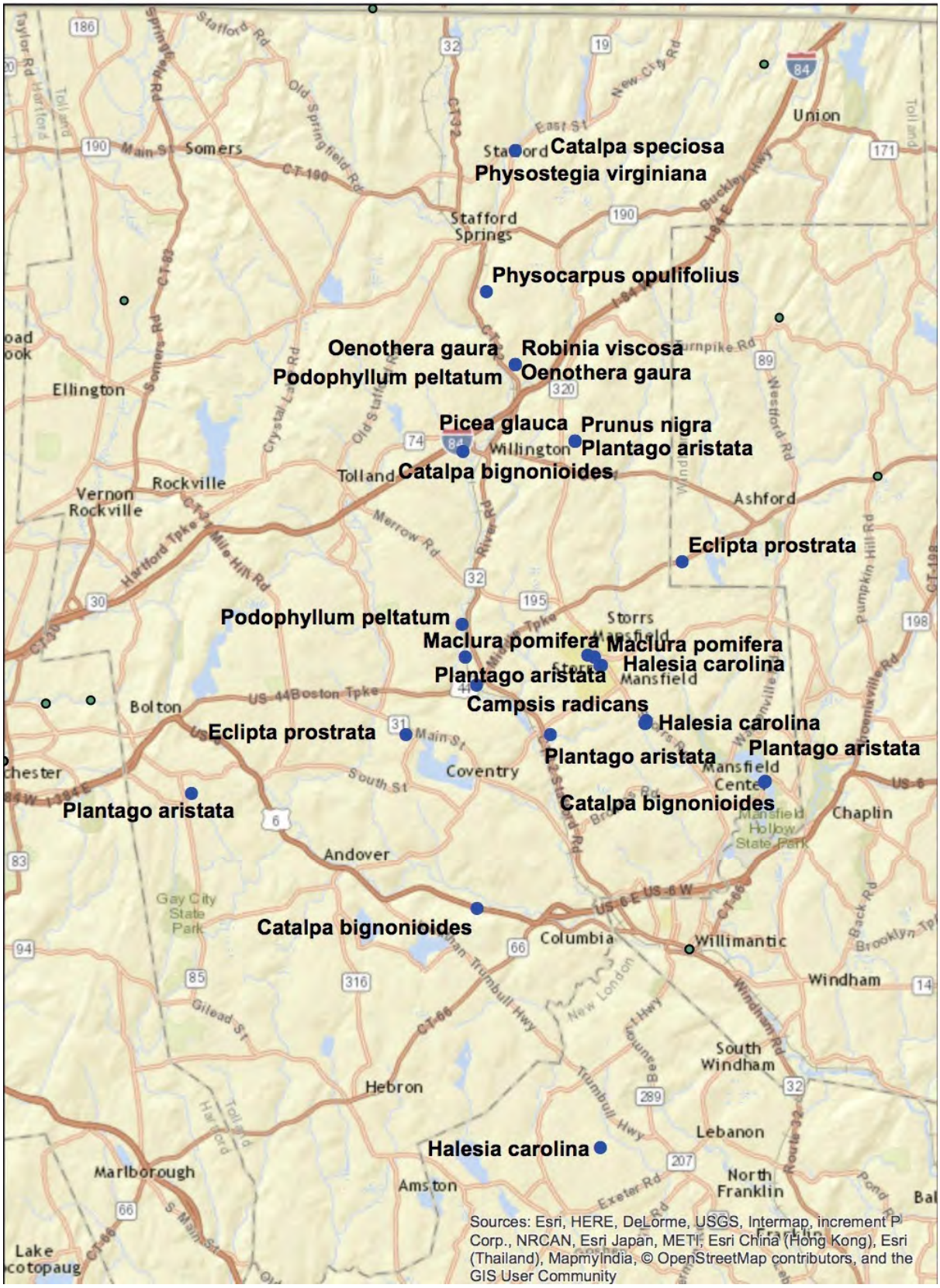
(Supported by

Advisor: Jesse Bellemare, Biology

References:

[1]Sax, D. F., R. Early, and J. Bellemare. "Niche Syndromes, Species Extinction Risks, and Management under Climate Change." Trends in Ecology & Evolution 28.9 (2013): 517-23.

Tolland County, Connecticut
Potential Adventive Populations



Investigation the Inversion Polymorphism on the X-Chromosome

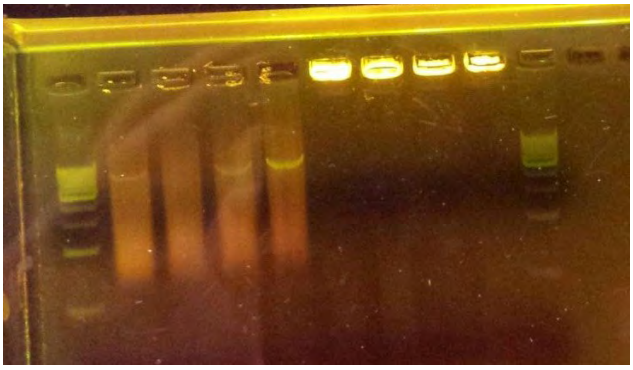
Jessica Haskins/UNH 2019

This summer I worked with a research team to gather data on an inversion polymorphism on the long arm of the X-chromosome in humans. The long arm has long inverted repeats (LIRs) that flank two genes.

The inversion is considered polymorphic in humans as there are two possible gene arrangements: the plus (which reads centromere, LIR, filamin gene, emerin gene, LIR, and telomere) and the minus (which reads centromere, LIR, emerin gene, filamin gene, LIR, and telomere). The lab's previous research suggests that the frequency of each orientation varies between populations. I helped to increase the sample size to strengthen the results. As this region is on the X-chromosome, females can be homozygous plus, homozygous minus, or heterozygous based on the X-chromosomes they get from their mother and father. Since males receive one X-chromosome, they are hemizygous plus or hemizygous minus.

I learned how to sample individuals by extracting my DNA and genotyping myself for the inversion using long PCR and iPCR. Long PCR is a presence absence assay, so we run a plus and minus reaction for each sample. The plus reaction only amplifies the DNA with the plus arrangement, and the minus reaction only amplifies the minus orientation. The DNA of heterozygous females is amplified in both the plus and minus reactions. Long PCR amplifies regions that are 12,000 to 13,000 base pairs in length, which makes them too similar in size to run the plus and minus reaction together. Inverse PCR (iPCR) confirmed the gene arrangement we found using long PCR. Although iPCR takes more time, it allows us to multiplex, or run the plus and minus reactions together. The DNA has to be digested, ligated, and then amplified using PCR. The primers are designed to point away from each other in the undigested/unligated genomic DNA, so that once the DNA is self-ligated, the primers amplify a region across the ligation site. The procedure is outlined in Kirby et al (in preparation).

I also helped with SNP PCR for male samples. Single nucleotide polymorphisms (SNPs) are variation at the base-level that are common enough to be detectable in the population. There are several on the long arm of the X-chromosome in humans. We used Sanger Sequencing to look for linkage disequilibrium for 18 of the SNPs on the long arm between the two LIRs. Linkage disequilibrium, or the non-random association between alleles, is the result of a lack of recombination. We only used male samples for sequencing because they are hemizygous. Jessica, need to say that the SNPs were in the region between the two LIRs. Do you have a gel photo to include with the abstract?



(Supported by the Smith College Committee on Faculty Compensation and Development (CFCD) and the Blakeslee Fund in the Biological Sciences)

Advisor: Robert Merritt, Biological Sciences

Potential Effects of Eastern Hemlock *(Tsuga canadensis)* Decline on the Hemlock-Associated Liverwort *Bazzania trilobata*

Michelle Jackson/2015

The decline of *Tsuga canadensis* connected to the invasive insects *Adelges tsugae* and *Fiorinia externa* has been shown to exhibit negative impacts on various communities of organisms. The forestry management technique of salvage logging is also contributing to abrupt changes within these tree canopies. Such intense light exposure and alterations in nutrient cycling could influence understory populations that rely on the cold, moist conditions created by *T. canadensis* trees. One potential example of a plant species affected by these sudden ecological changes is the bryophyte, *Bazzania trilobata*. *B. trilobata* is a leafy liverwort that is often observed in association with *T. canadensis* populations in the older growth forests of New England. To explore the possible effects on *B. trilobata* with the impending decline of *T. canadensis*, I conducted a two-year transplant experiment at Smith College's MacLeish Field Station. Samples of *B. trilobata* were moved from a source site near the field station and monitored with field surveys along transects for changes in stability and decline as influenced by abiotic and biotic factors including: soil moisture content, solar radiation, the total number of trees, and the number of *T. canadensis* trees at each transect point. Statistical analyses using individual and multivariate logistic regressions discerned the number of *T. canadensis* trees as the ultimate factor influencing the decline of *B. trilobata*. These findings suggest indirect negative effects associated with the decline of *T. canadensis* from *A. tsugae* and *F. externa*, as well as the first documented case of a plant species at risk from these effects.

Additional surveys will explore this complex niche of *B. trilobata* and possible impacts related to changes in the leaf-litter due to the succession of *Betula lenta* and other deciduous trees.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences)

Advisor: Jesse Bellemare, Biological Sciences

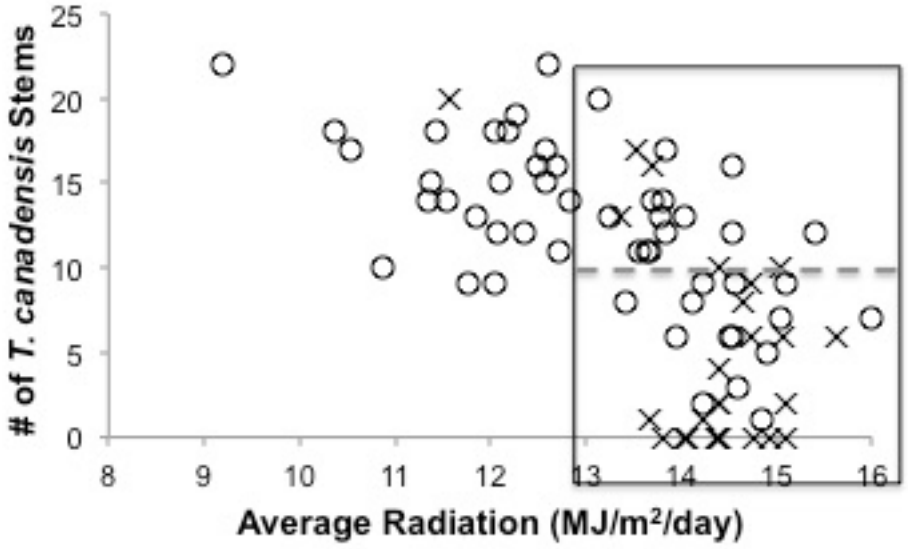


Fig. 1 The status of B. trilobata samples arrayed in an environmental space defined by average solar radiation and the numbers of T. canadensis trees at each transect point. Open circles (o) indicate stable samples and samples of B. trilobata in decline are designated by x's. Greatest sample decline was observed in areas with fewer T. canadensis trees (≤10) and high solar radiation (as outlined by subsample of specimens in the black square; n =56). As the number of T. canadensis trees increase, fewer samples decline which suggests a buffering effect in relation to a greater abundance of T. canadensis (>10 trees) at higher radiation levels (designated in the black square by the gray dashed line; samples below the line with ≤10 T. canadensis trees n = 37; samples above the line with >10 T. canadensis trees n = 19).

Phytoplankton Microcosm: an Oceanic Study on Algae Blooms and Ciliate Community Composition

Doris Juarez/2017

Text: In efforts to contribute to research pertaining to Microbes, we conducted an environmental study on the affects of algae blooms on ciliate communities. Due to the limited information that exists about how microbial communities function and their role in the overall food web, we are hopeful that this research project could contribute to those efforts. We questioned if difference in size of a microbe will influence community composition based on the basic principle that the bigger you are, the more you will eat. And if the starting community (non filtered) would be more diverse than other samples because the ciliates will not survive during these blooms.

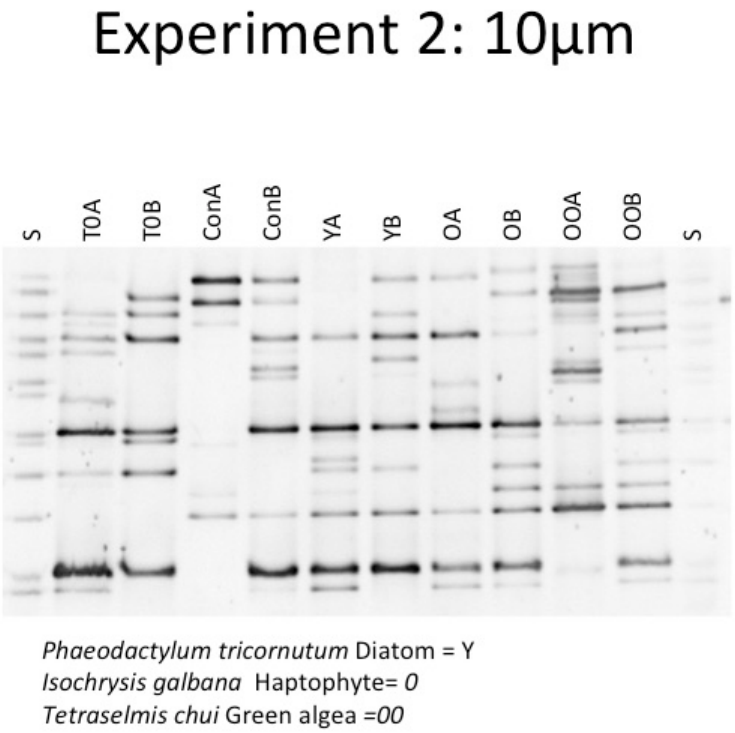
A microcosm allows researchers to simulate what would occur in the natural world under controlled conditions. To represent the blooms, there were four treatments: control, Phaeodactylum tricornutum, a diatom, Tetraselmis chuii, a green microalgae and Isochrysis galbana, a haptophyte. By using molecular techniques, DNA was extracted from the water samples. Using Ciliate specific primers, each sample was then used for PCR. After PCR, the product was used for DGGE (Denaturant Gradient Gel Electrophoresis). DGGE allows us to see a screen shot of what the ciliate community looked like based on composition and abundance (See Figure below).

Our findings suggest there is very little difference between filter sizes. We also see that there is one type of phytoplankton, T.chuii (green algae), which seems to have a more diverse community (00A and 00B). We also see that the starting community (T0) changes once it is placed into each treatment. Some haplotypes disappear, others dominate throughout, or new ones appear. This is only one third of the project; therefore we are hopeful that these results will be consistent in the two other experiments. DNA sequencing and Bioinformatics would be the next step in order to identify the taxa in these communities. These results are exciting because we are able to get a glimpse how algae blooms can affect key members of the oceanic food web.

Continuation of this work will be done during the 2015-2016 Academic school year as a McKinley Pre-Honors fellow.

(Supported by the National Science Foundation)

Advisor: Laura Katz, Biological Sciences



Effect of GPR30 Receptor Activation on Male Goldfish Mating Behavior

Jazmyne Keane/2016

Previous research has shown that estradiol positively effects social behavior of male goldfish on a rapid time scale.[1] The regulation of sexual behavior through steroids can occur from either genomic signaling with classical receptors or by non-genomic signaling pathways. Genomic signaling produces gradual physiological changes that involve gene expression; the changes can be measured on a scale of hours to days. Non-genomic signaling by hormones do not involve initial or direct influence on gene expression; the changes can occur on a scale of minutes. Estrogens, including 17b-estradiol, can act through non-genomic signaling to activate physiological changes at a more rapid rate than traditional genomic signaling.[2] GPR30 is a G protein-coupled receptor that facilitates non-genomic signaling.[2] The GPR30 receptor binds 17b-estradiol; this ligand additionally binds to other types of membrane estrogen receptors. G1, a selective agonist for GPR30, has been shown to increase sexually receptive behavior in female mice.[2] Mangiamele's lab researched if GPR30 activation via G1 would increase male goldfish social behavior.

For the experiment, we used EthoVision XT software to track social behavior of male goldfish assigned to different treatment groups over a course of two days. The experimental group of goldfish was injected with a vehicle solution on the first day and a G1 solution on the second day. The control group of goldfish was injected with only a vehicle on both days of the experiment. All goldfish on both days of the experiment had behavior tracked during a baseline period with no stimulus present followed by an experimental period with a female goldfish stimulus placed on a side tank next to the area the subject spent the least amount of time during the baseline. The amount of time the subject spent in the social zone adjacent to the female stimulus was recorded for both periods. A social proximity score was calculated for all animals for each day based on social zone time data.

For the second day of the experiment, goldfish that received G1 had a higher average social proximity scores compared to the control group goldfish that only received the vehicle treatment (Fig. 1). This suggests that GPR30 activation via G1 motivated the subject goldfish to socialize with other fish. Further research in the Mangiamele lab will investigate the molecular effects of G1 on the goldfish brain.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences)

Advisor: Lisa Mangiamele, Biological Sciences

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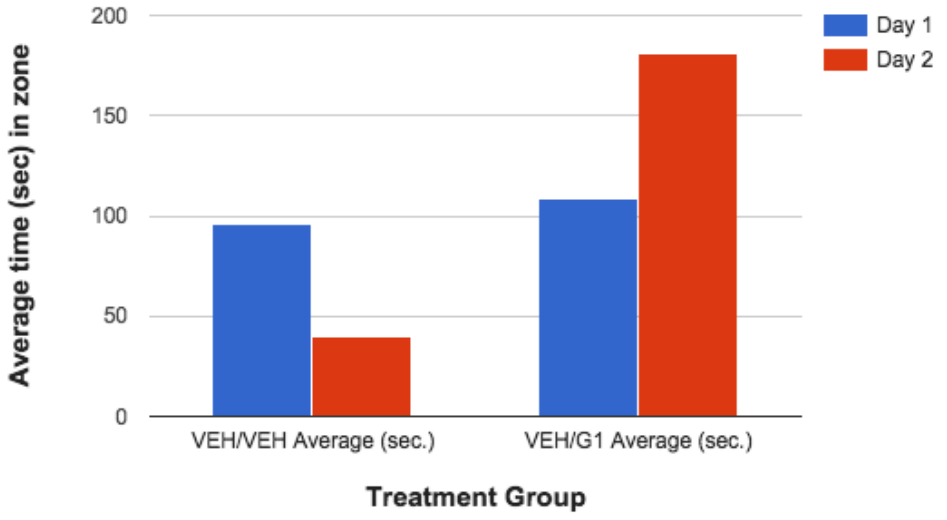

Figure 1. Average social zone proximity scores on day 1 and day 2 for the G1 treatment group and the control treatment group Neuroendocrinology 100:71-80.

Possible Host Switching in Seal Heartworm *(Acanthocheilonema spirocauda)*

Caroline Keroack/2016 and Kalani Williams/2018

Seal heartworm (*Acanthocheilonema spirocauda*) is a filarial parasite of many phocid seals, such as the charismatic harbor seal (*Phoca vitulina*). Seal heartworm has no singular definitive seal host species, and is distributed throughout the Northern hemisphere (Measures et al. 1997). Clinical manifestations of infection include anorexia, fatigue, dehydration, coughing/bronchiospasm and many other classical symptoms of filariasis (Daily, 2001). Complications include secondary bacterial infection, irreversible pathological changes, and possibly death. The parasite probably follows an indirect life cycle, requiring a vector for transmission. This vector is believed to be the seal louse (*Echinophthirius horridus*), an insect ectoparasite of pinnipeds. To date, seal heartworm is believed to be restricted to phocid hosts, and has only been observed in particular species (Leidenberger, 2007). Our preliminary molecular data suggests that seal heartworm infects gray seals (*Halichoerus grypus*) and the common harbor porpoise (*Phocoenca phocoena*), species that have never been reported to harbor the parasite (Leidenberger, 2007). Preliminary identification of A. spirocauda has relied on small, single bar-coding genes amplified by simple polymerase chain reactions (PCRs). The most widely used bar-coding genes, particularly in nematode species identification, are the nuclear *internal transcribed spacer 2* (ITS2) and the mitochondrial gene *cytochrome oxidase subunit 1* (COI) (Ferri, 2009; Derycke, 2010). In order to assign species with certainty, we need to expand the amount of genetic data analyzed; specifically sequencing and annotation of mitochondrial genomes will allow for absolute species elucidation. Work focused on isolating and amplifying full mitochondrial genomes for further analysis and diagnostic development. Thus far, we have amplified genomes from *Halocercus delphini*, *Otostrongylis circumlitis,* and most recently *Acanthocheilonema spirocauda* using long PCR. These mitochondrial genomes will enable the definitive identification of seal heartworm in both gray seals and harbor porpoises, as the gene order in the mitochondrial genome is species-specific (Moore, 1995). We plan to attempt to amplify the mitochondrial genomes of all parasites currently in our collection, then subject these genomes to next generation sequencing on the Illumina® platform. Full genomes will be used for comparative analysis and potential development of diagnostic tests to be used in the future on stranded and rescued animals.

(Supported by the Blakeslee Fund in the Biological Sciences)

Advisor: Steven Williams, Biological Sciences

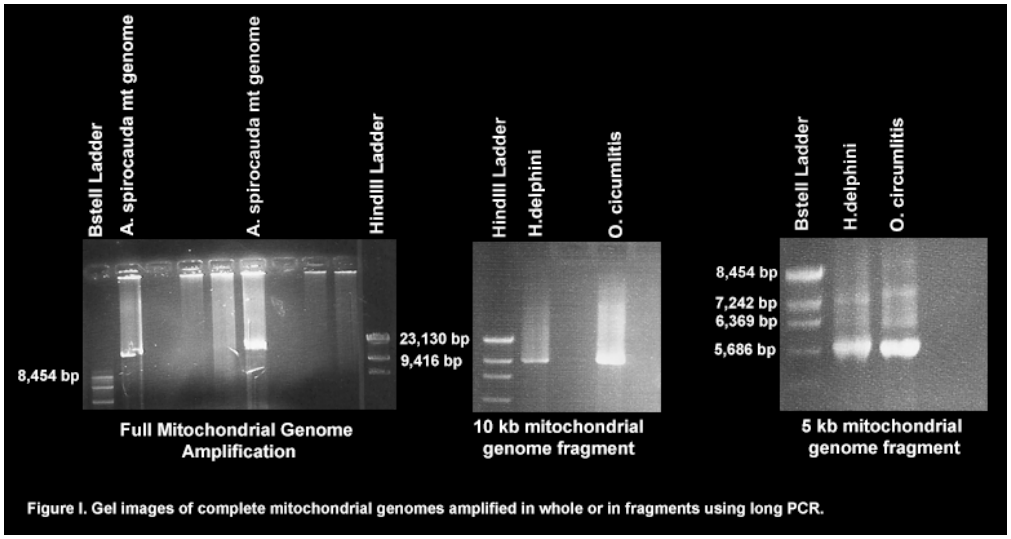

Figure I. Gel images of complete mitochondrial genomes amplified in whole or in fragments using long PCR.

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Applying Cre Recombinase Technology to Single-Cell Systems

Lydia-Rose Kesich/2016

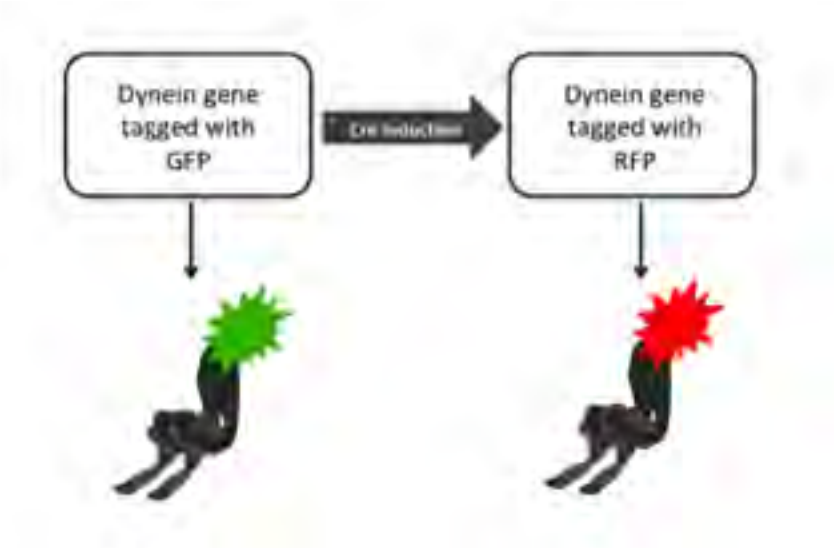

Figure 1. Experimental scheme, showing green florescent protein tagged dynein (left) being expressed before cre induction and red florescent protein tagged dynein (right) being expressed after.

The motor protein dynein performs the essential functions of moving cargo in and out of cells and helping cells divide.[1] Much of its behavior has been described, but an area of ongoing research is the localization of individual proteins throughout the course of their "lives"—do dynein motors localize to different regions after they are first assembled and before they are ultimately degraded?[2] To address this question, my group is building a tool that uses the Cre-lox recombinase system to generate a line of baker's yeast (Saccharomyces. cerevisiae) with dynein motors florescently tagged in a variety of colors.

Cre recombinase is an enzyme that originated in the PI bacteriophage[3]. It is capable of rearranging DNA in a site-specific manner via translocations, inversions, insertions, and deletions,[3] making it a highly useful enzyme for the creation of new reporter lines. We are working to generate a stable cre-expressing line and then modify it by inserting a cassette of two florescent proteins (FPs), along with a set of cre recognition sites, at the 3' end of the dynein gene. When cre is inactive, the translated dynein will be tagged with the first FP (left side of diagram). When cre is activated, dynein will be tagged with the second FP (right side of diagram). This will allow us to identify when a particular molecule of dynein was made.

We are currently working to confirm that we have successfully created a cre expressing yeast line. We are using several techniques, including Western blotting and DNA sequencing, to answer this question. Once it is confirmed that cre has been integrated we will proceed to fusing the florescent protein cassette with the dynein gene.

Our research is still in the early stages. Once we have successfully tested our new tool, we hope to apply it to proteins besides dynein. We believe that cre tools can be used to answer a variety of questions in cell biology, enable the study of protein lifetime, and potentially be adapted for cellular computing applications.

(Supported by the Howard Hughes Medical Institute)

Advisor: Nathan Derr, Biological Sciences

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Observation of Male Typical Sex Behaviors in Goldfish Influenced by Prostaglandin F2α

Seneca Lee/2016

Carassius auratus, also known as goldfish, have many seemingly in depth ways of communication when it comes to the reproductive cycle and social behaviors between male and females. In addition to visual and auditory stimulation, female goldfish release a mixture of pheromones believed to influence male social behavior. Pheromones are believed to quickly influence male typical social behavior (Sorenson, 1989) as rapidly as an hour or less. Male social behavior when exposed to prostaglandin F2α in solution and visual stimulation of a female goldfish was observed to determine how rapidly the pheromone affects the males.

Measurements of how long PGF2α took to effect a male goldfish social behavior was observed via a behavioral-time course. Male fish acclimated for five minutes, the PGF2α diluted solution was steadily pumped into the tank to simulate natural exposure, and the males social behavior and activity level was tracked after 10, 15, 30, 45, 1 hour post treatment. Using Nodlus Ethovision XT 11, behavior was measured by only tracking data when animal was three inches or less from female fish and tracking would last for five minutes at each time point.

A control of ethanol at the same dosage was used because ethanol does not have an effect on male fish (Sorenson, 1989) so this was used for comparison.

Results indicate that PGF2α does have a behavioral effect on the animal fairly rapidly, however, further research is planned to be conducted as there is not a significant difference between some time points. Figure 1displaying social behavior and Figure 2 displaying one measurement of activity shows an affect at 15 minutes and one hour.

To somewhat establish the time frame of the effects of PGF2α, this experiment required computer technique, animal care, and a variety or research methods. These in combination with more learning techniques hope to answer the question how does PGF2α influence male behavior specifically what signals are sent to the brain and how do these signals induce male typical sex behaviors? Individual animal brains were collected and are to be analyzed later this year.

(Supported by Committee on Faculty Compensation and Development (CFCD)

Advisor: Lisa Mangiamele, Biological Sciences

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A Study of the Xq28 Inversion Polymorphism in Eutherians

Jessica Magri/2017

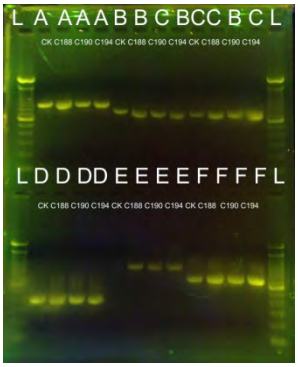

Figure 1: PCR products run on an agarose gel

On the long arm of the eutherian X chromosome, there exists a region where the orientation of the filamin (FLNA) and emerin (EMD) genes can be inverted due to recombination that occurs between inverted repeats (IRs) flanking the two genes[1]. Humans are polymorphic for this inversion and the two gene orientations are distinguished by single nucleotide polymorphisms (SNPs). When sets of SNPs exist consistently in the same region, they exhibit linkage disequilibrium, the non-random association of alleles at different loci. It was hypothesized that linkage disequilibrium exists between sets of SNPs that differentiate the plus (FLNA-EMD) haplotype from the minus (EMD-FLNA) haplotype.

To locate the SNPs, SNP PCR reactions amplified six segments (A-F) of the FLNA-EMD region of four female human individuals, and the PCR products were loaded onto a 2% agarose gel (Figure 1). Based on the expected size of the amplicons, the gel shows that the correct segments were amplified for all four individuals. After purification, the products were Sanger-sequenced and the resulting chromatograms were analyzed to determine the SNP locations (Figure 2).

My results suggest that the two different gene orientations exhibit distinct SNPs that differentiate one haplotype from the other. The homozygotes are identical at all but two SNP sites while the heterozygote is mostly distinct. However, the determination of SNPs was complicated by the presence of excess ddNTPs not eliminated during purification and the heterozygote chromatogram was unreliable because it only showed one base pair at each SNP site instead of two. More experimentation will need to be conducted before reaching a conclusion about the existence of linkage disequilibrium. In addition, I gained experience with genotyping eutherian individuals for the inversion polymorphism, and I also engaged in computer work that may aid in the genotyping of humans, dogs, cats, horses, and elephants.

This research experience was valuable to me because I was exposed to laboratory techniques that will be essential to my career goals. I hope to start research on a topic concerning human genetics this semester.

(Supported by the Blakeslee Fund in the Biological Sciences)

Advisors: Cait Kirby and Robert Merritt, Biological Sciences

[1]Caceres, M. 2007. A recurrent inversion on the eutherian X chromosome. Proc. Natl. Acad. Sci. U S A 104(47): 18571–18576.

ID #	Biological sex	Genotype	RXN A SNP 1	RXN A SNP 2	RXN A SNP 3	RXN A SNP 4	RXN B SNP 1	RXN B SNP 2	RXN C SNP 1	RXN C SNP 2	RXN D SNP 1	RXN D SNP 2	RXN E SNP 1	RXN F SNP 1
C182	Female	Plus homozygote	C	C	C	A	G	G	G	A	G	T	X	G
C188	Female	Heterozygote	G	C	G	C	G	T	C	G	A	C	T	C
C190	Female	Plus homozygote	C	G	G	A	C	G	G	A	G	T	C	C
C194	Female	Plus homozygote	C	G	G	A	C	G	G	A	G	T	C	C

Figure 2: SNPs found for each individual. The nucleotide bases are color-coded with X indicating the absence of a nucleotide in that particular position.

Tree of Life: Bioinformatics Pipeline

Jiaqi Mei/2016 and Zuliat Owoade/2016

The objective of our independent student research was the modification of a bioinformatic pipeline across the three domains of life. Since the hypotheses of Darwin, biologists have endeavored to create a comprehensive tree of life.[2] Yet, these evolving models of classification imply that phylogenetic taxonomy is in constant flux due to ongoing research in genomics. Therein, organisms are typically classified based on their morphological, structural, ecological, behavioral, metabolic, and genetic characteristics—all relative to the field of microbiology.[2] Yet, recent advances in molecular phylogeny have synthesized the creation of Bayesian models of phylogenetic "supertrees.."[2] One complication in these phylogenetic "trees," however, is the existence of lateral gene transfer (LGT). LGT refers to the nonvertical transmission of genetic material between species, and contrasts with the traditional view of vertical inheritance from parent to offspring.[2]

Our research project largely relies on bioinformatics-based methodologies and computational coding in investigating LGT events in genomes. For the purposes of our independent research, we relied primarily on Python and Seaview. In the initial run of the phylogenomic pipeline, there were 2972 genes trees, and these trees were and will continue to be refined as more criteria arises. Using Python, I (Zuliat Owoade) implemented some scripts that were used in filtering the data we had. Since one of the aim of this research was to have robust trees that includes as much taxa or at least include taxa we are interested in, I used the scripts to filter out trees that did not meet our criteria. In addition, most of the gene sequence we used in our analysis were not all whole genome, and hence I used Python scripts in analyzing how complete the genome in each gene tree were. I (Jiaqi Mei) began with analyzing the data within the phylogenetic gene trees produced by a phylogenomic pipeline that is available in the Katzlab.

Although, there are significant barrier in prokaryote to eukaryote LGT such as the presence of introns, lack of potential donors or interactions, or the viability of a transfer of genetic material.[1] Recent research studies, however, suggest traces of a feasible if complex relationship between LGT and eukaryotes.[3] Therefore, in the following academic semester, we plan to continuing our research as separate honors theses that employ the pipeline--examining the timing of the LGT or potential trends in fungal and SAR (Stramenophiles, Aveolates, Rhizaria) genomes. Yet, in order to trace and evaluate further consequences of LGT, continuation of streamlining the bioinformatics pipeline is crucial.

(Supported by the National Science Foundation, Mei; the Schultz Foundation, Owoade)

Advisor: Laura Katz, Biological Sciences

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Understanding Total Internal Reflection Fluorescence and Constructing a TIRF Microscope

Cadence Miskimin/2017

Research in microbiology, while increasingly relevant to our understanding of both the natural world and the human body, is limited by the technology available to scientists to visualize the objects and organisms they are studying. New technologies are now available with the capability to study single molecules in real time, and this is a crucial advantage to researchers. Total Internal Reflection Fluorescence, or TIRF, is one such innovation. For my research I investigated the technology behind TIRF microscopy and began constructing a low-cost TIRF model for use in teaching labs at Smith.

Our model system uses optical components purchased from Thor Labs, fixed on an optical "breadboard." It uses two low power diode lasers (405 nm and 532 nm), as well as a 100X/1.45 Nikon objective lens, a CCD camera and related optical and mounting components. Laser light passes through the objective to achieve TIR as it hits the interface between the coverslip and the water suspending the specimen. In order to be totally internally reflected, the laser light must hit these two media, first the higher index glass (~1.52) and then the lower index water (~1.34), at an incident angle larger than or equal to a specific critical angle according to Snell's law. When the critical angle is reached, the light will be confined to the higher index coverslip, and will be totally internally reflected at the interface between the two materials. An evanescent field occurs at this interface, which is less than 100 nanometers thick and causes only the fluorophores within the field to fluoresce. This allows us to view only the specimens in this small area immediately beyond the coverslip.

TIRF microscopes therefore have very high resolution at the single molecule scale, without needing to fix the sample as is the case with electron microscopy. Being able to view proteins moving in real time is beneficial for many different kinds of microbiology research, but the availability of lower cost and therefore more accessible options is still critically low. My research this summer sought to address this problem, and construct a functioning TIRF microscope for $15,000, less than 5% of the cost of most commercially available models. Together with my advisors, we hope that this low cost microscope design will help to increase understanding and use of this valuable technology.

(Supported by Committee on Faculty Compensation and Development (CFCD))

Advisors: Nathan Derr, Biological Sciences; William Williams, Physics

Reck-Peterson, S. L., Derr, N. D., and Stuurman, N. 2010. "Imaging Single Molecules Using Total Internal Reflection Fluorescence Microscopy (TIRFM)." Cold Spring Harbor Protocols, no. 3 (2010): pdb.top73. doi:10.1101/pdb.top73.

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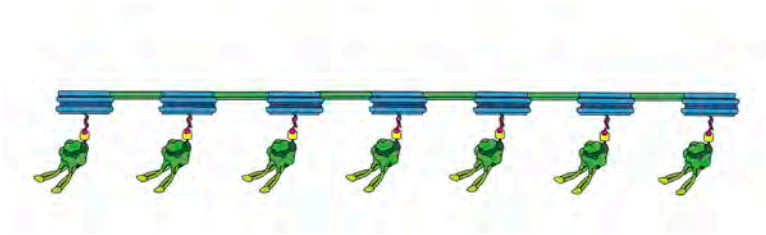
Rigid or Not So Rigid: The Effect of Two Different Molecular Frames on the Processivity of Motor Proteins

Jessica Morgan/2017



Segmented chassis with 7 dynein motor proteins attached.

Dynein motor proteins, utilized for intracellular transport in vivo, can be studied in vitro using synthetic cargos made from three-dimensional DNA origami, which control the number of motors under study at one time.

Previous results from Derr et al., showed a decrease in the velocity of dynein ensembles utilizing a rigid cargo.[1] It was hypothesized that this decrease in velocity was due to negative interference resulting from asynchronous stepping of motors and the communication between motors that promotes different microtubule-bound configurations.[2] For this reason, a "segmented" chassis was designed by members of the Derr Lab to eliminate the proposed negative interference. With this synthetic cargo, each motor would bind to its own segment and would not be able to relay forces to other motors through the cargo structure.

With the segmented chassis the velocity of a chassis with 7 dynein experienced an increase in velocity as the number of motors attached on the ensemble increased. Dynein anchored to the segmented chassis were expected to maintain a constant velocity. We are investigating the hypothesis about the effects of the motors' saltatory motion and how the individual motion of motors affects the ensemble motility.Saltatory motion is defined as rapid, discontinuous motion with rapid changes in velocity[4]. It is thought that each motor may occasionally pause. This will not impact the velocity of the entire ensemble. The segmented chassis prevents the coupling of motors and therefore the communication of pauses is not transmitted to each motor. To investigate the proposed saltatory motion, an ATP analog (AMP-PNP) was introduced, which would bind to an ATP binding domain on dynein and cause the motor to remain bound to the microtubule. Through this method we could exaggerate the saltatory motion experienced by individual motors on the chassis. Velocities and runlengths were determined on the single-molecule level using total internal reflection fluorescence (TIRF) microscopy. The mystery behind the increased velocities shall be answered in the fall semester as I continue this research as a Special Studies project, which will later be presented at Collaborations.

(Supported by the Blakeslee Fund in the Biological Sciences)

Advisor: Nathan Derr, Biological Sciences

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Slit-Roundabout Signaling in Commissure Formation during Zebrafish Forebrain Development

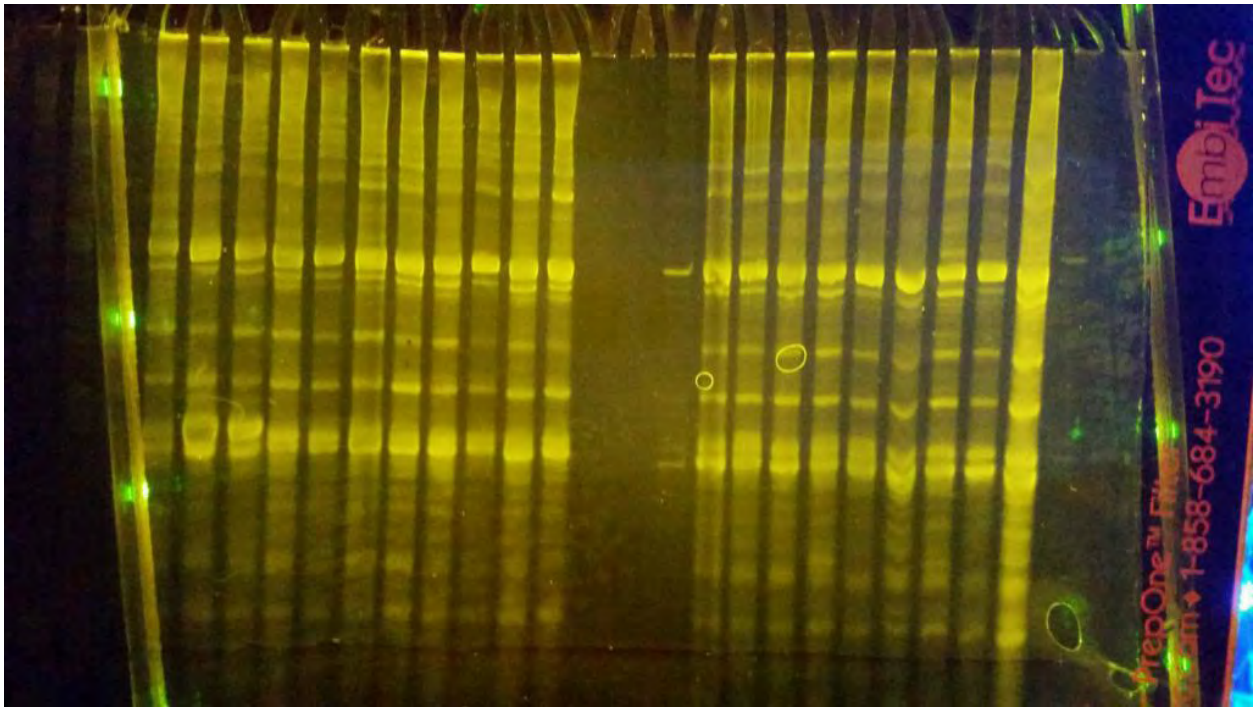
Vivian Morris/2018

Connections need to be made between the left and right hemispheres of the brain so that necessary communication can occur. To allow for this communication to occur neurons form commissures, tight bundles of axons that cross the midline of the brain over a substrate of astroglia cells. Slits are extracellular signaling molecules that work with Roundabout receptors at the midline to help guide axons, part of neurons that extend to make connections with other neurons. Previous research conducted suggests that a role for Slit1a is to promote axon growth. However, Slit2 and Slit3 repel axons and prevent them from growing in different directions.

In order to further understand how Slits function in regards to commissure formation, we wanted to create a genetic knockdown of the Slits starting with Slit1a to observe what happens when this protein is missing in comparison to when it is present. To do this we used CRISPR technology. CRISPR, Clustered Regularly Interspersed Palandromic Repeats, are places in the genome of bacteria that hold small parts of phage DNA that allow the cell to recognize and degrade that phage if it enters the bacteria. This function can be applied to other organisms such as zebrafish as a genome editing tool. We designed a CRISPR sequence that would target Slit1a in order to knock it down in our mutants. After injecting sgRNA and Cas9, an endonuclease that induces double stranded breaks after binding to target DNA, into embryos at the 1-cell stage, we had to confirm mutants. After selecting representative samples of injected embryos, we found mutants with small deletions suggesting a potential knockdown of the Slit1a gene. These mutants will then be used to further understand Slit1a's function in the formation of commissures in the forebrain of zebrafish.

(Supported by the National Science Foundation)

Advisor: Michael Barresi, Biological Sciences



Native Species Restoration Plantings Along the Smith College Waterfront

Abby Onos/2017

Native plants are vital to the health of their ecosystems where they help maintain biodiversity and habitat. However, many native populations have been disturbed due to the presence of invasive species which have known detrimental ecological effects. The waterfront owned by Smith College along Paradise Pond and the Mill River is inhabited by many invasive species. Beginning in 2010, an ongoing initiative to map and remove invasives has been underway in the effort to meet regulatory compliance as part of the agreement surrounding the construction of the synthetic turf field. This year, in the interest of moving away from regulatory compliance and towards waterfront stewardship, a contract with the New England Wildflower Society (NEWFS) provided the opportunity to create restoration plots in which native species were planted.

Research plots were selected based on habitat type and potential for planting sites. Habitats represented include: understory, meadow, wetland edge, and river shore. Each plot was measured, marked with PVC pipes, flagged, and mapped using GPS. The plots were then inventoried for invasive species. If found, they were recorded and removed by hand. Seven total plots were created. Plant preferences to habitat, soil moisture, and sunlight were considered when determining where to plant. With help from a crew of other Botanic Garden interns, approximately 600 plugs were planted with 12 herbaceous species represented.

The main purpose of this project was to establish a baseline protocol for restoration plots and collect spatial information in the hopes of future study, all while installing known populations of native plants. Throughout this I gained skills that helped me set up a protocol for field research and implement it. As part of the Management and Restoration Plan created by NEWFS, the plots will be revisited next year to record survivorship and vigor along with presence and percent cover of invasives. In the coming years, a continuation of data collection will allow us to determine which species have the greatest potential for permanent establishment and vigor. A focus on restoration and invasive removal could potentially lead to a healthier and more biologically diverse waterfront in the future.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences)

Advisors: Michael Marcotrigiano and Gaby Immerman, Biological Sciences

Fig. 1 Map showing locations of restoration plots. Fig. 2 Table describing preferences for habitat, light, and moisture for each native species (courtesy of Amanda Weise, NEWFS).

Fig. 2

Species Name	Habitat Preference	Light Preference (Full sun, part sun, partial shade, shade)	Moisture Preference (Dry, average, moist, wet)
Aralia racemosa ssp. racemosa	understory, wetland edge	Full sun to partial shade	Not too dry, not too wet
Asclepias syriaca	field, meadow	Full sun	Dry to average
Eupatorium perfoliatum	river shore, wetland edge	Full sun to partial shade	Moist to wet
Eutrochium (Eupatorium) maculatum	river shore, wetland edge	Full sun to partial shade	Moist to wet
Geranium maculatum	understory	Full sun to partial shade	Not too dry, not too wet
Iris versicolor	wetland edge	Full sun to partial shade	Moist to wet
Solidago odora	field, meadow	Full sun	Dry to average
Symphyotrichum (Aster) novae-angliae	field, meadow	Full sun to partial shade	Dry to average
Verbena hastata	wetland edge, river shore	Full sun to partial shade	Moist to wet
Agrostis perennans	understory, river shore	Full sun to partial shade	Dry to moist
Panicum virgatum	field, meadow, river shore, wet edge	Full sun to partial shade	Dry to average
Schizachyrium scoparium var. scoparium	field, meadow	Full sun to partial shade	Dry to moist, not wet

Biodiversity and RNA Editing in Testate Amoeba

Natalie Phillips/2016

We live in a very diverse microbial world where we strive to understand their purpose and interactions on Earth. Testate amoebae, single-celled protists found in soils, bogs and fens, are among the various microbes studied to better understand various things such as climate and pH, since they are bioindicators. My research this summer focused on observing the amount of biodiversity in Hawley Bog, a fen in Massachusetts, and Mclean Bog, a bog in New York,. I also focused on looking for evidence of RNA editing in the genetic makeup of different amoebae.

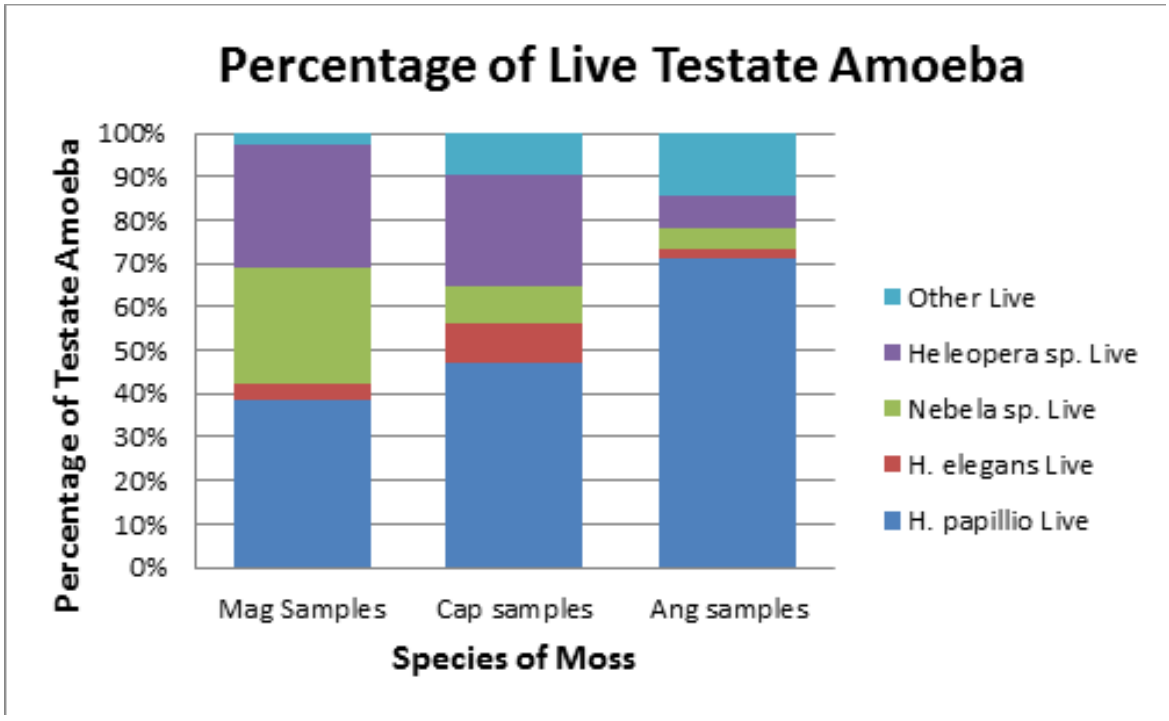
In order to assess the biodiversity of testate amoebae, I sampled at Hawley Bog and made nine observation plates and was given 60 samples from Mclean Bog. Based on the morphology of the testate amoeba, I observed the number of different species and genera in a 20 minute period per sample using light microscopy. I then picked amoebae of different species and genera using a mouth pipette and used PCR, WGA (whole genome amplification), and sequencing techniques to analyze their genetic data. To start looking for evidence of RNA editing, I used a RNA to cDNA kit to extract the RNA and convert it to cDNA. PCR, gel isolation, miniprep and sequencing techniques were also used to have the cleanest possible product to analyze the sequences.

Observing the Hawley Bog samples, I found two species and two genera, Nebela species, Heleopera species, Hyalosphenia papilio and Hyalosphenia elegans. The most abundant were the H. papilio where they dominated majority of the samples. From the Mclean Bog samples, there were three different species of moss that the testate amoeba came from and H. papilio also dominated all three species. However, Nebela sp. and Heleopera sp. were seen in higher abundances in two species of the moss. In the upcoming academic year, I plan to continue assessing the biodiversity by working on analyzing their genetic data and making phylogenetic gene trees for my honors thesis.

Using my RNA to cDNA kit, I was able to successfully receive cDNA and amplify it using Actin and rSSU (ribosomal small subunit) primers. I intend to test the products from this kit using mitochondrial sequences such as Cox1 primers amongst others to then further analyze the sequences for my honors thesis.

(Supported by the Howard Hughes Medical Institute)

Advisor: Laura Katz, Biological Sciences



Graph of Mclean Bog morphology data

The Effects of Diet and Development on Basal Metabolic Rate in Canidae and Leporidae

Katherine Pielmeier/2015

Basal metabolic rate (BMR) is the minimum rate of oxygen consumption in resting mammals within thermal neutral conditions.[1] Body mass is widely considered the primary determinant of BMR; when body mass increases, BMR increases.[2] However, other factors, such as food habits (carnivorous vs. herbivorous) can influence BMR.[3, 4] Because higher metabolic rates result in faster protein turnover, carnivores have higher basal metabolic rates than their herbivorous counterparts.[5] I compared the basal metabolic rates of Canidae, carnivores, and Leporidae, herbivores, to determine if food habits impact BMR.

Most studies on BMR include several mammalian taxa and therefore encompass a wide range of body masses. Thus, I sought to examine the relationship between body mass and BMR on a smaller scale. Canidae and Leporidae are the ideal carnivores and herbivores, respectively, for this study because they overlap with respect to body mass, thus allowing me to control for allometric effects on BMR and focus on how food habit affects BMR. I compiled body mass and BMR data for canids and leporids weighing 1–5 kg from the literature. Data were log transformed for normality and a general linear regression was conducted with log body mass as the covariate.

Surprisingly, leporids have higher basal metabolic rates than their canid counterparts. The literature overwhelmingly states that because herbivorous mammals consume high-fiber, and therefore less digestible, diets, herbivorous mammals have lower basal metabolic rates.[6] Furthermore, plants and grasses are not as efficiently digested as meat; theory predicts herbivorous diets cannot sustain high metabolic rates.[6] Another unexpected result was the negative correlation between body mass and BMR; according to the literature, BMR and body mass are positively correlated across all mammalian taxa. However, my results are statistically significant (general linear regression: log transformed: R^2 43.78% and $p = 0.017$).

The observed negative correlation may be due to the small scope of this research; the BMR literature includes a wider range of taxa and body masses than my research does. Thus, while the overall correlation between BMR and body mass in mammals is positive, some taxa may exhibit negative correlations on a smaller scale. Furthermore, development patterns (altricial vs. precocial) may have a greater influence in determining metabolism for some taxa; leporids are predominately precocial whereas canids are altricial. Thus, development can play a significant role in determining metabolism whereas food habits may not. Finally, food habits may not determine BMR as originally expected.

(Supported by the B. Elizabeth Horner Fund in the Biological Sciences)

Advisor: Virginia Hayssen, Biological Sciences

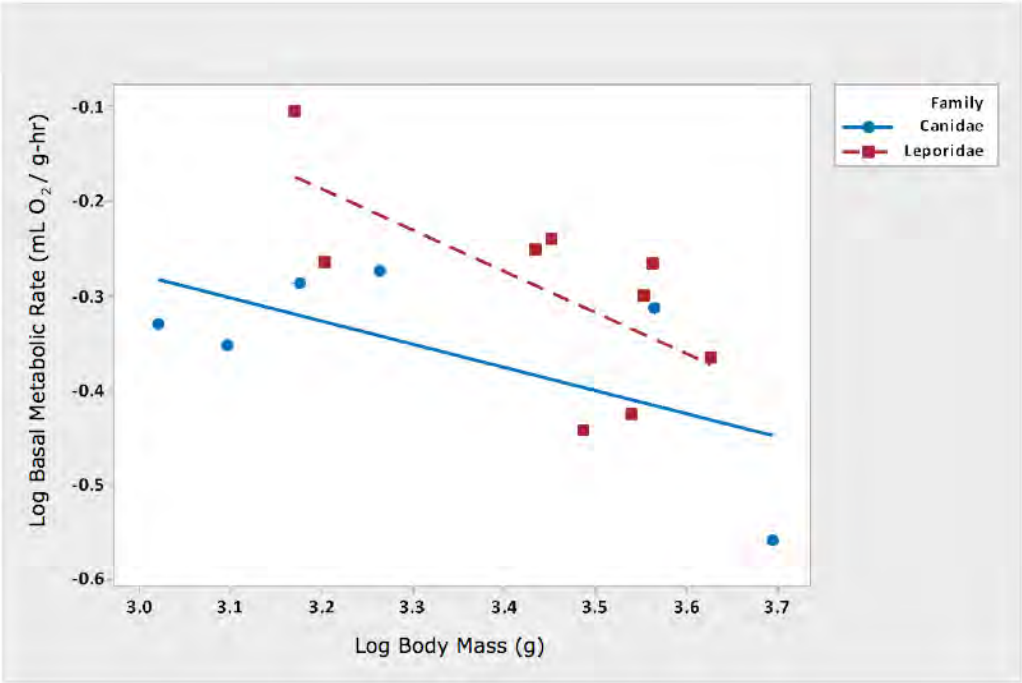


Figure 1: The correlation between basal metabolic rate and body mass in Canidae and Leporidae weighing 1–5 kg. Leporids (herbivores) have higher metabolic rates than canids (carnivores). Both leporids and canids exhibit a negative correlation between BMR and body mass although the trend across all mammalian taxa is positive.

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Protein Evolution in Ciliates

Olivia Pilling/2017 and Anna Rogers/2017

Ciliates are unicellular protists that are defined by cilia in at least one phase of their life cycle and by dimorphic nuclei (i.e. a somatic macronucleus and germline micronucleus). Our work with ciliates this summer sought to understand if/how genome structure affects patterns of DNA sequence evolution. Specifically, we study protein evolution in members of the class Heterotrichea, focusing on divergent paralogs (i.e. genes that differ in function due to an ancient duplication event). Heterotrichea have a unique method of nuclear division. They are designated postciliodesmatophora, indicating their microtubules for nuclear division are outside of the nucleus.[1]

Using PCR and cloning techniques we analyze sequences for genes of three species (*Blepharisma americanum, Spirostomum ambiguum* and *Stentor coeruleus*) that we are interested in. We chose to look at typically conserved eukaryotic proteins (elongation factor 1α, histone H3 and H4, and cytoskeletal proteins Actin, α-tubulin and β-tubulin).[2] We then analyze the data using MegAlign and HyPhy to determine how divergent the sequences are from one another. Preliminary data reveal *Spirostomum ambiguum* has at least two paralogs of the Actin gene (Figure 1). The highlighted region shows one amino acid substitution, Asparagine (N) to Serine (S), and three silent mutations at the third codon position, which does not affect the amino acid. This means there has been an ancient gene duplication and has some restraint to conserve the amino acids.

This study is important because ciliate genome structure and protein evolution can be a model for genome evolution across the tree of life. Further research may involve studying Karyorelictea, the even less studied and mainly uncultivable sister clade to Heterotrichea.

(Supported by the Howard Hughes Medical Institute)

Advisor: Laura Katz, Biological Sciences

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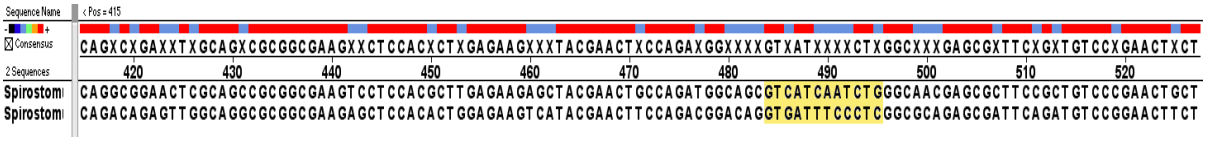
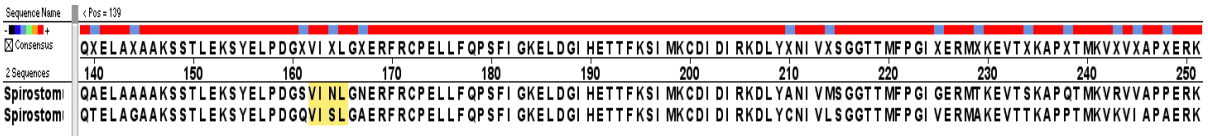


(A)



(B)

Figure 1. The sequences are two paralogs of the Actin gene in *Spirostomum ambiguum*, which show nucleotides (A) and amino acids (B). Highlighted are showing three silent mutations and one amino acid change. Sequences are aligned using DNASTAR MegAlign.

Temperature regulated mechanisms in *Escherichia coli*

Julia Reier/2017

Escherichia coli have developed complex molecular mechanisms to detect changes in their immediate environment to mediate cellular stresses. As such, bacteria have the ability to distinguish between host and non-host environments, which govern virulence factors and can induce infection in a host. Temperature is a critical environmental cue that affects the growth and pathogenesis of bacteria. In my research I studied the effect of temperature on gene expression and regulation in uropathogenic E. coli (UPEC) and enteropathogenic E. coli (EPEC).

After shifting pathogenic E. coli, from ambient temperature (23˚C) to human body temperature (37˚C); I isolated RNA from the cells and ran qRT-PCR to assess the effects of temperature change on expression of genes that contribute to infection and transmission including adhesion, biofilm formation, acid resistance and virulence, therefore identifying differences in gene expression between types of pathogenic E. coli.

I focused my research on genes that controlled the expression of pili and flagella in EPEC and UPEC, because those genes are crucial in the immediate attachment of E. coli in the host. The data I collected using qRT-PCR was compared to data collected by former students and genomic databases. By using basic bioinformatics that measured fold change and C_t (threshold cycle) values, I was able to analyze gene expression at different time points and temperatures in both pathogenic strains.

While I was able to show that several genes were temperature regulated in the UPEC strain, limiting amounts of RNA was isolated from cells grown in a biofilm hampered the experimentation and there were some conflicting results with previous data. In the EPEC qRT-PCR experiments, I initiated qRT-PCR showing that replicate B along with previous data shared similar gene expression involved in colonization when there was a shift in temperature.

In order to make any definitive conclusions about specific gene expression involved in colonization and biofilm formation during temperature shifts in EPEC and UPEC, a biofilm assay experiment and additional RNA isolation needs to be conducted. In addition, more primers will be designed to accommodate the different genes used in host colonization by UPEC and EPEC. By the end of the next school year I hope to present my findings to the American Microbiology Society and begin writing my thesis.

(Supported by the Schultz Foundation)

Advisor: Christine White-Ziegler, Biological Sciences

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[3]White-Ziegler, Area grant. Smith College

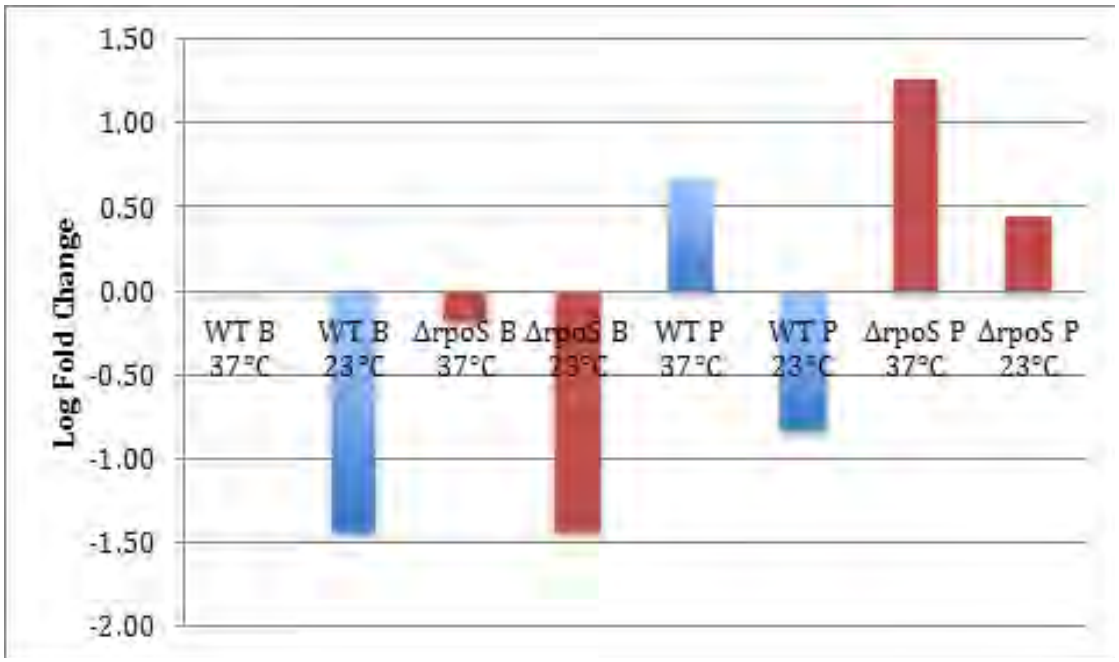


Figure 1. The level of expression of fimA in wildtype and mutant uropathogenic E. coli (UPEC).

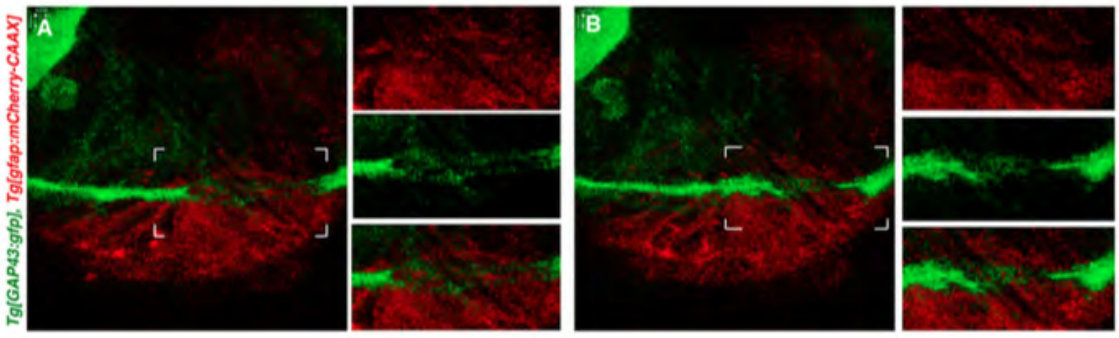
The Diencephalic Glial Bridge is Made Up of a Heterogeneous Population of Astroglia

Caitlin Schneider/2015

Although the birth of new neurons occurs throughout adulthood, the bulk of neural patterning is complete before an organism is even born. The underlying neural framework established during embryonic development is crucial to the proper functioning of the nervous system. To establish connections, neurons send projections called axons to find target cells and form synapses. In the bilateral organism, neurons oftentimes send axons across the midline to form connections with cells on the other side of the brain – these axons bundle to form commissures, which serve to connect the two sides of the nervous system. This midline crossing is a unique event, as neurons crossing the midline do so once or not at all. Little is known about the cell population at the midline that facilitates this crossing. We use the zebrafish model system to elucidate the nature of the cells, called astroglia. Cell transplantation techniques allowed us to visualize midline astroglia in the zebrafish forebrain, and we have identified three distinct morphologies of astroglia: mesenchymal, radial glia, and multi-process. These morphologies are found in different regions around forebrain commissures, and preliminary data demonstrates that they exhibit differential immunolabeling, suggesting they are molecularly distinct as well. In vivo imaging of developing zebrafish embryos demonstrates that developing axons make contact with the membranes of these midline astroglia as they navigate their environment. Future work will determine the behavior of the distinct morphologies during midline axon crossing; we will also identify the specific molecular differences amongst midline astroglia.

(Supported by Blakeslee Fund in the Biological Sciences)

Advisor: Michael Barresi, Biological Sciences



Midline crossing of axons (green). Developing axons contact the membranes of astroglial cells (red), indicating a role for astroglia in midline crossing.

Engineered Therapeutic and Diagnostic Proteins Targeting Tumor Biomarker Mesothelin

Allison Sirois/2016 J

In recent years, there has been significant progress in developing targeted cancer diagnostics and therapeutics, allowing for increased efficacy and reduced toxicity. For many cancers however, such as triple-negative breast, ovarian, pancreatic, or lung, targeted options are not yet available. Thus, new biomarkers for these cancers must be identified and appropriately translated for clinical application. Mesothelin (MSLN), a cell surface protein, is expressed at high levels on these tumors, with limited expression in healthy tissue. Furthermore, MSLN has been shown to bind another known tumor biomarker MUC16 (CA125), an interaction shown to facilitate cancer progression and metastasis. The differential expression pattern of MSLN, and its association with MUC16, makes MSLN a promising biomarker. We aim to engineer MSLN-targeting proteins to interrupt the MSLN-MUC16 tumor biomarker interface, with applications as both molecular diagnostics and targeted therapeutics.

Based on the non-antibody fibronectin scaffold, we are using directed evolution and yeast surface display technologies to engineer high-affinity proteins that target the domain of MSLN responsible for binding MUC16 (Figure 1). We have identified, recombinantly expressed in yeast, and purified the minimal binding domain of MSLN that binds MUC16.

Using magnetic- and fluorescent-activated cell sorting (FACS), we have identified fibronectin variants that bind the MSLN minimal binding domain with moderate affinity (K_D ~ nM). We have established in vitro assays to measure the engineered proteins' binding to tumor cell lines expressing MSLN or MUC16. Work in progress includes measuring the stability, binding affinity, and bioactivity of the candidate proteins, while developing assays to measure their biological activity on tumor cell lines. Future work will evaluate the engineered proteins as molecular imaging agents by injecting fluorescently labeled variants into tumor-bearing mice and measuring in vivo tumor contrast. We will also validate their therapeutic potential by measuring their effect on cell proliferation and apoptosis in tumor cell lines.

(Supported by the Schultz Foundation)

Advisor: Sarah Moore, Engineering and Biological Sciences

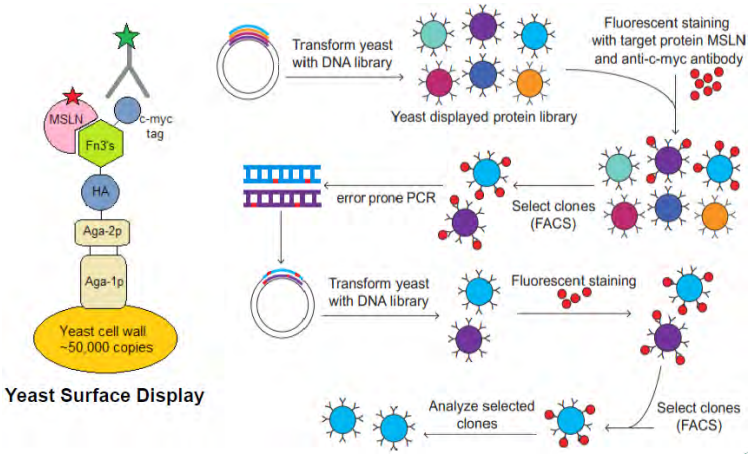


Figure 1: Schematic of project design. Yeast surface display is coupled with directed evolution and FACS to engineer novel binding proteins to block the MSLN-MUC16 interface.

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Phylogenetic Analysis of the Morphospecies *Rhipsalis baccifera*

Liz Tan/2016

Introduction *Rhipsalis baccifera* is a species of tropical epiphytic cactus endemic to both the New World[1] and the Old World; it is categorized into six subspecies: *erythrocarpa*, *horrida*, and *mauritania* in the Old World; and, *baccifera, hileiabaiana*, and *shaferi* in the New World. Do these subspecies merit separate species status? Elusive polymorphisms in the relatively rapidly evolving intergenic regions of the chloroplast genome (cpDNA) were used to investigate the correlation between phylogenetic divergence and the globally dispersed biogeographical regions of endemic growth. Determination of the polyploidization levels, using karyotyping techniques, was also used to examine possible genetic divergence across various samples.

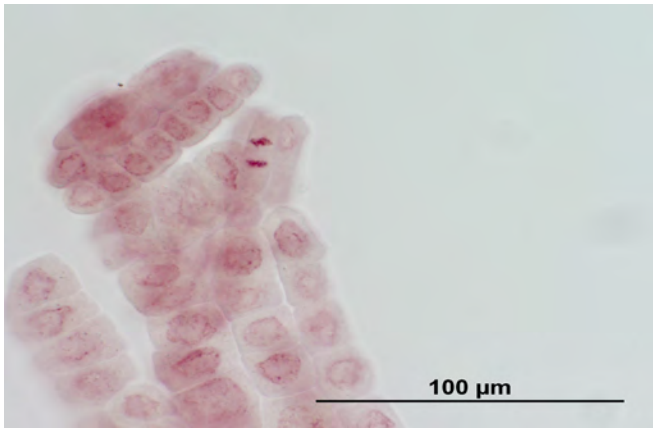

Figure 1. *Rhipsalis baccifera* root tip stained with aceto-orcein showing nuclei and a cell in telophase in the meristematic zone. The roots were fixed briefly, and hydrolyzed at 60° C for one minute with 1 N HCl.The chromosomes are lined up by their centromeres.

Methods Phire Plant Direct Polymerase chain reactions (PCR) were performed to amplify various intergenic regions of the chloroplast genome of *R. baccifera* samples provided by the Lyman Plant House. Direct sequencing yielded results that were analyzed for polymorphisms to determine if the samples are separate species. Cuttings of *R. baccifera* grown in wet sand, perlite, or water provided root tips used for microscopy. Finding a reliable, steady source of growing roots was a challenge. Karyotyping to find mitotic division and determine ploidy level in *Rhipsalis* was performed along with *Allium cepa* as a control. The Feulgen technique or aceto-orcein was used to stain the chromosomes and nuclei[2]. The mitotic arresters colchicine and 8-hydroxyquinoline were used in an attempt to both maximize metaphase figures and condense the chromosomes (Figure 1).

Results and Discussion Although PCR products and sequencing show high quality data, only a few polymorphisms have been found in the two different cpDNA sequenced regions, which is not enough to determine intraspecific taxonomy. The karyotyping figures show dividing cells in the root tips. Literature supports that the morning and early afternoon may lead to a higher proportion of metaphase figures. Techniques that both dissolve the cell wall, using hydrolytic enzymes, and spread the chromosomes out for crisper images will also be explored.

Acknowledgments I would like to thank Mr. Richard Briggs, for all of his help with the histological wet-lab guidance; Rob Nicholson, for introducing me to this project; and the Lyman Plant House staff, for collecting and caring for all of the samples used in this study.

(Supported by the Howard Hughes Medical Institute)

Advisors: Robert Merritt and Laura Katz, Biological Sciences

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Cryptic Diversity within Testate Amoeba and Genome Mapping

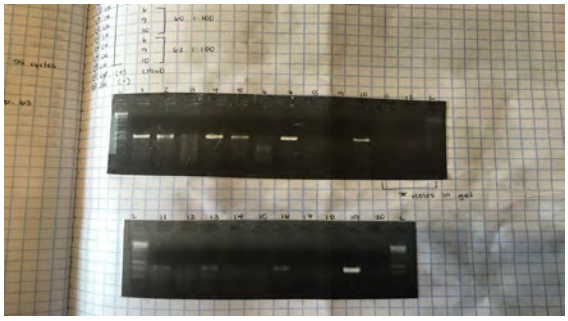
Monica Wilson/2017

Testate amoeba are unicellular microorganisms that serve as prominent bioindicators and top predators within their peatland environments[1], as well as potential vectors for parasites.[2] Past endeavors to distinguish, and phylogenetically group these microbes have been accomplished primarily through morphology; a practice which largely ignores nuanced discordances between phenotype and genetic distance, lateral gene transfer (LGT), adaptive radiations and the like. For my research, I focused on the intraspecific diversity within Quadrulella symmetrica, one of eight genera suspected to contain 'cryptic' species (i.e. morphology-molecule discordant species).[3] Examining these cryptic species may not only illuminate underlying factors of protist biodiversity, but aid in targeting parasitic genes within vectors that pose huge public health risks.

For the testate diversity component, I sampled Sphagnum spp. moss from various areas of Hawley Bog to simulate an assemblage of amoebae from various microclimates. I then recovered individual cells for later use in whole genome amplification (WGA), polymerase chain reactions, bacteria culturing, and gene sequencing. To assess possible bacterial LGT, I looked at multiple gene trees, protein alignments, and virtual genome constructions using SeaView alignment software and the National Center for Biotechnology Information (NCBI) database.

The data collected from this study showed robust support for possible LGT from bacteria into eukaryotes (e.g. Trichomonas vaginalis), given that they are not bacterial gene cassettes. I determined select protein sequences to show sufficient promise for LGT as they corresponded to bacterial genes found amongst clusters of almost exclusively eukaryotic genes. I attempted to assess the greatest degree of genetic divergence between individual Quadrulella sym. cells by using mitochondrial gene sequencing (COI) on samples that had previously been sequenced successfully for a basic eukaryotic gene, actin. Although no results were drawn from the mitochondrial gene sequencing, I repeated numerous PCRs for either gene in order to optimize results in the future.

I found this research experience incredibly helpful in allowing me to work both independently and in collaboration with others. I feel I've had adequate practice mastering familiar techniques and being introduced to new ones. I intend to continue with these skills, applying them to an Honors Thesis as a senior.



Gel electrophoresis of actin gene sequencing for individual Quadrulella sym. cells with dilutions of 1, 1:10, and 1:100.

(Supported by the National Science Foundation)

Advisor: Laura Katz, Biological Sciences

[1]Booth, Robert K. "Ecology of Testate Amoebae (protozoa) in Two Lake Superior Coastal Wetlands: Implications for Paleoecology and Environmental Monitoring." Wetlands 21, no. 4 (2001): 564-76.

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Understanding the Interaction Between Two Invasive Pests on Hemlock Trees

Jinyi Yang/2018 and Yuri Lee/2018

The New England forests house many different species in a complex ecosystem, and one of its key players is the eastern hemlock tree. However, in the past years, two exotic and invasive species of insects- the hemlock woolly adelgid (HWA) and the elongate hemlock scale (EHS) - have caused these important trees to drastically shorten their original life span. Hemlock woolly adelgids cause the eastern hemlocks to die off at a rate near a decade after infestation, while the elongate hemlock scales (although not a killing parasite to their host) make the trees much weaker.[1] Our project revolved around how exactly these insects affect the trees, how the two insects coexisted on the same tree, and other ecological changes that occurred to impact the ecosystem- mainly to the soil.

Our lab group visited the MacLeish Field Station every week to collect the volumetric water content from the soil collars in our black birch and eastern hemlock plots, and to collect branch samples from both old(taller than average breast height) and young(shorter than average waist height) eastern hemlock trees. These samples were viewed under the dissecting microscope, stereomicroscope and the scanning electron microscope to observe the EHS and HWA. The dissecting microscope was used to count the insects, while the stereomicroscope and SEM were used to view how the EHS and HWA were interacting/feeding off the trees.

After two months of data collecting and picture taking, we discovered that our selected hemlocks are under major attacks by the EHS. Relatively few HWAs are found on the leaves. We presume that the hemlock trees are under the first round attack by the EHS, and we expect that the number of HWAs will increase later in the summer. In addition, the SEM photos revealed some suspicious tubes that are interacting with the leaves. Unfortunately, so far we are unable to identify the physical interaction between the two insects. Interestingly, we also noticed some bacteria-like creatures inside dead EHS. We are curious how these creatures play a part in the HWA and EHS competition or cooperation. We still have many questions need to be answered. For one, because the specimen of our experiment are presumably all at immobile stages of the insects, we suspect that maybe the interaction between the two insects are during their crawler stages.

(Supported by the Margaret A. Walsh Grantham Fund, Yang; B. Elizabeth Horner Fund in the Biological Sciences, Lee)

Advisor: Danielle Ignace, Biological Sciences

[1]Gomez S. 2015. Interactions between invasive herbivores and their longterm impact on New England hemlock forests. Biol Invasions. 17:661-673.


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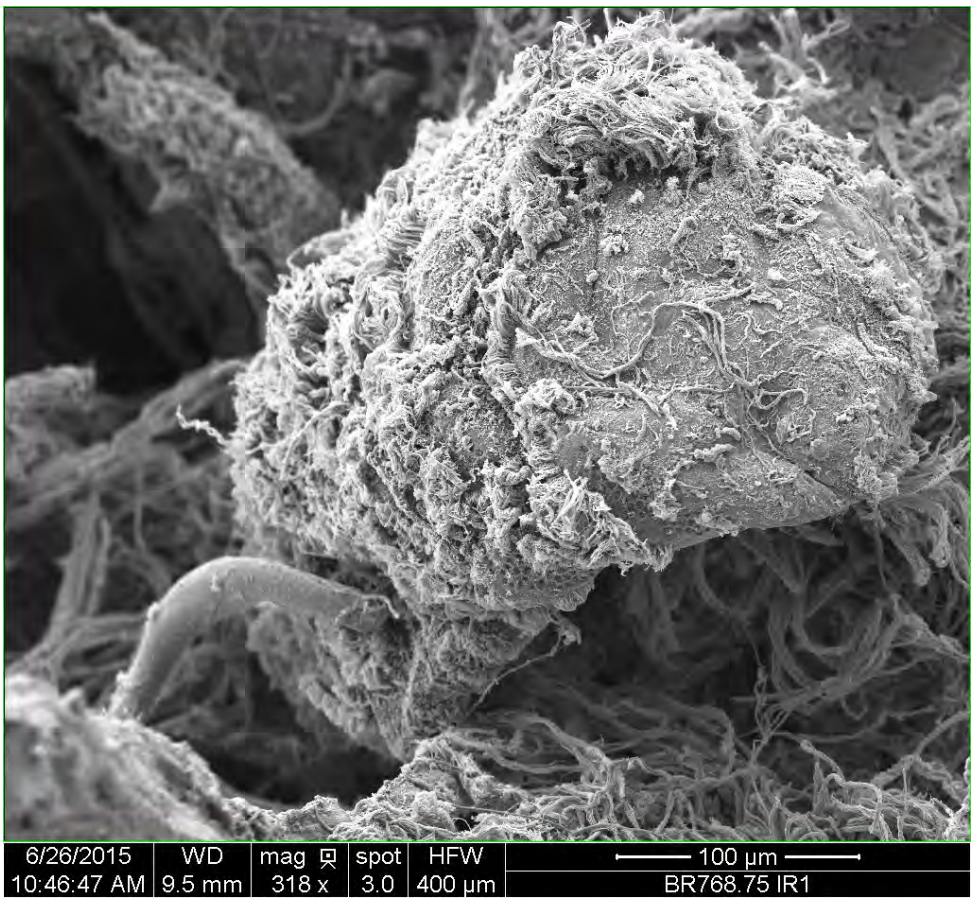
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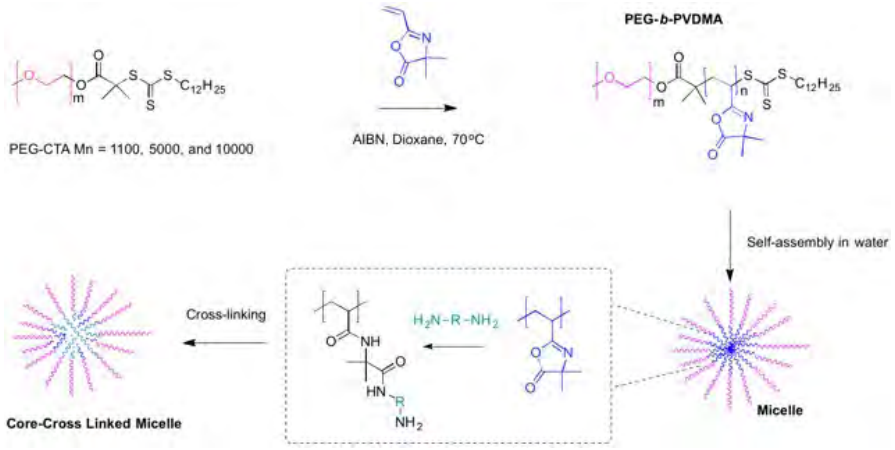
Stimuli-Responsive Polymeric Biomaterials for Controlled Drug Release

Quinn Anex-Ries/2017



Stimuli responsive biomaterials release encapsulated cargo when an external stimulus is applied. Controllable drug delivery helps to prevent premature drug release and allows for the targeting of specific tissues.[1] Many types of biomaterials can be synthesized using polymers. Hydrogels are cross-linked polymeric networks that swell in water. Micelles are formed from amphiphilic diblock copolymers, the hydrophobic block forms the core and the hydrophilic block forms the exterior of the macromolecule when introduced to water.[2,3] Vinyl dimethyl azlactone (VDMA) is an highly reactive monomer, which polymerizes to make PVDMA, with the ability to tether drugs that can be used to synthesize micelles and hydrogels.

Core cross-linking of micelles leads to increased stability, as well as stimuli-responsiveness. I worked with PEG-PVDMA diblock copolymers and cysteamine, which is a redox responsive cross-linker, and hexanediamine, which is non-stimuli responsive. The particle analyzer and the TEM microscope were used to characterize micelles. I encountered problems as I began cross-linking studies, as ATR-IR revealed that the diblock copolymers were hydrolyzing.

Hydrogels were synthesized using PVDMA and several crosslinkers: cysteamine, hexanediamine, and 400 polyethylene glycol (PEG). After successfully synthesizing hydrogels using all three cross-linkers I performed several different time studies. Dithiothreitol (DTT) cleaves the disulfide bond in cysteamine, causing hydrogels formed with cysteamine to fall apart. Cysteamine gels were placed in both water and DTT solutions, along with hexanediamine control gels. It was confirmed that only cysteamine gels in DTT solutions disassembled. Next, I studied the gel formation time as a function of cross-linking percentage for PEG gels.

I will continue to characterize gel formation kinetics for several different cross-linkers. I hope to resolve the issue of hydrolysis of the PEG-PVDMA diblock copolymers in order to continue micelle studies. I have now begun working on a biomathematics project that focuses on the computational modeling of micelle formation.

(Supported by the Schultz Foundation)

Advisor: Maren Buck, Chemistry

[1]Wu, L.; Zou, Y.; Deng, C.; Cheng, R.; Meng, F.; Zhong, Z. Intracellular release of doxorubicin from core-crosslinked polypeptide micelles triggered by both pH and reduction conditions. Biomaterials. 2013, 34, 5762-5272.

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Salivary Dopamine in Parkinson's Disease

Noah Blohm/2016

In Parkinson's disease, dopaminergic neurons in the substantia nigra die, with significant symptoms and diagnosis occurring when mortality reaches about 80%. The main mass of dopaminergic neurons is located in the substantia nigra of the brain; however, there is also a large concentration of such neurons in the enteric nervous system, a subdivision of the peripheral nervous system (PNS) found in the gut and having a key involvement in the digestive organs. Based on the hypothesis that dopaminergic neurons in the PNS will be affected prior to those in the central nervous system (namely, the substantia nigra), a drop in dopamine levels in the saliva (reflecting death of peripheral dopaminergic neurons) might provide an early-detection method for Parkinson's Disease. To test this, the Bickar lab has developed a procedure to measure concentration of dopamine in saliva samples.

However, enervation of the salivary glands by dopaminergic neurons projecting from either the CNS or the enteric nervous system has not been shown in mammals. Thus, the target question of my research this summer became, "Where is the dopamine detected in the saliva samples coming from?" My hypothesis is that there are undiscovered dopaminergic neurons directly connected to the salivary glands in mammals.

This hypothesis is supported by previous research showing involvement of the salivary glands in Parkinson's, beginning in early stages, and linkage between the salivary glands, PNS, and CNS (1). While hypersialorrhea is a common symptom of PD, it is due to decreased swallowing reflexes and an anteriorly flexed head position, while saliva production itself is depressed in advanced PD (1, 4). Treatment with L-dopa elicits a sialagogue response via interaction with central dopamine receptors in the striatum and adrenoreceptors located peripherally on the glands (5, 6). Treatment with intravenous dopamine also induces a sialogogue response, but this response is mediated only by α- and β-adrenoreceptors (6). Thus, I hypothesize that the source of salivary dopamine is, indeed, the peripheral nervous system, though the enervation is mediated not by dopaminergic receptors, but adrenoreceptors.

Using a Bicinchroninic Acid (BCA) micro-assay, I created an initial standard curve of absorbance (Fig. 2) to total protein concentration. As I continue this project as part of my honors thesis, I will determine when a significant change in dopamine concentration relative to total protein, electrolyte, and solute concentrations occurred, and thus could be attributable to PD, as the disease is specific to the dopaminergic system.

Fig. 1: Flowchart of proposed possible pathways for dopamine's affect on the salivary glands, and thus the presence of dopamine in salivary samples.

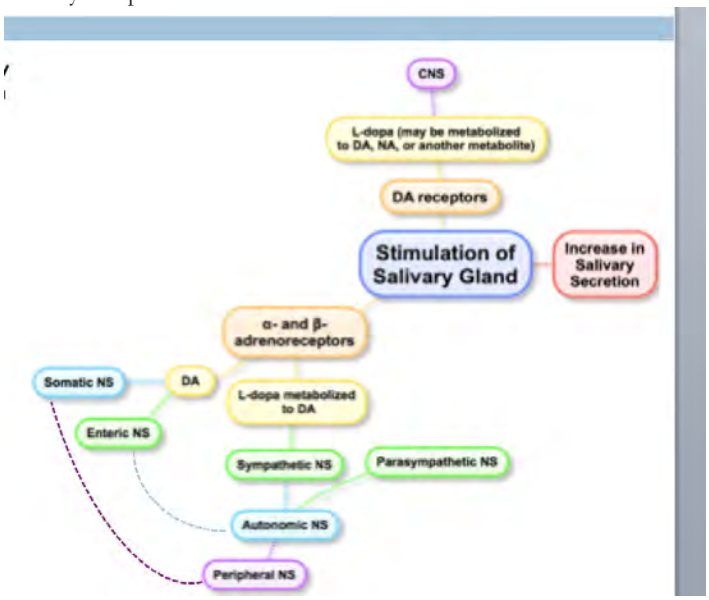
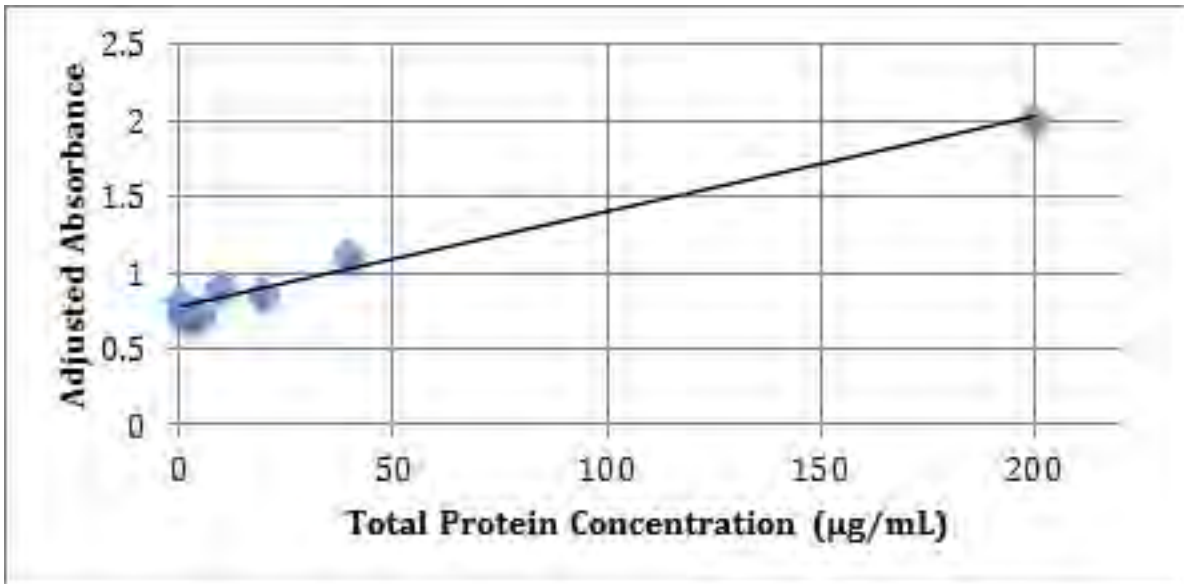


Fig. 2: Standard curve of absorbance at 562 nm for total protein.



(Supported by the Schultz Foundation)

Adviser: David Bickar, Chemistry

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Detection of Human Salivary Dopamine in 24-hour cycle

Hana Cha/2016J

Parkinson's disease is a neurological disease that results in the degeneration of dopaminergic neurons. This results in the inhibition of releasing dopamine in the brain, followed by very low levels of dopamine concentrations. It has been found that low level of dopamine is the source of the most common symptoms of Parkinson's disease: tremor, dyskinesia and drooling. Unfortunately, these symptoms emerge when 80-90% of the patient's dopaminergic neurons have already been degenerated, and the only treatment currently available for Parkinson's disease patients is administration of medications that enhances dopamine release in dopaminergic neurons that have yet been affected by the disease.

The current methodology for diagnosing Parkinson's disease is the visible common symptoms of the disease. However, there yet seems to be any technique or methodology that could quantitatively diagnose the disease in patients before the emergence of the Parkinsonian symptoms. Hence this research serves to detect dopamine in human saliva using Electrochemical Detecting High Performance Liquid Chromatography (ECD HPLC) as a non-invasive technique to observe levels of dopamine in non-Parkinsonian individuals. This project serves as a foundation for the research, where the salivary dopamine concentrations are measured throughout the 24-hour period to identify any observable trends.

Therefore in this particular project, human saliva was collected at specific hours of the 24-hour cycle in 4-hours intervals starting at midnight. Once collected, the sample was purified using a cation-exchange column, concentrated using a vacuum concentrator and then analyzed using a High Performance Liquid Chromatography. The data was then converted into concentrations, and when combined, a plot was generated that seem to identify two time periods during the 24-hour cycle when dopamine concentration was highest.

Although the concluding results of the research project points to the two periods in the 24-hour time period when dopamine concentrations are the highest, more samples need to be analyzed and data must be collected in order to obtain a more accurate plot for dopamine. In addition, the saliva samples were collected from one individual, where it would lack to represent the dopamine concentration for all human population. Hence in conclusion, further research is necessary to confirm the consistency of the project's results.

(Supported by the Howard Hughes Medical Institute)

Advisor: David Bickar, Chemistry

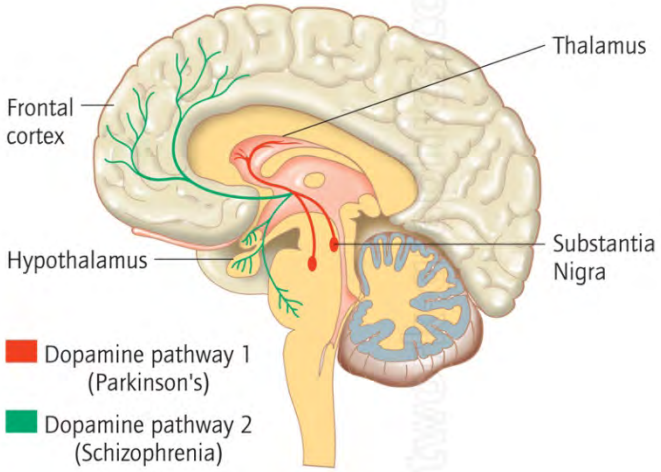

Fig. 1. Dopaminergic pathways in the brain, and their associative neurodegenerative diseases.

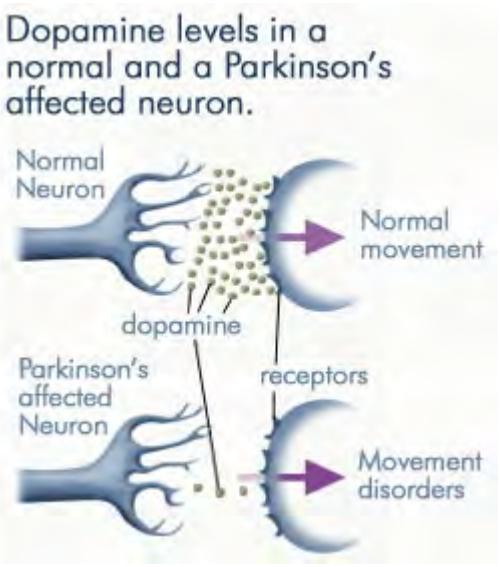

Fig. 2. Illustration of the involvement of dopamine levels in normal and Parkinsonian neurons.

Synthesis and Analysis of Polymer Hydrogel Biomedical Materials

Anna Carroll/2016

Modern medicine demands innovative therapeutics, such as hydrogel matrices for tissue engineering and regenerative medicine[1]. Novel hydrogel biomaterials can be formed using a unique and newly explored biocompatible and selectively amine-functionalizable polymer known as poly(2-vinyl-4,4'-dimethylazlactone) or PVDMA[2]. This approach creates gels with tunable mechanical properties that can be functionalized with numerous pharmaceuticals, proteins, and other useful agents[1].

The Buck lab synthesizes 2-vinyl-4,4'-dimethylazlactone (VDMA) monomer[3], which becomes PVDMA through a free-radical polymerization with azobisisobutyronitrile (AIBN) initiator at 70°C in dioxane[4]. This polymer, once precipitated into hexane or diethyl ether and collected by suction filtration, is dissolved in a 3:1 acetone : dimethylsulfoxide (DMSO) mixture, typically at 8 weight percent. Adding the desired equivalence of diamine cross-linker, in this case "Jeffamine," achieves hydrogel formation. Gels are functionalized by submersion in excess amine (ethanolamine is used for proof of concept studies), dissolved in additional DMSO. Gels are then washed in sufficient phosphate buffer (pH 7.5, 100mM) to soak out the organic solvents. In order to form gels directly in phosphate buffer (pH 7.5, 100mM), copolymers containing VDMA (which is hyrdophobic) as well as hydrophillic monomers including poly(ethylene glycol)methyl ether methacrylate, N-acryloyl-2-methylalanine, and methacrylic acid, were similarly synthesized in DMSO[5]. These polymers and hydrogels are then analyzed using infared spectroscopy (IR).

Large-scale VDMA syntheses yielded approximately 50% each, while PVDMA was consistently collected at nearly 100% yield. PVDMA homopolymer-based hydrogels formed readily in organic conditions and were functionalized with model amines, and the kinetic properties of this process with varied cross-linker percentage, temperature, and polymer concentration are continuously analyzed. While IR confirmed creation of VDMA-containing copolymers, a copolymer sufficiently hydrophilic to dissolve in phosphate buffer has not yet been obtained, and hydrolysis of azlactone domains during the synthetic process presents a challenge.

Successful formation, functionalization, and characterization of these dynamic PVDMA-based hydrogels represent vital steps towards producing biomaterials for future implementation in medicine. In addition to pursuing a water-soluble VDMA-containing copolymer in the future, existing hydrogels will be functionalized with fluorophores, anti-microbial agents (silver nanoparticles), and proteins ("RGD" cell adhesion peptides). Their practical properties will be evaluated as part of an honors thesis, testing their ability to repel and kill bacterial cells while promoting adhesion and growth of mammalian cells in culture.

(Supported by the Alumnae Gift Fund in Chemistry)

Advisor: Maren Buck, Chemistry

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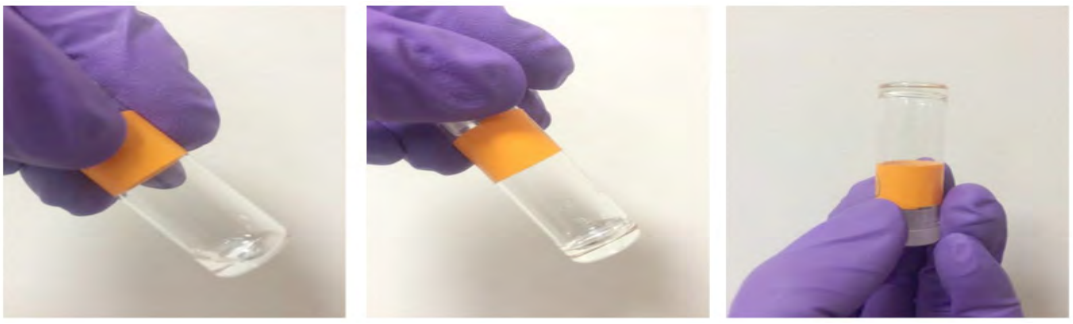
"Tilt Test" Determining Hydrogel Formation:



The Simultaneous Nanoscale Control of Surface Chemistry and Surface Topography on Si(100).

Charnice Charmant/2016

Nanoscale Topography has biological importance, as it influences a surfaces cells growth[1] and mobility. By combining nanoscale topography and the control of chemistry, we can influence the adsorption of biomolecules by chemically altering the surface. On Si(100), the surface goes through two stages of etching. In the first stage, the etching results in a dihydride species appearing on the surface, and the later stages of etching result in faceted hillocks. These hillocks allow biomolecules to attach to the surface. Oxidation and Hydrosilylation of surfaces were two experiments conducted that allow us to observe the chemical changes of the surfaces functional groups. Though oxidation is site specific, reacting less on fully oxidized surfaces, hydrosilylation is not site specific; it creates different layers on the surface. Dynamic contact angle was also used to probe the chemistry and topography of the surface. The advancing angle informs us of the sensitivity to the most hydrophobic parts of the surface, while the receding angle informs us of the sensitivity to the most hydrophilic parts of the surface. The difference of these values is the hysteresis, which measures the homogeneity of the surface. Multifunctionalization was another experiment conducted; by oxidizing and hydrosilylating the surfaces in one experiment, we were able to find that multifunctionalization of a rough surface – a surface that is already oxidized – results in well-ordered alkyl chains where SiO modes are detectable; the multifunctionalization of a flat surface does not result in well-ordered alkyl chains and SiO modes are not detectable. In conclusion, we can highlight that oxidation is site specific. Also, while hydrosilylation is not site specific, it creates different layers on the two surfaces. Multifunctionalized, rough surfaces have different characteristics than multifunctionalized, flat surfaces.

(Supported by the Schultz Foundation)

Advisor: Kate Queeney, Chemistry

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Ethoxylation of Indole and Its Derivatives by Ethylene Carbonate as a Greener Reagent

Peishan Chen/2016

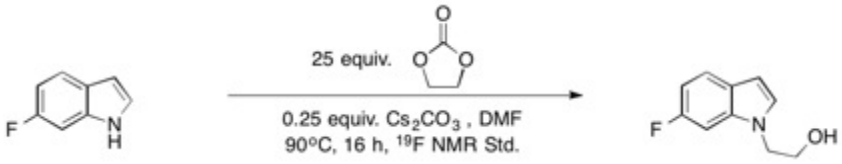
Greener and more sustainable chemical reactions are attracting scientists nowadays. For example, using a less hazardous starting material or a more environmentally friendly solvent is preferred according to the sustainable chemistry definition. In addition, the use of a less environmentally hazardous starting material is preferred because it can reduce the cost and time to process waste and avoid hazardous experimental procedures.

Ethylene oxide (oxirane) is widely used in industry, such as in the production of ethylene glycol (a coolant in automotive engines), glycol ether (an ingredient in cleaning compounds), ethanolamine (one of the ingredients in wax remover). Because of its highly strained ring structure, oxirane is not stable in ambient condition. It is acutely toxic, and carcinogenic, which leads to danger when using it as a reagent. It therefore results in a high-risk working environment for chemists.

It is necessary to discover a safer and more stable reagent that has similar functionality to oxirane and substitutes for it. We hypothesized that ethylene carbonate might play this role. Ethylene carbonate is a solid at room temperature, and has a low melting point. Therefore, the experimental procedure for ethoxylation with ethylene carbonate is much safer than one requiring oxirane. In order to develop an optimized experimental procedure for ethoxylation, reaction conditions were screened. The utilization of a ^{19}F NMR method enabled rapid quantification of the percentage of product formed. During SURF, we were able to optimize the reaction yield to 63%. The optimization experiments and investigations of other starting materials will continue to go on during the upcoming academic year.

(Supported by the Smith College Committee of Faculty Compensation and Development (CFCD))

Advisor: David Gorin, Chemistry



Investigation of the Base Pair Opening for Spiroiminodihydantoin (Sp) DNA Lesions

Luojun Dong/2017

Oxidative damage to DNA has been shown to be relevant to carcinogenesis, aging, and neurological disorders.[1] Many oxidative lesions derive from guanine because it has a low reduction potential.[2] 8-Oxoguanine (8-oxoG) is one of the guanine lesions that has been well studied. While 8-oxoG is similar in size and structure to guanine, it is highly mutagenic, prone to GC→TA transversions. 8-oxoG is also highly reactive toward further oxidation. Through one-electron oxidation, 8-oxoG can be oxidized into the spiroiminodihydantoin (Sp) lesion.[1] To obtain more insight into the enzyme repair mechanism of the Sp lesion, we measured the opening rates (aka imino proton exchange rates) of a normal G-C base pair and a Sp-C base pair in 11-mer DNA duplexes by 1D NMR.

As these duplexes have previously been studied at pH=7, this summer I mainly worked with the control GC duplex at pH=8. My hypothesis was that at higher pH and higher ammonia concentration, the imino protons in all base pairs would exchange with magnetized water at a faster rate. Hence, with the enhanced exchange rates, we would be able to better observe the different opening behavior between the normal G-C base pair and the Sp-C base pair. While the data collection is still in progress, I found that in base pair opening experiments, the signal resolution of the 1D NMR spectrum is highly sensitive to the shimming of the NMR instrument, which can be reflected by the water inversion spectrum. Also, at room temperature, the G imino proton signals at pH=8 are different from those at pH=7. At pH=8 and 8°C, no separation of G6 and G13 peaks was observed.

This research experiment was very helpful because I not only gained more knowledge about DNA, but also learned many useful laboratory and analytical techniques, such as advanced level operation of the 500 MHz NMR. During the academic year, I will continue on the data collection and improvement of the base pair opening experiments.

(Supported by the Howard Hughes Medical Institute)

Advisor: Cristina Suarez, Chemistry; Elizabeth Jamieson, Biochemistry

Reference:

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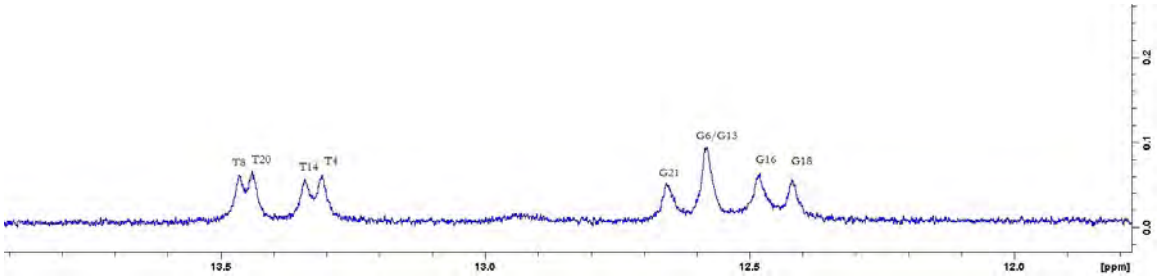

1D NMR spectrum of the imino protons of the control G-C duplex at 10°C.

Design and Synthesis of an Oxazole-Cyclic Peptide

Katherine Graham-O'Regan/2017

Cyclic peptides are diverse biological structures, many of which hold numerous therapeutic properties, such as antibacterial activity, anti-tumor activity, and prevention of neurological fibril formation. For decades biochemists have been inspired by cyclic peptides found in nature that hold profound health benefits, using these naturally occurring peptides as the inspiration for many pharmaceutical drugs.[1] My research was focused on creating a completely new molecule that would not only be a potential antibiotic but also hold other positive effects not normally present in cyclic peptides.

The cyclic peptide design was inspired by biological structures isolated from marine life containing *oxazole* and *thiazide* groups. Both groups are five membered rings that are believed to have antifungal and antiviral properties, in addition to the ability to reverse multiple drug resistance in cancer cells. An *oxazole* group can be easily made from *serine* and *phenylalanine*, thus I designed an eight residue cyclic peptide composed of four amino acids alternating in position. The *oxazole* rings are formed through coupling and oxidation of the amino acids. This synthesis was done using a solid phase strategy, a very common means of peptide synthesis. Solid-phase synthesis enables a drastic reduction to the synthesis time as compared to traditional synthesis in solution form. It is done by using small bead like objects as anchors (*resin*) on each of the numerous peptides formed.

As of now my results are inconclusive, further analysis will be done this fall to determine the success and future direction for the project. Both the synthesis and analysis of this cyclic peptide have given me an opportunity to become much more comfortable executing biochemical experiments. I have also been able to familiarize myself with such equipment as the NMR, UV-visible spectroscopy, and column chromatography.

(Supported by the Howard Hughes Medical Institute)

Advisor: David Bickar, Chemistry

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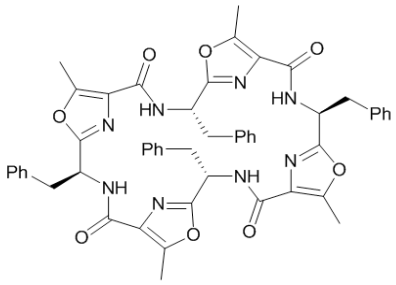

Aerobic Copper-Catalyzed Methylation of Aromatic C-H Bonds Using Methylboronic Acid

Clare Jacobson/2016

In recent years carbon bound methyl groups have proven to be both ubiquitous and important functional groups in pharmaceutical compounds. In 2011 a majority of the top small molecule drugs had at least one C-methyl group within the molecule.[1] Their presence has proven highly important in optimizing a drug's potency, solubility, and decomposition within the body, therefore strategies to install these moieties within small molecule drugs are valuable to the pharmaceutical industry. Most valuable to the industry are conditions that allow C-H methylation to be performed on a molecule at a late stage in its synthesis, allowing the method to be more practical to widespread optimization screening.

Therefore we are developing a protocol to install a methyl group onto a C-H bond contained within a functionalized aromatic ring via a Chan-Lam cross coupling mechanism. The Chan-Lam reaction uses a copper catalyst and an oxidant to cross couple a nucleophile and a boronic acid nucleophile.

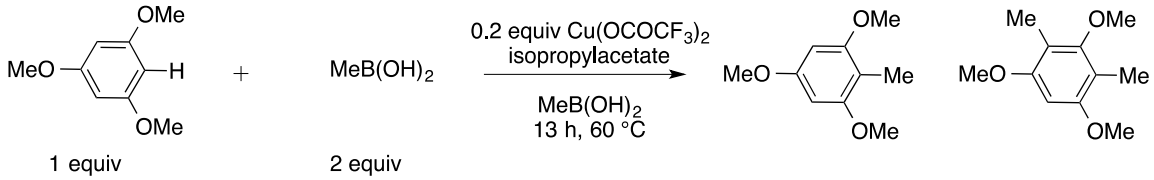

Figure 1: Reaction scheme for the current methylation conditions of 1,3,5-trimethoxybenzene.

We began developing our methodology based on literature precedent for other C-H bond activation using the Chan-Lam cross coupling. The only previously published study, by the Itamic Group, cited a successful cross coupling between aromatic C-H bonds and phenylboronic acid using copper(II)trifluoroacetate.[2] Using these published conditions for arylation we successfully methylated 1,3,5-trimethoxybenzene with methylboronic acid and have proceeded to further optimize the reaction conditions to the state in which they appear in Figure 1. Conditions were optimized using TLC, ^{1}H and ^{13}C NMR spectroscopy, flash column chromatography, and GC/MS spectrometry to monitor the reaction, characterize products and quantify yields.

While these initial optimization results are preliminary and there is a great deal of further work do be done, the successful methylation of an aromatic C-H bond is an exciting and promising first step to address the challenge of C-H methylation. I hope to further this work by continuing to optimize conditions as well as expand the substrate scope of this reaction while completing an honors thesis this fall.

(Supported by the American Chemical Society)

Advisor: David Gorin, Chemistry

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[2]Ban, I.; Sudo, T.; Taniguchi, T.; Itami, K. *Org. Lett.* **2008,** *10(16)*, 3607-3609.

Synthesis and Purification of 2,6-Diisopropylcyclohexanol for Use as a Potential Anesthetic

Ariel Li/2017

Propofol (Fig. 1) is a common intravenous anesthetic that binds to the $GABA_A$ receptors in the central nervous system.[1] Its biological activity is largely attributed to the aliphatic groups adjacent to the hydroxyl group.[1] With the goals of discovering anesthetics with fewer side effects and studying the anesthetic action and mechanism, Adam Hall's neuroscience lab investigated various isomeric mixtures of cyclohexanol analogs with aliphatic groups on 2,6 positions and obtained promising results. Inspired by menthol (Fig. 2), an entiomerically pure cyclohexanol derivative, the Hall lab is now interested in testing single stereoisomers to explore the possibility of $GABA_A$ receptors being stereo selective.

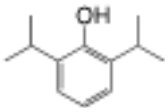

Figure 1. Structure of Propofol

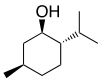

Figure 2. Structure of Menthol

Previous works in the Shea lab has focused on synthesizing and isolating stereoisomers of 2,6-dimethyl and 2,6-diethylcyclohexanol. The goal of the current project is to synthesize and isolate 2,6-diisopropylcyclohexanol isomers as the compound bears the most structural similarity to propofol. The scheme (Fig. 3) illustrates a double aldol condensation reaction[2], followed by hydrogenation of the conjugated enone[3] and separation of the cis and trans isomers. The isomers are to be reduced separately and the resulting stereoisomers are to be separated via flash column chromatography. The first aldol condensation was successfully achieved but the low yield raised questions on the scalability of the synthesis. Future direction for this scheme would be to continue the synthesis from Compound A.

An alternative synthesis route was explored, and the scheme consists of a one-step double aldol condensation followed by a conjugate addition, then separation and reduction of the cyclohexanone stereoisomers will be performed as planned. The aldol reaction was performed under 2 conditions: one by grinding up the reagents in a mortar[4] and another by stirring the reagents in ethanol. Both reactions produced the desired enone product but the mortar reaction was more efficient regarding time and yield. Continuing the synthesis with Compound B would be the priority of future investigations.

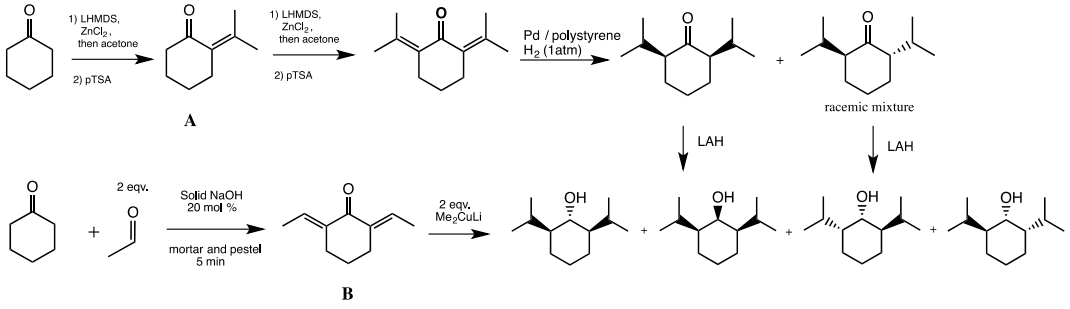

Figure 3. Reaction Scheme for the Synthesis of 2,6-Diisopropylcyclohexanol

(Supported by the Schultz Foundation)

Advisor: Kevin Shea, Chemistry

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Chemical Patterning of Nanoscale Surfaces

Kelsey Mack/2017

The chemical and topographical control of silicon surfaces through water etching has been proven to be very influential in a wide variety of areas, such as microorganism behavior.[1] However, there is still a lot to learn about the characteristics of silicon surfaces. Our current work, continued from past work in the Queeney lab done by Madeleine Beasley (2014) and Minhee Kim (2015), focuses on understanding and exploring the chemistry and topography of rough and flat multifunctionalized Si (100) surfaces.

All samples were prepared via a modified RCA SC-1 (hydrogen peroxide, ammonium hydroxide in 4:1 ratio) and SC-2 (hydrogen peroxide, hydrochloric acid in 4:1 ratio) cleaning method to remove impurities. Half of the surfaces were left as flat oxygen terminated surfaces, while the rest of the surfaces were subsequently etched in buffered oxide etchant (BOE) leaving rough hydrogen-terminated surfaces. The rough surfaces were prepared over a 24 hour etch using argon purged water as an anisotropic surface etchant to form nanotopographical features that retained the different silicon orientations of the original hydrogen terminated surface. Oxidation was performed on both rough and flat surfaces for various times (20, 40 and 60 minutes), depending on whether a full or partial oxidation of the surface was needed. This was done by using a box with walls of UV resistant material to keep out oxygen radical species that can oxidize the silicon surface at non preferential sites at a fast rate. Both rough and flat surfaces were hydrosilylated for 15 minutes in a round bottomed flask of heated 1-octadecene. Surface infrared spectroscopy (FTIR) provided detailed information of the topography through the identification of the different silicon hydride species on the specially ordered surface. Contact angle measurements were also utilized to determine the wettability of the surfaces.

Previously collected data was used to help come up with the hypothesis that the rough surface would have a higher density of CH bonds as well as SiO bonds after being multifunctionalized. As shown in the graphs below, hydrosilylation and oxidation did seem to occur more readily on the rough Si (100) surface as opposed to the flat. It can be seen in the CH and the SiO bond stretch region of the FTIR graphs that the rough surface has a larger peak area than the flat surface. However further investigations will be needed to uncover more information and extend this work to better understand the effect of this patterning on selectivity of the surface regions.

(Supported by the Howard Hughes Medical Institute)

Advisor: Kate Queeney, Chemistry

1, Beasley, M.S. "Simultaneous Control of Nanoscale Topography and Chemical Functionalization on the Si (100) Surface." Undergraduate Thesis, Smith College Department of Chemistry, 2014.

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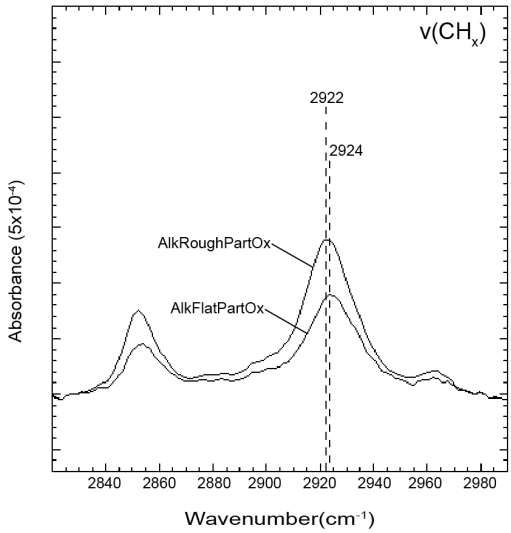
v(CHx)
2922
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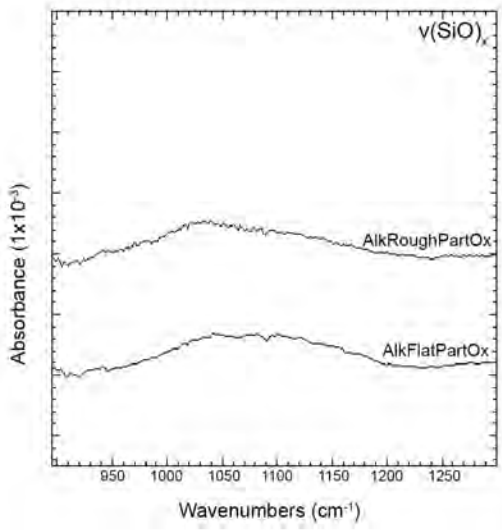

v(SiO)x
AlkRoughPartOx
AlkFlatPartOx
Absorbance (1x10-3)
950 1000 1050 1100 1150 1200 1250
Wavenumbers (cm-1)

Chemical Patterning of Nanoscale Surfaces

Nomfuneko Mafunda/2017

The clean, H-terminated surface of the silicon surface has served as a template for making widely used devices in the microelectronics industry. The Queeney Lab has been investigating the Si(100) surface chemistry and topography by altering the morphology. Our goal was to determine if there is a difference between the multifunctionalized rough surface and the multifunctionalized flat surface.[1]

The Si(100) samples were cleaned using a modified RCA clean; SC-1(4:1:1 ultrapure water: Hydrogen Peroxide: Ammonium Hydroxide at 70º-80ºC for 10min) and SC-2 (ultrapure water: Hydrogen Peroxide: Hydrogen Chloride). The samples were rinsed copiously with ultrapure water between the two cleanings. Some of the samples were etched for 24-hours with deoxygenated water to make hydrogen-terminated surfaces with hillocks of approximately 100nm in diameter while the remaining samples were etched with Hydrofluoric Acid to make a flat hydrogen terminated surface. This was followed by a one hour oxidation and a 15 minute hydrosilylation resulting in rough and flat multifunctionalized surfaces that were both oxidized and alkyl terminated.

The two rough and flat multifunctionalized surfaces were compared using a Fourier Transform Infrared (FTIR) spectroscopy and Contact Angle Goniometer. The FTIR was used to analyze the chemistry of the surfaces whilst the Contact Angle was used for the analysis of the surface's wettability and topography. Figure 1 shows the FTIR spectrum of the CH region (left) and the contact angle data graph (right) of the two surfaces. The CH region graph shows the rough surface to be blue shifted by 1cm^{-1} from the flat surface. The contact angle data show that the rough surface has a greater average hysteresis than that of the flat surface, 16º and 12º respectively. The contact angle results show that the rough surface is more heterogeneous than the flat surface.

These results show that the rough and flat multifunctionalized surfaces are indeed different and these differences can be analyzed using the FTIR and Contact Angle.

Although these results show that the surfaces are different, further experiments need to be conducted in the future to give more reliable results.

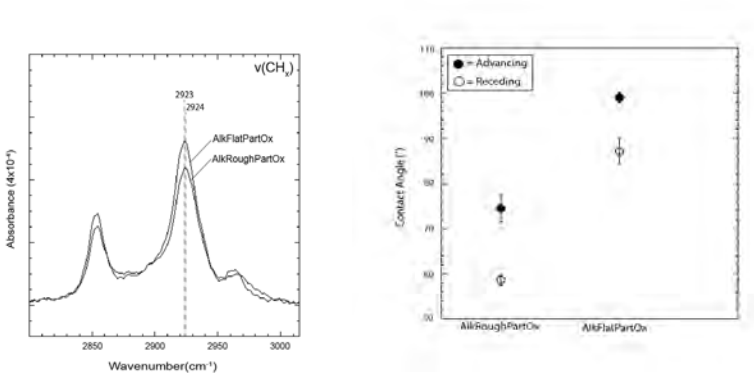


Figure 1: ν(CH_x) (left) and contact angle (right) graphs of flat and rough multifunctionalized surfaces\

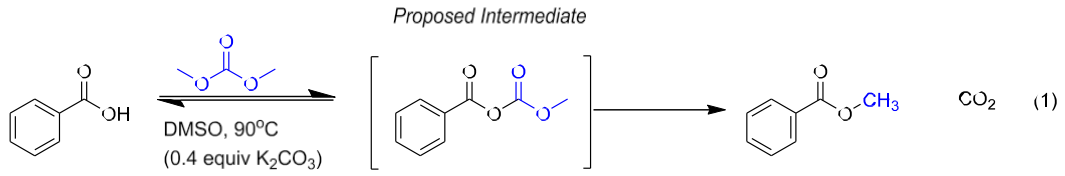
(Supported by the Dreyfus Foundation)

Advisor: Kate Queeney, Chemistry

1. Kim, M. "Simultaneously Controlling Nanoscale Morphology and Chemical Functionality on the Si(100) Surface" Undergraduate thesis, Smith College Department of Chemistry, 2015

O-Methylation using Dimethyl Carbonate: Mechanistic Studies

Noelia Martinez-Muñoz/2016



Methylation is widely used in synthesis of natural and pharmaceutical products. Currently used methylating agents, such as diazomethane, trimethylsilyldiazomethane (TMS diazomethane) and methyl iodide are all toxic, unstable, or both. Unfortunately, TMS diazomethane has caused the death of two scientists in recent years.[1] This problem motivated our lab to find a safer alternative to these methylating agents. Previous work in the lab optimized the conditions for methylation using dimethyl carbonate, a stable, non-toxic reagent, as the methyl source (eq 1).[2] My goal this summer was to gain further insight into the mechanism of this reaction.

Shieh and coworkers used dimethyl carbonate and DBU at 90 degrees Celsius to methylate oxygen nucleophiles.[3] They proposed the formation of an activated intermediate. Since our conditions are similar to the Shieh conditions, we also proposed an intermediate (Figure 1). To form product, one mechanistic possibility is that the reaction can proceed via an intermolecular SN2-like mechanism between the intermediate and the carboxylate anion.[4] Another possibility is a direct SN2 mechanism between dimethyl carbonate and the nucleophile without the formation of the intermediate.

This summer I did some experiments to see which pathway is more likely to occur. A Hammett Study was used to elucidate the electronic effects of the rate determining step of the reaction. To do this experiment, substituted benzoic acids were placed in a reaction flask with unsubstituted benzoic acid to watch the formation of product over time and calculate the ratio of rate constants between the different carboxylic acids. Preliminary results are consistent with the carboxylic acid acting as the nucleophile.

To further explore the mechanism, I added one equivalent of methanol to the reaction to see if it slows the reaction. Shieh found that the addition of methanol stopped the reaction which strengthened their hypothesis for intermediate formation. Methanol effects the reaction because there is an equilibrium for the formation of intermediate suggesting the rate determining step of the reaction under the Shieh conditions is the nucleophilic attack of the carboxylate anion on the intermediate. When I added methanol to the reaction under our conditions, I found that there was no effect on the rate of the reaction. This leads us to believe that if the intermediate forms, the rate determining step is different from the Shieh conditions. Based on the Hammett Study findings, the rate determining step may be the formation of the intermediate. There still remains the possibility that no intermediate forms and the reaction is a direct SN2 mechanism. I will continue to explore the mechanism and see if intermediate formation or direct SN2 is the more likely pathway.

(Supported by the American Chemical Society)

Advisor: David Gorin, Chemistry

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Distortion in $Mn(CO)_5X$ Compounds

Alexandra Maryashina/2017

Manganese pentacarbonyl compounds, $Mn(CO)_5X$, are important in understanding insertion reactions. They are observed to distort from octahedral geometry depending on the nature of the ligand X. Our calculations show that in compounds of appropriate symmetry, there are two equatorial X-Mn-CO angles – See Figure 1. From previous research we have learnt that the biggest distortion occurs when the ligand X is the best donor. To investigate this distortion we proposed to examine the donor-acceptor interactions between the ligand X and $Mn(CO)_5^+$ fragment using a method to partition the deformation density into different components (σ, π) of the chemical bond.

Our results show that the strength of the bond between the ligand X and $Mn(CO)_5^+$ fragment increases with the donor ability of the ligand X, which was measured by the magnitude of the distortion angle. The major component of the bond between fragments (approximately 70%) is the σ-type donation from the ligand X to $Mn(CO)_5^+$ fragment. Within this component there is a significant amount of charge donated into p_z orbitals on the equatorial carbons from p_z and s orbitals on acetylide carbon. The second and the third largest components of the bond is the π-type interactions between the filled p_x of acetylide carbon and empty π_z^* of xz-plane carbonyls ("B1") and the filled p_y of acetylide carbon and empty π_z^* of yz-plane carbonyls ("B2"). Thus, our findings suggest that there is a ligand-ligand bonding between acetylide carbon on the ligand X and equatorial carbonyls.

The second goal we pursued this summer was to analyze the energy surface map of combining the fragments into one molecular system. The molecule $Mn(CO)_5CCC(CHO)_2^-$ was divided into two chemically meaningful fragments: ligand $CCC(CHO)_2^{2-}$ and $Mn(CO)_5^+$ fragment. Single point calculations were then performed for each fragment. The fragments were ultimately combined into one molecular system and the energy was calculated for the whole molecule. Our results show that the symmetrical distortion is not energetically favored – See Figure 2. In contrast, the molecule energetically prefers to distort in a bifurcation manner, where one of the distortion angles appears large while the other stays relatively small or even becomes negative. We hope to continue this research during the upcoming academic year and ultimately understand why the bifurcation occurs.

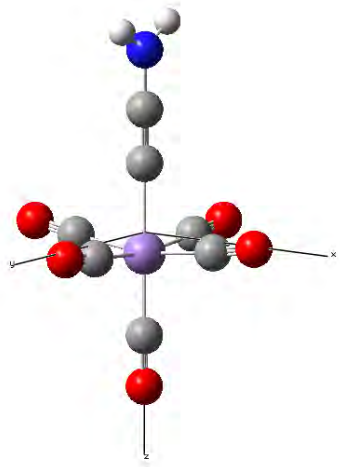


Figure 1: Distortion in $Mn(CO)_5CCNH_2$

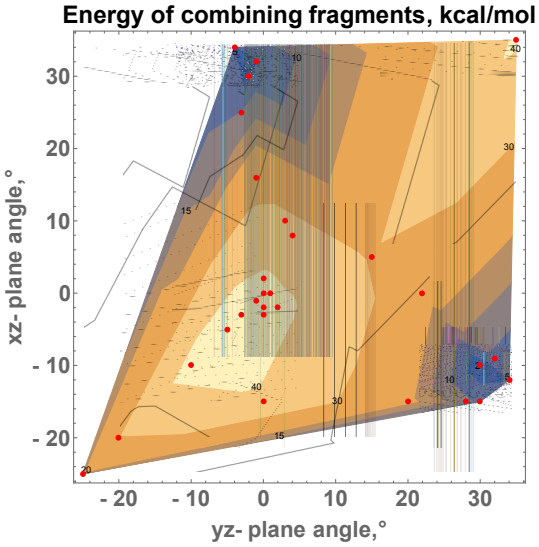


Figure 2: Energy surface map for fragmentation of $Mn(CO)_5CCC(CHO)_2^-$

(Supported by the Schultz Foundation)

Advisor: Robert Linck, Chemistry

Investigating the Effect of Lacmoid on Amyloid Fibril Formation Using FTIR

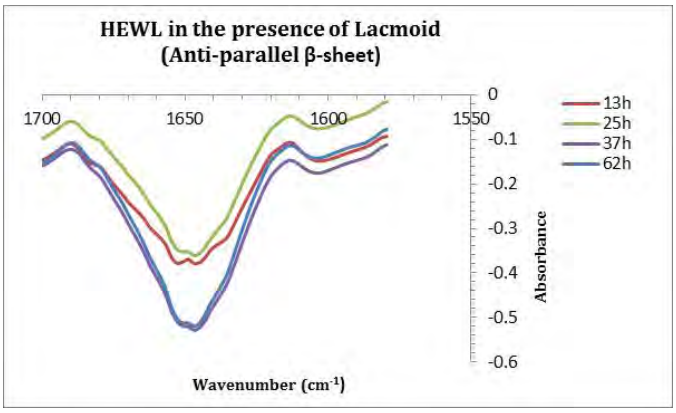
Rene Maserati/2015

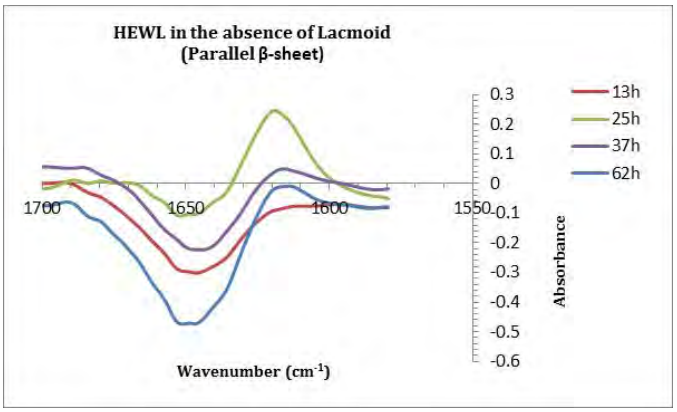
Amyloid fibrils are β-sheet rich, misfolded protein aggregates associated with diseases such as Alzheimer's and Parkinson's.[1] A buildup of amyloid beta peptide deposits has long been considered one of the primary contributors to the decline of neuronal function implicated in Alzheimer's disease.[1] However, recent studies suggest the soluble oligomer intermediate state of these peptide fragments is responsible for neurotoxicity and cell death.[1]

Multiple studies have been conducted using small molecules as potential inhibitors (or accelerators) of amyloid fibril formation, as they are easily modified and accessible, making them good therapeutic candidates.[1] However, many of these studies provide conflicting reports. Lacmoid, a pH indicator and blue dye, is one of the many small molecules that have been reported to both inhibit and accelerate amyloid fibril formation.[2, 3]

In this study, the transformation of hen egg white lysozyme (HEWL) into fibrils and oligomers in the presence and absence of lacmoid was investigated and Fourier Transformation Infrared spectroscopy (FTIR) was used to differentiate between parallel and anti-parallel β sheet conformation. An incubation solution of HEWL was prepared under acidic conditions and high heat in order to promote hydrolysis. After 24 hour incubation, lacmoid was added to half of the solution. Incubation at 62°C was continued and FTIR measurements were conducted in situ at time points over the course of a week.

HEWL in the presence of lacmoid maintained an anti-parallel β-sheet, oligomer conformation with a characteristic low frequency component at 1614 cm^{-1} and a high frequency component at 1689 cm^{-1}, whereas HEWL alone presented only a low frequency component at 1619 cm^{-1}, characteristic of a parallel β-sheet, fibril conformation.





The results of this study suggest that lacmoid inhibits amyloid fibril formation at equimolar concentrations (HEWL:lacmoid). Further investigation is necessary to determine if this is the case with an excess molar ratio of lacmoid:HEWL and vice versa. Future studies using FTIR could be useful in testing other small molecules as viable therapeutic agents.

(Supported by the Emma Bell Hauch Fund)

Advisor: David Bickar, Chemistry

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Extraction and Functionalization of Neurolenins from *Neurolaena lobate*

Katie McGeough/2016

Lymphatic filariasis (LF) is a neglected tropical disease that currently affects 1.3 billion people in 83 countries.[1] LF is caused by the parasitic roundworms *Wuchereria bancrofti, Brugia malayi,* and *Brugia timori* in the lymphatic system, and is transmitted by mosquitoes in certain stages of the worms' lives.[2] Current treatments for LF temporarily sterilize female adult worms and kill microfiliarae; thus there is a need for medications against the nematodes in all stages of their lifecycles.[3] Previously, neurolenins B, C, and D have shown anti-inflammatory as well as anti-filarial activity against the nematode *T. cruzi.*[4,5] Subsequent research at Smith College in 2014 demonstrated that mixtures of neurolenins, extracted from *Neurolaena lobata* native to South and Central America, showed anti-filarial activity against *B. pahangi* (a close relative of filarial nematode *B. malayi)* in all stages of its lifecycle.[6]

Research this summer focused on the extraction, classification, and purification of neurolenins from *N. loba*ta. It was experimentally determined, through the use of 2D NMR and HRMS, that *N. lobata* of Belize contains mainly neurolenin D (Figure 1). While reports indicate *N. lobata* of Trinidad contain mainly neurolenins A and B.[7] In addition to its purification and classification, neurolenin D was altered through an acetylation reaction; this reaction transformed both of the hydroxyl groups to acetate groups.

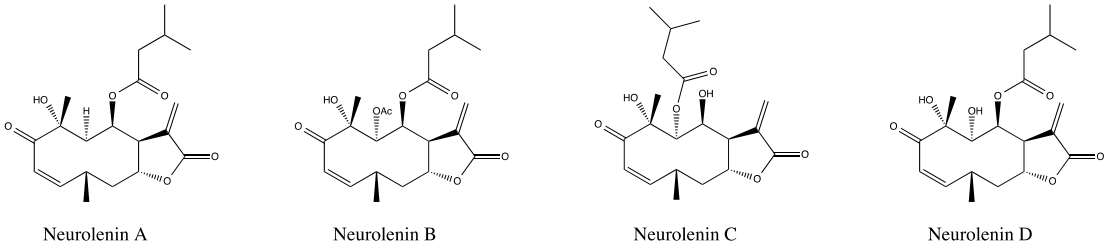

Figure 1. The chemical structures of neurolenins A, B, C, and D.

Future work for this project includes the extraction of neurolenins from *N. lobata* of Trinidad in attempts of obtaining pure neurolenin A and B. Additionally, neurolenin D, as well as its pure analog, will be tested against *B. pahangi* by the Williams lab in order to determine their biological activities.

(Supported by the American Chemical Society)

Advisor: Kevin Shea, Chemistry

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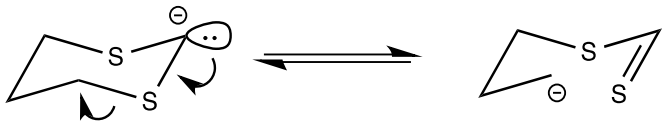
Understanding the Acidity of 1,3-dithiane

Megan Neubig/2017

Dithianes are a type of 6-membered heterocycle where two of the carbons are replaced with sulfur atoms. These compounds are often used in organic synthesis but to theoretical chemists, they present an interesting issue as well. In 1,3-dithiane, the central carbon between the two heteroatoms has been found to feature a proton with significantly higher acidity than in the oxygen equivalent of the molecule, 1,3-dioxane. This difference is hypothesized to be a result of the anomeric effect; a stereoelectronic effect that helps explain specific conformations and properties of 6-membered rings with endocyclic lone pairs. The origins of the effect itself are currently being debated but chemist believe it is either due to the stabilizing interaction between the lone pair on the carbanion and antibonding orbitals between the adjacent sulfur and carbon atoms (hyperconjugation), or the destabilizing interactions between the dipoles of the two groups (electrostatic effects).



Figrue 1. A visual depiction of hyperconjugation in 1,3-dithiane

To further explore the issue, I studied variations on the basic 1,3 substituted heterocycle. All molecules were optimized using the Gaussian 09 computer program. To analyze the acidities of each compound, the energy change upon deprotonation was compared to that of cyclohexane. Orbital interactions could be quantified through the natural bond orbital (NBO) calculations. Other changes in geometry, such as a difference in bond length and bond angle can be seen in Gaussview. Such changes can be used to see whether or not the structure of the molecule is adjusting in the way I would predict if orbital interactions were present.

I was able to conclude that the more electropositive the heteroatom, the greater evidence of hyperconjugation in the data and a greater relative acidity. This partially explains why 1,3-dithiane is more acidic than 1,3-dioxane. The properties and conformations of such compounds are important to understand when considering their reactivity, making this insight significant. However, the fact that the bond length and NBO data alone is not an accurate predictor of acidity suggests that there are other contributing factors left to be explored. Whether or not this confirms or refutes either side of the argument on the anomeric effect cannot be concluded from this data and thus, would require further investigation.

(Supported by the Dr. Marianne Tsuk Schiffer A.M. 1958. & Dr. J.P. Schiffer Advancement Endowed Fund)

Advisor: Robert Linck, Chemistry

Linkage Isomerization from Nitrito to Nitro of Cobalt(III) and Iron (0)

Jingyi Sui/2017

Nitrite can bind to metal complexes at either N or O end. For cobalt(III) pentaammine $(Co(NH_3)_5)^{3+}$, the nitro (N-bonded) complex is more stable than the nitrito (O-bonded) complex, and O to N isomerization takes place[1]. Jackson also discovered O to O isomerization, which is a faster process than the O to N isomerization.[2]

This study used Gaussian 09 to find the structures and energies of the nitrito complexes, nitro complexes of $(Co(NH_3)_5)^{3+}$ and $Fe(CO)_4$, and the transition states of the two linkage isomerizations. All the structures were calculated in the cc-pVTZ basis set. The result showed that the activation energy of the O to O transition was about half of the that of the O to N transition in both the cobalt and the iron complexes. Also both activation energies were fairly low, meaning two isomerization processes can take place easily. Figure 1 and 2 show the transition states of O to O transition and O to N transition in $Fe(CO)_4$ respectively.

Further study replaced the axial carbonyl of $Fe(CO)_4$ with $(CN)^-$ and $(NO)^+$ respectively to see how the activation energy of O to N transition changes with different ligands. The results showed that the activation energy increased about 3 kCal from $(CN)^-$ to (CO), and from (CO) to $(NO)^+$. Charge might affect the activation energy, but more ligands need to be tested.

The nitrite group in $Fe(CO)_4$ was then replaced with other ligands that could undergo similar isomerization, including NH_2CHO, $(NCS)^-$, (SO_2), and N_2. The energies of reactant, product, and the transition states were found, and the activation energies were calculated. The results showed that activation energies of all isomerization were between about 10 kCal and 30 kCal. Therefore, all these isomerization might have similar mechanism. The transition states were tested with IRC to see whether they went to the anticipated product or reactant.

(Supported by the Schultz Foundation)

Advisor: Robert Linck, Chemistry

Reference

1. Jackson, W. G., Lawrance, G. A., Lay, P. A., and Sargeson, A. M., Inorg. Chem., 1980, 19, 904.
2. Jackson, W. G., Lawrance, G. A., Lay, P. A., and Sargeson, A. M., J. Chem. Soc., Chem. Commun., 1982, 70.

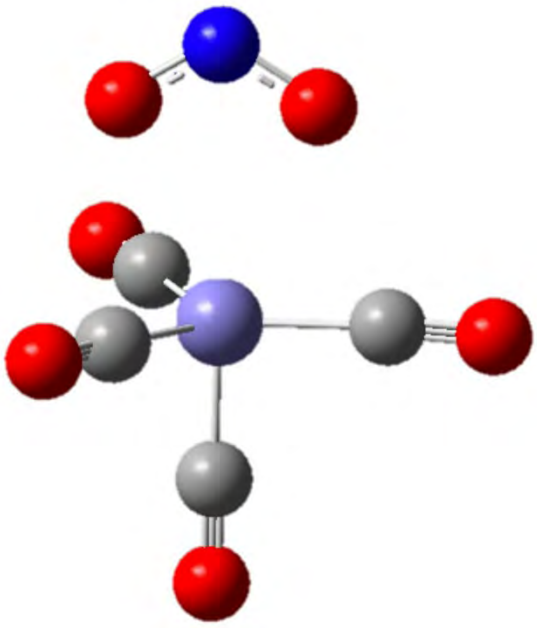


Figure 1 TS of O to O transition

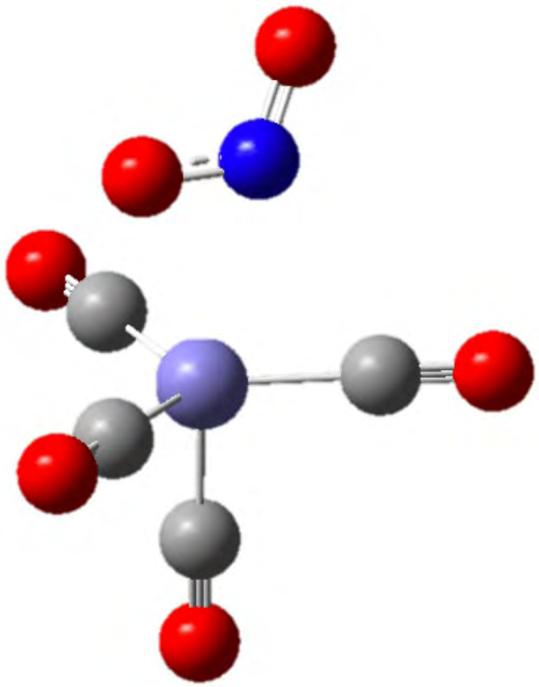


Figure 2 TS of O to N transition

Copper-Catalyzed Methylation of Phenol with Methyl Boronic Acid

Yingchuan Zhu/2017

Methylation is a form of alkylation ubiquitous in chemical research and pharmaceutical synthesis. However, the mostly used reagents, such as DMS, are usually either dangerous or toxic. Since electrophilicity is equal to toxicity in toxicology literature,[1] it is necessary to replace the current electrophilic reagent with a nucleophile. Gorin Lab has previously found that methyl boronic acid, which is a mild base and relatively stable nucleophile, can methylate carboxylic acid with copper catalyst.[2] One extension of this project is to find other oxygen nucelophiles. Therefore, my project in this summer has been focusing on methylation of phenol. Phenol methylation is also a useful strategy in research and industry, while the reagents that are widely used either are dangerous or require high temperature.

I first tried the reaction conditions for the methylation of carboxylic acid and screened the reaction with ^{19}F NMR. The data indicated that the reaction failed and a side product was formed. Then I began to search in the literature for Chan-Lam cross couplings done on N-nucleophiles, and I attempted to apply the similar reaction conditions on the alcohol. The phenol is successfully methylated by methylboronic acid when $Cu(OAc)_2$ is used as catalyst in the presence of Na_2CO_3, acetonitrile and bipyridine. The reaction requires to be heated at 55°C. Then I tried different copper sources to optimize the yield. It turned out that $CuBr_2$ gives the relatively better result. I also tried other types of solvents and pyridines, which did not affect the final yield.

However, at the current stage, the yield of this reaction is still very low, which makes it difficult to have a convincing structure characterization of the product. Therefore, one important part of the future work will be the optimization of the yield. I will also work on figuring out the mechanism of this reaction and explore the reaction scope.

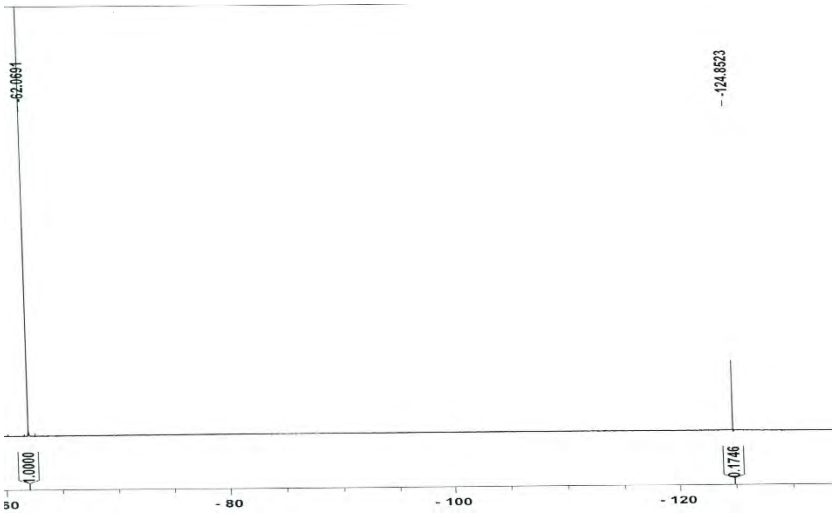
(*Supported by the Alumnae Gift Fund in Chemistry*)

Advisor: David Gorin, Chemistry

Reference:

[1] Schwobel, J.A.H. et al, Chem. Rev. 2011, 111, 2562

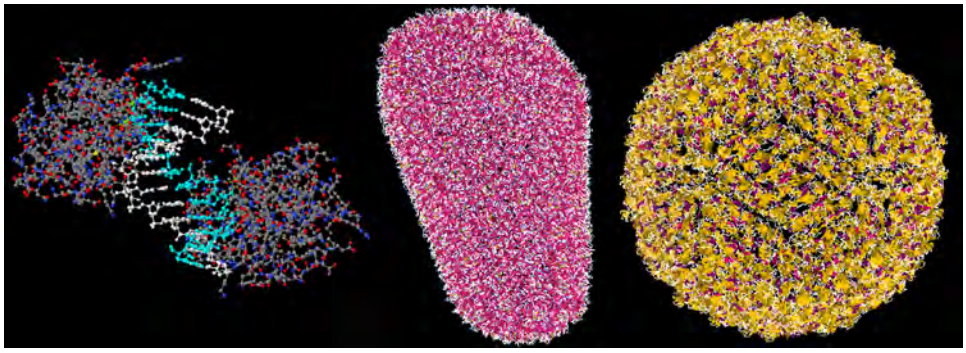
[2] J. Org. Chem., 2015, 80 (14), pp 7305–7310



The ^{19}F NMR result for the methylation of the phenol.

In Silico Extraction of Large Proteins' Property Information

Marina Cheng/2017



[1][2]

Proteins are macromolecules whose structures determine their chemical properties and essential biological roles in living organisms. In order to help biologists easily view and analyze such proteins, Professor Streinu and her LinKaGe lab created KINARI-Web that performs rigidity analysis of proteins and allows biologists to analyze a protein's rigidity and flexibility through Jmol, a Java biomolecule visualizer. [3][1] We are currently developing KINARI II that will, in addition to improved functionalities from KINARI I, perform rigidity analysis on extremely large proteins, particularly virus capsids. With fellow lab members, I created a Python program that uses MDAnalysis, an open-source object-oriented Python toolkit for molecular dynamics analysis of proteins, to extract information from extremely large proteins and output them in a form of a "summary." [4]

The first image above is a protein with the PDB ID 1ZBI, which is a small protein that KINARI I is able to operate with through Jmol. The image in the middle is a Jmol representation of several separate 3J3Y "bundle" files that contain the information for the whole protein in different files due to atom data storage limitations. The image on the right is the full biological assembly structure of the 1K4R protein. Our summary Python program allows biologists to see what their large "bundle" or biological assembly protein of interest is comprised of. KINARI II will then extract essential information necessary for further analysis and manipulation of the protein.

I also used MDAnalysis to create one of those secondary programs that KINARI II will run after the summary program. It is a Python program that hides or shows only certain parts of the PDB structure such as the DNA, RNA, or protein parts of the biomolecule, or of particular specified solvents, residues, or chains. For example, the DNA and RNA strands of the 1ZBI protein above are colored white and cyan respectively.

We are using MDAnalysis as it allows us to put information about the biomolecule in memory, and although it takes more time to load into KINARI initially, it allows us to quicken the processing process of the structure. If we use just Jmol, each step would take longer. KINARI II, once it is finished, will allow the user to choose between those methods.

We will continue to work with large data files of proteins that can be added to expand KINARI II.

(Supported by the Schultz Foundation)

Advisor: Ileana Streinu, Computer Science

[1] Jmol: an open-source Java viewer for chemical structures in 3D. www.jmol.org

[2] H.M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T.N. Bhat, H. Weissig, I.N. Shindyalov, P.E. Bourne (2000) the Protein Data Bank. www.rcsb.org

[3] Naomi Fox, Filip Jagodzinski, Yang Li, Ileana Streinu. KINARI-Web: A Server for Protein Rigidity Analysis, Nucleic Acids Research, 39 (Web Server Issue), 2011

[4] N. Michaud-Agrawal, E.J. Denning, T.B. Wolf, and O.Beckstein. MDAnalysis: Toolkit for the Analysis of Molecular Dynamics Simulations. www.mdanalysis.org

Global Proverbs: an Online Database for Computational Paremiology

Yumeng Wang/2017

Paremiology is the study of proverbs, which has a variety of uses in the study of such topics as philosophy, linguistics, and folklore. However, the existed online proverb collections failed to implement modern database and web technologies. For example, even a large quote site like "World of Quotes"[1] does not have much difference than the proverb collections in libraries. Therefore, the Global Proverbs Project I did this summer aimed to build a broad multilingual database annotated with useful metadata and multiple classification schemes. Built upon the Django web framework, the project allowed the proverbs to be annotated with cultural, explanation, date, geographic and thematic information. The Global Proverbs Project is an open resource to the internet community for proverbs research and its user-generated content also encourages interested individuals to contribute.

During the SURF program, I learned to work with Django, the high-level Python Web framework. By editing the settings, urls and templates of a project, I accomplished its internationalization so people can view a website in different languages. By the end of the program, I was more confident with Django and was able to do many tricks such as creating the database, internationalization, localization and user authentication.

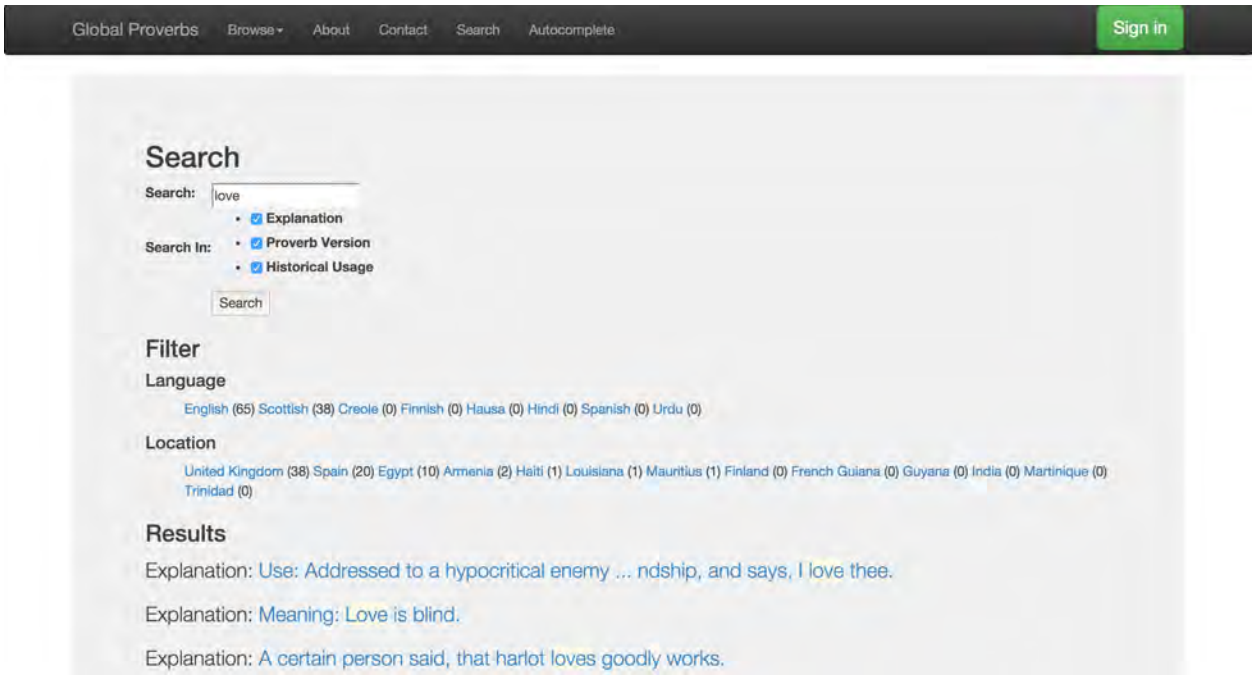
In order to use search in the project, I installed Haystack which makes integrating custom search as easy as possible while being flexible enough to handle more advanced use cases. I firstly used Whoosh, an easy search engine good for full-text search. Then I wanted to do more advanced search so I removed Whoosh and instead used Solr, a more complicated search engine with more features. Finally, I successfully customized the search form and applied model search and facet search on the same page. I also wrote my own highlighter to bring the readers a better view of the search results.

This SURF experience strengthen my problem-solving abilities as well as my confidence to do in-depth research on a specific project. It encourages me to do special studies in the same field in future academic year and continue graduate study in computer science.

(Supported by the 5 College Digital Humanities)

Advisor: Eita Mendelowitz, Computer Science

1,Famous Quotes, Quotations, and Sayings at WorldOfQuotes. (n.d.). Retrieved February 16, 2015, from http://www.worldofquotes.com/



Equipping the DesignLab@Smith to be a More Collaborative Space for Students and Faculty

Claire Adams/2016, Cindy Li/2018, Cecely Ogren/2016 and Ziqiu Zhang/2018

The overarching purpose of the DesignLab@Smith is to provide a space for students and faculty for "the active creation of the new realities that they have imagined as possible."[1] The summer of 2015, the Design Thinking group focused on designing and building the tools to equip a classroom for experiential interdisciplinary collaborative design work in any field. Currently, traditional classrooms lack adequate writing space and often contain permanent and/or heavy furniture that cannot be rearranged to specific needs. We tackled these challenges by creating more writing surfaces as well as building movable furniture.

Utilizing the book, Make Space, from the Institute of Design at Stanford to guide us in designing and building furniture for educational spaces in the Center of Design and Fabrication, we worked on three categories: working surfaces, writing surfaces and miscellaneous. For the first category, we built small group tables with 4 milk crates that serve as individual storage spaces. Furthermore, we built prototypes of whiteboard t-walls, z-rack, posts and movable whiteboards that could be hang on posts. Lastly, we decide to use milk crates for short term seating and then continued developing connectors that hold two crates together to serve as mini-storage units.

Through our work, we learned design is a continuous process. In order to make improvements, empathy for the user is critical. We learned, despite comfort being individualized, that we must conceive a comfort standard which a majority would be satisfied with. We discovered having adjustable components, such as height adjustable tables, are ideal. However, permanent fixtures are far more time efficient and practical. The typical classroom design creates an inconducive learning environment, therefore our solution is to utilize comfort and customizability to make classrooms more user-friendly.

Enhancing a classroom's design improves the usability of that space. For example, more whiteboard space allows students to better visualize concepts and problems. The next step is for DesignLab@ Smith to gather feedback from the students and faculty interacting with the prototypes in the teaching space. We will use their comments to continue improving our prototypes, as well as working on new designs to meet their needs. The DesignLab@Smith will be operating as a center for interdisciplinary collaboration and creative classroom design starting January of 2016.

(Supported by the Branta Foundation Grant)

Advisor: Borjana Mikic, Engineering

[1] Mikic, Borjana et al. 2015. Design Thinking and the Liberal Arts: a cross-campus initiative at Smith College. 2.

Investigating Renewable Energy Potentials in Jordan

Leen Hayek/2016

Jordan is a rapidly developing country located in the heart of the Middle East. Unlike many of its neighboring countries, Jordan is lacking in natural resources, specifically fossil fuels that are traditionally used for electricity generation. Due to increasing urban development and electric load, Jordan faces many challenges with regards to meeting its electric demand and allocating the financial resources necessary to do so. This serves as the motivation behind this research. As a result, I was working to incorporate renewable energy technology into the Jordanian electric system. The system was modeled using HOMER[1] software. Multiple scenarios were modeled including those where no renewables were utilized, those where 10% or 20% renewables were utilized, and those were only solar power was the only renewable utilized. This was done to investigate the effect of incorporating renewable technology on the price of electricity and to find scenarios where cleaner electricity could be provided for Jordan.

Initially, I created a map of all the generation facilities in the Kingdom, and gathered information about their capacities and fuel sources. However, I also needed to acquire multiple data sets to model the system. This included power demand data for the capital city, Amman. In addition, wind availability and solar availability studies were conducted to decide which areas were most suitable locations for wind turbines and solar farms. After examining the results, I selected the city of Aqaba as an appropriate location. Afterwards, solar radiation data and wind speed data were collected from Aqaba. The wind distribution data was modeled using Weibull Distribution to examine the probability of a certain wind speed occurring at the given location. After modeling the different scenarios, I compared the system and electricity costs, environmental impact and system reliability.

This research will be continued as a special studies project for the next semester and furthermore will utilize power data for the entire kingdom, rather than focusing on the capital city. The fuel cost data is based on current fuel prices in Jordan. However, in the future, I hope to incorporate price inflation and variations in fuel costs into my model.

(Supported by the Schultz Foundation)

Advisor: Judith Cardell, Engineering

1, HOMER. Computer software. Vers. Legacy.

2, "National Electric Power Company - NEPCO HomePage." National Electric Power Company - NEPCO

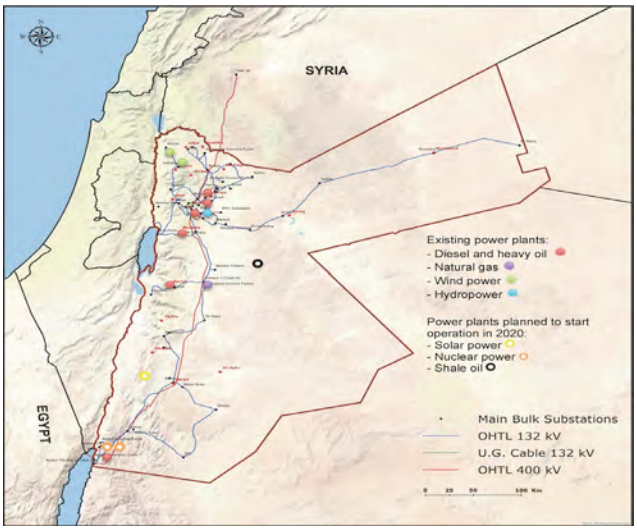


Figure 1: The transmission lines of the Jordanian grid[2]. The figure was updated to show installed power plants and those planned until 2020.

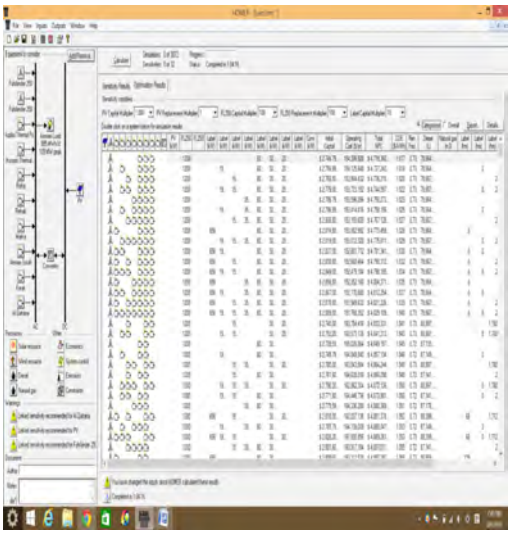


Figure 2: component diagram for one of the cases modeled by HOMER.

Wide Band Acoustics Immitance Database

Xi (Wendy) Jiang/2016

Wide band acoustic immittance (WAI) measures are an active area of research in which the goal is to develop these measures as a noninvasive auditory diagnostic tool for people of all ages. WAI measurements can be reported in many related formats, including: absorbance, admittance, impedance, power reflectance, and pressure reflectance. All can be calculated from a single ear-canal pressure measurement and a measurement of the source's Thevenin (or Norton) equivalent.

Over the summer, I was responsible to build a database and a database website. In particular, this database website hosts a database for WAI measurements made on normal ears of adults with age 18 and above. The measurements are data that had been published in a peer-reviewed format. The goal of the database is to enable auditory researchers to share WAI measurements and combine analyses over multiple datasets. Now this database has included data collected from one published paper and is ready for contributions of data from other researchers using instructions on the database website. A brochure including instructions for modifying the database and the database website was written for future use.

In the coming fall semester, I will continue adding qualified data to the databased and improving the database website as part of my honor thesis.

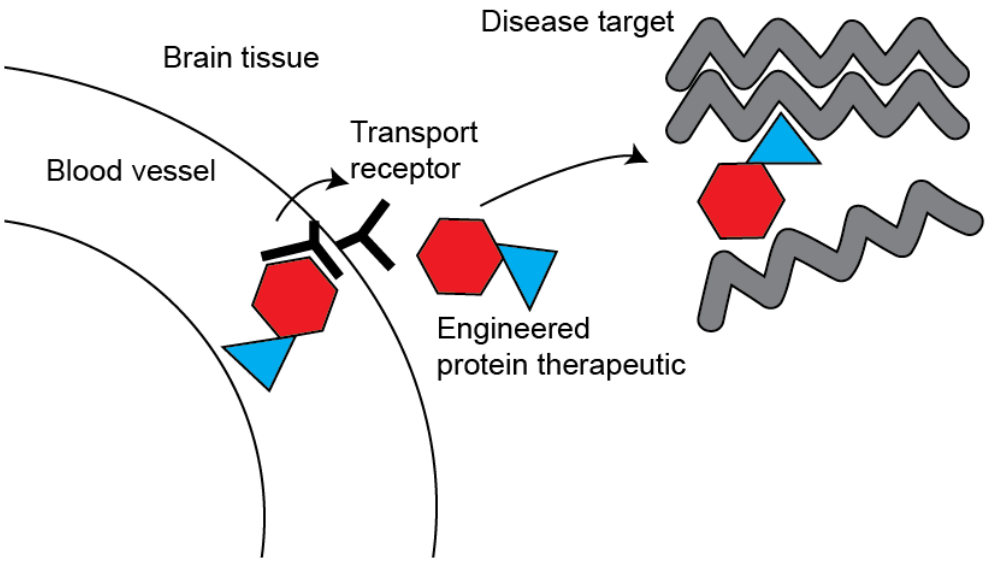
(Supported by the National Institutes of Health)

Advisor: Susan Voss, Engineering

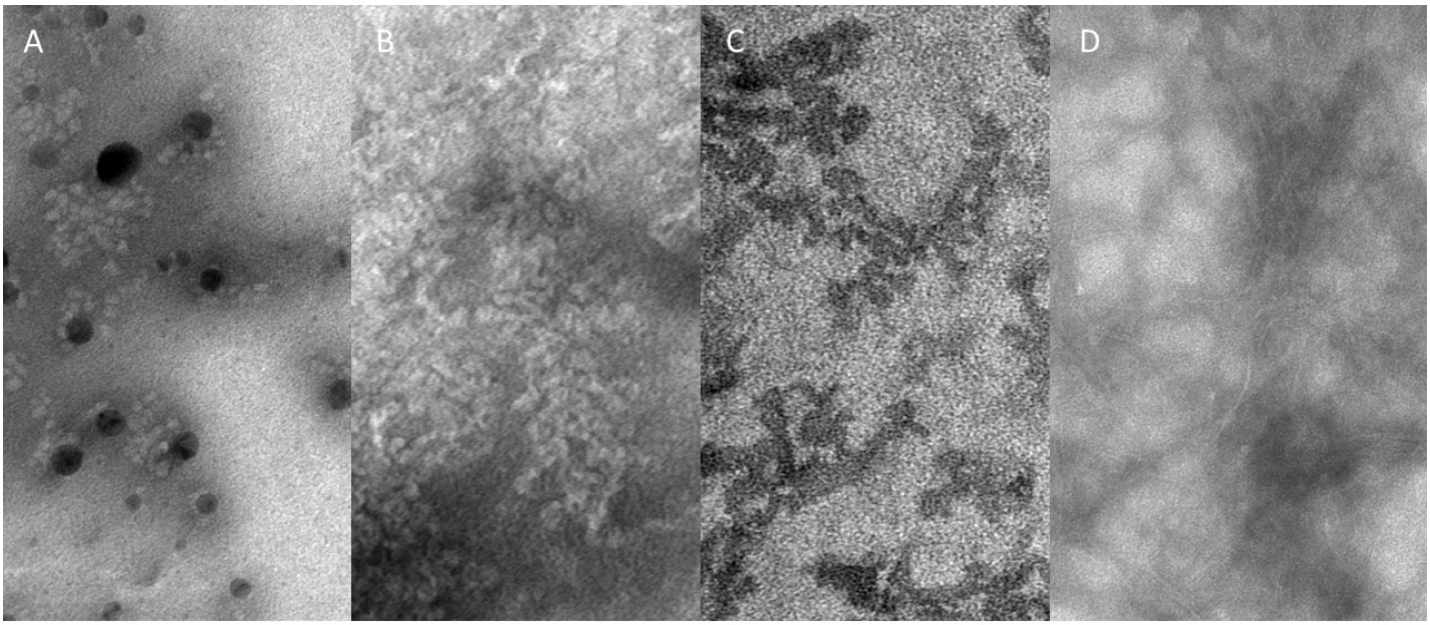
Engineering Proteins to Cross the Brain-Blood Barrier for Targeted Therapy in the CNS

Ayesha Khan

Target-specific proteins can be engineered to surpass the brain blood barrier and have therapeutic significance to help target and cure diseases of the central nervous system such as Alzheimer's disease. However, systematic cloning strategies must exist to engineer specific proteins that target and bind to the molecular aggregations shown by patients of Alzheimer's disease. We worked towards making aggregates of the amyloid-β peptide, then engineering a protein complex that contained linkers that would link together the amyloid-β binding receptor domain (the part of the molecule that will bind to the disease target) and the transferrin binding receptor domain (the part of the molecule that will help the protein surpass the blood brain barrier) into a protein complex.



We treated our amyloid-β monomer with tris buffer and heat (different times for different inductions) and used transmission electron microscopy to image and conclude that we had successfully developed both amyloid-β protofibrils and aggregates. A combination of transformation ligations, PCR, gel purifications and double digestions was performed to successfully produce gene sequences of the two selected linkers: EAAAK and GGGGS transformed into the Flag His tag. This gene sequence could potentially combine the amyloid-β binding domain and transferrin binding domain of our protein complex.



TEM images of aggregates grown from Aβ40. The scale bar is 200 nm wide and all images are shown at the same magnification. All samples were treated with 20 mM Tris–HCl, pH 7.4 and 100 mM NaCl (Tris-buffered saline, TBS) and incubated at 37°C under quiescent conditions. The protein concentrations and incubation times are as follows: (A) 199 μM Beta – Amyloid (1 - 42), *t* = 0 h. (B) 99 μM Beta – Amyloid (1 - 42), *t* = 6 h (C) 99 μM Beta – Amyloid (1 - 42), *t* = 12 h (D) 99 μM Beta – Amyloid (1 - 42), *t* = 24 h

After confirming the aggregation of amyloid-β, flow cytometry was used to measure the binding affinity of biotinylated amyloid-β to fibronectin binding domains. Methods used included growing the varying fibronectin cell cultures in SD and SG media and then dual labelling them with 9E10 and GTαMSPE antibodies, aggregated amyloid-β and strept-488 fluorophore tag. Some fibronectin variants were predicted to bind to the amyloid-β aggregates and some were not depending on the fibronectin loop variations. Flow cytometry determined if these labels had successfully expressed the c-Myc tag and the fibronectin binding domains were successfully binding to the AB aggregates. The flow cytometry results indicated that the c-Myc tag was being successfully expressed while there was variation in the expression of strept-488 between the different fibronectin loops calling for further study. To further continue this project, flow cytometry must be used to determine the binding affinity of all, amyloid-β monomers, protofibrils and aggregates ,with the different fibronectin amyloid binding loops. Variation in results between the monomer, protofibrils and aggregates will indicate which fibronectin loops bind best to which phase of amyloid-β hence helping us decide the protein sequence that would work best in targeting the amyloid-β clusters that cause Alzheimer's disease.

(Supported by the

Advisor: Sarah Moore, Engineering

Demand Response

Grace Lee/2017

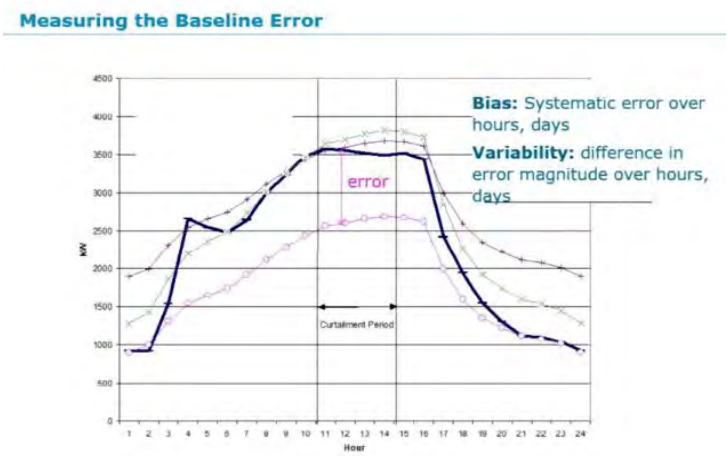


Figure depicting estimation of electricity usage vs. actual electricity usage. Emphasis placed on error.

Use of renewable energy sources has become a recent priority given that our unsustainable lifestyle heavily contributes to the detrimental effects of climate change. The concept of demand response, if successfully implemented, is just one method that will lead to a more sustainable future and lifestyle. Miriam Goldberg, a policy advisor and researcher for sustainable energy use, describes the concept of demand response as "how well we can measure what didn't happen and predict what won't". It is a practice that decreases the demand of electricity to meet the supply rather than the usual practice of increasing supply to match demand. Demand response encourages customers to reduce electricity usage during critical peak periods and utilize electricity during off-peak periods. The problem that Goldberg is addressing is incentive; because there's not an accurate way to measure electricity that is not used, it is hard to pay customers for saved electricity, and therefore harder to implement demand response into our daily lives. This is the fundamental challenge as seen in the figure above; there is no way to meter what was not used.

This means that when renewable energy sources, such as wind and solar, are producing electricity, customers are encouraged to continue their usual habits. Additionally, during peak periods when renewable energy sources are not able to produce as much electricity, consumers decrease their usage. Not only is this a more efficient and cheaper method of using electricity, but customers are also rewarded with a lower energy bill as well as reduced risk of outages [and other electrical interruptions]. It requires a more active participation in the market, but presents many advantages. Demand response is currently the most efficient solution for using renewable electrical sources and is a much cheaper alternative to building new power plants or installing electric storage devices.

(*Supported by the National Science Foundation)*

Advisor: Judith Cardell, Engineering

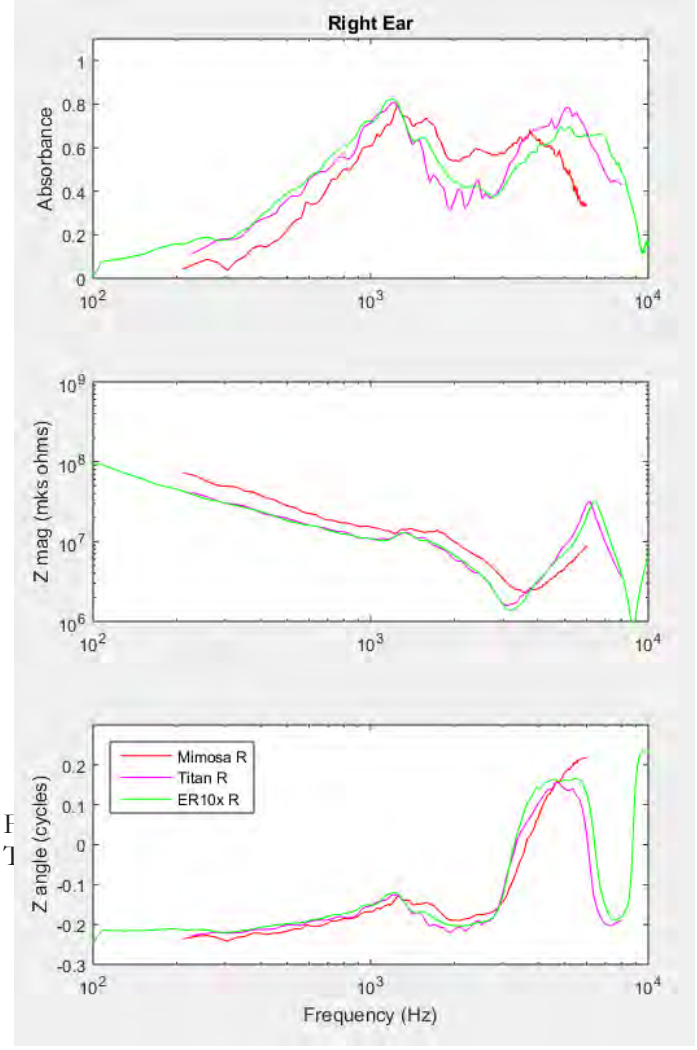
Wideband Acoustic Immitance

Annie Murillo/2016 and Audrey Ong/2016

Wideband acoustic immittance (WAI) is an emerging noninvasive auditory diagnostic tool that collects both power-based and impedance-based measurements. The potential use of these measurements includes the detection of middle ear problems such as otitis media with effusion (OME), which is characterized as the presence of fluid in the middle ear. The current pervasive auditory diagnostic tool is tympanometry; however a tympanometry measurement requires pressurization of the ear, and thus cannot be performed on infants as it may damage their eardrum. On the other hand, WAI does not require pressurization and is able to collect data over a higher range of frequencies, which is where the detection of most middle ear problems occurs.

Current FDA-approved devices that can measure WAI are the HearID from Mimosa Acoustics and Titan from Interacoustics. Another WAI device that is undergoing development is the ER-10X system from Etymotic Research - while currently only being used for research purposes, it has the intention of also becoming medically licensed by the FDA. For this study, we were interested in determining if WAI measurements taken varied depending on which of the three instruments was used to measure WAI. The study is also interested in quantifying if parameters such as age, gender, and race have an effect on WAI measurements. These findings will help WAI researchers share data among each other more effectively.

Over the summer, we were responsible for getting the HearID, Titan, and ER-10X systems ready and running for the clinical research trials that will take place over the course of the next school year. Since the ER-10X system is a research unit, we needed to make sure that it worked correctly and was ready for the clinical trials. As part of the process, we have learnt how to read the pressure and Thevenin magnitude and angle graphs generated by a WAI measurement, and also learnt to identify measurement problems such as leaks, non-linearity, and noise. We also collaborated with the researchers and engineers that developed the WAI instruments to solve the unexpected difficulties that were encountered. A few of the breakthroughs to get the ER-10X to work were changing the method used to calculate the Thevenin equivalent on Matlab, and also modifying the measurement procedure.



In the Fall, Annie will continue with the research as a special studies project and will be part of the team that will conduct the WAI measurements on adult human subjects.

(Supported by National Institutes of Health)

Advisor: Susan Voss, Engineering

Design and Testing of PEM Fuel Cell Stacks for Meteorological Balloons

Julieanna Niu/2016

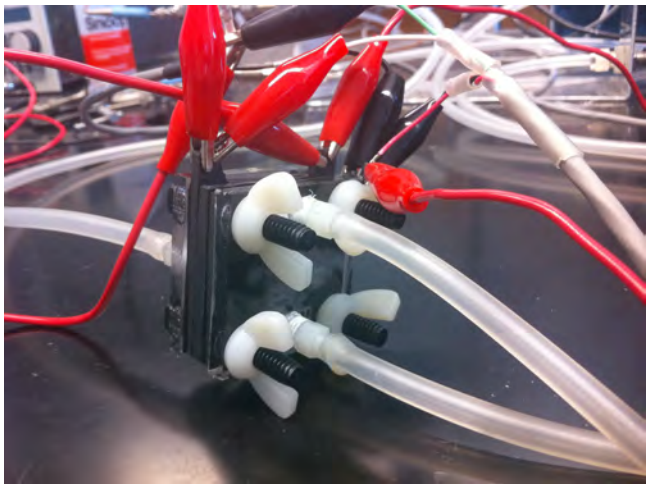
A fuel cell is an energy conversion device that takes chemical energy from an input fuel (hydrogen) and outputs electrical energy and water through an electrochemical reaction. Proton electrolyte membrane fuel cells (PEMFCs) can potentially be used as an alternative to lithium-ion batteries for powering controlled meteorological (CMET) balloons, which are a type of unmanned aerial vehicle used in atmospheric research. Lithium-ion batteries meet these needs but have the drawback of being caustic, which can cause adverse environmental effects if not recovered after a flight. A PEMFC is a promising alternative option to meet the energy needs of CMETs, in addition to being an efficient and clean power system that runs on a renewable fuel. Ultimately, a successful PEMFC system for this application must achieve specific power and energy densities comparable to those of lithium-ion batteries (approximately 80mW/g and 300 Wh/kg respectively).

To this end, two types of 2-cell stacks were fabricated and constructed, with one cell utilizing Buna-N gaskets and ELAT cloth gas diffusion layer (GDL), and the other utilizing silicone gaskets and Sigracet paper GDL. Both stacks were tested under a variety of conditions, including initially testing without membrane wetting, without clamping, and at various air flow rates. In all tests, the stack successfully held pressure, indicating that the stacks were well sealed. Stack performance for most tests appeared to be stable at low currents; however, at higher currents (typically 0.7A and above) instability became more apparent as the two cells operated at noticeably dissimilar voltages. All stacks exhibited significant performance degradation after the addition of water to the cell, suggesting that cathode flooding may be a problem. Cell performance also generally improved after the addition of a c-clamp, suggesting that a better compression method can be implemented. The effect of using different gasket/GDL combinations could not effectively be determined due to the difficulty of delineating the effects of multiple factors under current testing conditions.

Because the stacks did not perform as well as can be expected, the next step will be to identify and delineate the factors that are causing the current design to operate at this sub-standard level, and to adjust the design accordingly. Ultimately, the stack should operate at 0.5V per cell at 300 mA/cm^2, and exhibit better stability. Possible avenues where cell performance can be optimized include an investigation into cathode flooding and air humidification. This work will continue into the next academic year as an honors thesis.

(Supported by the Schultz Foundation)

Advisor: Denise McKahn, Engineering



Design Thinking

Cecely Ogren/2016

The objective of the design thinking project is to research, design, and fabricate a space where anyone who is part of the Smith College community can go to design and build projects collaboratively. This is very important because every other design and fabrication space on campus has clearly defined departmental or divisional affiliations; thus, Smith College needs an interdisciplinary design space.

The majority of the preliminary research we, my team members and I, did was through reading Maker Space by Scott Doorley and Scott Witthoft and fabricating our own variations of their design oriented furniture to be placed in the design space/classroom.[1] Once the piece was fabricated, we would use the furniture in the space temporarily allotted to us to see how our designs held up and to see how they could be improved to be more conducive to an open, creative atmosphere.

Maker Space explained that movable furniture helps get students into a creative mindset, and whiteboard space allows people to write down and work through problems. With this is in mind, we made a table that is on wheels for mobility and also has removable crates for storage and for transporting small projects from place to place, as shown in the photo below. We also built was a T-shaped, whiteboard covered wall on wheels to be used as a mobile partition and white board for groups sharing a space.

The Design Thinking project is giving all Smith College students a place to design and build. This project is also giving research students the opportunity to find out what kind of atmosphere is most conducive to effective design and creative solutions and the opportunity to work with their hands by physically building such an atmosphere and testing what variations of designs work best in that situation. There is still plenty of building to be finished and research to be done on design efficiency, which makes it very likely that one of my younger team mates will continue this into the new academic year as a special studies or as an honors project, or perhaps another group of summer researchers will continue with it next summer.

"Crable"

(Supported by the Branta Foundation Grant)

Advisor: Borjana Mikic, Engineering

1 Doorley, Scott, and Scott Witthoft. Make Space: How to Set the Stage for Creative Collaboration. Hoboken: John Wiley & Sons, 2012. Print.

Extracting Energy From Forest Residues Using Biomass Conversion Technologies

Anna Partridge/2016

Forest residues are consistently burned on the hillside in the United States, releasing energy that could be used to generate electricity or thermal power. Currently, the cost of storing, chipping and transporting these logging waste products is not economically viable for the forestry industry. My research team is researching the conversion of wood chips into a more valuable product, which may ultimately be more economically feasible and environmentally sustainable, while providing a reliable renewable energy source.

Both a literature review of biomass gasification technologies as well as field-testing of a pilot scale torrefier, dryer, and briquetter were done during this project. Torrefaction increases the mass and energy density of the wood chips so that they may be co-fired with coal after pelletization.[1] Briquetting uses high pressure to densify the wood chips into blocks to increase transportability and increase the energy content of the wood on a per mass basis. A test matrix including three different species of wood at different chip sizes and moisture contents was used to determine the conditions which produce the most energy dense and durable briquettes, while the same three species of wood were tested in the torrefier at varying moisture contents, temperature and residence time conditions.

In order to determine the impact of input parameters on product characteristics, a thermo-gravimetric analyzer (TGA) and bomb calorimeter will be used to determine the proximate analysis, ultimate analysis, moisture content, and higher heating value. These measures of product quality will be related to the temperatures and residence times within the reactor as well as the moisture content of the wood chips before entering the reactor.

The research team hopes to develop recommendations for the optimal input conditions to increase the energy content and economic value of the resulting products. This information will be published in technical reports and scholarly articles. My Senior Honors Thesis will be a continuation of this work, intended to investigate the thermal profiles inside the torrefier and provide design recommendations to improve the control systems which govern the high-temperature torrefaction process and therefore give the operator direct control over the quality of the torrefied product.

(Supported by the Schultz Foundation)

Advisor: Denise McKahn, Engineering

References: Kleinschmidt. C. 2011. Overview of international developments in torrefaction. Central European Biomass Conference.

Briquetter and feedstock piles at remote test site.

Engineering Theranostic Protein for Tumor Biomarker Mesothelin

Deepal Patel/2017 and Elsie Odhiambo/2017

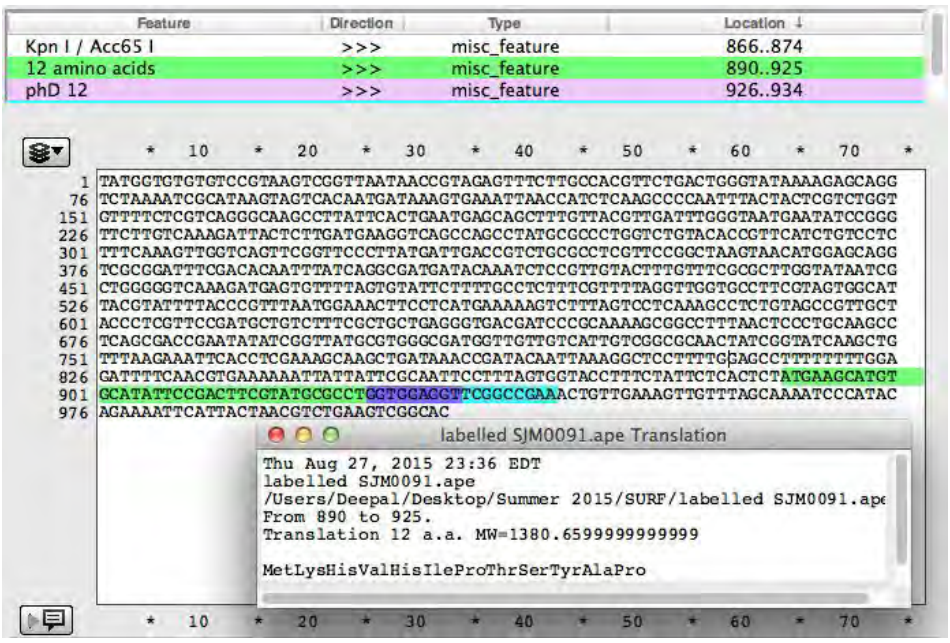
Can we find the genotype of a protein that has been shown in previous research to bind most effectively to a tumor biomarker: Mesothelin (MSLN).[1] Is it possible to use that protein as a theranostic for triple negative breast, ovarian, lung, and pancreatic cancer where MSLN is overexpressed? How can we

determine if this protein binds well to MSLN in vitro and in vivo? These questions have been at the root of our summer research. They are important for the development of a target specific; in this case MSLN; protein based drug.[2] So far, there are no such drugs that have been approved by the FDA.

A previous researcher collected phage samples that bound to MSLN through panning.[3&4] Eluate from each wash, up to the fourth, was collected and stored. Through the process of plating and phage

amplification we isolated and amplified individual peptide sequences; incorporated in bacteriophage; that hypothetically bind strongest to MSLN (from the 4th eluate). We then applied Sanger sequencing to determine their genotypes. Afterwards, we performed multiple ELISA tests to investigate whether the obtained proteins bind to MSLN and how well they are binding.

Image showing the peptide sequence retrieved that potentially binds strongest to MSLN.



Phage samples that we isolated and successfully sequenced all yield the same peptide sequence that is highlighted above. In the future, we are planning further ELISA tests for this sequence having determined the type of plates to use as ELISA results showed possible plastic binding. In order to have a diverse range of peptide sequences to choose from for future applications, we will sequence phage samples from the third and second eluate.

The protein we isolated could potentially be used as a theranostic for the aforementioned cancer types. It could possibly be modified via incorporation into other scaffolds for diagnosis and drug delivery. Such scaffolds include larger protein scaffold and even polymers. We plan to continue this work over the semester as a special studies in order to run the aforementioned ELISA assays as well as develop other aspects of this project.

(Supported by National Institutes of Health)

Advisor: Sarah Moore, Engineering

Engineered Therapeutic and Diagnostic Proteins Targeting Tumor Biomarker Mesothelin

Allison Sirois/2016 J

In recent years, there has been significant progress in developing targeted cancer diagnostics and therapeutics, allowing for increased efficacy and reduced toxicity. For many cancers however, such as triple-negative breast, ovarian, pancreatic, or lung, targeted options are not yet available. Thus, new biomarkers for these cancers must be identified and appropriately translated for clinical application. Mesothelin (MSLN), a cell surface protein, is expressed at high levels on these tumors, with limited expression in healthy tissue[1]. Furthermore, MSLN has been shown to bind another known tumor biomarker MUC16 (CA125), an interaction shown to facilitate cancer progression and metastasis. The differential expression pattern of MSLN, and its association with MUC16, makes MSLN a promising biomarker. We aim to engineer MSLN-targeting proteins to interrupt the MSLN-MUC16 tumor biomarker interface, with applications as both molecular diagnostics and targeted therapeutics.

Based on the non-antibody fibronectin scaffold, we are using directed evolution and yeast surface display technologies to engineer high-affinity proteins that target the domain of MSLN responsible for binding MUC16 (Figure 1). We have identified, recombinantly expressed in yeast, and purified the minimal binding domain of MSLN that binds MUC16[2].

Using magnetic- and fluorescent-activated cell sorting (FACS), we have identified fibronectin variants that bind the MSLN minimal binding domain with moderate affinity (K_D ~ nM). We have established in vitro assays to measure the engineered proteins' binding to tumor cell lines expressing MSLN or MUC16. Work in progress includes measuring the stability, binding affinity, and bioactivity of the candidate proteins, while developing assays to measure their biological activity on tumor cell lines. Future work will evaluate the engineered proteins as molecular imaging agents by injecting fluorescently labeled variants into tumor-bearing mice and measuring in vivo tumor contrast. We will also validate their therapeutic potential by measuring their effect on cell proliferation and apoptosis in tumor cell lines.

(Supported by the Schultz Foundation)

Advisor: Sarah Moore, Engineering

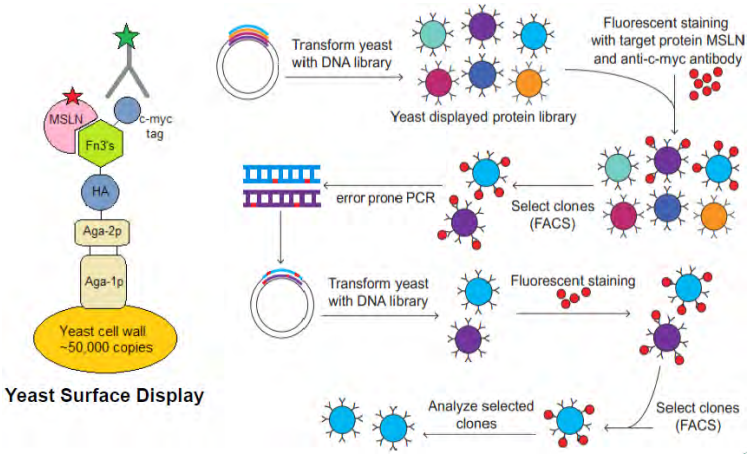


Figure 1: Schematic of project design. Yeast surface display is coupled with directed evolution and FACS to engineer novel binding proteins to block the MSLN-MUC16 interface.

[1]Chang, K., et al. (1992) Isolation and characterization of a monoclonal antibody, K1, reactive with ovarian cancers and normal mesothelium. Int J Cancer. 50, 373-81.

[2]Kaneko, O., et al. (2009) A binding domain on Mesothelin for CA125/MUC16. J Biol Chem. 284, 3739-49.

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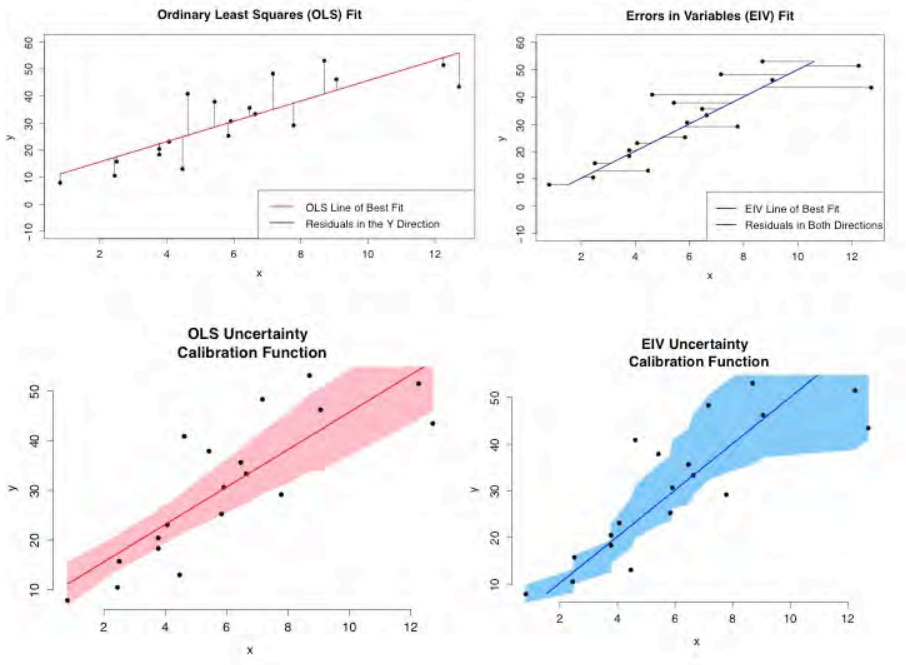
2. Ho, M. Feng, M. Fisher, R. Rader, C. Pastan, I. A novel high-affinity human monoclonal antibody to mesothelin. International Journal of Cancer 2011
3. Moore, S.J. Engineering Cystine-Knot Peptides for Molecular Imaging of Cancer. Stanford University Bioengineering 2012
4. George, K.S. Engineering Diagnostic and Therapeutic Microproteins Targeting the Interface of Tumor Biomarkers Mesothelin and MUC16. Smith College Biochemistry 2015

"Big Force" Calibrations: An Errors in Variables Approach

Sara Stoudt/2015

Measuring forces is key to commerce (weighing truck loads at truck scales), to manufacturing (shaping automotive body panels using presses), and to transportation (thrust of aircraft jet engines). Forces are measured using devices called force transducers, which convert an applied force to the deflection of an indicating mechanical pointer, or to an electrical signal (also called a deflection, by analogy). These devices are elastic, in the sense that they return to their original condition once the force is removed. Calibrating such a device means establishing a mapping between applied forces and instrumental indications. The National Institute of Standards and Technology (NIST) uses machines with large weights to calibrate transducers capable of measuring forces of up to 4.5 million newton (the weight of 180 Humvees!). NIST calibrates force transducers by applying known forces that the earth's gravity exerts upon very large stainless steel disks, and relating these forces to the corresponding deflections using a calibration curve. When the force transducer is used in practice, the user observes a deflection and uses the calibration curve to determine the corresponding force.

Currently, an ordinary least squares method is used to fit a curve (usually a polynomial of low degree) to the calibration data. However, this method does not account for the uncertainty in the applied forces, which can bias the fit. I have developed and implemented an alternative errors-in-variables (EIV) method that takes into account uncertainties in both the applied forces and the deflections. I also implemented a procedure for uncertainty quantification that produces a confidence band for the entire calibration curve. Both this EIV method and the procedure for the evaluation of measurement uncertainty are currently being incorporated into the NIST force calibration services.



(Supported by the National Institute of Standards and Technology)

Advisor: Antonio Possolo, National Institute of Standards and Technology (NIST)

Potential Methods for Data Anonymization

Angela Upreti/2016

Researchers in many fields anonymize the identity of research participants to maintain the privacy of the participants. The assurance of anonymity makes it easier for the participants to provide their information. Effective anonymization in context of a computer network has a lot of implications in the process of information gathering. If anonymization is done effectively, it should be impossible to link individual users in the computer network to their specific activity in the network. Hence, the participants are protected from the fear of their information being misused and moreover, the available information can then be used for benefit of the larger society. For SURF, I researched potential methods for data anonymization within a computer network.

Based on Professor Cardell's suggestion, I mostly looked at how pseudonymity is achieved in the Bitcoin Network. Bitcoin Network is a giant P2P network that has supported the alternative digital currency, Bitcoin since 2008. The network masterfully tackles the traditional problem of 'double spending' that kept other digital currencies from being prominent. In addition, I also looked at other P2P networks like TOR to learn more about how they protect user's identity.

With the help of some literature and online lecture series on Bitcoin, I was able to learn the underlying cryptographic and hashing principles used in the network and also the weakness and strengths of the network. I also got to download the entire bitcoin block chain which was about 20 GB of data and a bitcoin wallet. Being able see the workings of the block chain and the walled helped me better understand how public keys support the network. At the end, I was able to recognize that complete anonymity is not achievable in the Bitcoin network. Public key clustering can be used to track the flow of Bitcoins.

Researching Bitcoin and TOR gave me a lot of ideas about data anonymization. I plan to develop on these ideas for my honors project and code a simulator based on my idea.

(Supported by the National Science Foundation)

Advisor: Judith Cardell, Engineering

Wind Power Integration and Smart Grids

Jin Rui Yap/2016

It is estimated that renewable energy currently consists of approximately one fifth of world electricity production in the world.[1] The endeavour to increase this number is of paramount importance as the world population continues to rise while the earth's resources remain on a decline. The consumption habits of human beings are unsustainable in the long term, and renewable energy options are deemed by many as the solution to solving this crisis. I chose to focus my research on wind energy and its integration into conventional power grids. I also worked on deepening my understanding of the function of Smart Grids.

My first step was to understand the process and the science behind wind power generation and integration into conventional power grids. I watched online course videos on the science behind wind turbines, read texts on the topic recommended by Professor Cardell, as well as conducted an overall literature review on the use of wind power generation as a mainstream source of electricity as well as the issues associated with that. Subsequently, I used the HOMER software to better analyse off-grid hybrid power systems, running cost analyses on combinations of wind turbines, diesel generators, converters, inverters and batteries. Lastly, I focused my research on the use of JAVA Agent Development Framework (JADE) in Smart Grids.

Through the literature review, I learned that the integration of wind energy into the grid creates potential technical challenges that affect the Power Quality of the system, largely due to the intermittent nature of wind energy. Some of the issues associated with this includes load management, developing effective storage systems as well as forecasting and scheduling.[2] I also learned that, for off-grid hybrid systems, it is important to have the correct combination of components with the right capacities in order to ensure cost effectiveness. Lastly, I gained a beginner level competency in JAVA so as to better understand the structure of JADE.

In order to increase the viability of wind power generation as a means of mainstream power generation, it is important that the barriers highlighted above are taken to into account and resolved. This research experience has been enlightening for me as I have gained a deeper understanding of the functions of conventional power grids and wind energy generation systems, as well as the technology that is at the forefront of this field.

Sensitivity Results | Optimization Results

Double click on a system below for simulation results.

AIR	Label (kW)	S4KS25P	Conv. (kW)	Initial Capital	Operating Cost ($/yr)	Total NPC	COE ($/kWh)	Ren. Frac.	Diesel (L)	Label (hrs)
	1000	10	500	$ 40,000	1,241,739	$ 15,913,592	4.666	0.00	1,242,325	8,015
2	1000	10	500	$ 65,000	1,242,172	$ 15,944,121	4.675	0.00	1,241,860	8,012
4	1000	10	500	$ 90,000	1,242,604	$ 15,974,651	4.684	0.00	1,241,395	8,009
6	1000	10	500	$ 115,000	1,243,656	$ 16,013,096	4.695	0.00	1,241,550	8,010
8	1000	10	500	$ 140,000	1,244,243	$ 16,045,604	4.704	0.00	1,241,240	8,008
10	1000	10	500	$ 165,000	1,245,140	$ 16,082,070	4.715	0.00	1,241,240	8,008
	1000	8	500	$ 35,000	1,269,173	$ 16,259,295	4.767	0.00	1,270,070	8,194
2	1000	8	500	$ 60,000	1,269,451	$ 16,287,845	4.775	0.00	1,269,450	8,190
4	1000	8	500	$ 85,000	1,269,884	$ 16,318,375	4.784	0.00	1,268,985	8,187
6	1000	8	500	$ 110,000	1,270,781	$ 16,354,841	4.795	0.00	1,268,985	8,187
8	1000	8	500	$ 135,000	1,271,523	$ 16,389,327	4.805	0.00	1,268,830	8,186
10	1000	8	500	$ 160,000	1,272,110	$ 16,421,835	4.815	0.00	1,268,520	8,184
	1000	6	500	$ 30,000	1,292,581	$ 16,553,518	4.853	0.00	1,293,785	8,347

Picture 1: Optimization results for a hybrid power system consisting of a diesel generator, a converter, wind turbine, inverter and wind turbine.

(Supported by the National Science Foundation)

Advisor: Judith Cardell, Engineering

[1] "International Energy Statistics - EIA," International Energy Statistics - EIA.

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Through My Window: Imaginative Education and Teaching Through Narrative

Zoe Zandbergen/2018

Selection of illustrations made for project

Engineering and technological advances power our society. America is quickly recognizing that to make informed choices and understand our world, all citizens should have at least a basic understanding of the processes and uses of engineering. In a review of K-12 engineering education in the United States, the National Academy of Engineering and the National Research Council reported that "engineering education may even act as a catalyst for a more interconnected and effective K–12 STEM education system in the United States."[1] While engineering may at first seem an unpalatable topic for children, it can be sweetened through Imaginative Education- specifically, engaging narratives. This summer, I worked to develop both plot and art assets for the narratives created in the Through My Window project.

I used digital drawing software to create both a linear "graphic novel" subsection and a nonlinear interactive game subsection of a narrative meant to teach the principles of the engineering design cycle, based off the Next Generation Science Standards. I made my illustrations expressive and peppered my work with details to intrigue and immerse the reader, plus a tablespoon of humor. The fantastical yet human narrative separates this project from other engineering education initiatives. Another core goal of the project is representation of marginalized groups, as we would like any child to be able to see a future as an engineer; my art and character designs were made with this in mind. Simultaneously, I helped my coworkers plot a future narrative meant to teach children engineering ethics, acting as a creative consultant.

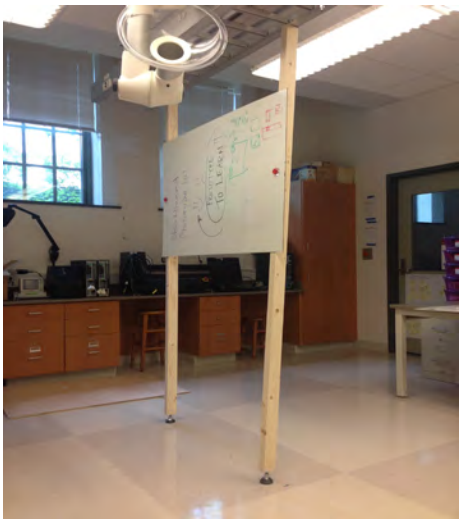
The narrative meant to teach principles of design is on track to be finished by January; without my participation, it may have taken a year longer. With the help of my increased knowledge of the project's organization, we can move forward on producing more learning adventures more efficiently.

When the adventure is completed and made available to schools, the project will gather data on how effectively the narrative teaches and how the students absorb the engineering concepts. This in turn will help us improve our future learning adventures, teaching children ideas from bioengineering to sustainability.

(Supported by the Schultz Foundation)

Advisor: Glenn Ellis, Engineering

1.L. Katehi, G. Pearson and M. Feder, (Eds.), National Academy of Engineering and National Research Council, Engineering in K–12 Education: Understanding the Status and Improving the Prospects, The National Academies Press, Washington, D.C., 2009.



Prototyping Tools to Support Creative Collaboration and Design Thinking in the Classroom

Ziqiu Zhang/2018

Usually, there aren't many spaces available on college campus for collaborative work. Spaces are either built for specific lab setting or professional faculty meeting. For example, at Smith College, collaborative spaces are built individually for each discipline. Outside of that discipline, students do not have access into the room or the building at all.

Inspired by the book "Make Space: how to set the stage for creative collaboration" (Doorley and Witthoft), I began to design tools that are useful for classroom collaboration. As a team of four, we explored the furniture that are listed on the Make Space book, such as, T-Wall, Prototyping Cart, Jacks, Shortboards, Periodic Table, and Z-Rack. We also modified the products according to our needs for the space.

Our finished products were installed in Dawes House on Smith College campus, and some of our products were brought to the Nelson Library as part of the group study area.

The Research experience was very inspiring because as we continued to explore the prototypes, we reached a better solution for our problems at the end. This experience will help me to better understand space and collaboration on college campus.

(Supported by the Branta Foundation Grant)

Advisor: Borjana Mikic, Engineering

A Study of Load Prediction in Demand Response

Ning Zhu/2017

Demand response refers to an action that customers change their consumption behaviors according to the changes in electricity costs. This is an exceptionally practical and promising idea since power plant is always at its lowest efficiency when the peak demand occurs.[1] By applying demand response, people can save electricity bills, and at the same time, the power generation system will become more reliable. This summer I mainly did research about demand response, and I particularly studied about the load measurement and prediction. Load forecasting is a crucial part in demand response because people need first to know where the peak will be in order to identify proper opportunities.

An energy-monitoring device was installed in the kitchen on the third floor of ford hall. The device was connected to the refrigerator for several days in order to observe a consumption pattern. Additionally, I also did some literature research in order to have an idea of what the current research status in the field of demand response was. Meanwhile, I studied some statistical models in order to know how to analyze the data and make the prediction.

The monitoring device went pretty well and the data looks good. There appeared several peaks during a day as expected. The next step will be analyzing the historical load shapes and make some predictions. In this way people will be able to assess potential demand response opportunities. I will continue my summer research project as a special study next semester.

(Supported by National Science Foundation)

Advisor: Judith Cardell, Engineering

1. Alt, Lowell. 2006 Energy Utility Rate Setting. P. 66

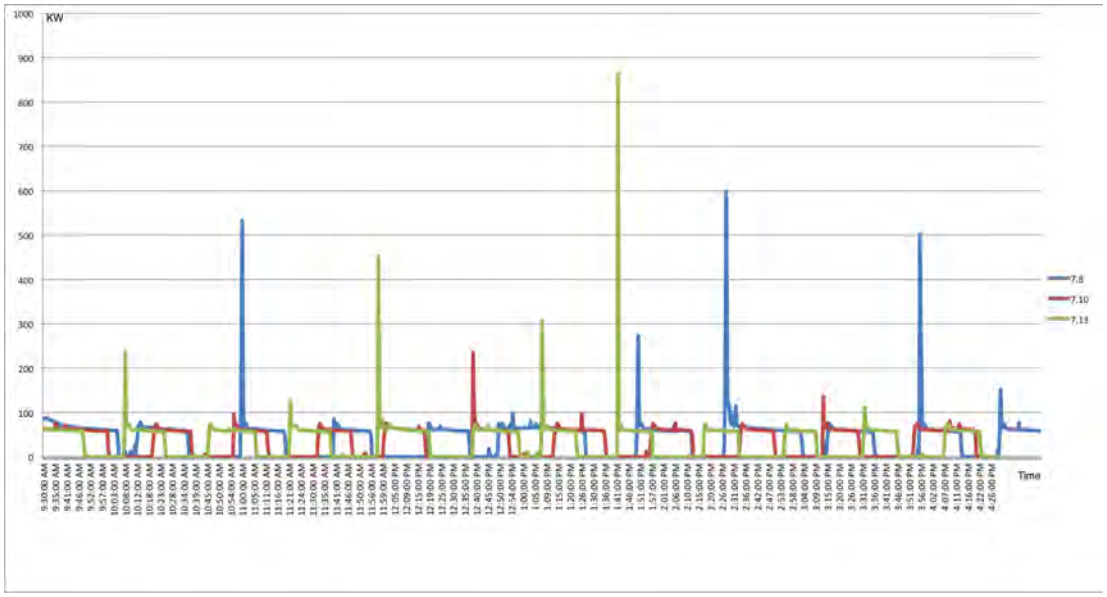


Figure 1: The electricity consumption data of the refrigerator on 7.8, 7.10 and 7.13.

Creating Resilient Communities: Habitat Restoration and Climate Change Monitoring in the Hawaiian Islands

Siiri Bigalke/2016

The Office for Coastal Management (OCM) at the National Oceanic and Atmospheric Administration (NOAA) monitors, collects, and translates scientific information to support resource management decisions. My internship at OCM focused on the intersection of how to sustainably manage resources, promote climate change resiliency, and utilize geospatial technology to make informed decisions in partnership with local communities and organizations.

The Sentinel Site Cooperative, a NOAA-wide initiative, aims to build coastal community resilience to sea level rise and coastal inundation. At the Sentinel Site He`eia, where non-native species now dominate the watershed, several partner organizations are working to restore the native habitat by rehabilitating the agricultural fields and fishpond that once provided food security to the native Hawaiian population. I helped to gather a collection of elevation data of the watershed. LiDAR data (which stands for light detection and ranging, a remote sensing technology to obtain elevation data from an airplane flyover) were already available for the area. However the dense vegetation in He`eia lowered the precision of the pre-existing data. We surveyed taro fields with GIS specialists to get very precise GPS and elevation points that will be referenced to the LiDAR data to create more accurate elevation models. These elevation models will be of great value to NOAA and its partners for a number of projects aimed at increasing our understanding of how to sustainably restore the ecosystem and monitor impacts of climate change.

I also worked on a number of short-term projects requested by partner communities. I helped to conceptualize and gather data for a new webpage for two OCM initiatives. Additionally I helped create maps for partner organizations that did not have the capacity to do geospatial analysis and learned the importance of finding reliable data with accompanying metadata.

During this internship I gained valuable experience in balancing the needs of communities and ecosystems in the face of climate change. I also gained experience in geospatial analysis and remote sensing. Above all we learned the importance of community engagement, which is especially important in Hawai`i where native values are so intrinsically tied with environmental stewardship.

(Supported by the Agnes Shedd Andreae 1932 Research Internship Fund)

Advisors: L. David Smith, Environmental Science & Policy, and Douglas Harper, National Oceanic and Atmospheric Administration (NOAA)

Coral Reef Ed-Ventures Program

Riley Gage/2015, Elena Karlsen-Ayala/2016, Emily Volkmann/2016, Laura Henry/2016, Shabnam Kapur/2016, and Mandy Castro/2017

This was the 16th summer of the Coral Reef Ed-Ventures Program (Coral Ed) in San Pedro, Ambergris Caye, Belize. Coral Ed is sponsored by Smith College's Environmental Science and Policy Program in collaboration with Ambergris Caye's Hol Chan Marine Reserve. The program goal is to promote awareness of and learning about natural marine ecosystems of the island. Six Smith students provided a place-based learning experience to the children of San Pedro through two free summer camps. The two-week youth camp (ages 7-12) and one-week advanced camp (12+) were run by the Coral Ed team.

The Mesoamerican Barrier Reef provides invaluable benefits for Belize. Coral Ed emphasized these services in their work with young campers. Highlights of advanced camp this year included a nature scavenger hunt and boat ride through the mangroves with guides from the American Crocodile Education Sanctuary (ACES). Youth camp included presentations from local organizations: Oceana, which studies offshore drilling; Mar Alliance, which works to educate about threatened marine animals and clarify myths about sharks; ACES, who gave campers interesting crocodile and safety facts; and Ecologic Divers, who reinforced the message about the importance of the reef and its conservation. Youth Camp concluded with a glass-bottom boat trip where campers viewed creatures and places they had been learning about all week. Students in youth camp culminated their week with a graduation celebration with their parents.

In addition to teaching, the Coral Ed team participated in research projects with Smith faculty, including GPS/GIS technology to help map the distribution of mangrove propagules and photography and videos on scuba to measure and map coral mounds and sea fans. Documentation of coral abundance, diversity, and the health at Mexico Rocks, an area recently designated a marine protected area, will provide baseline data, which will be used to document future changes associated with protected status. The team also aided John Caris, Smith's Spatial Analysis Lab Director in using GPS photography from a drone to map turtle nesting beaches. They also participated in a conch survey with Miguel Alamilla, Marine Biologist and Manager of Hol Chan Marine Reserve, in the reserve's no-take zone. Several of the research projects introduced new methodologies that will be refined in the future. This year's project was presented at Smith and will be showcased in several special studies projects this upcoming school year.

(Supported by the B. Elizabeth Horner Fund and Margaret W. Grantham 1875 Fund, The Center for the Environment, Ecological Design and Sustainability, and a gift from Linda Salisbury '78).

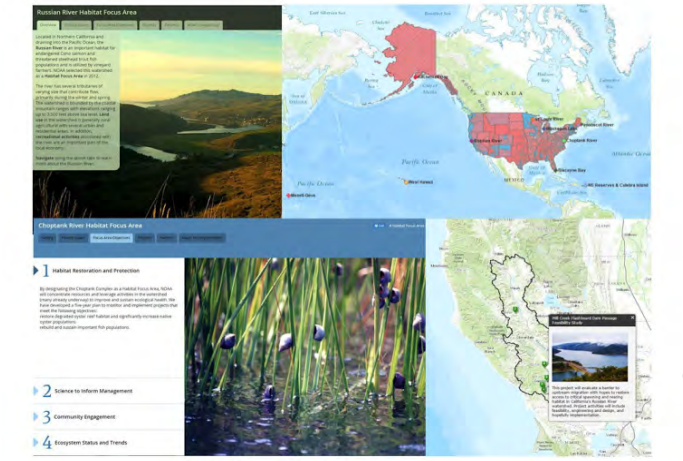
Advisors: L. David Smith, Environmental Science & Policy, Denise Lello, Biological Sciences, Al Curran, Geosciences, and Miguel Alamilla, Jr., Hol Chan Marine Reserve

Coral Ed students (from left to right) Riley Gage, Laura Henry, Shabnam Kapur, Emily Volkmann, Elena Karlsen-Ayala, and Mandy Castro advertise for camp with creative sea creature costumes.

Diver records data about nearby coral mound.

Bringing Narrative Maps to NOAA's Habitat Focus Area Initiative

Julia Graham/2016



Collage image of my story maps

My internship at the National Marine Fisheries Service (NMFS) office in NOAA headquarters in Silver Spring, Maryland was to develop story maps for NOAA's ten Habitat Focus Areas. A story map is a communication tool for publishing information on websites that combines narratives (stories) with maps, photographs, video, graphs, charts, tables and other graphic representation of information. Habitat Focus Areas (HFAs) are representative habitats in coastal areas managed by NOAA scientists and staff to enhance habitat conservation and provide additional resources to NOAA offices and regional partners. Story maps offer an effective multimedia means of communication for NOAA to show to the public and to partners what activities are taking place at the HFAs.

Throughout the story map development process, I worked with the regional HFA implementation teams to gather data and images about priority issues affecting the area, the HFA objectives, past and current conservation projects, and partner relationships. Since many HFAs did not have this information organized or gathered in a central location, I collaborated with them to create project lists and text documents to help compile the information that would go into the story map. In the meantime, I used ESRI ArcGIS online story map software to build story maps for each HFA, working directly with regional teams to personalize the story maps for their use. While I did not have enough time to finish all ten story maps, I made considerable headway in collecting data and creating web maps for future use by working with regional NOAA employees to develop a story map template and compile what information will be necessary to include.

(*Supported by the Agnes Shedd Andreae 1932 Research Internship Fund*)

Advisors: Daniel Farrow, National Oceanographic and Atmospheric Administration (NOAA),
Robert Newton, Environmental Science & Policy

Coral Reef Ed-Ventures Program

Shabnam Kapur/2016

This was the 16th summer of the Coral Reef Ed-Ventures Program (Coral Ed) in San Pedro, Ambergris Caye, Belize. Coral Ed is sponsored by Smith College's Environmental Science and Policy Program in collaboration with Ambergris Caye's Hol Chan Marine Reserve. The program goal is to promote awareness of and learning about natural marine ecosystems of the island. Six Smith students provided a place-based learning experience to the children of San Pedro through two free summer camps. The two-week youth camp (ages 7-12) and one-week advanced camp (12+) were run by the Coral Ed team.

The Mesoamerican Barrier Reef provides invaluable benefits for Belize. Coral Ed emphasized these services in their work with young campers. Highlights of advanced camp this year included a nature scavenger hunt and boat ride through the mangroves with guides from the American Crocodile Education Sanctuary (ACES). Youth camp included presentations from local organizations: Oceana, which studies offshore drilling; Mar Alliance, which works to educate about threatened marine animals and clarify myths about sharks; ACES, who gave campers interesting crocodile and safety facts; and Ecologic Divers, who reinforced the message about the importance of the reef and its conservation. Youth Camp concluded with a glass-bottom boat trip where campers viewed creatures and places they had been learning about all week. Students in youth camp culminated their week with a graduation celebration with their parents.

In addition to teaching, the Coral Ed team participated in research projects with Smith faculty, including GPS/GIS technology to help map the distribution of mangrove propagules and photography and videos on scuba to measure and map coral mounds and sea fans. Documentation of coral abundance, diversity, and the health at Mexico Rocks, an area recently designated a marine protected area, will provide baseline data, which will be used to document future changes associated with protected status. The team also aided John Caris, Smith's Spatial Analysis Lab Director in using GPS photography from a drone to map turtle nesting beaches. They also participated in a conch survey with Miguel Alamilla, Marine Biologist and Manager of Hol Chan Marine Reserve, in the reserve's no-take zone. Several of the research projects introduced new methodologies that will be refined in the future.

This year's project was presented at Smith and will be showcased in several special studies projects this upcoming school year.

(Supported by the Margaret A. Walsh Grantham Fund)

Advisors: L. David Smith, Environmental Science & Policy, Denise Lello, Biological Sciences, Al Curran, Geosciences, and Miguel Alamilla, Jr., Hol Chan Marine Reserve)

The Effects of Nutrient Addition and Predator Exclusion on Epiphyte Loads on Artificial Seagrass Units

Anastasia Konefal/2017

This summer I worked as a NOAA intern at the Northwest Fisheries Science Center assisting with a variety of projects centering on eelgrass (Zostera marina) populations in Puget Sound. I spent most of my time working on a field experiment at four different sites in the sound. We wanted to see if a nutrient addition and predator exclusion affected what epiphytes colonized on an artificial seagrass unit (ASU). Eelgrass is a very important habitat for macroinvertebrates like caprellids, gammarids, gastropods, and polychaetes, as well as for crabs and salmon. This experiment will give insight as to what makes eelgrass an appealing habitat, and if and how different nutrient and predator dynamics might create bottom up effects on species like crab and salmon.

Eight 40m electrical lines were prepped with three control units and three nutrients units. The ASUs consisted of two 30cm ropes attached to a PVC pipe, and a mesh bag that was either filled with 50g of osmocote (nutrient) or nothing (control). Six units were then lined in an alternating pattern along the electrical line. Two lines at each site were set up parallel to the shoreline. After two weeks, we checked on the lines to make sure that they were still intact and took nutrient samples using a 50ml syringe. Two weeks later, more water samples were taken along with part of the ASU. Ten centimeters were cut off the top of the rope and put in a Ziploc bag. Then, one of the two remaining ropes at each of the treatments were caged for a predator exclusion experiment.

After analyzing epiphyte loads on the ten centimeter ropes, we found no significance between control and nutrient enriched ASUs. This result suggests that nutrient concentrations are not a major factor in colonization by epiphytes. However, we have not yet analyzed the predator exclusion data. If we find significant differences between ASUs protected from predators and those accessible by predators, this could tell us a lot about the Puget Sound food chain. By excluding predators, different species may colonize on the eelgrass, and give us a wider sense of the diversity of species that live in the sound.

(Supported by the Agnes Shedd Andreae 1932 Research Internship Fund)

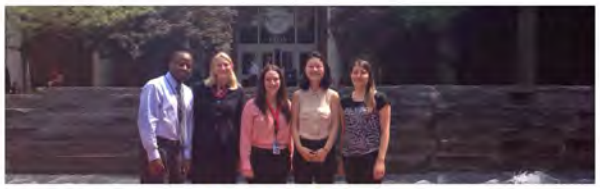
Advisors: Robert Newton, Environmental Science & Policy, and Jameal Samhouri, National Oceanic and Atmospheric Administration (NOAA)

Photographs: Adrian Stier

Operational Oversight at the National Oceanic and Atmospheric Administration

Kimberly Lu/2017

My internship was with the Formulations and Congressional Analysis (FCA) team within the Office of Oceanic and Atmospheric Research (OAR), one of the six Line Offices that constitute NOAA (National Oceanic and Atmospheric Administration). My main responsibility was to assist with a comprehensive operational and management review of the year-to-year operations of each of OAR's seventeen labs and programs. The review involved extensive information on their operations, including details about their vision and mission, key activities and deliverables, and the status of their workforce and funding. OAR's senior leadership's goals for the review were to find ways to improve the office's business model and to assess the research of each lab/program. In particular, the oversight team focused on the transition from research to operations (the "R2X" funnel) for each lab/program's key activities. My role in the project involved assembling the review's raw data into PowerPoint and Word documents that displayed them in a concise and coherent way. I transformed Excel tables into easy-to-understand graphs, and standardized the information presented among all seventeen labs/programs. Each review culminated in a two-hour meeting between the lab/program directors, the FCA team, and OAR leadership.



Key Activities:

Activity Title	QOSAP/ OSSE	HFIP	Hurricane Observations	Global Ocean Observations	Climate	Weather	Ocean and Coastal Circulation and Ecosystems	Ocean Acidification	Coral Monitoring	Microbiology
PPA	Weather Labs & Cis	Weather Labs & Cis	Weather Labs & Cis	Climate Labs & Cis	Climate Labs & Cis	Weather Labs & Cis	Ocean, Coastal, & Great Lakes Labs & Cis	Ocean, Coastal, & Great Lakes Labs & Cis	Ocean, Coastal, & Great Lakes Labs & Cis	Ocean, Coastal, & Great Lakes Labs & Cis
Programmatic Theme	Assessment	Forecast & Prediction	Observations	Observations	Assessment	Monitoring	Exploration/ Discovery	Observations	Monitoring	Product Development/ Emerging Technology
Collaborations	Inter-disciplinary with federal and non-federal partners	Inter-disciplinary with federal and non-federal partners	Inter-disciplinary within federal agencies	Inter-disciplinary with federal and non-federal partners	Inter-disciplinary with federal and non-federal partners	Unique to NOAA	Inter-disciplinary with federal and non-federal partners	Inter-disciplinary		Inter-disciplinary with federal and non-federal partners
Products and Services used by other NOAA Offices	All of NOAA, NWS, NESDIS, NOS, and NMFS	NWS	NWS	NWS	NWS	Tropical Analysis and Forecasting Branch of the NWS – National Hurricane Center	NWS – National Data Buoy Center, NOS, Fisheries	Coral Program		NMFS, NOS, Coral Program
R&D Maturity	TRL 3-5	TRL 6-8	TRL 3-5	Research	Research	Mature	Research	Research		Research/ Application
FY2014 Total Funding										

Image: FCA team (top); example figure from O&M reviews (bottom)

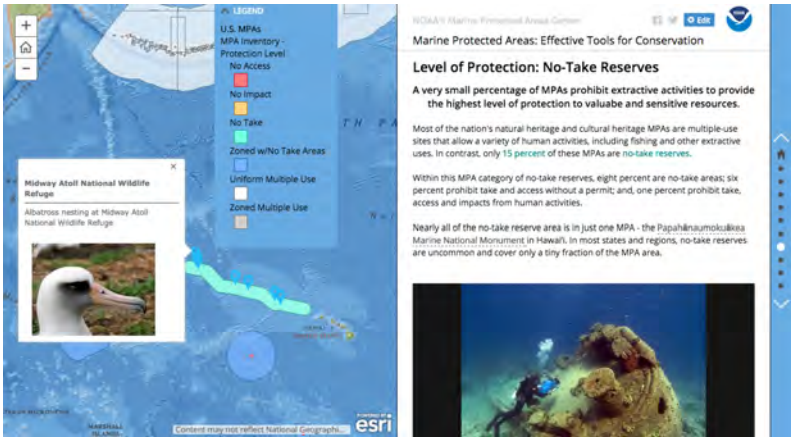
Beyond my work with the O&M reviews, I also reviewed and edited the proposed OAR budget for fiscal year 2016, legislative reports for Congress, and interagency memorandums. I watched hours of live C-SPAN video on the debate in the Commerce, Justice, and Science committee for the U.S. House of Representatives on NOAA's appropriations bill. I went to several Senate briefings on Capitol Hill to take notes on Asian Carp and ocean observations. Finally, I became well acquainted with the various offices and operations within NOAA by visiting sites such as Science On A Sphere and the National Weather Service. My office was involved in projects and legislation that focused on conservation, sustainability, environmental justice, and community resilience, which closely complement the knowledge and interests I am pursuing at Smith. I also gained valuable insight on the inner-workings of a federal agency, especially one that is based in science but still endures the barriers of bureaucracy and politics. Finally, I gained a deeper appreciation for the tireless work scientists and policymakers are doing to better understand the Earth, as well as our role on this planet.

(Supported by the Agnes Shedd Andreae 1932 Research Internship Fund)

Advisors: Anne Wibiralske, Environmental Science & Policy and Merriam Norris, National Oceanic and Atmospheric Administration (NOAA)

Communicating Marine Protected Areas: Using Story Maps and Online Tools to Share Information about MPAs

Danielle Opatovsky/2016



NOAA's National Marine Protected Areas (MPA) Center manages coastal and marine geospatial data across the country on over 1,700 MPAs, maintaining baseline information for policy makers, managers, and researchers. The MPA inventory is managed through the office of Marine Sanctuaries in Monterey CA where I worked to create interactive public "story maps" to strengthen the public's awareness of MPAs, support the development of the National System of MPAs, and demonstrate the utility of the breadth of geospatial data for coastal decision-making. ArcGIS Story maps are communication tools that combine geospatial data with online content for publication online. I worked on a team that made two separate story maps: "Marine Protected Areas: Effective Tools for Conservation" and "Marine Protected Areas: Building Resilience to Climate Change Impacts." The former provides a brief overview of MPAs and the MPA inventory; the latter illustrates how MPAs can provide coastal resilience to climate change through sentinel sites, long term monitoring, and protection of resources.

I used ArcGIS online, a platform that lets users import web maps as well as data from ArcGIS desktop to make interactive online maps that included textual content, images, videos, and links. For each story map, I organized the structure and laid out each chapter, wrote corresponding content for each chapter, and found additional resources and videos. I constructed a map for a chapter on no-take reserves that included point data on various marine species and their habitats in Papahānaumokuākea Marine National Monument to illustrate the importance of the area as a no-take reserve. I also edited maps on MPAs categorized by government level, as well as a map describing legal level of protection by area.

Story Maps are a powerful way to present geospatial information that is dynamic and appealing to people who may be unfamiliar with mapping tools. The MPA inventory hosts a wealth of data well suited for story maps, as story maps provide space for explanation and a platform to display map data. Our team was the first to make a representative summary map of the MPA program, offering an overview as to why the MPA Inventory is an important conservation tool. This story map will be featured on the new Marine Protected Areas Center website.

(Supported by the Agnes Shedd Andreae 1932 Research Internship Fund)

Advisors: L. David Smith and Anne Wibiralske, Environmental Science & Policy and Mimi D'iorio, National Oceanic and Atmospheric Administration (NOAA)

Consistently Key Habitat Variables on Rocky and Coral Reef Fish Assemblages

Grace Peralta/2016

Many studies have been published that assess and analyze the effect of habitat variables on fish populations. These studies have looked at both rocky, temperate reefs and tropical, coral reefs. Despite the extensive research on reef habitat characteristics, a coherent summation of what habitat variables consistently affect fish populations has yet to be developed. At the NOAA laboratory in Beaufort, North Carolina, our goal was to identify the habitat characteristic(s) that most consistently have shown a significant affect (positive or negative) on fish populations, and to assess whether those characteristics were consistent across both reef types.

We conducted an extensive literature review, analyzing over one hundred peer-reviewed research papers describing studies relating reef habitat variables to fish metrics. We looked for papers with information on habitat features (such as vertical relief, rugosity--a measurement of the roughness and diversity of texture on the substrate surface, patch-size, and extent of coral cover) and how those features effect fish metrics (including species richness, evenness, diversity, abundance, and biomass). We compiled the data from our literature review in an Access database, wherein we could analyze the dataset findings from many studies.

Our analysis has demonstrated that certain habitat features and fish metrics are in fact consistently correlated across both coral and rocky reefs. Preliminary analyses indicate that rugosity, coral cover, depth, substrate type, and presence and proximity of seagrass beds are most consistently correlated with changes in fish populations. In features such as rugosity and coral cover this correlation tended to be positive; with increased rugosity, there is increased abundance of fish. When the full analysis of the dataset is complete we will have a firmer assessment of these correlations. We will also be able to identify habitat characteristics that have consistently shown little or no affect on the fish populations studied. Drawing on the findings from our literature review, we hope that future research on reef fish assemblages can be simplified. By identifying which habitat features are the key predictors (and which are not) for stable, increasing, or declining fish populations, future research on reef fish populations can be streamlined by focusing on increasing our understanding of the dynamics of the necessary elements. Our conclusions could also be useful in choosing sites for new Marine Protected Areas, assist in the design and placement of artificial reefs, and contribute to fishery management policies.

(Supported by the Agnes Shedd Andreae 1932 Research Internship Fund)

Advisor: Anne Wibiralske, Environmental Science & Policy and Todd Kellison, National Oceanic and Atmospheric Administration (NOAA)

I also had opportunities for fieldwork outside my project. Here we are taking blood samples from a green sea turtle we caught while gill netting in the seagrass beds.

Environmental Resilience: A Three-Part Interdisciplinary Study

Andrea Schmid/2017

My SURF research this summer consisted of three different projects. The first project was a short exploratory study that I conducted with Professor Washington-Ottombre in Ambergris Caye Belize. I helped her put together a survey which we used to interview people to access the island community's perspectives on social and environmental issues. We conducted eight interviews which helped us get an idea of the issues that major stakeholders on Ambergris Caye cared the most about.

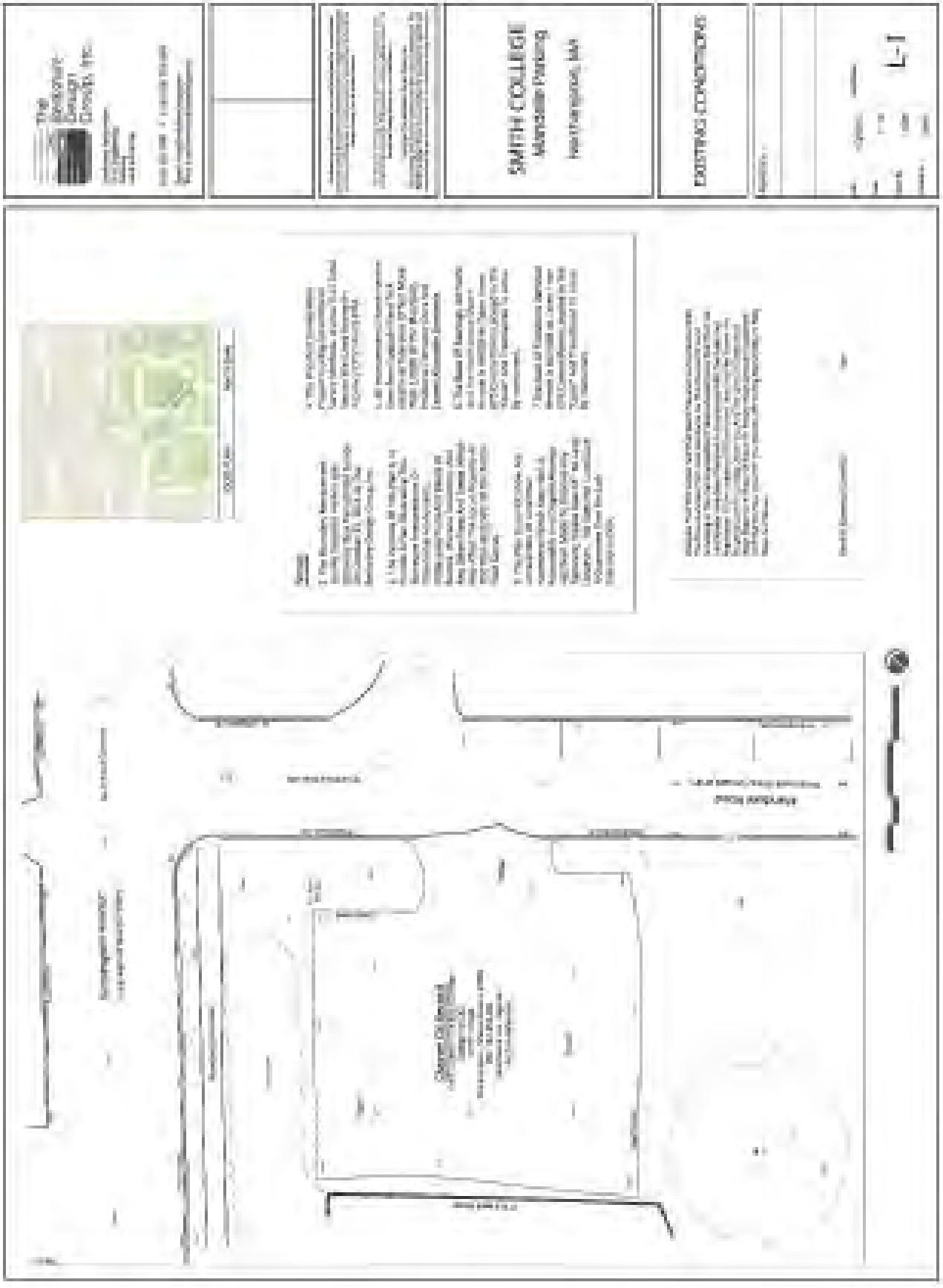
The second project if my SURF research involved creating a conceptual design for the permeable pavement parking lot that will be installed on campus in the quadrangle. I worked with Dano Weisbord and Peter Gagnon from Capital Projects, along with engineers and landscape architects from Berkshire Design Group who were hired for this project.

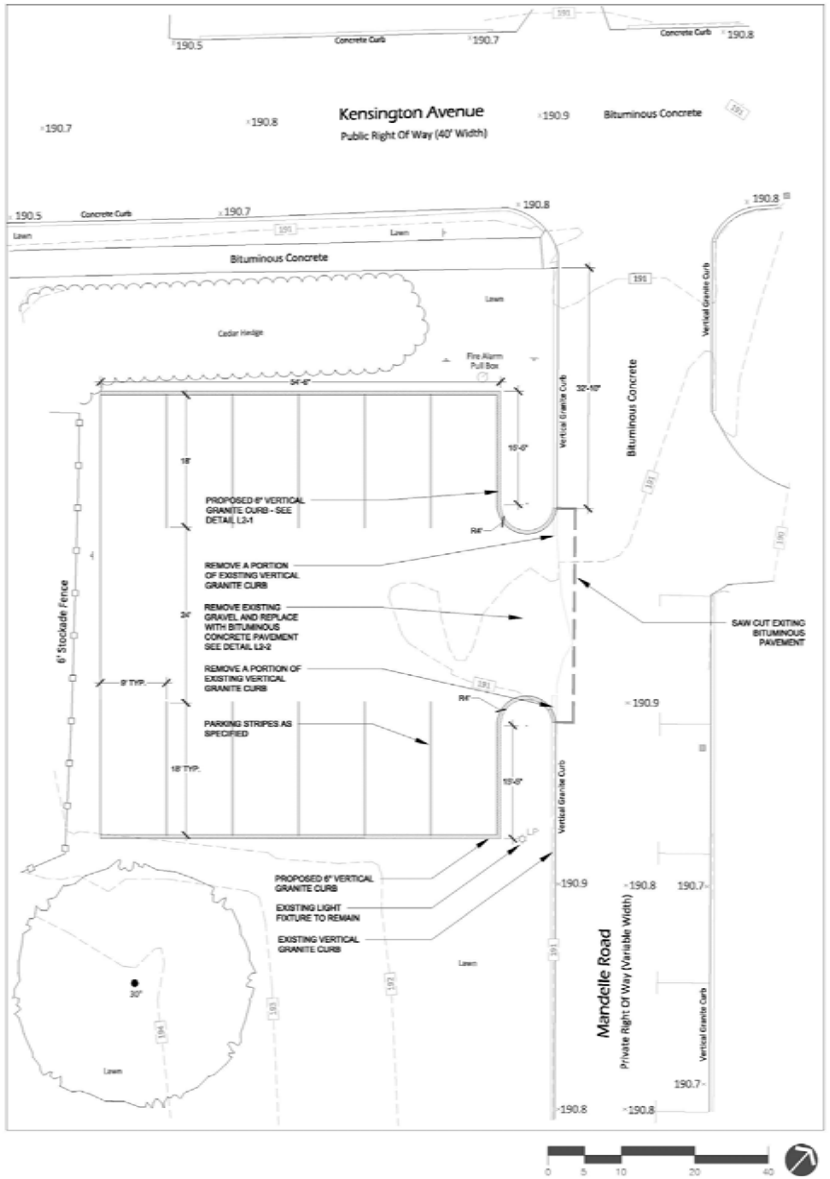
Finally, the third part of my research was more centered on GIS digitizing and georeferencing two maps of an irrigation scheme in Kenya. My advisor Professor Washington-Ottombre proposed the project to me as a way to help her and the farmers whom she worked with in Kenya during her research on the irrigation scheme. I spent a significant amount of time with this project, major roads and rivers on Google Earth and ArcMap and aligning printed maps of the irrigation scheme with the true coordinates of its location so that further research and analysis can be done of the area.

With this said, my SURF experience was unconventional in that it did not consist of a single project for the whole summer. I was involved in interdisciplinary projects that challenged me and introduced me to different fields of environmental science and allowed me to grow as a student in my interests and research skills. Additionally, while these projects might seem unrelated, they all fall under the common theme of environmental resilience, through design, research, and technology.

(Supported by the Schultz Foundation)

Advisor: Camille Washington-Ottombre, Environmental Science & Policy


SMITH COLLEGE
EXISTING CONDITIONS



LAYOUT NOTES

1. Do not scale drawings for quantity take-offs or construction. Use written dimensions only. If dimensions are incomplete, contact The Berkshire Design Group, Inc. for clarification.

2. All lines or points are perpendicular or parallel to lines from which they are measured unless otherwise noted.

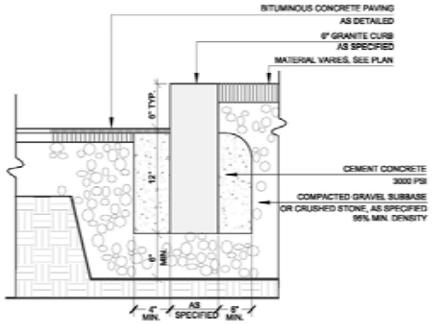
3. The Contractor shall verify all layout, dimensions, grades, and inverts prior to construction; report any and all discrepancies to the Landscape Architect. All discrepancies shall be resolved in writing prior to beginning work.

4. All areas disturbed from construction activity to be raked, smoothed, fertilized and seeded with perennial turfgrasses unless otherwise noted.

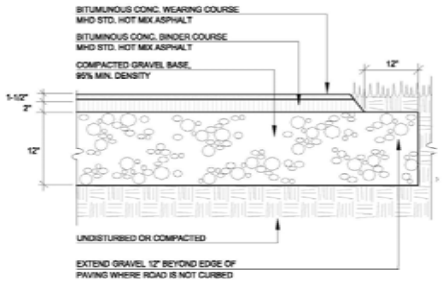
5. All new walks and surfaces to meet existing walks and surfaces with smooth, continuous line and grade.

6. The Contractor shall not install concrete during adverse weather conditions (rain, sleet, etc.) unless otherwise directed by the Landscape Architect.

This project requires coverage under the EPA NPDES General Permit for Stormwater Discharges from Construction Activities. Contractor and Owner are responsible for finalizing a Stormwater Pollution Prevention Plan (SWPPP) and filing for the NPDES Permit and for review by the City of Northampton DPW prior to the start of construction. All work shall conform to the requirements of the Permit for this project. All clearing, grading, drainage, construction and development shall be conducted in strict accordance with the SWPPP.



1 VERTICAL GRANITE CURB
SCALE: NTS



2 BIT. CONC. PAVING
SCALE: NTS

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SMITH COLLEGE
Mandelle Parking

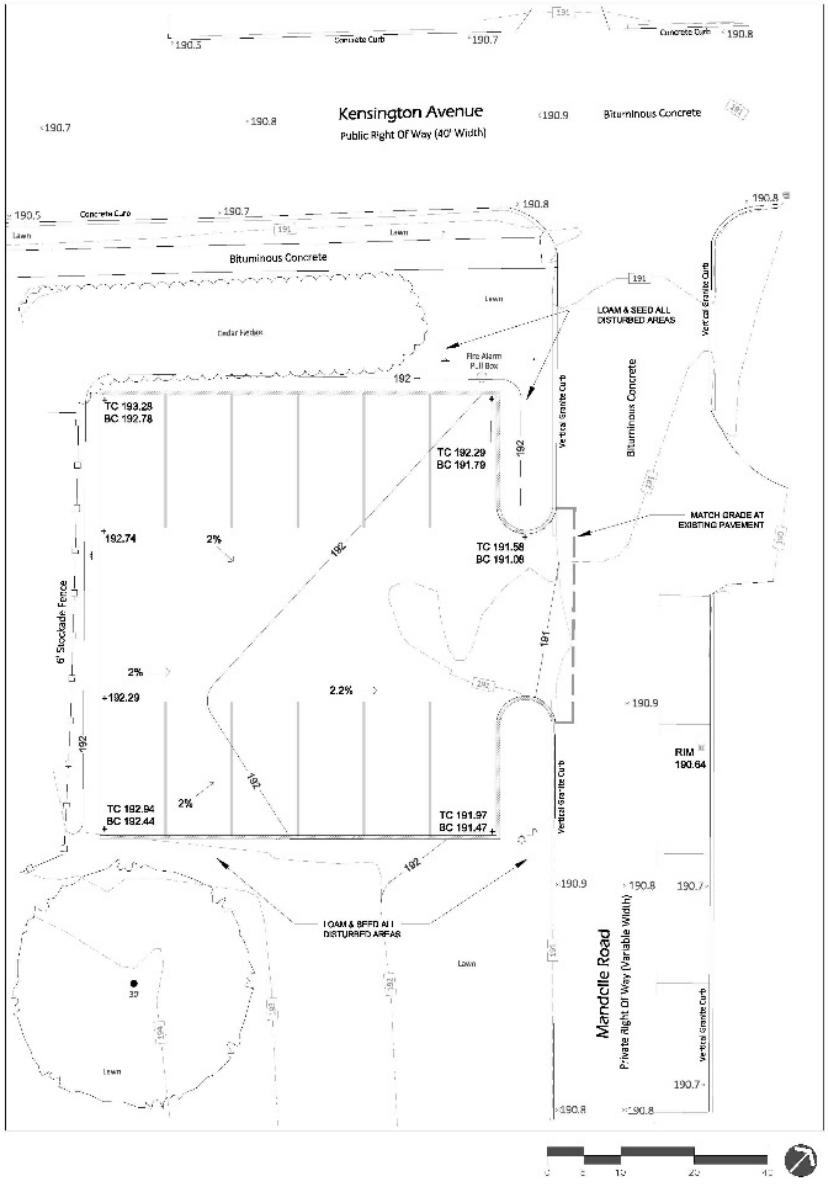
Northampton, MA

SITE LAYOUT PLAN

Revisions

Date:	03/10/15
Scale:	1"=10'
Drawn By:	ESW
Checked By:	RMK

Sheet Number: L-2



GRADING NOTES

1. All sidewalks/walkways shall conform to the Massachusetts Architectural Access Board's (AAB) requirements. Sidewalk/walkway cross-slope is 1.5 % minimum, 2.0% maximum. Maximum slope in any direction shall be 5.0%. Slopes shall not exceed 2% across any accessible parking space or adjacent aisles.

2. All materials and construction methods shall conform to the construction standards and specifications of the City of Northampton and the Massachusetts Highway Department.

3. All dimensions, elevations and layout shall be verified in the field by the contractor and approved by the Landscape Architect prior to beginning work.

4. All new or adjusted manholes, gas gates, water gates and water services to be flush with finished grade.

5. All new or adjusted catch basin rims shall be set 1/2" below finished grade unless otherwise noted. Inlets within water quality swales shall be set 4" above adjacent finished grade.

6. Notify the Landscape Architect of any discrepancies prior to construction.

The Berkshire Design Group, Inc.
Landscape Architecture
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SMITH COLLEGE
Mandelle Parking

Northampton, MA

SITE GRADING PLAN

Revisions

Date: 03/10/15
Scale: 1"=10'
Drawn By: ESW
Checked By: RMK
Sheet Number: L-3

Architecture and Urbanism CEEDS Campus Space Planning! Survey of Study Space on the Smith College's Campus

Geneva Strauss-Wise/2016

This research project is a critical-analysis of existing study spaces on Smith College's campus, with an eye towards the Neilson Library renovation and its future study space designs. Questions of focus include: What is the quality of existing study spaces on campus? What factors make them successful and encourage regular use? What sites have the potential to be study swing-space during the renovation? What small-scale changes could be made to best meet students study needs during this time? And lastly, how can we incorporate what we learn from these pre-existing spaces' usage into the design of study space in the new Neilson Library?

Sites were photographed and evaluated based on qualitative criterion. This information was synthesized into a spreadsheet, numeric values were assigned to some criteria, this mixed analysis was in turn was used to generate a Google- map that filters sites based on their potential to be swing space during the Neilson Library renovation. In addition, student and staff interviews were performed which helped to illuminate how issues of design connected to larger challenges in creating a healthy, and sustainable in campus study culture at Smith College.

Based on my research and the information collected two primary observations were made: First, many study spaces are not living up to their potential for use due to minor design flaws, and second, there are almost no permanent spaces of student design, or where students can continue to influence the nature of the space on campus. In addition, several minor observations about space use became apparent after analysis and visualization of the data: many spaces have an insufficient number of accessible electrical outlets, are not open for early morning and late night study, have insufficient ergonomic furniture, lack sustainable, healthy snack options outside of dining hall hours, and tend to be kept at very cool temperatures. !

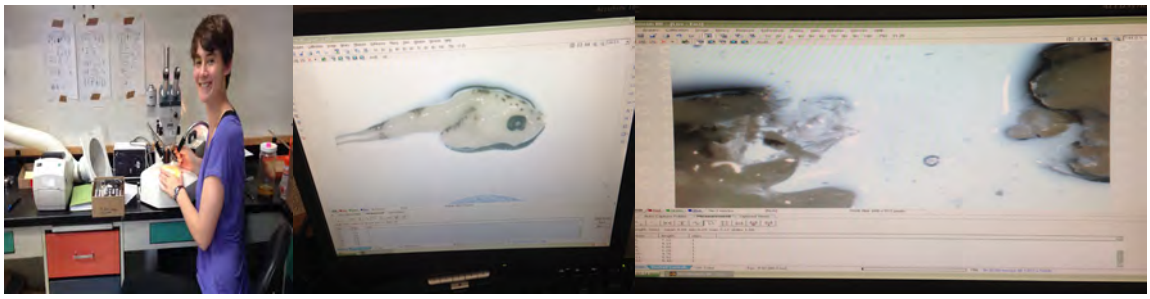
These results can be used in several ways. Firstly, the study identifies potential study swing spaces for during the Neilson Library renovation, secondly, the observations and data can easily be translated into other projects, for instance, the creation of a "space-scout" project for students to find alternative study spaces during the Neilson Library renovation, and lastly, the information is useful for thinking about the design of future healthy, sustainable study spaces specific to the Smith College campus.

(Supported by the Center for the Environment, Ecological Design and Sustainability, (CEEDS))

Advisor: Steven Moga, Landscape Studies

Using Otoliths to Establish an Age-Length Ratio for Silver Hake *(Merluccius bilinearis)* in the Northwest Atlantic

Celeste Venolia/2017



Silver Hake (Merluccius bilinearis) is a groundfish species found from Newfoundland to South Carolina. Ocean temperatures influence Silver Hake movement patterns and potentially influence growth rates.[1] Establishing a relationship between age and length allows for estimations of the ages of larvae by simply measuring lengths. With accurate estimates of age, a larval index, which estimates the spawning stock biomass, can be calculated and used by stock assessors in the development of management recommendations.

Fish ages are determined using otoliths, calcium carbonate deposits in fish heads that are used in balance and hearing. Many fish species deposit daily layers, or increments, on their otoliths during the larval stage.[2] The number of increments on an otolith is an approximate larval age.

The Northeast Fisheries Science Center conducts shelf-wide plankton surveys from Cape Hatteras, North Carolina to Cape Sable, Nova Scotia. I sampled 100 larval Silver Hake, measuring their length from jaw tip to notochord tip using Nikon imaging software. I removed their sagittal otoliths and mounted the otoliths on microscope slides. Two people read the number of increments on the otoliths. Precision criteria using the coefficients of variation of the pairs of readings were used to determine which of our estimated ages were significantly different.[2] We re-read otoliths with significantly different readings and repeated the statistical process. Two otoliths were polished with fine sand paper to improve readability. Samples that were still significantly different were rejected. A total of 95 otoliths (95%) were used to develop an age-length relationship based on a linear regression of the data. A t-test showed that our linear model of growth was significantly different from the relationships for larval Silver Hake from the Scotian Shelf[3] and juvenile Silver Hake off the coast of New York and New Jersey.[4] An ANCOVA was also calculated to compare the variance of the regression lines. Based on both analyses, our data were significantly different from the Canadian larval data and the juvenile data. The difference between the juvenile data and the larval data can potentially be attributed to differences in growth rate at various life stages. Our larval data set differs from the Canadian larval data either because of differing interpretations of otolith increments or differing growth rates from genetic or environmental factors. This age-length relationship will aid in the creation of a silver hake larval index.

(Supported by the Agnes Shedd Andreae 1932 Research Internship Fund)

Advisors: L. David Smith, Environmental Science & Policy and Harvey Walsh and Katey Marancik, National Ocean and Atmospheric Administration (NOAA)

References:

[1]Northeast Fisheries Science Center. 2011. 51st Northeast Regional Stock Assessment Workshop (51st SAW) Assessment Report. US Dept Commer, Northeast Fish Sci Cent Ref Doc. 11-02; 856 p.

[2]Stevenson, David K., and Steven E. Campana. Otolith Microstructure Examination and Analysis. Ottawa: Dept. of Fisheries and Oceans, 1992.

[3]Jeffrey, Jennifer A., and Christopher T. Taggart. "Growth Variation and Water Mass Associations of Larval Silver Hake (Merluccius bilinearis) on the Scotian Shelf." Canadian Journal of Fisheries and Aquatic Sciences 57.8 (2000): 1728-738.

[4]Steves, Brian P., and Robert K. Cowen. "Settlement, Growth, and Movement of Silver Hake Merluccius bilinearis in Nursery Habitat on the New York Bight Continental Shelf." Marine Ecology Progress Series 196 (2000): 279-90.

Investigating Slow Slip Events with GPS Velocities

Elias Bergman/2017

The Olympic Peninsula is located on the overriding plate of the Cascadia subduction zone between the North American and Juan de Fuca tectonic plates. With GPS technology, the movement of tectonic plates can be monitored and measured in 3 dimensions, often with only millimeters of uncertainty. During subduction, areas of the plates moving towards each other periodically become stuck together, or coupled, and then release some of the strain. Earthquakes occur when these releases are sudden and fast, but GPS position data show that strain can be released much more slowly. These releases are known as "slow slip events" (SSEs), and occur over 2-4 weeks, instead of seconds, as earthquakes do. This phenomenon is not observed in every subduction zone, but in Cascadia, SSEs occur about every 14 months. Greater understanding of SSEs and the subduction zone's behavior may provide insight into the earthquake cycle and hazard reduction for the area.

Daily position data from GPS stations anchored throughout the Olympic Peninsula have been collected for the past 20 years. The overall trends in these data show consistent eastward movement of the overriding plate, with reversals of motion and decreased velocities at regular intervals, which are the signatures of SSEs. In previous research on SSEs using GPS position data, SSEs were identified subjectively by eye using time vs. position graphs. I created an algorithm that compares the best-fit slopes before and after each day relative to the mean velocity of the station in order to identify potential SSEs, then compares the selected events with neighboring stations to filter out false positives in noisy data. (Figure 1.) Once identified, data from the SSEs were removed, and a line with both periodic and linear components was fit to the remaining inter-event position data. Spatio-temporal changes can be identified by looking for patterns in these inter-event velocities.

Having an objective, reproducible method for identifying SSEs is essential to future research on this little-understood aseismic process. SSEs are occurring in many places around the world, though each region of slow slip has a unique recurrence interval and typical change in velocity for each event. The threshold of identification in the algorithm is easily modified to accommodate more subtle or pronounced changes in velocity and direction, while maintaining consistent, objective criteria for identifying SSEs. Without these, comparing the results between researchers, even those working on the same region, is inaccurate and inconsistent. I will continue identifying patterns inter-event velocities and coupling patterns as Special Studies in the spring, with a possibility of using this research for a senior thesis.

(Supported by the Schultz Foundation)

Advisor: Jack Loveless, Geosciences

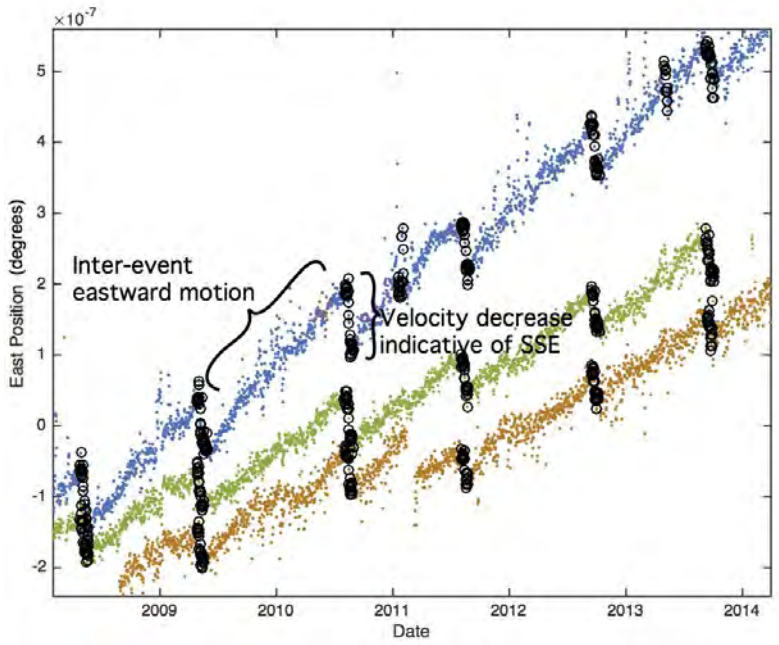


Figure 1: Time vs position graph of eastward component of motion for 3 GPS stations. Each point represents one day's recorded coordinate location, and black circles are the SSE days chosen by the algorithm.

Creating a Guide to Building Stones on Smith College Campus

Sarah Dester/2016

The building stones of Smith College Campus can serve as a unique educational tool for providing a glimpse into earth history. This project is about creating a guidebook to inform and educate about the geological origins of these stones and their history of quarrying and use as building material.

This summer I researched the geological and cultural significance of the building stones on Smith's Campus, including utilizing the Smith Archives for historical building references. Red sandstone and Indiana limestone dominate Smith's early architectural designs.[1] These two stones, for example, are found on the windowsills and arches of College Hall. More recent Bass Hall is particularly noteworthy for its Indiana limestone entrance. Red sandstone, or "brownstone," was largely quarried in Portland, Connecticut and used across the Northeast, mostly in row housing in areas of Boston and New York City.[2] This stone was deposited into what geologists call the Portland Formation during the breakup of Pangea in the Jurassic period, almost 200 million years ago. Geologically, red sandstone is an arkosic wacke, which means that many of its sand grains are made of the mineral feldspar embedded in a muddy, Fe-oxide rich matrix. Indiana limestone formed in a shallow, warm inland sea that covered what is currently the Midwest of the United States during the Carboniferous period about 350 million years ago. This limestone is a fossiliferous grainstone, meaning that it is made of sand-size fossils of marine organisms such as brachiopods, crinoids, and bryozoans cemented together with the carbonate mineral calcite. This stone was used for building many post offices nationwide, and for repairs on The Lincoln Memorial, and the White House in Washington D.C.[2] Using this information I have started drafting entries for the guidebook, considering both organization by various stone types and by individual buildings on Campus.

This fall I will continue this work as a special studies project. Further tasks involve obtaining samples to make petrographic thin sections for viewing, describing, and photographing the stones under a microscope. I will continue searching for relevant information in the College Archives and the Facilities Management office. I will also take photographs of various examples across the Campus and create maps of their locations. Together with additional geological facts, all this information will be gathered and compiled in an attractively illustrated and popularly written guidebook. This guidebook will be offered in a PDF format on the Smith College Geosciences Department website.

(Supported by the Schultz Foundation)

Advisor: Bosiljka Glumac, Geosciences

References:

[1]Lincoln, Eleanor Terry, and John Abel Pinto. This, the House We Live In: The Smith College Campus from 1871 to 1982. Northampton: Smith College, 1983.
[2]Williams, David B. Stories in Stone: Travels through Urban Geology. New York: Walker Publishing Company, Inc., 2009.

Left: College Hall. Arches in red sandstone and Indiana limestone. Windows trimmed with Indiana limestone. Built by Peabody & Stearns, 1875.
Right: Front entrance of Bass Hall carved of Indiana limestone. Built by Shepley, Bulfinch, Richardson and Abbott, 1991.

Metamorphism and Assimilation of Xenoliths of the Cuillin Centre, Isle of Skye, Scotland

Emily DiPadova/2016

During the formation of new crust during continental rifting, magmas crystallizing within the crust may evolve by incorporating pieces of surrounding rocks. These rock fragments (called xenoliths) are metamorphosed by the high temperature of the magma and can undergo variable amounts of melting, resulting in chemical contamination of the surrounding magmas. If the xenoliths can be matched to nearby source rocks, there are potential opportunities to compare the metamorphosed and partially melted xenoliths with their original source rocks and examine the changes they have undergone. This comparison may provide insights into how mafic igneous rocks are metamorphosed and melted at extremely high temperatures.

Fieldwork was conducted on xenoliths in the plutonic igneous rocks of the Cuillin Centre, a large magmatic intrusion that crystallized deep in the crust on the Isle of Skye, Scotland, and has since been exposed by erosion. Several different types of xenoliths were identified (Figure 1). Some are clearly pieces of the lava flows that surround the intrusion, with mineral-filled volcanic gas bubbles still visible as spots on the rock surface (Figure 1E). Others are fragments of dikes, in which magmas filled open fractures that cut through older rocks (Figure 1D). Many others, however, are of more ambiguous origin (Figure 1A,B,C). Thin sections were made of 24 xenolith samples using the laboratory facilities at Smith and whole rock compositions of 25 samples were determined using X-ray fluorescence (XRF) spectroscopy at UMass.

For my honors thesis I will examine the thin sections and analyze their mineral compositions using petrographic and scanning electron microscopy, and will compare the whole rock compositions to previously published data on the lavas and other rocks surrounding the intrusion. I will use this data to model the processes of partial melting, metamorphism, and hydrothermal alteration that affected these xenoliths and examine how partial melting may have contaminated the surrounding magma.

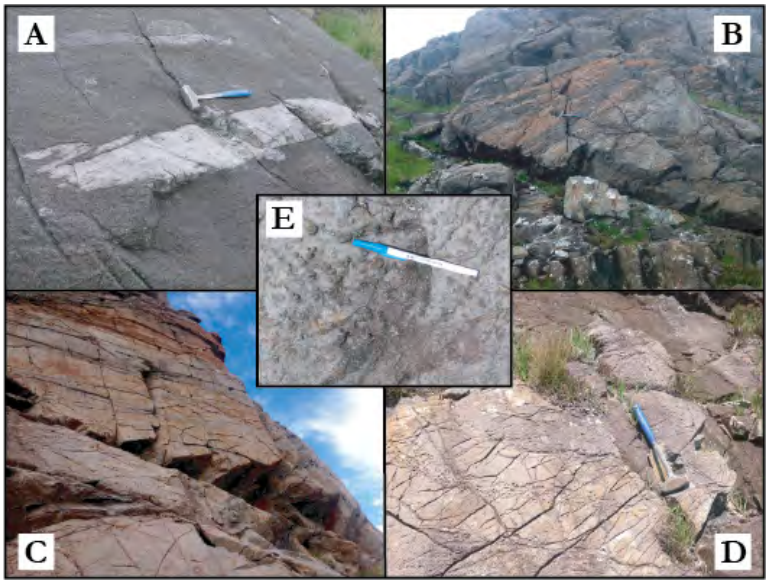


Figure 1: Different types of xenoliths found in the Cuillin Centre on the Isle of Skye, as described in the text.

(Supported by the Schultz Foundation)

Advisor: Mark Brandriss, Geosciences

Metal Content of Paradise Pond Sediments

Maya Domeshek/2018

Smith College's Paradise Pond accumulates sediment because sediment suspended in the fast moving water of the Mill River comes out of suspension when it enters the slower waters of the pond. In the past, the college has removed the sediment approximately every eight years by draining and dredging. But this is neither cheap nor environmentally friendly, so sediment sluicing has been proposed as an alternative. Sluicing would involve opening the gate in the dam during a high flow event and allowing the water to wash the sediment downstream. The hope is that releasing sediment downstream would more closely mimic the Mill River's natural system. To avoid injury to downstream sights, however, Paradise Pond sediments must be measured for pollutants.

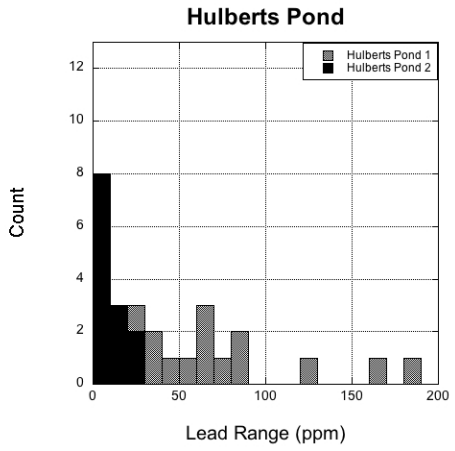
Sediment cores from Paradise Pond were compared to sediment cores from Hulberts Pond downstream. The cores were taken using a uwitech gravity corer and a drive core, then segmented into 2.5cm pieces and dried at 50°C. The segments were digested using EPA method 3050B in which 1-2 grams of sediment were heated with nitric and hydrochloric acid and oxidized with peroxide. The extract liquid was then analyzed for ten heavy metal contaminants, chiefly lead, using an Inductively Coupled Plasma Optical Emission Spectrometer (ICP-OES).

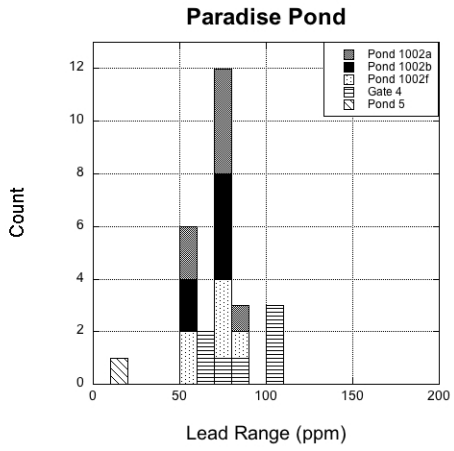
The average amount of lead measured in the Paradise Pond samples was 72.5ppm (sd = 18.7) while that measured in the Hulberts Pond samples was 47.1ppm (sd = 49.2). It is unlikely that the difference between these two averages is significant given the high standard deviations, but they cannot be compared using a t-test, as the data distribution is non-normal. The non-normal distribution and low average lead in Hulberts Pond may be because Hulberts Pond 2 with average lead 10.9ppm (sd = 6.51), was taken from the bottom of the swiftly moving channel, while Hulberts Pond 1 with average lead 80.8ppm (sd = 47.6) similar to Paradise Pond, was taken from a muddy bar. It is likely that the majority of Hulberts Pond sediment is like Hulberts Pond 1, as the pond is mostly pond, not channel.

So far, there is insufficient evidence for a significant difference in contamination between Hulberts Pond and Paradise Pond, although analysis of more cores would increase certainty. All of the samples, save two from Hulberts Pond, had acceptable levels of lead, bellow ~160ppm. It seems sluicing sediment from Paradise Pond would not harmfully increase lead levels downstream.

(Supported by Smith College Center for the Environment, Ecological Design and Sustainability, (CEEDS))

Advisor: Robert Newton, Geosciences





Searching for Potential Microfossils from the Bitter Springs Formation, Australia

Kimberly Du/2018

Microfossils are the resulted formation of microorganisms from millions of years ago embedded in some type of rock. Being able to come across microfossils will enable us to understand what kind of life lived in a specific area and how they thrived and fed. This summer, rock residue from the Bitter Springs Formation from central Australia were analyzed thoroughly from different depths of the formation. To analyze the residue, a light microscope was used to identify specimen that seemed to have a distinct shape and the Scanning Electron Microscope (SEM) was used to confirm whether or not the specimen actually had a distinct shape as well as look at chemical composition.

While canvassing through several samples of rock residue using a light microscope, I found many specimen that were slightly oval, slightly round, and even hexagon-like. Taking these specimen up to the SEM, which required hours of patience, resulted in much disappointment. It seemed that the samples I looked through did not have promising microfossils though what was interesting was the abundance of hexagon-like specimen. It is not known whether or not these hexagon specimen could be potential microfossils but these specimen do have a distinct hexagon shape. These specimen lead to the question: are these hexagons potential microfossils or are they just a coincidence of atoms put together in a hexagon shape?

Through this summer experience, I was able to do hands-on work in a field completely new to me, learning about rocks and how to master two important microscopes: the light microscope and the SEM. For my upcoming fall semester, I will continue to conduct research in the geosciences area but work on a similar project. With this research experience, I will be able to carry my enhanced skills of being patient and becoming more detail-oriented to the classroom and to other research as well.

(Supported by the Howard Hughes Medical Institute)

Advisor: Sara Pruss, Geosciences

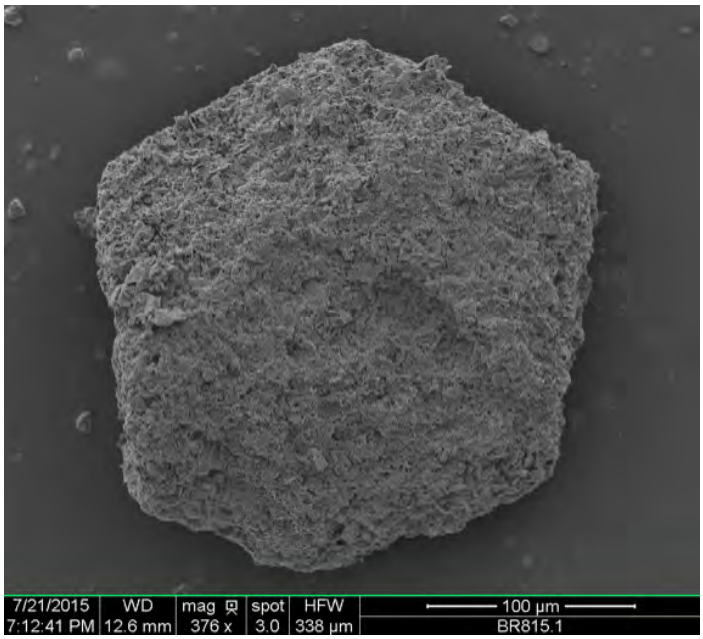


Figure 1. A hexagon-looking specimen and a potential microfossil pulled from one of the rock samples from the Bitter Springs Formation.

Salty Bogs: A Baseline Analysis for CEC and ESP Percentage of Peat

Hannah Francis/2016

Road salt application to roadways before winter storms is a precaution that has the potential to contaminate wetlands. Sodium from road salt adsorbs to organic material, causing it to accumulate and be retained by wetlands. The level of sodium adsorption should vary with the concentration of Na^+ and other cations in groundwater, as has been demonstrated for clay minerals. However, the equilibrium constants for these cation exchange reactions on peat, which define the thresholds to which sodium can adsorb to peat surfaces by removing a previously adsorbed cation, are not constrained. Also unknown is if the ability of Na^+ to adsorb varies with the ionic strength of the solution, as well as the concentration of divalent cations that may be abundant in groundwater of alkaline wetland environments.

We designed a study to determine the cation exchange behavior of Na^+–Ca^{2+} on peat (equation 1), based on methods used by Kopittke et al. (2006) that measured the exchange of sodium and calcium on different clay minerals. We wanted to expand this to a peat substrate.

$$2Na^+ + Ca_{exch} \rightleftharpoons Ca^{2+} + 2Na_{exch} \quad (1)$$

Eight sodium adsorption ratio (SAR) solutions, each having an ionic strength of 0.01M, were created using $CaCl_2 \cdot 2H_2O$ and NaCl to target SAR values of 1, 2.5, 5, 7, 10, 20, 40, and 60 (Equation 2). This ionic strength mimics the groundwater characteristics of other peatlands in Massachusetts that receive road salt runoff (Rhodes and Guswa, in review). We determined the exchangeable sodium percentage (ESP) for peat equilibrated with different SAR solutions (Equation 2). The results are used to calculate the Vanselow selectivity coefficient (K_v) to determine the preference for sodium or calcium on exchange sites (equation 3).

$$SAR = \frac{[Na]}{\sqrt{[Ca+Mg]}} \qquad ESP\% = \frac{Na_{meq/L}}{TotalCEC_{meq/L}} * 100 \quad (2)$$

$$Kv = \frac{XNa * a_{Ca}^{0.5}}{XCa^{0.5} * a_{Na}} \quad (3)$$

(3) XNa or XCa are exchangeable Na and Ca concentrations and a_{Na} or a_{Ca} are activities of Na and Ca in the SAR solution.

Peat for the exchange reactions was collected from a floating sphagnum moss peat mat at Hawley Bog (Hawley, MA) because it is remote from roads and should have low concentrations of sodium and divalent cations. Our measurements of groundwater from the Hawley Bog peat mat confirmed this hypothesis, although Na^+ is slightly elevated (peat pH= 3.8–4.5, Ca= 0.28-0.51 mg/L, Na= 0.88-1.54 mg/L; ANC= 15.6 μeq/L).

Cation exchange capacity of peat ranged from 43.2-82.4 $cmol_c/kg_{peat}$. The exchangeable sodium percentage (ESP) values ranged from 10.8-58.30% between the lower and higher SAR solutions, suggesting that as sodium increases in solution, it also increases on exchange sites. The SAR solution with the highest sodium concentration (up to 576.2 mg/L Na, and 4.0 mg/L Ca) received just under 60% sodium on cation exchange sites (Figure 3). This suggests there is a limit to the amount of sodium that can adsorb to the exchange sites. Most K_v values for each SAR reaction (except SARs 1 and 2.5) are greater than 1 (mean K_v= 1.89), showing a preference for sodium on exchange sites when Na^+ in water is proportionally high. While the data collected provide insight into the cation exchange chemistry of peat, future work is needed to explore SAR solutions at different ionic strengths to see if K_v and ESP values change with lower and higher ionic strength solutions.

(Supported by the Shultz Foundation)

Advisor: Amy Rhodes, Geosciences

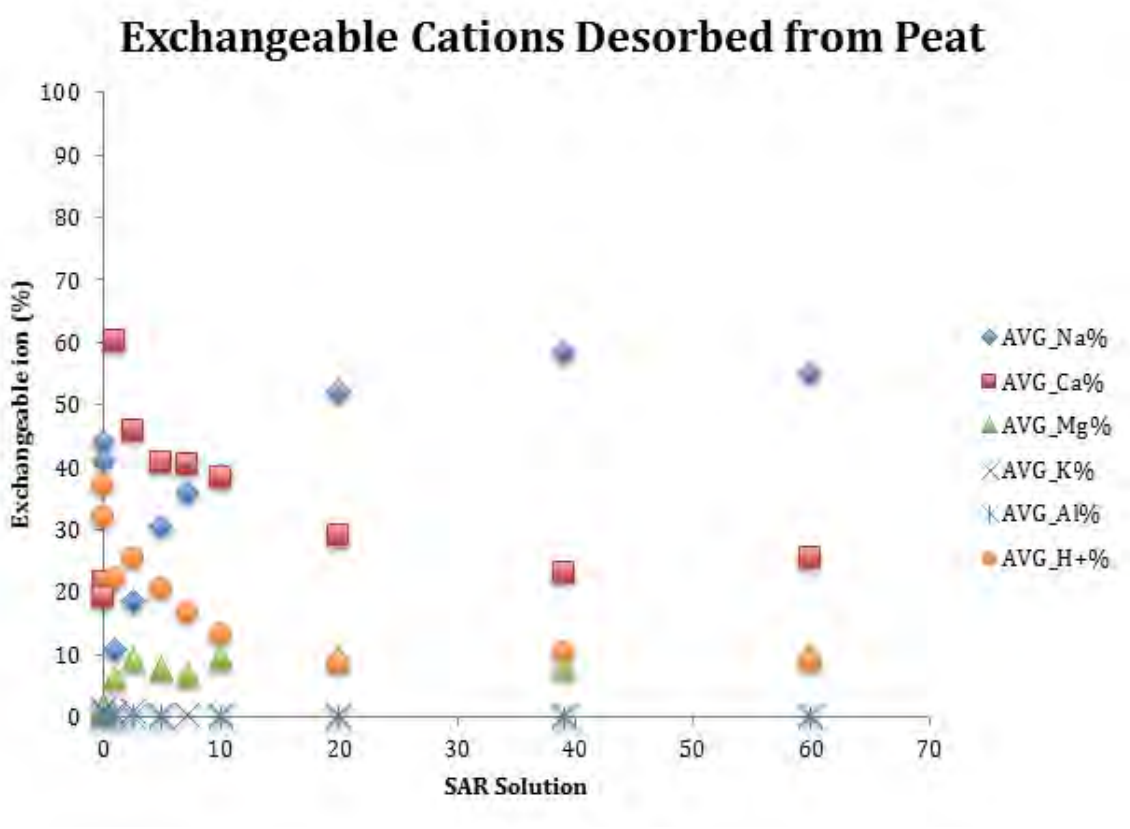


Figure 1. The ion that exchanges with sodium in solution is primarily calcium. Sodium and calcium are the ions present in the greatest proportions. Hydrogen ions decrease in solution until they reach a similar composition in solution to magnesium. Aluminum and potassium comprise a negligible proportion of ions in solution.

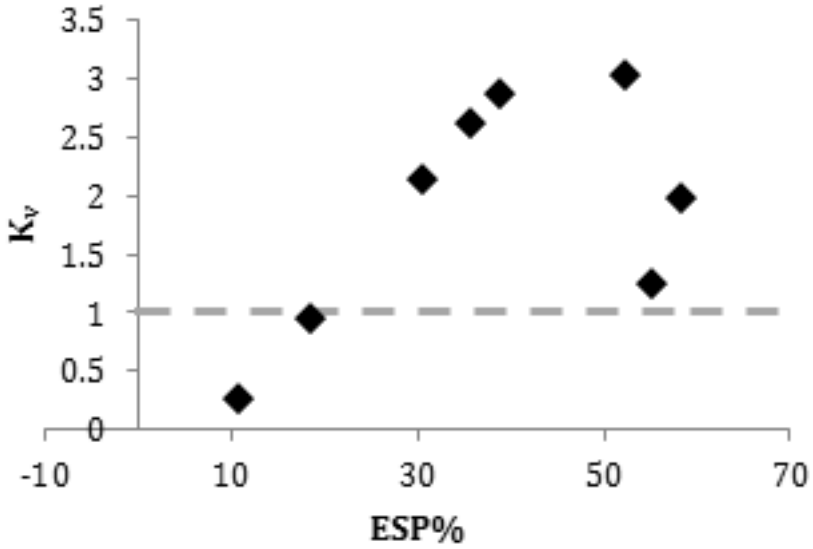


Figure 2. Variation of the Vanselow exchange coefficient (K_v) with different exchangeable sodium percentages (ESP) resulting from the various sodium adsorption ratios (SARs). Values of K_v>1 show a preference for Na^+ on the exchange sites over Ca^{2+}.

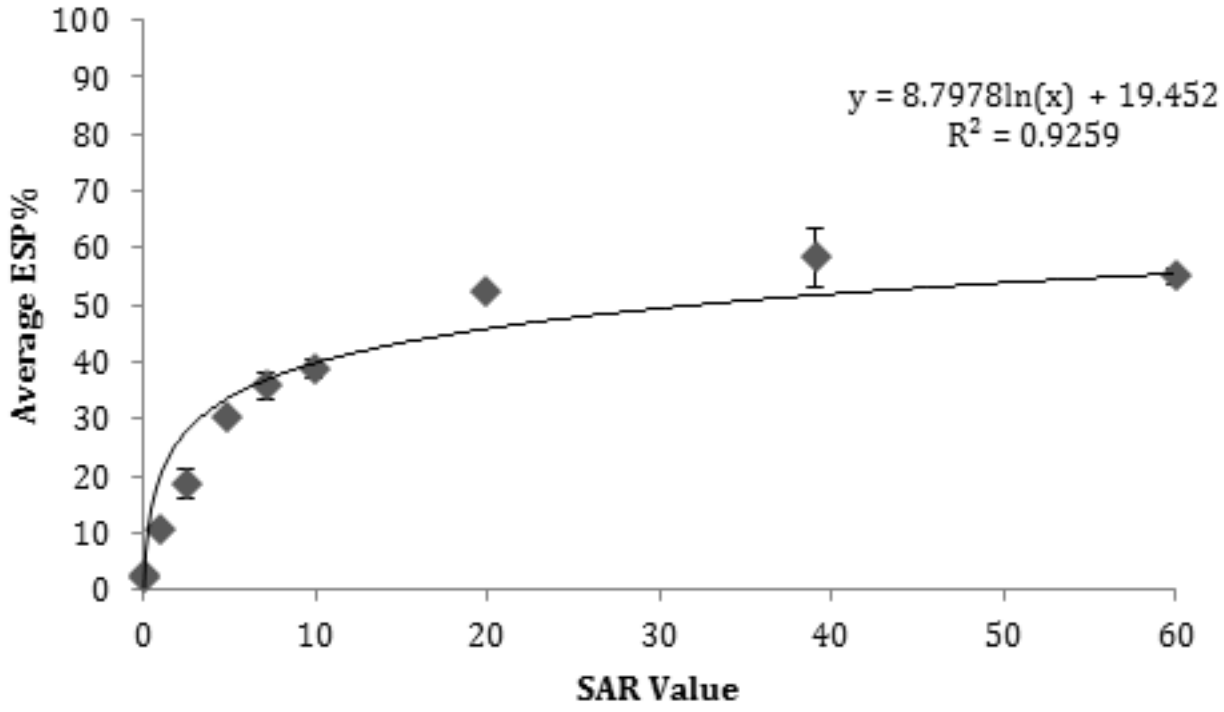


Figure 3. The entrained solution of SAR-equilibrated peat (at I=0.01M) vs. average exchangeable sodium percentage (ESP%) displays a generally positive logarithmic correlation. As SAR values increase (up to SAR 20), ESP% increases, showing an increase of Na on exchange sites when Na concentrations in the solution are greater. ESP% values reach a limit just below 60%, suggesting a preference of Na on the exchange sites, but a limitation by Ca^{2+} or other ions at high Na:Ca ratios.

Relative Element Mobility in Pseudomorphs after Lawsonite from the Schists of Syros, Greece

Clementine Hamelin/2015

Lawsonite, of formula $CaAl_2Si_2O_7(OH)_2 \cdot H_2O$, is an index mineral of high-P, low-T metamorphism, characteristic of subduction zones. It is rarely preserved during exhumation[1] and commonly occurs as pseudomorphs.[2] Pseudomorphs after lawsonite occur in the schists of Syros, Greece, a part of the Cycladic blueschist belt. In the field, they occur as fine-grained whitish aggregates of minerals replacing original lawsonite crystals, which broke down at or close to peak metamorphic temperature. Because the lawsonite crystal structure incorporates up to 12 wt.% water, lawsonite growth and subsequent breakdown is considered a substantial mechanism for water transport down to great depths in subduction zones. However, this process and the chemical reactions controlling it are not well understood. The goal of this project is to model these reactions physically and thermodynamically to understand the relative mobility of different elements at play in the lawsonite breakdown and preservation of the pseudomorphs in the schists of Syros.

Thin section maps showing element and mineral distribution in the rocks were produced using a scanning electron microscope with energy dispersive x-ray spectrometry (SEM/EDS) (Fig. 1). Pseudomorphs are dominantly composed of epidote-group minerals and white micas with minor amounts of chlorite, quartz and albite. Thermodynamic modeling suggests that lawsonite reacted with matrix minerals - glaucophane, Mg-rich phengite and/or pyroxene to produce the minerals observed in the pseudomorphs. Analysis of the element maps show a low Al-mobility (Fig. 1) relative to other elements – such as K (in phengite) and Na (in paragonite), and minor amounts of Mg and Fe – which do not occur in lawsonite, yet are present in the pseudomorphs. These elements must therefore have moved from the matrix to the pseudomorphs during the pseudomorphing reactions. In epidote-rich pseudomorphs, Ca has remained relatively immobile, whereas in white-mica rich pseudomorphs, Ca has moved into matrix glaucophane in small but significant amounts.

These results suggest that Al was relatively immobile during the pseudomorphing process, preserving the original lawsonite crystals shape; however, Al must have been more mobile in order to grow the original lawsonite crystals from an originally homogeneous matrix. The observed change in phengite compositions from celadonite (Mg-rich) in the matrix to muscovite (Mg-poor) in the pseudomorphs also suggests that a continuous reaction requiring dissolution of phengite in the matrix and growth of new mica in the pseudomorphs occurred. The consistency of thermodynamic modeling with observed textures and modes suggests that the pseudomorphing reactions account for element mobility between pseudomorphs and matrix. These reactions can be considered to have taken place in a 'closed system' on the thin section level, suggesting that larger-scale metasomatism is not required to justify the pseudomorphing process as well as the distribution of elements in the pseudomorphs.

This project builds on previous KECK and independent research projects led by students and faculty, and is the continuation of a previous SURF summer project. Results will be presented to students at Smith in a talk, as well as at the national GSA conference in Baltimore, MD in the fall of 2015. A peer- reviewed journal article presenting our results is in preparation and will be submitted for publication in the near future.

(Supported by the Schultz Foundation)

Advisor: John Brady, Geosciences References:

References:

[1] Keiter, M., Ballhaus, C., and Tomaschek, F. (2011) A New geological map of the Island of Syros (Aegean Sea, Greece): Implications for lithostratigraphy and structural history of the Cycladic Blueschist Unit: Geological Society of America Special Papers 481.

[2] Schumacher, J.C., Brady, J.B., Cheney, J.T., and Tonnsen, R.R. (2008) Glaucophane-bearing marbles of Syros, Greece: Journal of Petrology, v. 49, p 1667-1686.

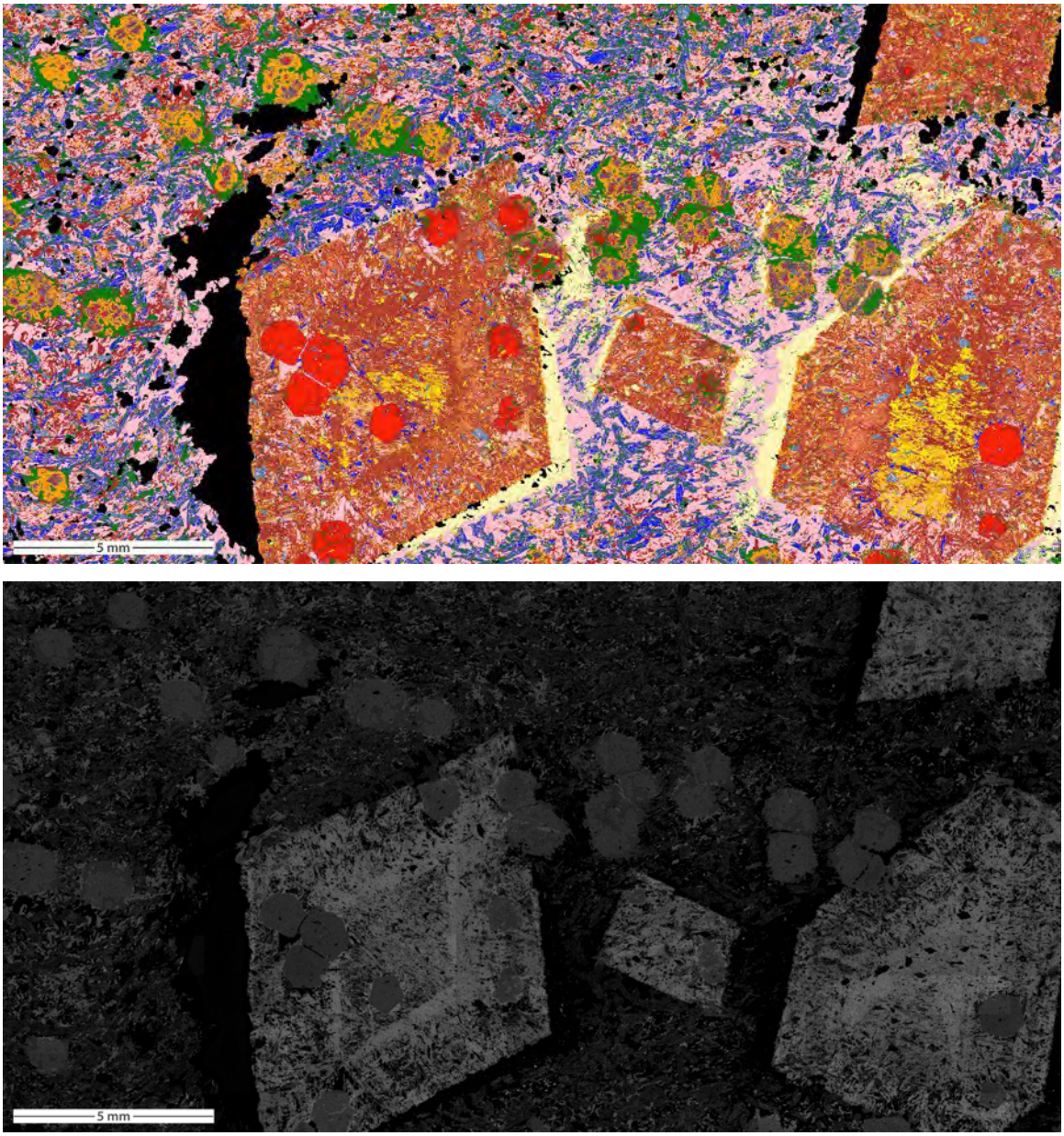


Figure 1 – Thin section phase map (top) and Al-distribution map (bottom) in sample LMA-00-12B. In the top image, note the pseudomorph in the center, which is ~ 1-1.5 cm long, with a calcite-filled pressure shadow around the edges (light yellow), indicating the volume loss resulting from the breakdown of the lawsonite and release of water from the crystal lawsonite structure during breakdown. Ca-rich minerals (epidote-group) are concentrated in the core of the lawsonite whereas the outer part of it is mostly composed of white micas (K- and Na-rich phases) requiring movement of these elements from the matrix into the pseudomorphs during lawsonite-breakdown. In the bottom image, high-Al (light grey) content is concentrated in the diamond shape of the pseudomorphs, retaining its original distribution in the formerly present lawsonite porphyroblasts, indicating that the relative immobility of Al is responsible for the preservation of the lawsonite shape.

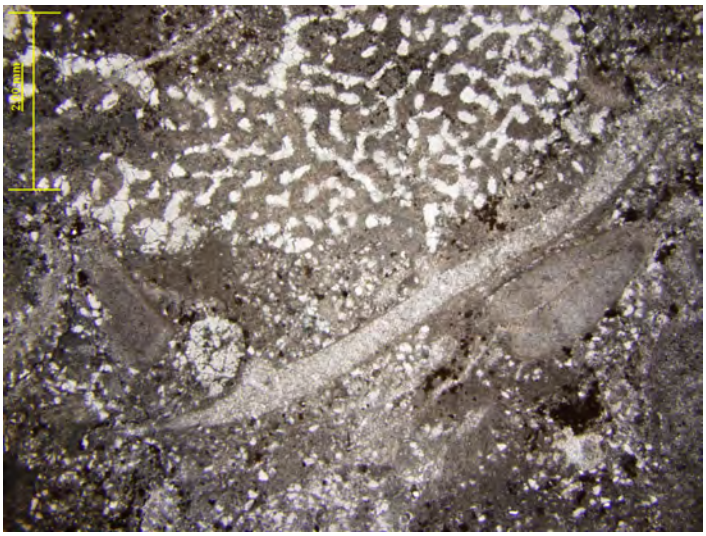
Top map color code: red = garnet; brown = phengite; salmon = paragonite; pink = quartz; blue = glaucophane; green = chlorite; orange = albite; yellow/gold = epidote-group minerals (epidote/zoisite/clinozoisite); steel blue = titanite.

New Archaeocyathan Reefs and Chemostratigraphy of the Lower Cambrian Wood Canyon Formation, Death Valley, USA

Tessa McGann/2016

Archaeocyathans, the first calcifying metazoan reef-builders, thrived in tropical/subtropical oceans across the globe during the early Cambrian. To investigate the role of archaeocyathans in early Paleozoic carbonate production, we analyzed previously undescribed archaeocyathan patch reefs in the lower Cambrian (Series 2) Wood Canyon Formation in the western United States. Thirty-eight samples were taken from 4 laterally correlative patch reefs found in Titanothere Canyon, Death Valley National Park. From these samples, 33 thin sections were point counted to quantify the skeletal components of the reefs and the surrounding facies. Additionally, samples were taken through stratigraphy to generate a carbon isotope curve from this carbonate-rich part of the Wood Canyon. On average, skeletal material is found to account for 10% of the points counted from samples taken from the reefs; of the 10%, archaeocyathans account for 51%, while echinoderm and trilobite fossils make up 29%. In the grainstone-wackestone beds flanking and immediately below the reefs, skeletal material accounts for an average of 14%, with archaeocyathans producing ~ 21% of the skeletal carbonate and echinoderm fossils producing 73%.

Biostratigraphy and carbon isotopes provide constraints on the age of this part of the Wood Canyon Formation. The biostratigraphy places the upper Wood Canyon in the *Fallotaspis/Nevadella* zones, making this part of the section correlative with the Campito Formation of the White-Inyo successions. Carbon isotope values shift from -3‰ -0.6‰ in the basal ~15 m of this exposed section and then plateau at about -1.3‰ up to 55 m. Values show a small excursion to -3.8‰ at 75 m and then shift back to a plateau around -2.3‰ for the remainder of the section. These values, in concert with the biostratigraphy, places the archaeocythan reefs in Stage 3 (Atdabanian) of the Cambrian. The study provides both a link between Cambrian sections of the Death Valley region to the White-Inyo successions and otherwise supports previous findings that archaeocyathan reefs were ecologically complex systems, contributing to the skeletal production of marine carbonate by providing a habitat for a diverse community of calcifying animals.



Photomicrograph of a thin section made from a sample taken from the reef, displaying archaeocyathan and other skeletal material in a micritic and quartz-rich matrix.

(Supported by the Schultz Foundation)

Advisor: Sara Pruss, Geosciences

Pond Project

Mia Ndama/2017

In efforts to find a cost-efficient method to periodically dredge Paradise Pond, Smith has proposed to install a sluice gate to flush contaminated sediment down the Mill River which will hopefully empty into the Connecticut River. The sluice gate will operate for high flow rates of at least 200 cubic feet per second (cfs). In order to determine whether the contaminated sediment successfully empties into the Connecticut River, we have proposed to investigate the health of the Mill River before and after sluicing. In this study, the health of the Mill River is determined by the abundance and biodiversity of its macroinvertebrates. For this project, we have established a baseline health of the Mill River before sluicing.

Macroinvertebrates were collected at seven different sites along the Mill River (Figure 1). Two methods were used to take quantitative samples at the seven sites: Hester Dendy sampling and kick net sampling. At each site, three Hester-Dendys were placed in the river (facing upstream) for four weeks to collect benthic macroinvertebrates (Figure 2). At the end of four weeks, Hester Dendys were pulled out of the river and the macroinvertebrates were immediately preserved. At five sites, kick net sampling was performed with a one mm mesh hand net. For each sample, the net was placed on the riverbed (facing upstream) and the riverbed was disturbed (kicking motion into the net) for approximately 30 seconds. Twenty kick net samples were performed at each of the five sites. These invertebrates were also immediately preserved. After collecting and preserving the invertebrates, they were identified and classified by genus using dichotomous keys. The abundance of each genus was used to find the Water Quality Index (WQI) and Shannon Diversity Index (SDI) at each of seven sites.

Overall, the Water Quality Index and the Shannon Diversity Index revealed that the Mill River has high water quality and is moderately diverse. As demonstrated in Table 1, the average WQI for kick net sampling at the five sites was 72.64. According to the standard, the range 60 to 79 is considered "good" water quality. We found the highest WQI at site 1, which was 86.5. According to the standard, the WQI at site 1 is "excellent." We found the lowest WQI at site 5, which was 61.2. According to Table 1, we found relatively low diversity at site 4, where the SDI was 2.11. The SDI values for all other kick net sampling sites were all intermediate at approximately 2.6. A bootstrap two-sample KS test was performed to compare the difference between the SDI for site 4 and the SDI for the other four sites. The p-value for this test was less than 0.05 which demonstrates that there is a significant difference in diversity between site 4 and all other sites. The macroinvertebrates collected from the Hester Dendys are still undergoing classification. Results from this sampling method are still pending.

According to our results, before the installation of the sluice gate, the Mill River is in relatively good health with high water quality and moderate biodiversity. However, there may be a few preliminary signs of potential sediment accumulation at site 4 where we found a significantly lower diversity of macroinvertebrates. We would want to continue to monitor this site after the sluice gate has been installed. To do this, we would use the same sampling methods to examine biodiversity and abundance of macroinvertebrates.

(Supported by the Center for the Environment, Ecological Design, and Sustainability (CEEDS))

Advisor: Robert Newton, Geosciences

Figures and Tables

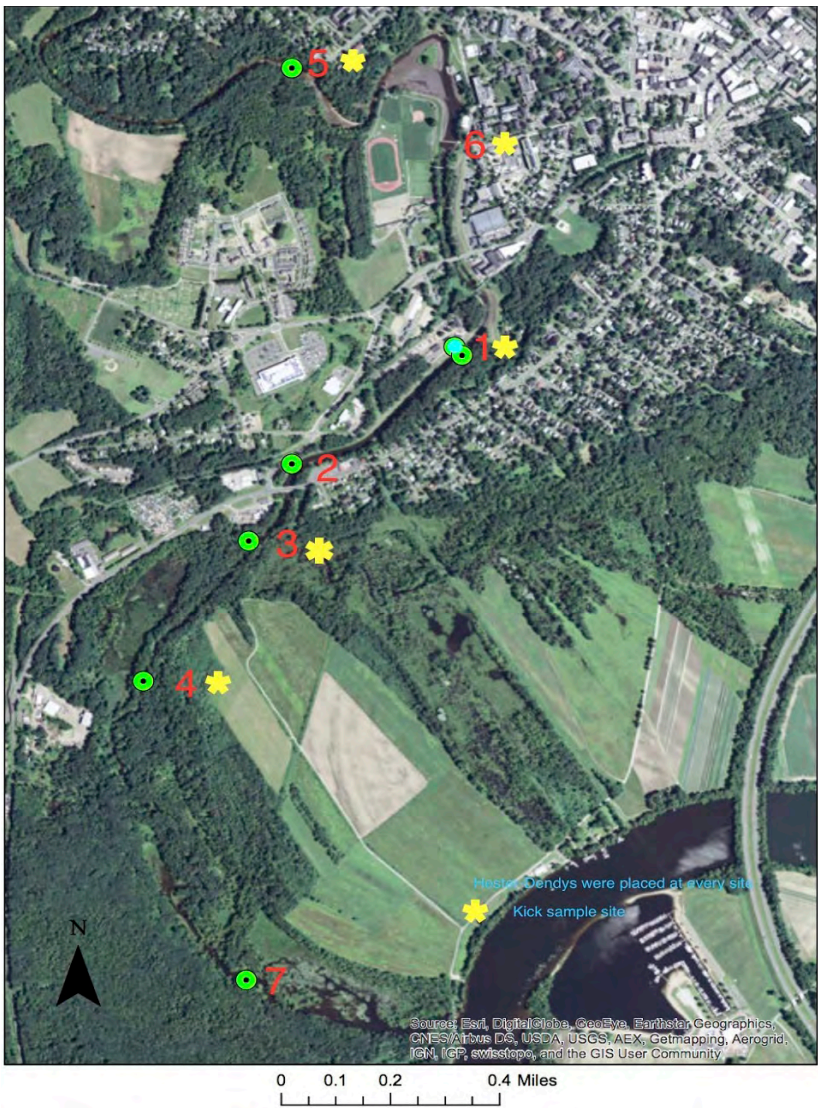


Figure 1: Map of the seven sampling sites along the Mill River. The yellow stars indicate where kick net sampling was performed

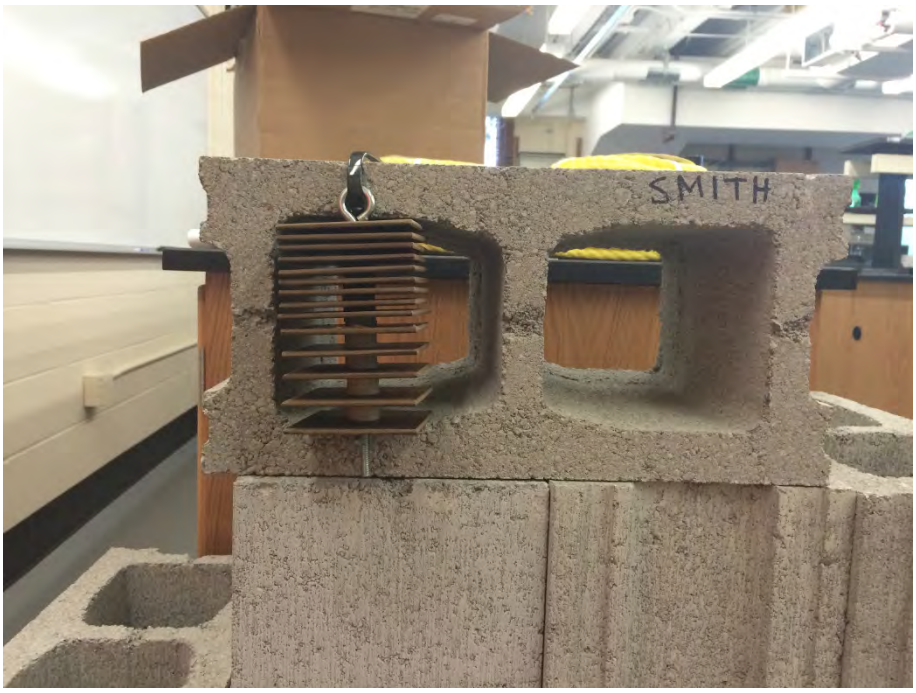


Figure 2: An example of one Hester Dendy which was used to resemble benthic substrate and collect macroinvertebrates

	Site 1	Site 3	Site 4	Site 5	Site 6
WQI	86	73	68	61	72
SDI	2.624	2.648	2.111	2.638	2.975

Table 1: The WQI and SDI found for each kick sampling site based on the diversity and abundance of the genus of the macroinvertebrates collected

Assessing the Risk of Sluicing on the Biotic Health of the Mill River

Molly Peek/2018

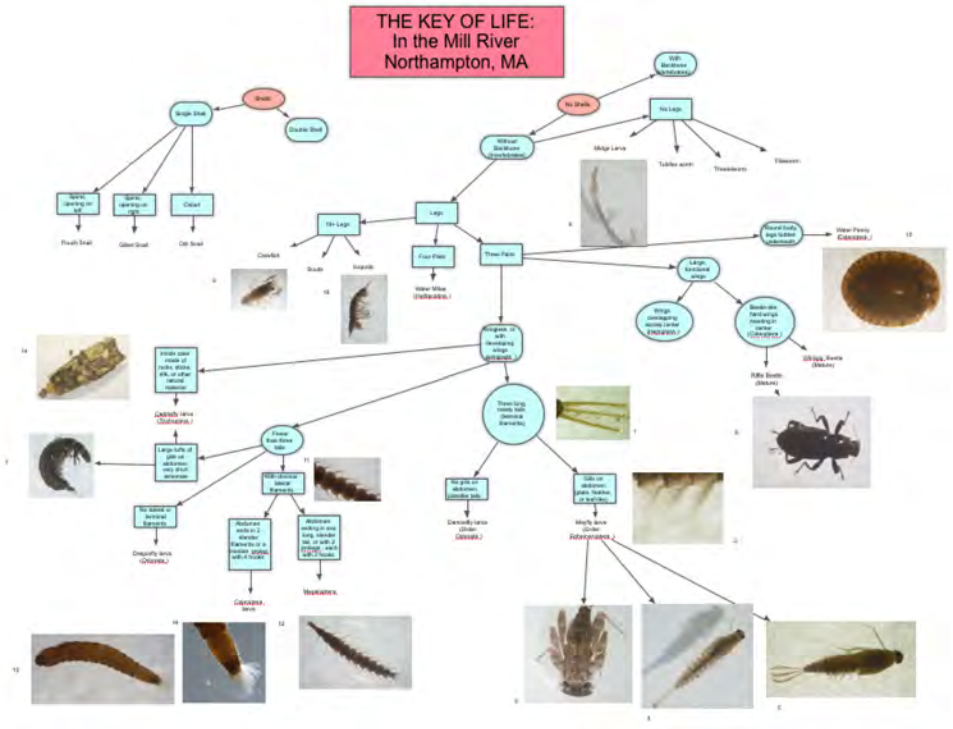
The Mill River in Northampton, MA, is dammed at Smith College, creating Paradise Pond. For a cost-efficient solution to periodic dredging of the campus landmark, Smith has proposed a sluice gate for flow events 200 cfs or greater to flush out fine-grained and possibly contaminated sediment. This study assesses current stream health and potential harm posed by sluiced sediment using biotic testing at six downstream and one upstream site. Macroinvertebrates were collected using Hester-Dendy samplers deployed for four weeks at all seven sites, and kick sampling techniques at five suitable sites. Macroinvertebrates were identified to genus and their abundances provided a biotic Water Quality Index (WQI) and a Shannon Diversity Index (SDI). Initial measurements of mussel length and number of growth rings were preformed using systematic sampling methods on Elliptio complanata and Lampsilis radiata to monitor the effect of sluiced sediment on density and age patterns in the populations. Mussel sampling was also preformed in the nearby Manhan River as a control.

Macroinvertebrate kick sampling yielded an average WQI of 72.64. Site 4 yielded low diversity with 2.11, and other sites had intermediate SDIs. Site 4 also had the lowest (14%) EPT score for the sum of indicator organisms. Historic mussel collection data shows fluctuating age populations and declining Lampsilis radiata populations. Mill River mussel density was significantly greater than the Manhan river ($p=0.32$), as was mussel length ($p=0.00045$), although number of growth rings was not ($p=0.32$).

Kick sampling indicates the Mill River is in consistently "good" health at each site before the sluice gate is installed, although lower health scores at site 4 indicate that the pattern of sediment accumulation may exacerbate harm from increased flow. Mussel density and length was greater in the sand-gravel Mill River substrate than in the fine-grained Manhan River, indicating that mussels respond to substrate and prefer coarser materials. These tests will continue in order to monitor stream health and diversity after sluicing begins, and catalogued macroinvertebrates will be used to perfect a Mill-River specific dichotomous key for identifying macroinvertebrates.

(Supported by the Center for the Environment, Ecological Design and Sustainability, (CEEDS))

Advisor: Robert Newton, Geosciences



Sedimentation in Paradise Pond

Marcia Rojas/2018

Rivers naturally carry sediment. At certain velocities, as shown in the Hjulström Diagram below, sediment of varying sizes are deposited. Due to excess sedimentation, Paradise Pond must periodically have sediment removed. Doing away with the costly and obstructive methods of dredge excavations and hydraulic dredges, the Mill River Project aims to alleviate sedimentation in the pond by making use of the river system itself. The goal of the project is to open the dam gate when there is much erosion occurring, such as a storm, and allow for the accumulated sediment in the pond to continue down the Mill River.

Three research components I worked on along with the Mill River Project research team were gathering data for discharge levels, moving bed tests and bathymetry of the pond. My individual focus was sediment grain size analysis. The core samples analyzed were obtained during the 2014-15 academic year from varying areas of interest in the pond. All samples were wet sieved through a No. 230 (63) sieve and samples with high sand content were dry sieved.

Out of the 119 sediment samples analyzed from Paradise Pond, 84 of them are more than fifty-percent sand. From moving bed tests, it was determined sediment movement did occur after high flow events. To ensure the safety of downstream habitats, lab analyses of the sediment for mercury, lead and phosphorus were also performed. Amounts of the materials were found to be under regulation levels. These and other results of the project will be presented by our research team this year at the New England Graduate Student Water Symposium.

Sand being the majority grain size present in the samples gives a view into what kind of velocities are required for the sediment to move from those general regions of the pond. Further analysis must be done to specify what the sand size distributions are. Additionally, it is important to note that some cores were larger than others, rendering a need for further statistical analysis of the data. For the upcoming 2015-16 academic year I plan on continuing my involvement in this project. My primary goals will be to gather more precise data on the grain size of the samples and to create meaningful statistical measures of the data.

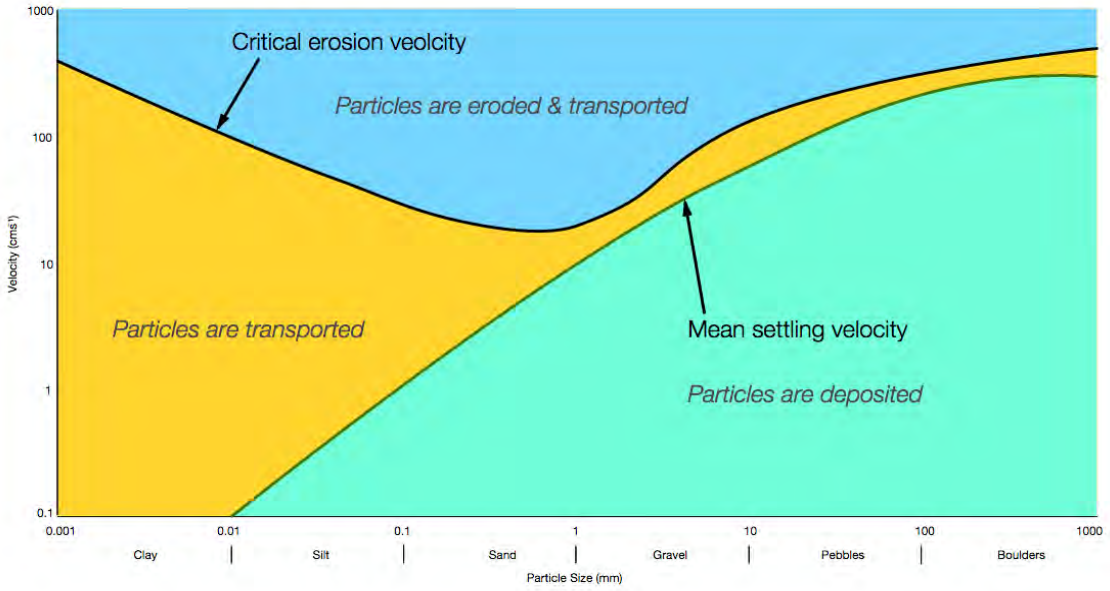


Figure 1: Hjulström Diagram

(Supported by the Center for the Environment, Ecological Design and Sustainability, (CEEDS))

Advisor: Robert Newton, Geosciences

The Advent of the Coral Reef: Animal Abundance in Upper Ordovician Lourdes Formation Reefs, Western Newfoundland

Emma Roth/2017

During the Middle to Late Ordovician, carbonate reefs changed drastically. Corals and other metazoans began constructing reefs for the first time following the long-term microbial reef resurgence of the Cambro-Ordovician interval. The Lourdes Formation of western Newfoundland is a 75-m thick Upper Ordovician (late Whiterockian to early Mohawkian) mixed siliciclastic-carbonate unit exposed on the southwest coast of Long Point on the Port au Port Peninsula. In the Black Duck 3 Member of the Lourdes Formation, coral bioherms are well developed.

The buildups measured in this work are up to 5 m-thick, ~5 m wide and occur through 16 m of stratigraphy. Here, we mapped and sampled 3 reef bioherms at 1 locality were the Black Duck 3 Member was well exposed. We measured and sampled each reef in detail, extracting 42 samples from the reef core, grainstone channels that form under and around the reefs, and the surrounding sediments. Each sample was thin sectioned and a subset of 26 well preserved samples were point counted.

In general, fossil points accounted for 37.4% of all points counted from reef samples. The coral, Labyrinthites, makes up the most skeletal material in the reef core (83% of fossil points). Crinoids make up 7% of fossil points with ostracode, brachiopod, stromatoporoid, and bryozoan material making up 10% of the remaining fossil counts. Fossil material in the grainstone channels is composed of crinoids (66%), bryozoans (16%), and brachiopods (12%), with small amounts of ostracodes and trilobites (6% combined). Crinoids (48%) and brachiopods (26%) make up most of the skeletal material in the surrounding sediments, but in general, skeletal material was less abundant (11%) than in the reef.

Our initial analysis of these bioherms confirms earlier work indicating corals are abundant in the reef core, likely acting as framework builders, and that crinoids are ubiquitous components of this reef ecosystem, probably serving as sediment bafflers. Additionally, we suggest that even at this early stage in coral bioherm development, an ecologically complex reef system developed in western Newfoundland where diverse skeletal material is much more prominent in these ecosystems than in any reefs that existed before this time.

I will be continuing this project in the fall semester and presenting a poster at the GSA annual conference in November.

(Supported by the Committee on Faculty Compensation and Development (CFCD))

Advisor: Sara Pruss, Geosciences

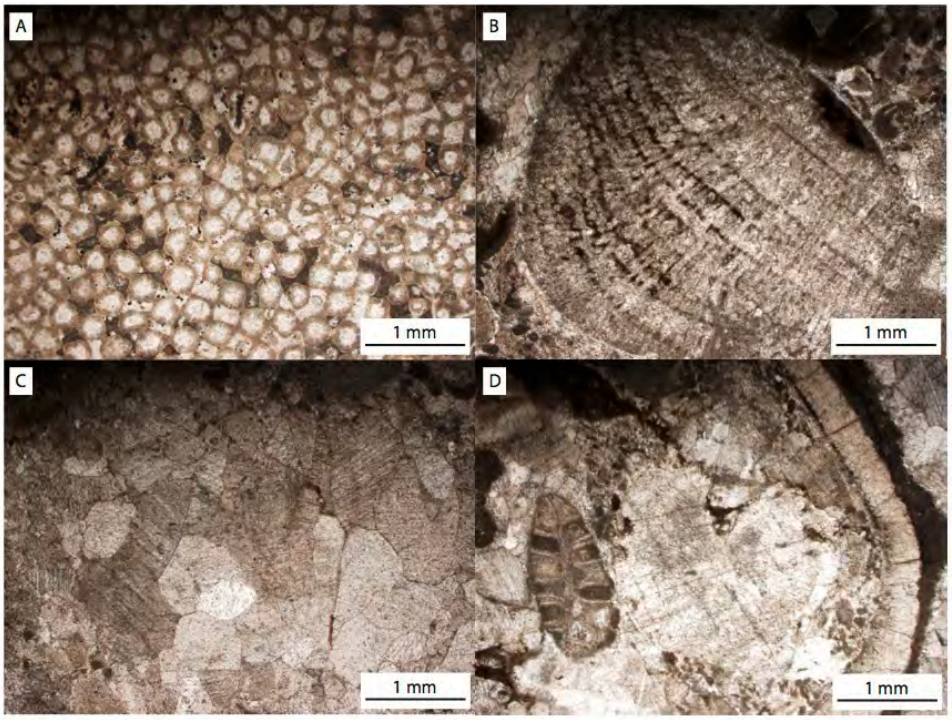


Figure 1A: Thin section of coral from a reef core.

Figure 1B: Thin section of a stromatoporoid from a reef core.

Figure 1C: Thin section of crinoid material from a grainstone channel.

Figure 1D: Thin section of a bryozoan colony, crinoid material, and a brachiopod from a grainstone channel.

Management of Sediment Accumulated in Paradise Pond, Smith College

Lizzie Sturtevant/2018

Rivers have a balance of sediment inflow and outflow. However, the construction of a dam such as the one used to create Paradise Pond, disrupts this balance by lowering water velocities, resulting in deposition and accumulation of sediment.[1]

Paradise Pond is traditionally dredged every 8-10 years and the accumulated sediment is transported to a landfill. As an alternative to dredging, it may be possible to utilize the sluice gate at the base of the dam to flush sediment downstream. Opening the gate during high flow events would increase water velocity and carry suspended sediment through the gate.

To assess potential risks of contamination with sediment release, nine cores were collected from Paradise Pond and two sediment cores from Hulbert's Pond, a downstream site. Cores were analyzed for mercury, lead, and phosphorus. Cores were segmented, dried at 50°C, homogenized, and analyzed for mercury by thermal decomposition cold vapor atomic absorption using a Hydra IIC Mercury Analyzer. Core samples were also acid digested, then analyzed for extractable metals such as lead using an Inductively Coupled Plasma Optical Emission Spectrometer.

Additionally, cores were analyzed for grain size. Grain size is determined by the velocity under which sediment is deposited. Samples were wet sieved through a No. 230 (63 μm) sieve and then dried at 50°C. Percent sand and mud in each sample were obtained using the recorded weights before and after drying.

A bathymetric map was created to establish sediment distribution in the pond. Additionally, moving bed tests were used to record sediment movement. Downstream reference stations were also established to monitor sediment accumulation after a sluicing event. Baseline data includes cross-sectional profiles of reference stations and discharge measurements. Stream health and macroinvertebrate diversity were also monitored at downstream sites.

No significant difference was found in Pb and Hg concentrations between Paradise Pond and Hulbert's pond. Paradise Pond sediment is coarser than that found in Hulberts Pond (39% mud vs 66% mud). Moving bed was detected in the channel upstream of the dam as well as at the inlet to the pond during events of 360-470 cfs. Overall stream health prior to opening the sluice gate was classified as "good" using a biotic water quality index. Now that we have collected this baseline data, we are prepared to test the sluice gate and measure the subsequent sediment deposition downstream.

(Supported by the Center for the Environment, Ecological Design and Sustainability (CEEDS))

Advisor: Robert Newton, Geosciences

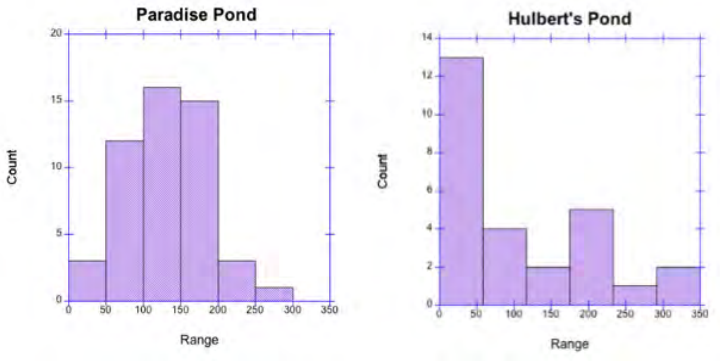


Figure 1. Histograms of total Hg concentrations from Paradise Pond and Hulberts Pond core samples. Highest concentrations were found in Hulberts Pond although there was no statistically significant difference between the 2 sites.

[1]Batuca, Dan G., and Jan M. Jordaan. *Silting and Desilting of Reservoirs*. Rotterdam, Netherlands: A.A. Balkema, 2000. Print.

Sediment Movement and Accumulation in Paradise Pond

Lyn Watts/2017

Paradise Pond, on Smith College's campus, is traditionally dredged regularly to remove accumulated sediment (the last dredging occurred in 2007). This project investigates the viability of flushing sediment downstream through the sluice gate in the dam as an alternative to dredging. Sluicing sediment during storm events mimics a normal river system. The conditions under which sediment moves in the pond were investigated using a Teledyne RDI RiverRay Acoustic Doppler Current Profiler (ADCP) to measure Water velocity and the rate of moving bed (sediment movement on the bottom of the pond).

To analyze current sediment accumulation, a bathymetric map was created using an Innerspace Model 455 survey grade depth sounder coupled to a Trimble GeoXH receiver running TerraSync software. Positions were obtained from a Trimble R1 GNSS Receiver and differentially corrected using Trimble Pathfinder Office software. A Leica geosystems TPS1200 Total station measured elevations where the water depth was less than two feet. The merged datasets were used to create an elevation map of the pond in ArcGIS.

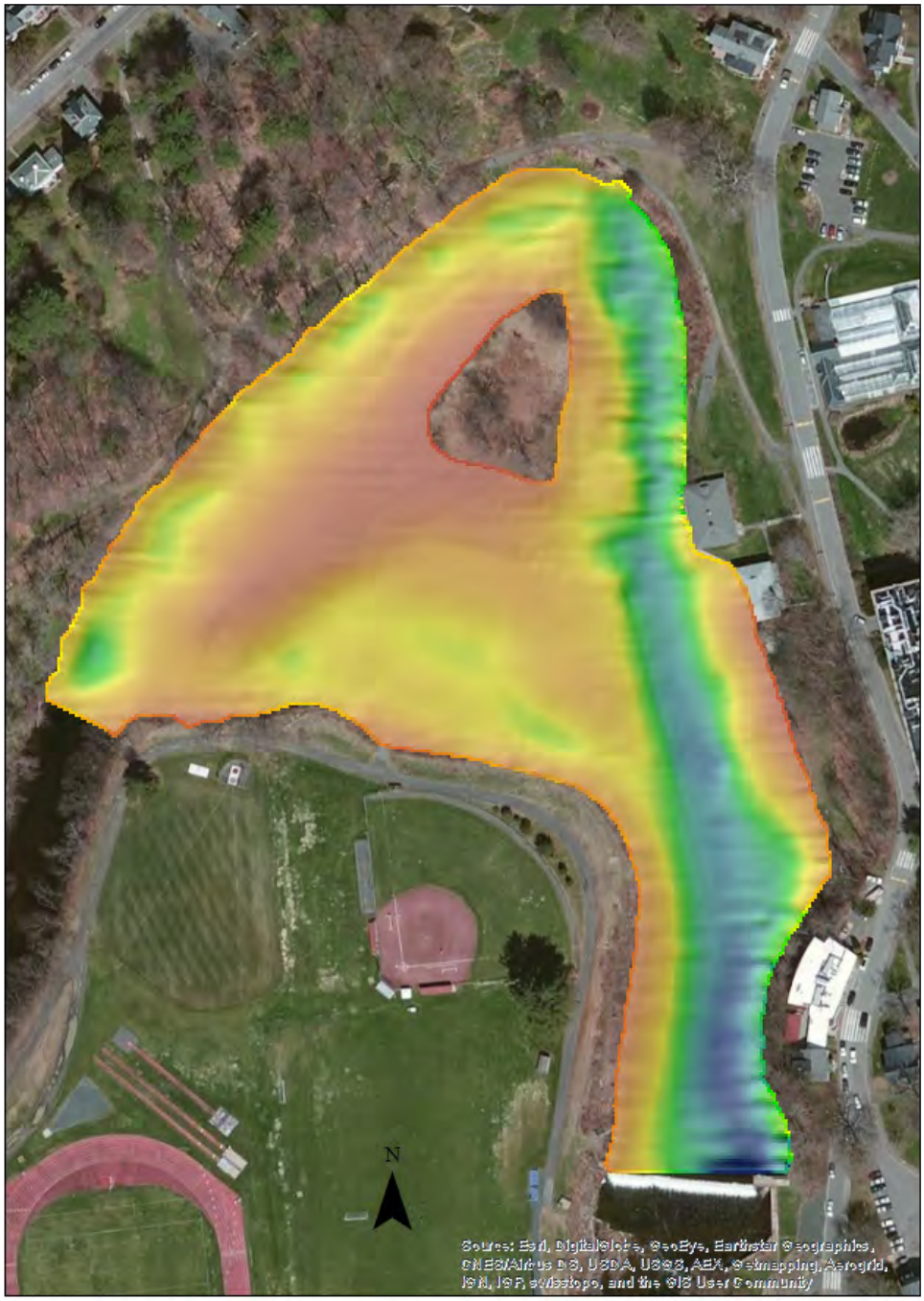
The bathymetric map shows the deepest part of the pond forms a channel along the left bank, where there is greater velocity. Compared to a map created in 2014, over two feet of sediment has accumulated. Two sand bars compose most of the total accumulated sediment and between 0- 1.5 feet of additional sediment is distributed throughout the pond.

Moving bed tests were conducted during high flow conditions (360 to 470 cubic feet per second (cfs)), and confirmed where the pond width is narrow. Tests were also conducted in front of the sluice gate when the gate was open 30% and the discharge was low (140-150 cfs). Moving bed was recorded at five meters from the gate where the velocity was 0.48 ft/s, but not at 20 meters. Moving bed directly in front of the open gate demonstrates that while sediment movement is possible without high water velocity, a storm event is necessary to move large quantities of sediment. During measured events, sediment is moving, but not in wider areas where bathymetry shows higher sediment accumulation.

Thus far, location is the only predictor of moving bed. To determine the best conditions for moving bed (before or after a storm, what velocities are necessary in different areas, etc.), more moving bed tests will be conducted under higher discharge conditions in the fall semester.

(Supported by the Center for the Environment, Ecological Design and Sustainability (CEEDS))

Advisor: Robert Newton, Geosciences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Miles

Sand Transport and Dynamics at Popham Beach, Central Coastal Maine

Jane Weinstock/2016

Popham Beach is a bedrock-bound sand bar system adjacent to the Kennebec River estuary in central Maine. While the sands that make up Popham Beach have previously been sustainably circulated in the estuarine system (between the estuary mouth, an offshore sand shoal, a beach sand bar complex, and back into the estuary),[1] in 2009 the tidal Morse River to the west of the beach eroded the beach back over 100 meters (figures 1 and 2). Due to the sand circulation system and conservation efforts, the beach has largely returned to its original size, but the back-beach dune environment is still in its infancy.[2,3] The goal of this project was to document this recovery process as it unfolds. This project joins a larger effort to document the sand dynamics at Popham Beach in order to achieve a better understanding of how bedrock-bound estuarine systems can change over time and to better inform policies regarding the area's future as a tourist destination.

Beach profiles were measured in the summer of 2015 using a Trimble Leica Geosystems TPS1200 Total Station along eight lines defined by a Trimble GeoXH Global positioning system (GPS) receiver. The eight lines (figures 3 and 4), which are measured annually each spring by the Smith College geomorphology class, were measured three times over an eight week period. Additional data were collected along the beach's low tide line and on either side of the Morse River every 1-3 weeks, and dune growth was mapped every 2-3 weeks.

Initial results show the sand is returning to eroded areas and the dunes are reforming, but the bulk of data analysis will be carried out using ArcGIS software upon return to Smith College in September. Results will be used to determine which areas of the beach are being built up and whether any are at risk of eroding back into existing infrastructures. This information will further geomorphic knowledge regarding bedrock-bound estuaries, as modern dynamic systems, ecologically, and sedimentological records of paleoenvironments.

(Supported by the Schultz Foundation)

Advisor: Robert Newton, Geosciences

References:

[1]FitzGerald, D.M., Buynevich, I.V., Fenster M.S., McKinlay, P.A. (2000) Sand dynamics at the mouth of a rock-bound, tide-dominated estuary. Sedimentary Geology 131: 25-49.

[2]Newton, R.M. (2015) Personal correspondence

[3]Personal observations

Figure 1: Aerial photograph from 2003 showing original size and shape of Popham Beach. North is up.

Figure 2: Aerial photo from 2009 showing major erosional event. North is up.

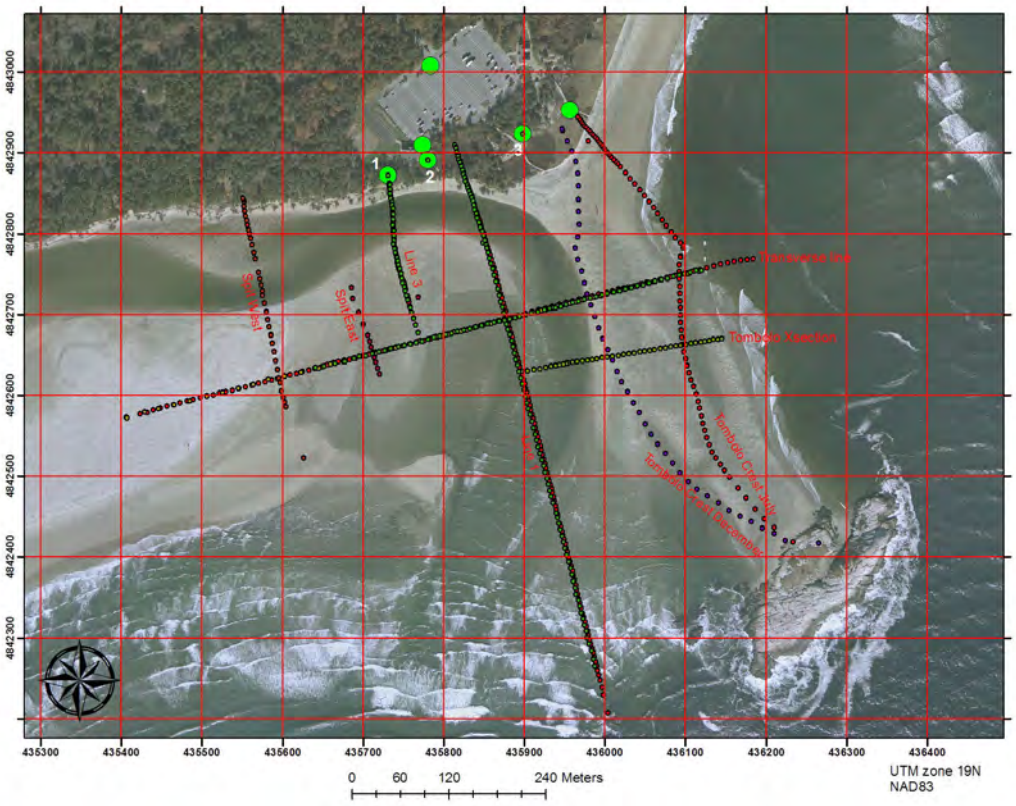

Figure 3: Aerial photo (2009) showing six of the eight transects measured (the seventh, SpitEast, was not used).

Figure 4: Aerial photo showing two additional transects at Hunnewell Beach, directly northeast of Popham (parking lot shown in both photos). North is up.

Design and Construction of a Parking Lot, Testing Various Permeable Materials at the Ada and Archibald MacLeish Field Station in Whately, MA

Laura Krok-Horton/2017

Pervious pavements are a sustainable alternative to impervious materials such as asphalt and concrete, which add to the urban heat island effect and groundwater pollutants. By allowing the movement of stormwater through the surface, permeable materials reduce runoff, control pollutants, and are more aesthetically pleasing. This summer, the research I did focused on the design, budget, and construction of a 14-car permeable-surface testing parking lot at the Ada and Archibald MacLeish Field Station in Whately Massachusetts.

I researched parking lot layouts after analysis of the site, and I created designs for the 6,000 sq. ft. cleared field, located at the entrance of the property. I also researched various sustainable parking lot designs, such as permeable materials and site preparation.

With the research collected, four types of permeable surfaces were selected to be tested: TurfStone, TrueGrid, GrassProtecta, and an innovative material (yet to be determined) that will question the concept of permeability. Lysimeters under each material, will collect water that has passed through the material to test for effects on ground water. The durability of the materials will be analyzed to understand the effect of snowplowing on each material in the winter.

Along with initial construction of the testing site, I learned how to prepare the site by drawing plans, compiled an inventory of labor and materials, and scheduled and supervised the work on site. The installment of the permeable pavers and water collection systems will occur in the Spring of 2016.

(Supported by the Center for the Environment, Ecological Design and Sustainability, (CEEDS))

Advisor: Reid Bertone-Johnson, Landscape Studies

Mathematical Models of Intracellular Cargos and Motors

Sara Kacmoli/2017

My summer research was focused on testing and creating mathematical models that mimic the behavior of the molecular motors kinesin and dynein. These molecular motors are responsible for the transportation of different vesicles and organelles inside our cells. When they are attached to the same cargo, they can engage in what is commonly known as a "tug of war" where kinesin pulls the cargo anterogradly and dynein retrogradly.

The first model that was analyzed was a cargo-based model. We used Matlin to stochastically produce graphs of position and velocity as functions of time based on a velocity probability matrix that was obtained experimentally.[1] We then shifted our attention to a motor-based model which took into account constant binding and unbinding rates of the motors to the microtubule track. We performed simulations by implementing the Gillespie algorithm to keep track of the binding and unbinding of motors to the track while also updating the velocity and location of the ensemble from one reaction time to the next. The next layer of biological details added to this simple model was the effect of loading forces on the unbinding rate and velocity. These types of models are commonly known as "mean-field models,"[2] built upon two main assumptions: (i) opposing motors act as a load, and (ii) this load is shared equally among identical bound motors. Building upon existing models, we then relaxed the second assumption as well as the linear relationship between the exerted force and the unbinding rate. Monte Carlo simulation was used for computation where we updated the states at every fixed time step.[3]

The results from single-motor simulations were generally less than recent in-vitro experimental results.[4] From simulations, we gathered mean values of velocity, position, and percentages of time spent bound or unbound to the microtubule. We also collected simulation results for multiple-motor and performed parameter analysis, which generally confirmed our expectations. The next step in terms of future work would be modeling a more flexible cargo, which would perhaps merge the two points of view we have taken: cargo and motor-based modeling

During this project I learned valuable technical skills such as creating mathematical models and using Matlab to simulate them as well as gathering, presenting and interpreting data. I also learned about a new topic that I expect to prove helpful in my engineering career.

(Supported by the Committee on Faculty Compensation and Development (CFCD))

Advisor: Nessy Tania, Mathematics and Statistics

[1] Brown, A. "Stochastic Simulation of Neurofilament Transport in Axons: The "Stop-and-Go" Hypothesis." Molecular Biology of the Cell 16 (2005): 4243-255. Nature.com. Macmillan Publishers Limited. Web. 08 August 2015

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[5] Hancock, William O. "Bidirectional cargo transport: moving beyond tug of war." Nat Rev Mol Cell Biol 15 (2014) Nature.com. Nature Publishing Group, a division of Macmillan Publishers Limited. Web, 08 August 2015

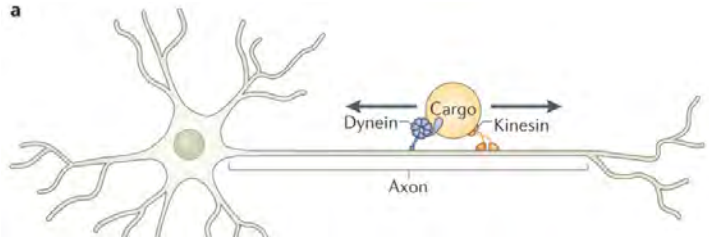

Fig 1: Membrane-bound vesicles transported bidirectionally by kinesin and dynein motors in both axons and dendrites[5]

Tuberculosis Disease Modeling in the USA

Ellie Mainou/2017

Tuberculosis (TB) is caused by the bacterium *Mycobacterium tuberculosis*. Latently infected individuals are neither symptomatic nor contagious. Individuals with active TB show symptoms, and may transmit the disease through the air. Despite worldwide efforts, TB remains a major global health problem with one third of the world's population being infected with TB. The greatest challenge concerning the disease is the emergence of strains resistant to common antibiotics (e.g. isoniazid and rifampin), constituting treatment difficult and costly. So far, mathematical models (e.g. Hill *et. all*) look at drug-susceptible TB only (3). We wanted to develop a predictive model in the US population that incorporates single- and multi-drug resistance.

We developed three departmental models that include the different groups of the population (susceptible, latently infected, actively infected, dead of TB), as well as the possible ways in which an individual can move from one group to another. Each model contains different strains of TB: drug-susceptible strains; drug-susceptible and isoniazid-resistant strains; and drug-susceptible, isoniazid-resistant, rifampin-resistant and multi-drug resistant strains. The change in the number of individuals in each compartment was described by a differential equation. The model was fitted to data obtained by the Center for Disease Control (CDC) for the years 2000-2012(1, 4). To account for uncertainty in parameter estimation and to better fit our model to data, we drew random parameter values from specific distributions whose ranges constitute epidemiological knowledge, keeping the values that produce better fits (2, 3, 5).

Figure 1a shows the best fit model for drug-susceptible strains against data. Most of the dots fall within the line, indicating that our model is a good fit for the total US population, the active TB cases and TB deaths each year. Figure 1b shows our predictions for active and latent cases, and deaths due to TB for the model containing drug-susceptible strains until 2100. According to the graphs there is a decline in the number of TB cases, leading to elimination of the disease in 2100.

Although the single-strain model provides a good fit to data, it is not representative of the reality, because of the absence of drug-resistant strains. It is expected that the incorporation of such strains will greatly alter our predictions. This is why our future work includes parameter estimation of the remaining models. Our ultimate goal is to identify effective methods for the elimination of TB. To achieve this we will analyze predictions for the four-strain model up to 2100, and manipulate parameters to evaluate the effects of different TB control strategies.

(Supported by the Schultz Foundation)

Advisors: Robert Dorit, Biological Sciences; Dylan Shepardson, Mathematics and Statistics

1)Bennett, D. 2008. Prevalence of Tuberculosis Infection in the United States Population. American Journal of Respiratory and Critical Care Medicine. 177:348-355.

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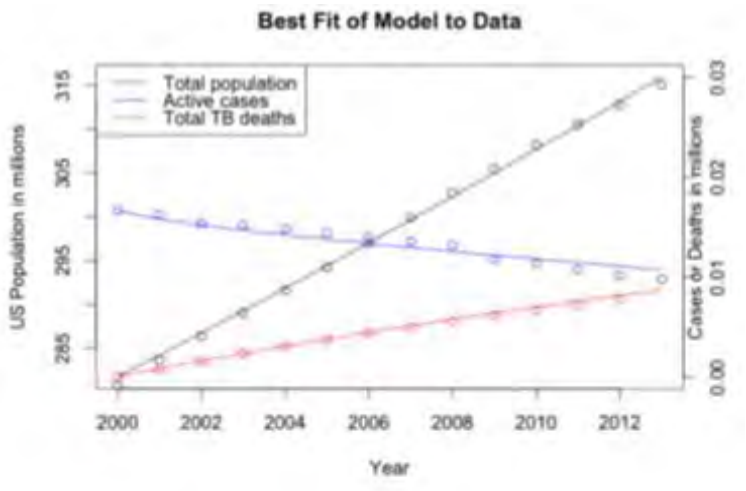


Fig 1a

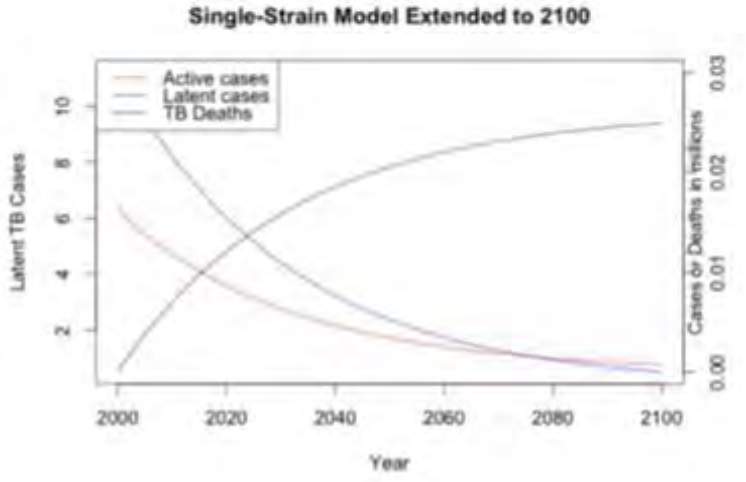


Fig 1b

Fig1a: Dots represent real data, and lines depict the best fit model to data. This model contains drug-susceptible strains only.

Fig 1b: Model predictions until 2100 for the model containing drug-susceptible strains.

Introduction to Splines

Megan Perry/2016'AC

Generalized splines are a graph labeling that meet a specified criteria. Splines are especially found in abstract algebra and are applied in many important fields including architecture, engineering, and significantly in digital media. Traditionally, splines are defined over polynomial rings. There are also many long unanswered questions about splines over these rings. Recently, research extends splines to the integers and integers modulo n. The latter is the focus of the survey paper I completed this summer.

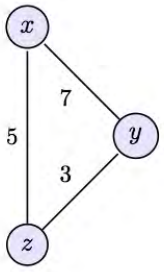
Meeting with my advisor throughout the summer I worked to clarify concepts for myself, and to articulate them clearly and succinctly for any audience. My work was mostly independent, though I enjoyed collaborating with another student working on splines, as well as with visiting mathematicians. I wrote this paper for anyone with some interest in mathematical research, but possibly lacking specific background; my goal was to give readers a strong enough foundation to begin their own research into splines. The paper is also useful for those with advanced degrees whose own work has not touched on these areas of mathematics in a long while.

There are still many unanswered questions about splines at this level. I hope that by answering these questions we are able to shed light on larger open questions as well.

(Supported by the Susan M. Rambo 1905 Fund)

Advisor: Julianna Tymoczko, Mathematics and Statistics

Example 7.2. Algorithm results for each prime power using trivial spline for first vector on a prime edge-labeled graph in $\mathbb{Z}/315\mathbb{Z}$



$\mathbb{Z}/315\mathbb{Z}$

$$\mathbb{B}_{\mathbb{Z}/9\mathbb{Z}} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix} \begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix} \begin{pmatrix} 3 \\ 0 \\ 0 \end{pmatrix} \right\}$$

$$\mathbb{B}_{\mathbb{Z}/5\mathbb{Z}} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix} \begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix} \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix} \right\}$$

$$\mathbb{B}_{\mathbb{Z}/7\mathbb{Z}} = \left\{ \begin{pmatrix} 1 \\ 1 \\ 1 \end{pmatrix} \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix} \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix} \right\}$$

FIGURE 11. The graph and generating sets from section 6

This is an example of a graph worked with to determine all splines of a specific edge labeling.

Splines Over the Integers Modulo a Prime Power

McCleary Philbin/Post-Bac 2015

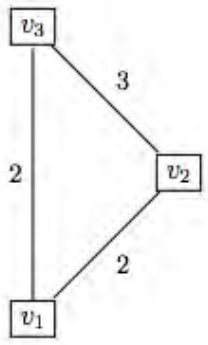
Given a graph with edges labeled by ideals in a ring R, a generalized spline is a labeling of each vertex by an element in R such that adjacent vertices differ by an element in the ideal associated to the edge connecting them. When the ring R is the integers, we can think of a spline as vertex-labeling such that the difference between any two adjacent vertices is a multiple of the label on their connecting edge. We give an example of an edge-labeled graph and a spline on that graph in the figure below. Splines appear in many areas of mathematics including geometry, topology, and analysis. Questions about splines include how to construct bases and determine the minimum number of generators for splines over a particular graph. Those studying equivariant cohomology using GKM theory also ask questions about the multiplicative structure of splines and try to determine multiplication tables and structure constants.

The base ring R can be any ring. In our research we primarily consider splines over the integers and the integers modulo a prime power and answer the aforementioned questions in this context. We present an algorithm to produce minimum generating sets for splines on connected graphs over the integers modulo a prime power. A graph theoretic corollary of this algorithm quickly determines the minimum number of generators for splines over the integers modulo a prime power. We complete the classification of splines over the integers modulo a prime power with multiplication tables of the minimum generating set elements given by the aforementioned algorithm. We give an extension of our algorithm to produce minimum generating sets over the integers modulo a prime power that produces bases for splines over the integers.

We give an inductive proof that the algorithm produces minimum generating sets for splines over the integers modulo a prime power. We prove our results about the minimum number of generators and multiplication tables for splines over the integers modulo a prime power by observing particular characteristics of the algorithm. These results lead us to questions about splines over different base rings R. In particular, we believe these results may be extended to splines over principal ideal rings, which are rings in which every ideal is generated by a single element.

(Supported by the Susan M. Rambo 1905 Fund)

Advisor: Julianna Tymoczko, Mathematics and Statistics



Below is an example of a vertex-labeling that is a spline on this graph

$$v_3 = 11$$

$$v_2 = 5$$

$$v_1 = 3$$

Do Actively Managed Funds Continually Outperform the Market?

Jing Xia/2017

Whether the actively managed and the passively managed funds are able beat the market in the long term has long been a debate between economists; however, for people who are interested, but have little background knowledge in economics, the online journals or research reports may be too obscure. In this summer research, I focused on analyzing the performances of different actively managed and passively managed (index) funds compared to their corresponding market benchmarks. By applying the statistical tool, R, and using the data collected through Yahoo Finance, I was able to observe and compare more than 7,000 different stocks. One of the important goals is that the research findings were obtained through a method that can be easily understood—and reproduced—by anyone with math modeling skills.

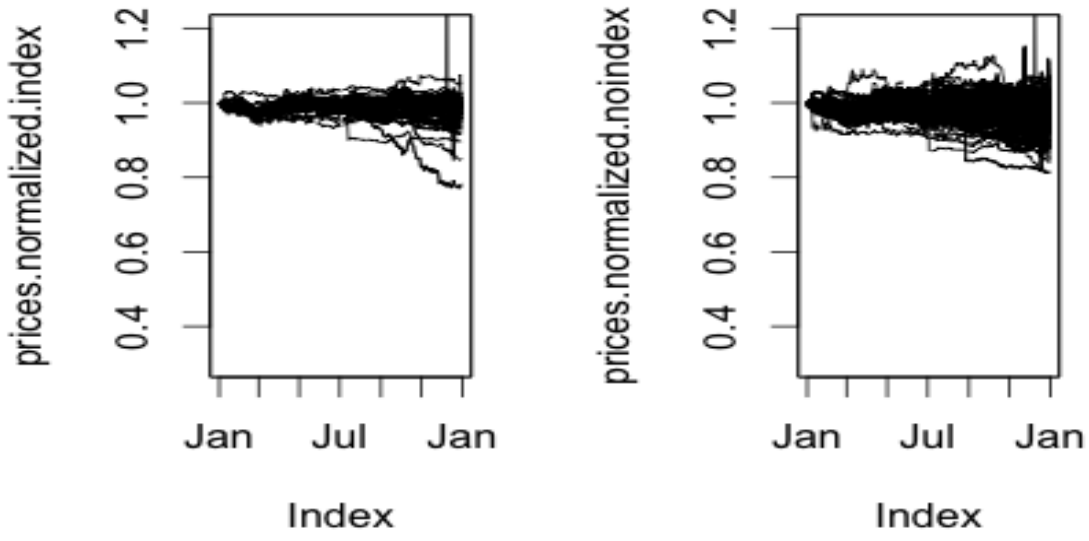
The daily end prices for each of the stock, which are included in the following 9 groups (all combinations of Large/Mid-Cap/Small and Blend/Growth/Value), were downloaded and each was compared to the corresponding average market price tracking index. The diagrams, one of which describes the relation between index funds and the market indexes, and the other of which portrays the relations between non-index funds and market indexes, were constructed using R. In the course of this research, I learned some general purpose R programming, as well how to use some packages specific to times series data.

From the diagrams, I can conclude that the index funds track the market indexes reasonably closely as predicted while the non-index funds' performances fluctuate by a wider range. By doing background research, I also found out the huge drops of certain funds shown were caused by the lack of ability of recovery from the companies' monthly dividend. Through this research, I learned the method of obtaining and processing the data collected from other resources, further explored different useful commands and packages in R, and approached an economics question from a mathematical/statistical perspective.

Through this summer research, I not only was able to gain a better understanding on the efficient market hypothesis and explain it to anyone with no previous economics background, but also improved my statistically related skills, which is essential for my future study and career. Certain topics still need to be further explored such as survival bias, long-run optimal risks, and how to exclude all passively from actively managed funds.

(Supported by Ellen Borie Fund in Mathematics and Statistics)

Advisor: Ben Baumer, Statistical and Data Sciences



Stress Hormone Levels and Prosocial Behavior in Rats

Katrina Blandino/2017

Empathy plays a key role in the social experience of humans, yet it is not well understood. Previous studies display empathy-like behavior in rats by creating a scenario in which a rat learns to open a restrainer to free a cage mate [1]. The purpose of this SURF research was a continuation of a study that aimed to further develop that model and examine personality traits of the rat, which may play a role in the empathy like behavior. In this study, 32 (16 male, 16 female) Long Evans rats were used to examine behavioral correlates of prosocial behavior and this summer a corticosterone Enzyme-Linked InmmunoSorbent Assay (ELISA) was run to determine if there was a relationship between overall stress response of free and trapped rats and prosocial behavior.

Results of the ELISA were correlated with the results from last three days of prosocial testing, as these days demonstrated a frequency of openings that was representative of the rat's prosocial behavior. Results showed a positive correlation between the peak concentration of female rats ($p=0.0174$) and the fraction of restrainer openings in the last three days of testing. There was also a positive correlation between the overall stress response (area under the curve) and the fraction of openings in the last three days of openings ($p=0.0253$). There was a significant difference between the overall stress response of female trapped and free rats, with trapped rats showing higher overall levels of stress hormone. Male rat corticosterone levels did not correlate with prosocial behavior. Behavior that were not scored during the semester included learning and memory (operant conditioning) and social interaction. These correlates were scored and analyzed. No significant correlations were found between these measures and prosocial behavior.

Other extensions to the study that were completed during the summer were modifications to the design of the restrainer door and preparation of the Leica 1900 Cryostat. Further studies will use the optimal door design to explore what cues from the trapped rat (visual, auditory, olfactory etc.) facilitate prosocial behavior. The cryostat will be used in a planned project to slice brain tissue harvested from the focal (free) rats of the study, utilizing autoradiography to relate oxytocin receptor density with prosocial behavior.

(Supported by the Frances Baker Holmes Internship Fund)

Advisor: Annaliese Beery, Neuroscience

References:

[1]Ben-Ami Bartal I, Decety J, and Mason P, (2011) Empathy and pro-social behavior in rats, Science 334: 1427-3

Three different door designs that were tested

Assessing Rat Corticosterone and the Prosociality Model

Katherine Freitas/2016

Rodent models have been often used to study pro-social behavior, typically to evaluate social preferences and social contact. New research has devised a model to study empathy-like behavior in rats that examines a free rat's inclination to release a restrained rat.[1]. The model utilized in this study found that an unrestrained rat would learn to intentionally free a cagemate, even when social contact between the two rats has been prevented.[1] This behavior is believed to show that rats respond to cagemate distress. As a result, an evaluation of this stress reaction was necessary to understand the behavioral patterns being observed. Stress responses were assessed in both the free and trapped rats with a corticosterone (CORT) assay.

Plasma corticosterone levels were analyzed and compared the rat's trapped or untrapped status, sex, and correlative data various behavioral tests. For the female rats, it was determined that there is a positive correlation between the fraction of restrainer door openings by the free rat in the last three days of testing (test was repeated for 12 days to incite rat learning over time) and CORT peak concentrations and overall stress response measure ($p=0.0174$; $p=0.0253$). It was also determined in females that there is a significant difference between trapped and free rat over all stress response (area under curve of CORT time course data) ($p=0.0486$). For the male rats a significant positive correlation was found between number of state changes and center entry in an open field anxiety test and basal CORT levels ($p=0.0059$).

Following our analysis of this initial study, we tried to assess the model used to understand why we were seeing discrepancies in results from other researchers.[1] We believed the door design of the restrainer used was flawed in that it was possibly too easy for the rat subjects to open, not allowing the rats to learn over a time period. Altering the door would potentially remove an extraneous variable in the experiment. We designed, constructed, and piloted several new doors each varying in difficulty for the free rat subject to learn to open. A new door design was finalized that, as such, performed in a way that we believe will lead to more consistent learned behavior trends that could be well utilized for similar studies in the future.

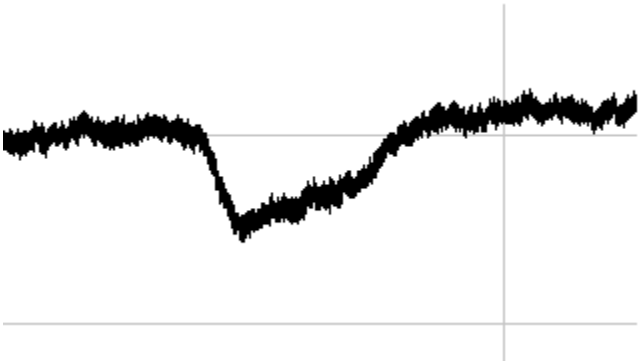
(Supported by the)

Adviser: Annaliese Beery, Neuroscience

Ben-Ami Bartal I, Decety J, and Mason P, (2011) Empathy and pro-social behavior in rats, Science 334: 1427-30

Mutant α7 Nicotinic Acetylcholine Receptor Current Response to Acetylcholine: a Patch-Clamp Study.

Erin Walch/2016



Current deflection observed after a 30μM dosage of Ach applied to an HEK cell expressing α7 nAChR receptors.

Neuronal nicotinic acetylcholine receptors (nAChRs) are involved in synaptic transmission in the mammalian CNS. The binding of the neurotransmitter acetylcholine (ACh) to the receptor triggers the influx of cations that act to excite neurons. Agonist ACh binds to nAChR, initiating a conformational change of the pore complex that gates the ionic current. G proteins recently demonstrated to be associated with α7 nAChR homopentamer undergo further conformational changes with the binding of ACh, and are thought to act through the release of secondary messengers and thus as an additional signal mechanism. The lab recently acquired constructs containing mutant α7 receptors from the Kabbani lab at George Mason Univ., VA. The mutant receptors are unable to bind to the G protein complexes and therefore abolish this form of signaling upon binding of ACh to the nAChR.

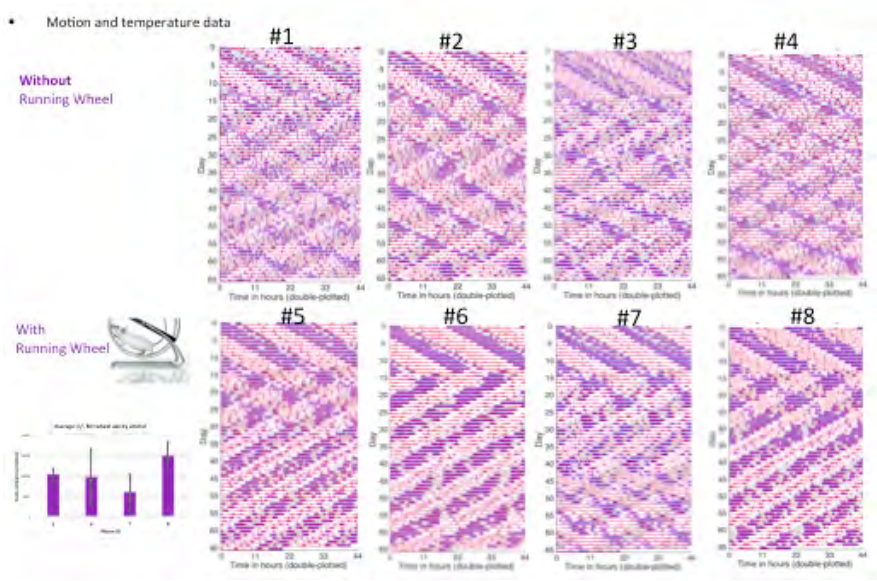
In the Hall lab, my goal is to compare the wild type and mutant α7 receptor currents using patch clamp electrophysiology to elucidate differences in receptor response to ACh. Whole cell patch clamping controls internal voltage of a cell through a glass pipette sealed onto the membrane. A dose response of ACh [1, 3, 10, 30, 100, 300 μM] is applied to a voltage-clamped human embryonic kidney cell expressing either wild type or mutant nAChRs. The binding of ACh to receptors produces a current deflection as a result ion flow across the membrane. Increased concentrations of ACh are expected to enhance the currents of wild type α7 receptors, while mutants may respond differently to the agonist. This collaborative project is important for understanding how the neurotransmitter ACh acts on its receptors and ultimately shapes neurotransmission in the mammalian brain.

(Supported by the Schultz Foundation)

Advisor: Adam Hall, Neuroscience

Exercise Alters Organization of Circadian System in Female Mice Housed Under 20H Light Cycles

Wanqi Wang/2017



Motion and temperature data of each individual mouse

Circadian disruption is a common factor in modern life, with frequent exposure to light at night, sleep restriction, jet lag and social jet lag. Health problems, such as disruption of metabolism and incidence of type 2 diabetes, are linked with this circadian disruption. We examined how frequent exercise versus a more sedentary lifestyle interacts with the coherence of the circadian system by exposing mice to a cycle with 10h of light and10h of dark. The circadian clocks of mice are typically unable to entrain to such 20h cycles; however, exercise can strengthen the circadian system[1] and can extend the ranges of cycle periods the circadian system is able to entrain to[2].

We housed female mice under 10:10 LD, either with or without a running wheel that can induce high levels of voluntary exercise. We hypothesized that exercise would enable animals to entrain to the exotic light cycle. We measured rhythms from peripheral tissues (esophagus, thymus, spleen) and from central pacemaker tissue using mice with a per2-luciferase transgene. We analyzed locomotor activity and body temperature as reported by i.p. implanted telemetry probes. Maximum entropy spectral analysis revealed multiple periodicities within some records, particularly in those of mice unable to entrain to the 10:10 LD. We also measured the spectral coherence to assess coordination between the temperature and activity rhythms at each of the periods present. Tissues exhibited circadian rhythms in vitro with widely varied times of peak. These studies provide evidence for an interaction of spontaneous voluntary exercise with entrainment as well as internal circadian synchrony.

(Supported by the Frances Baker Holmes Internship Fund)

Advisor: Mary Harrington, Neuroscience

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Designing a Magneto-Optical Trap for Heavy Metal Lanthanides

Darby Bates/2018

The long-term goal for this project is to design an apparatus capable of trapping neutral Terbium (Tb), Dysprosium (Dy), Holmium (Ho), Erbium (Er), Thulium (Tm), Ytterbium (Yb), Berkelium (Bk), Californium (Cf), Einsteinium (Es), Fermium (Fm), Mendelevium (Md), and Nobelium (No). Typically a neutral atom trap is capable of trapping only a few elements, making this design unique. The Williams lab is designing this apparatus to include an oven, Zeeman slower, and magneto-optical trap. The final apparatus will be work both using the oven for stable isotopes and connected to the output of an accelerator for the radioactive isotopes.

To begin the design, information about known properties of the elements we are interested in trapping were compiled. This included known electron configurations of each elements of interest for laser cooling and trapping, the wavelengths of their respective energy level transitions in nanometers, the Einstein coefficients for those levels, and the melting point of each metal. Many of the elements had two possible laser cooling and trapping frequencies. This information will be useful when determining the necessary temperature of the oven and the wavelength of the lasers to be used in the Zeeman slower and magneto-optical trap.

In order to model the total atomic flux out of the oven, we first needed to confirm that the results of an existing Er trap the mathematical relationships and the dimensions, temperature, and other parameters stated in Schindler's thesis.[1] After that model was verified, we used those relationships to predict the ratio of atoms that emerge from the oven to the total atoms released from the metal. We were also able to model the distribution of the atomic flux on a plane perpendicular to the length of the collimating tube at specified distances away from the end of the tube.[2] By combining the results from both models, we are now able to predict both the atomic flux and atomic distribution of atoms coming the oven at a particular temperature.

The next step is to use these calculated atomic beam distributions and model the behavior as the atoms travel through the Zeeman slower and into the magneto-optical trap.

(Supported by the Schultz Foundation)

Advisor: William Williams, Physics

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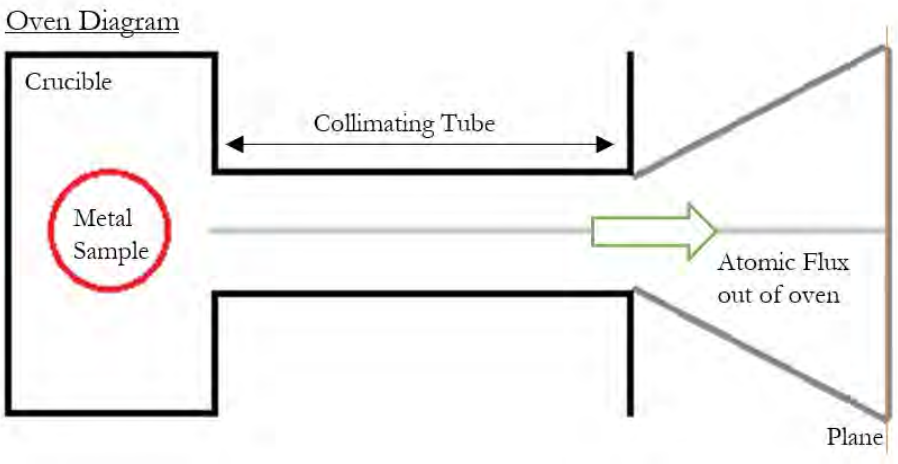


Figure 1: Diagram of oven design including collimating tube.

Studying Oscillons in Scalar Fields

Suroor Seher Gandhi/2018

In our project, we worked with conditions existing right after inflation (a brief period of exponential expansion of the universe after the Big Bang) ended, a period known as reheating. Immediately after inflation, almost all the energy density was contained in the homogenous inflaton field (the scalar field that caused inflation, denoted by). Reheating is the name given to the process through which the energy of the inflaton decayed into other forms. In our simulations, decayed into another scalar field (denoted by). There are many proposed models of reheating, and interaction between scalar fields is controlled by the potential of a model. Usually the plots of and show that both are randomly fluctuating. But several years ago, a peculiar phenomenon was observed in a model called two-field-m: under certain unknown conditions, there would appear patches where would simply stop fluctuating and remain at value zero, whereas would have very large oscillations in the same location. These patches were called oscillons, and although they had been observed before, it was for the first time that they had been found in the two-field-m model. However, at that time this was an unexpected finding in the middle of a completely different project, so not much investigation was possible. That is what turned into our project for the summer—to gather as much information about why oscillons form, and what are the conditions necessary for them to exist.

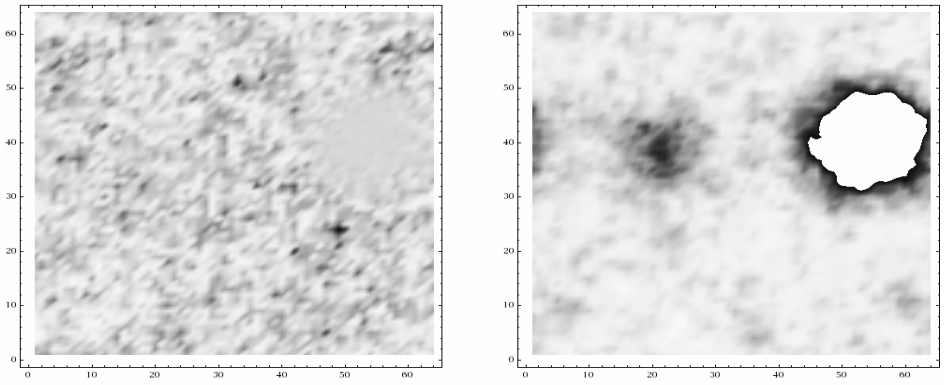
We simulated conditions of reheating using a C++ program, Latticeeasy, and plotted the results using Mathematica. We tried to determine what affected the oscillons and how. In order to do so, we changed both physical and computational parameters. The first type of parameters were designed to actually modify the manner in which the fields evolve and might really affect the occurrence of oscillons. Those of the second type were adjusted so that we could capture and study the evolution of the fields in the most suitable manner. For instance, we tried to see if simulating a non-expanding universe still caused oscillons, or what effect different random number seeds had.

We found that oscillons only needed an expanding background during the initial conditions, and they still appeared if expansion was turned off after some time. Also, oscillons did not seem to end abruptly, it might be that they reduce one at a time by merging with each other, but this needs to be further verified and studied. We also found that their location in the fields is almost certainly random.

As a result of our study, we now have a better idea of what conditions cause oscillons, but surely a lot still remains to be done. It was a great learning experience to work on a project from scratch, because that only increased the chances of being surprised; hard as it may have been to find the right direction, every step was a small discovery in itself.

(Supported by the Committee on Faculty Compensation and Development (CFCD))

Advisor: Gary Felder, Physics



The box to the left is a grayscale plot of φ and the one to the right is of χ. The circular patch to the right (light gray in φ, white in χ) is an oscillon.

Exploration of Superconductor Properties Under Low Temperatures

Lucy Liang/2017

With the development of quantum theory, superconductivity is theorized to be due to the cooper pairs (electron pairs) forming conducting layers within a material. Therefore, to destroy superconductivity, the cooper pairs need to be broken, which requires energy. The energy is provided through a strong magnetic field, and the field required to break the superconductivity is the Pauli-limited critical-field. This information can be collected and observed on a Pauli-limited critical-field phase diagram. We are looking for when the upper critical-field exceeds the Pauli-limited critical-field at a certain orientation of the sample crystals, which was theorized around 40 years ago, but never proven experimentally.

To be able to conduct such an experiment on a sample material, a calorimeter that will hold the sample and contain all the required sensors needs to be made. Most of my summer was spent on making a calorimeter that is about the size of a pill, which would fit in the tiny workspace that is available inside a 35T magnet that will be used to provide the magnetic field. The calorimeter consists of a calibrated thermometer (CT) for calibration, a platform thermometer (PT) and a platform heater (PH) for control, a sample thermometer (ST) and a sample heater (SH) monitoring and controlling the temperature of the sample, and a sample that sits between the ST and SH.

During data collection, the field was swept up and down several times with different orientations of the sample to find the exact angle we want it to be at. Then, critical-field measurements and heat capacity were taken at several different low temperatures for further analyzing.

Analyzing of the data is still in process, and further experiments will continue on into the semester. The final results of this experiment could be of help for theoretical physicists in the discovery and understanding of quantum physics.

(Supported by the Schultz Foundation)

Advisor: Nathanael Fortune, Physics

Attempt of Spectroscopy on Nobelium Ion inside a Linear Paul Trap

He Claudia Yun/2017

The aim of this project is to design an apparatus to measure two ground state transitions in the Nobelium (No) ion. Once measured, these transitions can be used to laser cool the ion to then perform high-resolution spectroscopy on other transitions. The physical motivation is to determine various nuclear parameters such as dipole moments, isotope shifts, and charge radii. At the moment, the only things that are known in the isotope chain are the nuclear spins and masses. Our proposed experimental setup is to create a dual species ion trap with Barium (Ba) and Nobelium. Initially, the apparatus will be tested using Ytterbium (Yb) in place of the radioactive Nobelium ion. During this summer, we explored the cooling time of Yb inside the linear Paul trap. The Yb ion is cooled via the Coulomb interaction with a laser cooled Ba ion, a process known as sympathetic cooling. The ions are observed to go through two stages during the cooling process: a fast and a slow one. We believe the borderline to be the crystallization of the ions. During the fast cooling stage, the temperature of the Yb ion was lowered from room temperature to approximately 2.5 K in less than 3.5 ms. During the slow cooling stage, the decay of the temperature has a time constant of ~130 s. We also explored an idea to perform spectroscopy on the unknown transitions using electron bombardment. This work shows this method of spectroscopy will not be sufficient.

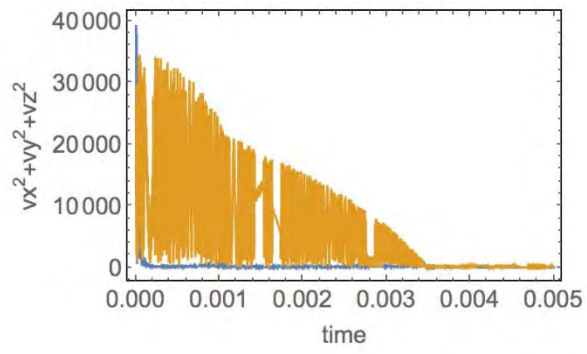


Fig. 1: This plot shows the velocities of the ions as time evolves. Blue (the curve whose amplitude drops dramatically at the beginning) represents the laser-cooled ion while yellow (the curve whose amplitude drops more slowly) the sympathetically cooled ion. We can see the rapid cooling stage and the slow cooling stage and the borderline is at around 3.5 ms.

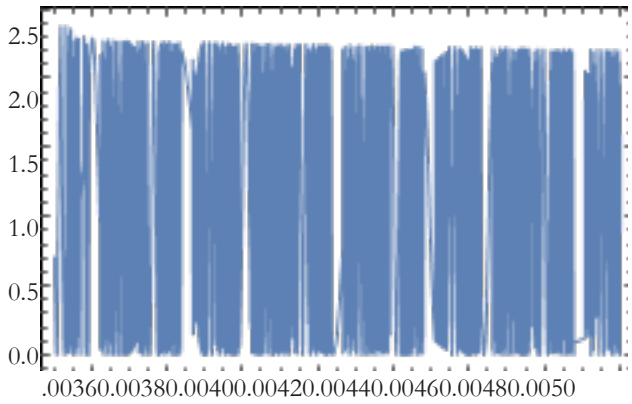


Fig. 2: This plots shows the energy (shown as temperature on the y-axis) of the sympathetically cooled ion versus time during the slow cooling stage (after 3.5 ms). We can see the slight decrease in the amplitude of the oscillation. The decay has a time constant of ~130s.

(Supported by Schultz Foundation)

Advisor: William Williams, Physics

Self-Compassion Buffers Low Social Status Internalization

Alexa Barriga/2016

People in lower social status have poorer physical and psychological functioning[1], which may be amplified when they internalize their social status[2]. Health promotion experts work to create more equitable social arrangements in societies with large status disparities. In the meantime, researchers and practitioners are eager to identify cost-effective, teachable strategies so people can buffer themselves from the health-damaging effects that come with low social status. Self-compassion is defined as "being kind and understanding towards oneself in times of pain or failure, perceiving one's own suffering as part of a larger human experience, and holding painful feelings and thoughts in mindful awareness."[3] A well-established body of research finds that self-compassion predicts improved health-related affect, cognition, and behavior—minimizing feelings of depression, anxiety, and distress, while increasing feelings of social connectedness and health promoting behaviors.[4] We hypothesized that greater self-compassion would buffer internalization of low social status.

We surveyed female participants 18-35 years old via Amazon's Mechanical Turk. In a 2x2 experimental design, participants were randomly assigned to one of four conditions (social status [low or high] x degree of internalization [low or high]), and asked to imagine and write about what their lives would be like if these assignments were true (N= 195). Participants completed a 26-item self-compassion scale[5] in addition to an item indicating the degree to which they resisted internalizing their status assignment. Independent of assigned social status, higher self-compassion predicted greater resistance to internalizing social status ($b=.40$, $SE=.20$, $p=.049$). Follow-up analyses of the condition x self-compassion interaction ($b=-.19$, $SE=.08$, $p=.024$) revealed that people assigned to highly internalize their low social status resisted doing so only when they had greater self-compassion ($t[44]=49.0$, $p<.001$). Findings from this study suggest that greater self-compassion helps buffer internalization of low social status.

This research will be extended throughout the 2015-2016 school year in Professor Jackson's Society, Psychology, and Health Laboratory.

(Supported by the Schultz Foundation)

Advisor: Benita Jackson, Psychology

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Coping Strategies and Hoarding

Kavita Bhandari/2017, Kimone Coley/AC, Hannah Saltzman/2016, Meredith Davis/2015

Cognitive theories of hoarding suggest that avoidance of negative emotions contribute to the development and maintenance of hoarding symptoms (Frost & Hartl, 1996, Timpano et al., 2014). These emotionally driven reinforcement patterns motivate acquiring, saving and difficulty discarding behavior (Frost & Gross, 1993; Shaw et al., 2015; Steketee & Frost, 2003). For example, acquiring or keeping an object represents avoidance of the negative emotional states that may result from not collecting or discarding the object (Timpano et al., 2009). Attempts to cope with discomfort by using avoidance strategies may be a vulnerability factor for hoarding disorder (Timpano et al., 2009). The aim of the current study was to investigate the role of coping styles in hoarding for a nonclinical sample (N=139). Measures included the Saving Inventory-Revised (SI-R) and the Active and Avoidant subscales of the Ways of Coping Scale –Revised (WOC-R). Results indicated that the active coping subscale was negatively correlated with the clutter, difficulty discarding, and acquisition subscales of the SI-R, while the avoidant coping subscale was positively associated with each subscale. Regression analysis revealed that avoidant coping emerged as a significant predictor of difficulty discarding, acquisition, and clutter independent of active coping. The active coping subscale was not found to be a significant predictor of hoarding independent of avoidant coping. These results are consistent with a cognitive behavioral model of hoarding that stresses emotional processing variables, such as avoidance behavior, as central to hoarding behavior (Frost & Hartl, 1996). Future research is needed to determine whether emotionally triggered maladaptive patterns of behavior serve as etiological or maintaining factors of the disorder.

(*Supported by the Frances Baker Holmes Internship Fund*)

Advisor: Randy Frost, Psychology

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The Relationship Between Perfectionism and Psychopathologies: The Mediating Role of Coping

Kimone Coley/2016

Perfectionism is two-dimensional, including: (a) Personal Standards (PS), which represents striving for high standards and is considered an adaptive component of perfectionism, and (b) Evaluative Concerns (EC), the maladaptive component which is defined by concern over critical evaluation.[1] EC is consistently associated with psychopathology. Although the role of perfectionism in psychopathology is unclear, research suggests that avoidant coping may impact this relationship.[2] We predicted that coping would mediate the relationship between perfectionism and generalized anxiety disorder (GAD), and social phobia (SP), depression, and eating disorders (EDs).

Participants included 139 undergraduates (87% female), aged 17 to 61 years (M = 21.52, SD = 6.2). They completed an online survey consisting of Brief PSWQ,[3] Short form Version of DASS-21 Depression scale,[4] Eating Disorder Inventory,[5] Frost Multidimensional Perfectionism Scale,[6] Brief Version of FNE Scale for Social Anxiety,[7] and Active and Avoidant Coping Scales.[8]

Correlational analysis indicated that EC was positively associated with avoidant coping and all forms of psychopathology measured, and was negatively associated with active coping. All forms of psychopathology maintained negative correlations with active coping and positive correlations with avoidant coping. Mediational analyses showed both active and avoidant coping mediated the relationship between EC and depression, while only avoidant coping mediated the relationship with EDs. Neither active/ avoidant coping mediated the relationship between EC and SP or GAD. Results suggest that coping styles may play a role in perfectionism's relation to depression and EDs, but anxiety may rely on different mechanisms. Assessing for perfectionism and subsequently targeting avoidant coping strategies in treatment for perfectionistic individuals may reduce the likelihood of depressive and ED pathology. Co-authors: Shalini Abayasekara, Hannah Saltzman, Meredith Davis, Randy O. Frost, and Alexandra M. Burgess

(Supported by the Frances Baker Holmes Internship Fund)

Advisor: Alexandra Burgess and Randy Frost, Psychology

Active and Avoidant Coping

	DASS-Depression	PSWQ-Generalized Anxiety Disorder	FNE- Social Phobia	EDI- Eating Disorder
Evaluative Concerns (EC)	PM .0616	NOT	NOT	PM .0845
Personal Standards (PS)	NOT	NOT	NOT	NOT

Note: PM = Partial mediation NOT = No mediation
FM = Full mediation # = Total Indirect Effect

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Evaluating the Psychometric Properties of the Graves Anthropomorphism Task Scale (GATS)

Lucy Graves/2015

Anthropomorphism is defined as the tendency to attribute human-like traits, motivations, characteristics, or emotions to nonhuman agents.[1] Examples of these nonhuman agents vary widely from animals to supernatural or religious figures to common place objects. Though anthropomorphizing may seem like a rare occurrence it is utilized in a variety of fields including advertising, marketing, robotics, environmentalism and law.[2] However, while anthropomorphism may be common, many of the measures of anthropomorphism currently available are unique to their respective studies. Few widespread measures have been developed and of those that do exist, they all have several drawbacks. For example, many of the measures do not address specificity or the subject of ownership and others conflate the item content with the agent anthropomorphized. Thus, the aim of the present study was twofold. First, to create a new measure of anthropomorphism, the Graves Anthropomorphism Task Scale (GATS), dealing with specific possessions owned by the subject that could be applicable in a variety of circumstances. Second, to evaluate the psychometric properties of this new measure.

Participants were recruited from an all women's liberal arts college. They were invited to take an online survey asking about their attitudes towards their possessions, their levels of social connection and their collecting and saving behaviors. Measures of anthropomorphism, loneliness, and hoarding were included.

Exploratory factor analyses of the GATS produced a three-factor solution. These three factors were represented by the three different entities subjects' anthropomorphized: a technology item, a comfort item and a past or present pet, if applicable. Each GATS subscale demonstrated good internal consistency (α above .85). To establish concurrent and convergent validity, the GATS was correlated with another measure of anthropomorphism, the Anthropomorphism Questionnaire (AQ) and with measures of hoarding. Strong correlations were found.

Overall, the GATS factored as expected. These results reinforce that it is the agent, and not the question, that is of importance. The GATS also exhibited good reliability and validity. It's flexibility and ability to be administered in multiple circumstances advocates for its continued use. Future studies ought to distribute the GATS, particularly in more diverse samples, in order to continue to evaluate the scale. A manuscript is in progress to publish the GATS and its psychometric properties so it can be circulated to others.

(Supported by the France Baker Holmes Internship Fund)

Advisor: Patricia DiBartolo, Psychology

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A Qualitative Pilot Study of Drinking Game Participants' Reasons for Targeting Other Players to Drink

Kelcie Grenier/2016

Many young adults play drinking games. For example, as much as 91% of college students who identify as drinkers and preparty or drink before going out to a social gathering or even where alcohol may not be available, have played a drinking game.[1] Although participation in drinking games is common, the practice is not without risk. In order to better understand and potentially prevent the negative consequences that can occur as a result of playing drinking games, we must first learn why players are targeted. The purpose of this research was to begin to answer that question.

Prior to the beginning of this research project, survey data pertaining to the research question was collected as part of a larger survey. Participants included 434 young adults (18-25 years) who had played a drinking game in the past month. Participants responded to open-ended survey questions asking for the top three reasons why players were chosen to play drinking games. A codebook was developed in order to analyze the participant's responses which followed procedures used for qualitative research.[2] Following completion of the codebook, reliability was achieved with another student in order to ensure the codebook's reliability. Kappas lower than .90 for the broad categories (see Table 1) were recoded independently and disagreements were resolved by consensus. The data was then coded in its entirety for analysis purposes

The data showed that the most frequently-cited reasons players believed others were chosen, believed they were chosen, and why they chose others fell into our "Personal Characteristics" category (see Table 1 for descriptions and examples of these responses).

The findings of this research project will be used to guide the development and design of an experimental study which will be conducted as part of a Special Study in the fall.

(Supported by the Frances Baker Holmes Internship Fund)

Advisor: Byron Zamboanga, Psychology

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Table 1

Descriptions of Broad Coding Categories

	Category	K	Examples
Alcohol related reasons for targeting	Target is chosen for reasons related to alcohol consumption such as tolerance, drinking style, or the type of drunk they become.	0.98	"They had a high tolerance"; "I'm always willing to drink"
Game related reasons for targeting	Target is chosen for strategic purposes in the game such as high or low skills or ability or chosen due to the rules of the game.	0.98	"They're good at beer pong"; "The game rules say I have to choose them"
Group context reasons for targeting	Target is chosen due to the group context in which the game is being played, and may include attraction between players, group membership, and status-related reasons.	0.97	"I wanted to sleep with them"; "Because I'm Irish"
Personal characteristics reasons for targeting	Target is chosen for qualities independent of the game, alcohol, and group context. This may include personal characteristics such as physical attributes or personality.	0.98	"I'm fun and outgoing"; "They're good-looking"

The Effectiveness of ACT for PTSD at the Brattleboro Retreat

Meadeshia Mitchell/2016

Posttraumatic Stress Disorder (PTSD) is a mental health problem that occurs as a result of traumatic events such as war, assault, or disaster. Treatments for PTSD include Acceptance and Commitment Therapy (ACT), cognitive therapy, and Eye Movement Desensitization and Reprocessing (EMDR)[1]. The purpose of this research project is to understand the effectiveness of Uniformed Service Program (USP) at the Brattleboro Retreat in Vermont. There has been no formal evaluation of the effectiveness of USP for treating PTSD symptoms, and thus this study was conducted to determine: Does the USP produce significant change in PTSD symptoms? What factors predict change in PTSD symptoms in the USP?

Thirty-eight patients completed all of the measures necessary to be included in this study. Patients reported demographic information and completed self-assessments of DSM-IV PTSD symptoms using the Posttraumatic Stress Disorder Checklist (PCL)[2] at the beginning and end of treatment. The treatment involves six hours of ACT sessions that take place a week. The USP activities (meditation, yoga, self care, and sleep and stress reduction therapy) complement the core principles of ACT. The self-report data were imported into SPSS for analysis and statistical tests were conducted to answer the research questions.

Analyses revealed that patients showed statistically significant pre-post therapy symptom reduction. Also, several demographic (e.g., ethnicity and employment), stressor (e.g., work problems and physical health), and behavioral factors (e.g., worry, not being acknowledged at work, and unsatisfied with daily responsibilities) predicted change in PTSD.

The results that were obtained are consistent with the notion that the BR USP successfully reduces PTSD symptoms. However, this study lacks a control group to determine whether the magnitude of change exceeds what might occur in alternative treatments. Hence, future research should compare these results with a control group and conduct follow-up assessments of these patients. With this in mind, this is a rare and understudied sample (uniformed personnel) and it is the first study of a rare but long-standing treatment program.

(Supported by the Francis Baker Holmes Internship Fund)

Advisor: Nnamdi Pole, Psychology

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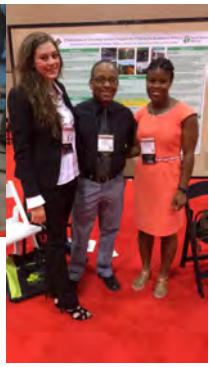

Effectiveness of Uniformed Service Program for PTSD at the Brattleboro Retreat

Hannah Saltzman/2016

The Brattleboro Retreat (BR) in Brattleboro, VT was founded in 1834 as one of the first private psychiatric hospitals in the United States to base their philosophy on the moral treatment of the mentally ill. This longstanding tradition is reflected today in the BR's Uniformed Service Program (USP), which treats service-related mental health difficulties (e.g., posttraumatic stress, substance abuse) in a variety of uniformed professions (e.g., police, firefighters, national guard, etc.). Uniformed professionals typically report heightened stigma about seeking mental health treatment. The USP provides a unique, restorative, and holistic healing environment in which patients can enjoy and benefit from peer support. The USP offers a 10-20 day residential transdiagostic treatment regimen based in Acceptance and Commitment Therapy (ACT) and supplemented with mindfulness based stress reduction, mindfulness based relapse prevention, mindful exercise, sleep therapy groups, peer support groups, and outdoor wellness-oriented recreation therapy. Though evidence supports some of these interventions for some of the conditions commonly seen in this population, until now, there has been no formal evaluation of the effectiveness of the USP for treating PTSD symptoms. The following study was conducted to determine if the USP produce significant change in PTSD symptoms, and what factors predict change in PTSD symptoms in the USP.

Over several years, patients reported demographic information and completed self-assessments using the Posttraumatic Stress Disorder Checklist (PCL) and the Treatment Outcome Package (TOP) at the beginning and end of treatment. The TOP is a self-report measure that includes demographics (e.g., age, gender, race, employment) stressors (e.g., death, abuse, work, conflicts, school) physical health (e.g., headaches, blood pressure, cancer), and behavioral problem questions (e.g., worried about things). The self-report data were imported into SPSS for analysis. These data were collected for clinical purposes and were not originally intended for research. After obtaining permission from the Smith College Institutional Review Board (IRB), we reviewed the descriptive statistics; we computed correlations, and conducted t-tests to answer our research questions.

Thirty-eight patients completed all of the measures necessary to be included in this study. The sample was predominantly White, male, and middle aged. Analyses revealed that patients showed statistically significant reductions and large pre-post effects in total PTSD symptoms ($d = 1.32$). The factors that predict change include ethnicity, unemployment, work problems, medications for headaches, worry, not being acknowledged at work, and being unsatisfied with daily responsibilities.

These results are consistent with the notion that the Brattleboro Retreat's Uniform Service Program effectively reduces PTSD symptoms. Work status (work problems, not being acknowledged at work, being employed) were all negative factors. The USP may heighten sensitivity to triggering work-related trauma memories. Headaches were a negative factor and worry was a positive factor. The USP includes specialized mindfulness techniques to address anxiety and pain management. These may be particularly useful for worriers but problematic for those with chronic headaches. Racial minority status was a positive factor. Non-White patients showed more PTSD improvement. This surprising result warrants further study. However, the study lacks a control group to determine whether the magnitude of change exceeds what might occur in alternative treatments or with no treatment. These issues will be addressed as next steps in this program of research. This research will be presented at the American Psychology Association in Toronto in August 2015.

(*Supported by the Frances Baker Holmes Internship Fund)*

Advisor: Nnamdi Pole, Psychology

A Roll of the Dice: Acculturation and Drinking Games Participation in Asian American Young Adults

Cara Tomaso/2016

Acculturation is the process of cultural, psychological, and social change that takes place when people of different ethnic/cultural backgrounds come in contact.[1] With respect to acculturation, it is important to account for dimensionality: while a unidimensional view assumes that as a person acculturates, her/his heritage culture is replaced with the host society's culture, a bidimensional approach is preferred because it allows for retention of one's heritage culture and the simultaneous acquisition of the host society's culture.

It is reasonable to expect that as Asian Americans acculturate into U.S. society, they may adopt U.S. cultural practices vis-à-vis drinking behaviors. However, research examining the link between acculturation and general drinking behaviors in Asian American young adults is mixed, and to date, no studies have examined the link between acculturation and drinking games participation in a sample of Asian American young adults. It is important to study drinking games as a correlate of acculturation because this activity is associated with a number of negative consequences, with some games imposing greater harm (e.g., extreme consumption games such as Chugging or Keg Stands) than others (e.g., verbal games such as Never Have I Ever).[2]

Thus, the present study uses a bidimensional conceptualization of acculturation to examine how acculturation is associated with drinking games participation and negative gaming consequences in a sample of Asian American young adults (N = 122; M_{age} = 22.1, SD = 1.97, age range = 18-25). Participants took an anonymous survey online. Results indicated that lower levels of acculturation were indirectly associated with increased negative gaming consequences, through its relationship with increased frequency of participation in consumption and dice games. All analyses controlled for age, gender, college student status (i.e., whether participants were currently enrolled in college), and typical alcohol use on non-gaming occasions. These findings suggest that when working with Asian American young adults, counselors and other health professionals could measure involvement in specific drinking games, in addition to levels of acculturation and familiarity with drinking games, in order to identify gamers who are at particular risk for negative drinking consequences.

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Advisor: Byron Zamboanga, Psychology

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Was That Really a Bad Investment, or a False Estimation From Others?

Yaqi Xiong/2017

An image of 3D brain map record of EEG data

Escalation of commitment refers to the tendency for individuals to persist with failing courses of action. This phenomenon is prevailing in stock investment and even relationships among people. In this summer research with Professor Blanchard, we hypothesized that the extent of escalation of commitment is overstated by the hindsight bias of observers. According to Fischhoff (1975), hindsight bias is people's exaggerated sense of inevitability after outcomes are known, relative to foresight expectations when results are unknown.

My research was mainly composed of two parts: literature review and learning a new piece of technology device called Emotiv and relevant software called EEGLAB, which works with Matlab. During the literature review, I cross searched and read articles about escalation of commitment and hindsight bias. Professor Blanchard and I met regularly to discuss our findings. From the previous researches, we realized that observers who show hindsight bias may also engage in counterfactual thinking. Previous researchers have rarely put them together. With such enlightenment, we shifted our focus to counterfactual thinking and decided to add it to our observer's hindsight bias paradigm. In order to identify counterfactual thinking, I began to learn a new device called Emotiv that could help us measure negative emotions and surprise.

Emotiv includes desktop applications and a headset with nine motion sensors to detect facial expressions and brain waves. We mostly focused on an application named 3D Brain Map to record and extract raw electroencephalogram (EEG) data, so that we could import and analyze the data in EEGLAB. EEGLAB is a Matlab extension that is composed of several data analysis options.

To add on previous researches about the relation between escalation and commitment and hindsight bias, my future experiment will introduce counterfactual thinking as a new variable to the classic paradigm. We will use EMOTIV and EEGLAB to record and analyze surprise and negative emotions, such as shame or frustration. We will finish designing and conduct a new study in the coming semester.

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Advisor: Fletcher Blanchard, Psychology

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