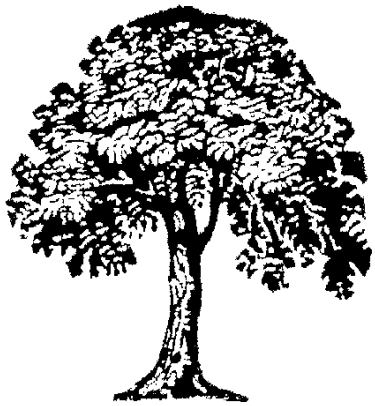

28th ANNUAL COLSA UNDERGRADUATE RESEARCH CONFERENCE

Memorial Union Building
Granite State Room and Theatre II

April 27, 2019
7:45 am – 12:45 pm

University of New Hampshire

ORAL PRESENTATION ABSTRACTS

28th ANNUAL COLSA UNDERGRADUATE RESEARCH CONFERENCE

5

Epidemiology of Staphylococcus Bacteria from Pets and Wild Carnivores in New England

Sharlene Amador, Cheryl Marie P Andam, Colin J McGonagle

In the United States, antibiotic resistance bacteria cause at least 2 million infections and approximately 23,000 deaths annually (1). Majority of these pathogens originate from animals (called zoonosis) and are transmitted to humans through direct contact or through food, water and environment. One important cause of infection in hospitals and communities worldwide is methicillin-resistant *Staphylococcus aureus*(MRSA), which can cause serious damage to skin and soft tissue. MRSA in animals has raised concern over their role as potential reservoirs or vectors for human MRSA infection in the community.Other species of *Staphylococcus*are widespread in animals and are potentially transmissible to humans, although there is limited epidemiological data about them. In this project, we aim to characterize the prevalence and distribution of different species of methicillin-resistant (MR) and methicillin-susceptible (MS) *Staphylococcus*isolated from domesticated (pets and livestock) and fur-bearing wild animals. We will be mentored by Dr. Cheryl Andam (MCBS Department), in collaboration with Drs. Robert Gibson and David Needle from the NH Veterinary Diagnostic Laboratory (NHVDL). Using epidemiological, phylogenetic and genomic data, we show that antibiotic resistant *Staphylococcus* species are genetically diverse and prevalent in multiple animal species. Our findings have important implications to animal and human health.

The Neural Correlates of Frustration

Amanda H Bagnardi, Caitlin S Mills

Frustration is a common emotional response specified by the presence of goal-blocking accompanied by the omission of a reward. Although prior research has linked feelings of frustration with aggression, social exclusion, and stress, the neural processes in the brain that are thought to produce frustration have not been well conceptualized to date. We conducted a quantitative meta-analysis of neuroimaging studies that were believed to induce frustration using activation likelihood estimation (ALE) to identify areas of the brain that were consistently activated across studies. Studies were included in the analysis if they involved an omission, loss, or exclusion condition which corresponded with increased difficulty or inability to complete a task. The ALE analysis revealed that certain areas of the brain were consistently recruited during "frustrating" tasks, such as the frontal gyri, insula, anterior cingulate cortices (ACC), and temporal gyri, among others. These are the first such meta-analytic results on the neural correlates of the complex, yet common affective state of frustration. We discuss these results in terms convergence and divergence from other well-known affective states that relate to frustration, such as anger and stress.

8

Using Stable Isotope Analysis of Methane in the Bubbles and Sediment Porewater of Ponds to Determine Methane Production Pathways

Ruth K Varner, Kathryn A Bennett
Earth Science, UNH Durham

Arctic and subarctic ecosystems in the northern hemisphere are warming faster than any other region of the globe. Rising temperatures, in this region, are causing changes in the natural cycles of these systems, such as the thawing of permafrost. As permafrost thaws it forms ponds that emit methane (CH_4), a potent greenhouse gas, predominantly through ebullition. Microbes present in these systems produce CH_4 through two primary pathways, acetoclastic methanogenesis forms CH_4 using organic carbon (C) sources while hydrogenotrophic uses inorganic C. Stable isotopes can be used to characterize the relative importance of these two pathways for overall CH_4 production, providing information that can improve modeling of current and future CH_4 emissions.

This study uses stable isotopes carbon-13 (^{13}C) and deuterium (D) to determine the presence of acetoclastic or hydrogenotrophic methanogenesis in this system. Isotope analysis was performed on porewater and ebullition (bubble) samples taken from seven ponds in a subarctic peatland located in the discontinuous permafrost region of northern Sweden. The seven ponds vary in physical attributes related to their formation, allowing observations to be made on the relationship between these attributes and CH_4 production pathways. Five years of unmanned aerial vehicle imagery and additional satellite imagery allows for determination of potential pond formation age and vegetation cover around the ponds to be compared with the isotopic characteristics. Minimal literature exists on the types of microbes and metabolic pathways present in subarctic ponds, therefore, conclusions drawn from this study will inform how ponds contribute to the global CH_4 budget.

6

The Effects of Calorie Restriction on the Development of Anxiety in Female Rodents

Robert C Drugan[2], Colleen Maeve Donovan[1]
[1]COLA/COLSA, UNH Durham
[2]PSYC, UNH Durham

Anorexia Nervosa is an eating disorder that affects over 30 million people in the United States, most of whom are women. Recent research indicates that anxiety, a separate mental disorder which disproportionately affects women, is frequently present before the development of an eating disorder. It is suspected that this correlation is due to the anxiolytic effects of caloric restriction, and that the self-starvation is reinforcing for those who are in the first phases of an eating disorder. Although females are especially vulnerable to both disorders, very few studies have been completed that specifically assess female reactivity to stress in relation to calorie restriction. We utilized female rodents in a traumatic stress paradigm in order to assess how calorie restriction affects their ability to cope with a stressor as well as its ability to induce stress resilience. Our findings indicate a stress-resilience effect as a result of calorie restriction when exposed to a traumatic stressor. This may indicate that positive reinforcement might play a role in the development of disordered eating as the reduction in calories allows for better coping with stress symptoms.

3

Developmental Pattern of Primary Cilia in the Mouse Adrenal Glands

Amanda M Kabel, Xuanmao Chen

Primary cilia are non-motile, centriole-derived organelles found in neurons and many other vertebrate cells. Defects in primary cilia cause many diseases in humans including polycystic kidney diseases and various developmental disorders. ARL13B is a protein marker for astrocytic primary cilia, and it is involved in cell division and organogenesis. Type 3 adenylyl cyclase (AC3) is mostly expressed in neuronal primary cilia and mediates ciliary cAMP signaling. The adrenal glands are composed of three structures (capsule, cortex, and medulla), each with their own unique function. The medulla mediates the body's fight-or-flight response by releasing epinephrine from neuroendocrine cells into the bloodstream. We found that neuroendocrine chromaffin cells in the adrenal medulla represent a good model to study AC3 in neuronal primary cilia because they lack neurites that normally interfere with the signaling from the primary cilia. Through immunostaining primary cilia in mouse adrenal glands, we examined the changes that the adrenal gland structures undergo during mouse postnatal development. We used two common protein markers for primary cilia (AC3 and ARL13B) with different expression patterns and functions and compared them in the three layers of the adrenal gland. Our preliminary data shows that the expression pattern and morphology of primary cilia changes as the adrenal gland develops postnatally. This research helps reveal how primary cilia affect the adrenal gland's development, and additionally, can provide useful clues for the study of AC3 in the brain.

1

Effect of Selenomethionine hydroxy analog (Se-MHA) in the form of Selisseo (2% Se) on the concentration of selenium in milk and in blood for mid and late lactation Holstein dairy cows

Jessica R Sexton, Nancy L Whitehouse

Selenium is a micromineral mineral that works in conjunction with Vitamin E to form an antioxidant called glutathione peroxidase which helps protect cells from destruction, especially in the case of mastitis. In the Northeast region of the United States, selenium is deficient in the soil, so it is commonly supplemented in dairy cattle rations to compensate for the deficiency in forages grown in the selenium deficient soils. The supplemented selenium product (Product A) commonly used is hydroxy-selenomethionine (HMSeBA), an organic selenium source produced by yeast. A new organic product (Product B), Selenomethionine hydroxy analog (Se-MHA) in the form of Selisseo was developed and required testing to receive FDA approval before use in the United States. The objective of this study was to the assess Selenium levels in blood and milk of the cows, to determine if the products would be safe for human consumption. Each of the following results will be shared in the order of control, product A, and then product B. The study found that there was a significant difference between treatments in milk yield (kg/d) (31.7^{b}, 33.6^{a}, 32.3^{b}), milk fat (kg/d) (1.39^{b}, 1.43^{a}, 1.40^{b}), milk true protein (kg/d) (1.08^{b}, 1.14^{a}, 1.11^{ab}), milk lactose (kg/d) (1.51^{b}, 1.62^{a}, 1.53^{b}), somatic cell count (58^{a}, 69^{a}, 31^{b}), energy corrected milk (kd/d^{2}) (36.5^{b}, 38.3^{a}, 37.0^{b}), and milk selenium (ng/mL) (57.1^{c}, 97.1^{b}, 116.3^{a}). There were also significant differences in blood selenium levels (ng/mL) (120.0^{c}, 134.1^{b}, 141.7^{a}).

2

Winter Tick Parasitism of Moose: Influence on Adult Cow Productivity and Winter Calf Mortality

Cody Symonds, Patrick Fitzgibbons, Owen McGovern, Brent Powers, and Peter Pekins Department of Natural Resources and the Environment, UNH, Durham

Moose (*Alces alces*) in New Hampshire have experienced slow population decline in the last decade. The principal cause is from the effects of the winter tick (*Dermacentor albipictus*) that has caused epizootics (>50% mortality of 10 month-old calves in March-April) and reduced productivity of yearling and adult cows. As part of a larger research effort to investigate the impact of winter ticks, we measured birthrates of 35 radio-collared adult cows and summer calf survival in northern New Hampshire. We also measured tick loads on hides collected from 10-month old calves dying in March-April. Productivity measurements required field monitoring from mid-May through July using radio-telemetry techniques to stalk and directly observe the study animals. Tick loads were measured by complete counts of 50% of each hide (n = 9). The calving rate was 60% which was lower than the range in 2014-2017 (73%-78%). Calf survival rate to July 1 was 66%, slightly lower than that measured in 2017, but within the 5-year range (64%-93%). As in past years, neonatal mortality was concentrated in the first week of life, after which, survival was >90% until March-April. The average tick load measured on hides of deceased calves was 35,691 (range =17,412-49,414). This range was similar to that measured in past years and is sufficient to induce mortality from acute anemia associated with concentrated massive blood loss and protein imbalance. Our data corroborate the individual and population impact of winter ticks on moose.

4

Dynamic Causal Modeling of the Speech Network in Stroke-Induced Apraxia of Speech

Donald A Robin[1], Avery L Van De Water[2]
[1]Communication Science and Disorders, UNH Durham
[2]Communication, Sciences & Disorders, UNH Durham

Apraxia of speech (AOS) is a motor speech disorder caused by the inability to effectively translate kinematic parameters required for speech production (McNeil et al., 1997). In adults, it is typically caused by a left hemisphere stroke, though a progressive form exists as well. Little is known about the underlying neuropathology of the disorder. Three key regions of interest are hypothesized to be associated with apraxia: the bilateral inferior frontal gyrus (IFG), premotor cortex (PM), and anterior insula (aINS). Previous work quantified resting state functional MRI network functional connectivity strengths between these regions and found that AOS was defined by reduced connectivity strength between left and right PM cortices as well as negative connectivity between left PM and right aINS. In order to enhance our understanding a primary network underlying AOS, the resting state fMRI data from 31 human subjects with history of left hemispheric stroke (15 with AOS, 16 non-AOS) was further modeled here. This investigation used a Bayesian-based modeling approach, dynamic causal modeling (DCM), to determine the causal relations among the previously mapped regions. In support of our hypothesis, findings indicate that the PM, not the IFG, is the node responsible for driving connectivity strength and direction. These data support involvement of the regions of interest previously described (bilateral PM and aINS) and further define the nature of that relationship, more specifically informing a neurobiological model of AOS that may fuel future investigations and treatment methods and/or outcomes.

POSTER PRESENTATION ABSTRACTS

28th ANNUAL COLSA UNDERGRADUATE RESEARCH CONFERENCE

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Using Cardiac Assay Techniques and Immunohistochemisty to Determine Whether American Lobsters (Homarus americanus) Have Extraocular Photoreceptors in Their Central Nervous System

Winsor H Watson, Brienna Elizabeth Achorn, Kerri Lynne Strobeck

Crustaceans, such as crayfish, horseshoe crabs, and lobsters have complex visual systems. In certain species such as crayfish (Procamborus clarkii), light-sensitive opsin proteins are located in both the eyes and cell bodies in the cerebral ganglia, suggesting that decapods may have opsins that allow for photosensitivity throughout their central nervous system. The goal of this study was to test this hypothesis in American Lobsters (Homarus americanus) by using a cardiac assay technique, as well as immunohistochemistry. In the cardiac assay experiments, the lobster's eyes were covered and they were placed in an aquarium in a dark room with IR lighting and an IR sensitive camera. Changes in their heart rate and behavior were monitored while subjecting them to different lights of different wavelengths (green, blue, red, white and UV). The data obtained demonstrated that they do, in fact, has extraocular photoreceptors. In order to try and identify the location of these photoreceptor neurons, we removed the CNS of juvenile lobsters, fixed them, and exposed them to antibodies directed against various opsins and cryptochromes. Preliminary data indicated cryptochromes are located throughout the CNS, but at this time, the opsin studies have not been completed. Overall, our data indicate that lobsters have photoreceptors in many locations other than their eyes, and we are not attempting to determine their role.

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Epidemiology of Staphylococcus Bacteria from Pets and Wild Carnivores in New England

Sharlene Amador, Cheryl Marie P Andam, Colin J McGonagle

In the United States, antibiotic resistance bacteria cause at least 2 million infections and approximately 23,000 deaths annually (1). Majority of these pathogens originate from animals (called zoonosis) and are transmitted to humans through direct contact or through food, water and environment. One important cause of infection in hospitals and communities worldwide is methicillin-resistant *Staphylococcus aureus*(MRSA), which can cause serious damage to skin and soft tissue. MRSA in animals has raised concern over their role as potential reservoirs or vectors for human MRSA infection in the community.Other species of *Staphylococcus*are widespread in animals and are potentially transmissible to humans, although there is limited epidemiological data about them. In this project, we aim to characterize the prevalence and distribution of different species of methicillin-resistant (MR) and methicillin-susceptible (MS) *Staphylococcus*isolated from domesticated (pets and livestock) and fur-bearing wild animals. We will be mentored by Dr. Cheryl Andam (MCBS Department), in collaboration with Drs. Robert Gibson and David Needle from the NH Veterinary Diagnostic Laboratory (NHVDL). Using epidemiological, phylogenetic and genomic data, we show that antibiotic resistant *Staphylococcus* species are genetically diverse and prevalent in multiple animal species. Our findings have important implications to animal and human health.

103

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Amanda H Bagnardi, Caitlin S Mills

Frustration is a common emotional response specified by the presence of goal-blocking accompanied by the omission of a reward. Although prior research has linked feelings of frustration with aggression, social exclusion, and stress, the neural processes in the brain that are thought to produce frustration have not been well conceptualized to date. We conducted a quantitative meta-analysis of neuroimaging studies that were believed to induce frustration using activation likelihood estimation (ALE) to identify areas of the brain that were consistently activated across studies. Studies were included in the analysis if they involved an omission, loss, or exclusion condition which corresponded with increased difficulty or inability to complete a task. The ALE analysis revealed that certain areas of the brain were consistently recruited during "frustrating" tasks, such as the frontal gyri, insula, anterior cingulate cortices (ACC), and temporal gyri, among others. These are the first such meta-analytic results on the neural correlates of the complex, yet common affective state of frustration. We discuss these results in terms convergence and divergence from other well-known affective states that relate to frustration, such as anger and stress.

16

Exploring the diversity of antibiotic-producing *Streptomyces* bacteria from Odiorne Point State Park salt marsh and drowned forest

Cheryl Marie P Andam, John T Ball, Krista M Mastrogiacomo

We collected *Streptomyces* from the Drowned Forest Beach and salt marsh at the Odiorne Point State Park in Rye, NH. Since *Streptomyces* is commonly found in the soil, then we should also be able to find them in the sand of a once very lush forest. The Drowned Forest at one time was an extensive forest until it sank after the end of the Wisconsin Glaciation and subsequent rise in temperature. The trees eventually died because they cannot grow in salt water when the Atlantic Ocean overtook it. We were able to isolate and culture *Streptomycin* from these areas and show that they are genetically diverse. Our study suggests that previously unrecognized ecological niches, such as the Forest beach and salt marsh, are important sources of antibiotic producing bacteria.

43

Assessing Gross Depolymerization and Immobilization Rates Using a 15-N Isotope Pool Dilution Assay

Bethany Balstad, Scott Greenwood, Lauren Breza, Bennett Thompson, & Stuart Grandy
Natural Resources, UNH Durham

Nitrogen (N) is an important nutrient for plant production in agriculture, but excess amounts of plant-available N are often mobile and can be transported to nearby aquatic ecosystems where they are detrimental. In natural systems, soil microbes mediate the availability of N through a process known as depolymerization: the breakdown of complex organic N into smaller plant-available units such as amino acids. A delicate balance must be maintained between depolymerization processes and plant consumption to optimize agricultural yields and avoid off site transport of excess N. This study utilizes a novel ^{15}N isotope pool dilution method to measure gross depolymerization rates. The soils used in this project were sampled from experimental plots in eastern Nebraska and included two different crop treatments. Half of the samples had experienced continuous corn cropping while the other half had a more diverse treatment including oat, sorghum, soy, and corn; an addition of rye litter was used as a source of complex N to the microbes in the soils. It was hypothesized that the diverse treatment soils would have higher rates of depolymerization and a more diverse amino acid composition, because continuous corn cropping can decrease soil microbial diversity over time thus affecting their N transformation efficiency. The results of this experiment indicated necessary points of improvement and a future direction for this developing methodology.

106

The Student-Athlete Wellness Study: An Analysis of Sleep, Diet Quality, and Perceived Stress as Risk Factors for Injury in Division I Student-Athletes

Jesse Stabile Morrell, Morgan P Baumgartner
Nutrition, UNH Durham

During the demanding transition to early adulthood that occurs while in college, student-athletes must find a way to deal with the pressure of excelling in their academics as well as their respective sports. These external stressors lead to added duress that has caused a large portion of NCAA student-athletes to report feelings of anxiety and depression, which may affect their mental and physical health. Additionally, the literature suggests that a careful balance of sleep and nutrition play large roles in the overall health of student-athletes, including risk for injury. This study aims to assess how sleep, nutrition, and perceived stress relate to risk for injury in Division I student-athletes at the University of New Hampshire. Male and female varsity sport athletes (n=23) were assessed twice: once in-season and once out-of-season, using a survey, anthropometric measurements, and via 24-hour dietary recalls. Data analyses will be used to identify significant relationships between self-reported injury and diet quality, sleep quality, and perceived stress and to compare the differences in these factors between seasons. The study's findings have the potential to inform administrators and coaches regarding risk factors associated with student-athlete injury and to create policies that can improve the health and wellbeing of college students at UNH and beyond.

90

Measuring the effect of drought on water use in Red Maple (*Acer rubrum*) trees.

Emily A Beard, Matthew A Vadeboncoeur, Heidi Asbjornsen
Natural Resources and the Environment , UNH Durham

An increase in drought duration, severity, and frequency in the Northeastern United States is a likely part of our future climate. Drought effects on forest tree species remains largely unstudied aside from the University of New Hampshire DroughtNet project. This study builds on the current DroughtNet project by analyzing drought effects on Red Maple (*Acer rubrum*) trees, a common understory tree species. This study was conducted at Thompson Farm in Durham, New Hampshire. Trees (n=12) were under either a throughfall exclusion structure, limiting ground water by 55%, or in a control plot. The exclusion structure simulated a 1 in 100-year drought, forcing trees to limit water use. Heat Ratio Method (HRM) Sapflow sensors measured the rate of water uptake across all plots. This study contributes to the DroughtNet project and helps to fully understand water dynamics in a New England forest experiencing prolonged water shortage.

31

Fertilizer Regime for Organic Strawberry Production

Lise L Mahoney[1], Aidan R Benner[2]
[1]Agriculture, UNH Durham
[2]COLSA, UNH Durham

Strawberry breeding research work was conducted in organically certified fields at the UNH Woodman Research Farm. Enviro 12-0-1, an organically approved fertilizer that is Organic Materials Research Institute (OMRI) listed, was applied throughout the 2018 growing season. Enviro 12-0-1 contains mainly a nitrogen dosage (12%), with no phosphorus and a very small amount of potassium (1%). The fertilizer was dissolved in water, and injected into a drip irrigation system using a Mazzei injector. The fertilizer was administered on a weekly basis during the months of June, July, and August, into three fields at varying amounts based on the area irrigated. During the season, phenotyping was completed on which basis plant selections could be made for the next round of breeding. We did this work to trial various breeding lines of strawberries, to see how they performed in this organic setting. The soil management for these field will be presented.

116

Using Stable Isotope Analysis of Methane in the Bubbles and Sediment Porewater of Ponds to Determine Methane Production Pathways

Ruth K Varner, Kathryn A Bennett
Earth Science, UNH Durham

Arctic and subarctic ecosystems in the northern hemisphere are warming faster than any other region of the globe. Rising temperatures, in this region, are causing changes in the natural cycles of these systems, such as the thawing of permafrost. As permafrost thaws it forms ponds that emit methane (CH_4), a potent greenhouse gas, predominantly through ebullition. Microbes present in these systems produce CH_4 through two primary pathways, acetoclastic methanogenesis forms CH_4 using organic carbon (C) sources while hydrogenotrophic uses inorganic C. Stable isotopes can be used to characterize the relative importance of these two pathways for overall CH_4 production, providing information that can improve modeling of current and future CH_4 emissions.

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60

Do RPA-dependent Epigenetic Modifications Regulate Early Flowering in *Arabidopsis thaliana*?

Emily S Berry, Kevin Michael Culligan

Epigenetics is the study of heritable changes not found in the DNA sequence. Most of these inheritance mechanisms are caused by the addition of a methyl group to cytosine nucleotides in DNA and prevent gene expressoin. The model organism *Arabidopsis thaliana* (abbreviated *A. thaliana*) is commonly used in genetic experiments, and its usefulness is extended to research in epigenetics. Previous research from the Culligan lab focused on genes involved in DNA damage and repair, such as BRCA2 and the RPA1A/B/C/D/E genes. While conducting this research, investigators noticed that the RPA1C/E double-mutant typically expressed the phenotype of early flowering despite there being no changes made to the nucleotide sequence or environment compared to the other strains. One possible explanation to this phenomenon is the methylation of of certain regions of DNA associated with flowering. The goal of this experiment is to identify any possible epigenetic differences between the Col-O wild type and RPA1C, RPA1E and RPA1C/E *A. thaliana* mutants that play a role in early flowering in RPA1C/E. From this research, different DNA methylation patterns could be identified in these RPA1 mutants, and the results could help researchers better understand how DNA methylation and histone modifications affect the development of an organism. Early flowering can also be seen in agricultural settings and can severely affect crop yields.

66

Effects of Storage Time and Temperature on Molecular Analyses of Soil Fauna Communities

Jessica G Ernakovich, Christina A Lyons[1], Nathan D Blais[2]
[1]Natrual Resources , UNH Durham
[2]Natural Resources, UNH Durham

Soil mesofauna are important soil quality indicators making them vital tools for land managers. In the past it has been laborious to identify and determine diversity of soil fauna, but new molecular techniques have streamlined this process. The application of new techniques for examining faunal diversity has been limited to fresh soil; but resource availability can make it difficult to run analyses immediately after sampling. Moreover, many long-term ecological studies archive air-dried soils. It is unknown if faunal analysis can be performed after long-term storage. Here we examine how storage duration and temperature affect DNA-based soil fauna diversity analysis compared to extractions on fresh soil. To test this, soil DNA was extracted shortly after sampling (control) and then after storage for 2- and 4-weeks at three temperatures (25°C, 4°C, -20°C). PCR was used to amplify the 18S rRNA gene (to target soil fauna) which was then sequenced; community composition and diversity were then analyzed. We hypothesize that (1) -20°C samples will have similar diversity relative to the control because freezing reduces microbial degradation of DNA (2) increased duration of storage will reduce diversity relative to the control due to enzymatic breakdown of DNA.

95

Quantifying the Effects of Forest-to-Pasture and Forest-to-Silvopasture Conversions on Supporting and Regulating Ecosystem Services

Nathan D Blais[1], Alexandra R Contosta[2]
[1]Natural Resources, UNH Durham
[2]Research Center of Earth Sciences, UNH Durham

This project seeks to investigate the effects of land use changes in New England. Due to recent increases in demand for local agricultural production, forested portions of farmland are being converted to other uses. This study is interested particularly in forest-pasture and forest-silvopasture conversions. These changes may have negative implications on the ecosystem services forests provide. In this study I seek to assess changes in major regulating and supporting ecosystem services that may be occurring because of these land use changes. Measuring Carbon and Nitrogen mineralization and nitrification rates I will quantify possible changes in nutrient cycling and storage. This will be done using 30-day incubations of soil samples collected from several land use treatments. My results will aid in gaining a better understanding of how land use effects ecosystem services vital to the New England area and fill in knowledge gaps to inform farmers and land managers in making the best choices for their agricultural and forested lands.

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Evaluation of Antibiotic Use in Shelter Cats With Upper Respiratory Infection: A Prospective Study

Sarah E Proctor, Jillian R Broadhurst

Feline Upper-Respiratory Infection (URI) is commonplace in most animal shelters, and its endemic presence is problematic for the animals as well as for veterinarians and other shelter personnel. Despite the fact that viruses are responsible for the majority of these infections, many cats with URI in shelters are still treated with antibiotics. Antibiotic treatment in the absence of bacterial infection and the overuse of antibiotics can lead to antibiotic resistance among feline populations. The aim of this research was to compare duration and severity of URI in shelter cats treated with and without antibiotics. Cats showing clinical symptoms were randomly assigned to two groups, one receiving antibiotic treatment and the other receiving no antibiotics. Cats were monitored daily and the severity of their ocular and nasal symptoms scored on a numerical scale. The duration of their clinical symptoms was also recorded. Pharyngeal swabs were taken from some of the study population to determine whether or not bacterial infection was present. The mean severity and duration scores and standard deviations were calculated for each group and an unpaired t-test performed. No significant difference in the severity of URI and the duration of the illness was found in cats who did and did not receive antibiotic treatment. These findings support the need to change the protocol for treatment of feline URI in order to improve the quality of care provided to the shelter cats. Furthermore, these findings provided additional evidence to support the need for enhanced antibiotic stewardship in both veterinary and human medicine.

59

Distribution and Abundance of *Crassostrea virginica* larvae in the Great Bay, NH

Nicole E Bumbera[2], Jenn Dijkstra[1]
[1]Center for Coastal & Ocean Mapping/Joint Hydrographic Center, Jere A. Chase Ocean Engineering Lab
[2]Chase Oceanic Engineering, UNH Durham

The eastern oyster, *Crassostrea virginica*, is a ecosystem engineer that provides multiple ecosystem services that include bio-filtration, erosion alleviation, and habitat for other species. In Great Bay, oysters support the local economy by providing jobs through commercial fishing. Presently, oysters from 15 oyster farms are sold to local and regional restaurants. Since the early 1990s, the standing stock of oysters has declined by 89% (State of the Estuaries Report 2018) due to pollution, disease, invasive species, rising temperatures and over harvesting. Restoration efforts have shown low survival rates of oyster spat with a 39% survival rate in 2016 and a 64% in 2017 with varying recruitment levels at differing sites (Eckert 2016). The goal of this study was to examine the abundance and distribution of oyster larvae at four reefs (Nannie Island, Squamscott, Lamprey and Woodman's Point), in Great Bay. The sites chosen leveraged on-going restoration and recruitment efforts by UNH, TNC and Fish and Game. Oyster larval collection was weekly from June 27th until Aug 20th with 3 replicate samples obtained per reef. Collections were made using bongo nets, 30x90 cm, with a mesh size of 64µm that were horizontally towed for 5 minutes 1-2 meters beneath the water's surface. Filtered volume of water averaged 14.71m^3. Results indicate spatial differences in the abundance of larvae as well as two peak oyster spawning periods.

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The Path to a Sustainable Meal

Jacob Capraro[1], Todd Guerdat[2]

[1]Sustainable Agriculture and Food Systems; [2]Department of Agriculture, Nutrition and Food Systems

Have you ever wondered what a truly sustainable meal looks like? What about a restaurant that is completely farm-to-table? A sustainable restaurant does more than buy its vegetables from a local farmer. The chef, farmer, and consumer need to co-exist in a sustainable cycle. This research paper examines the cycle of a sustainable meal served by a farm-to table restaurant and how the definition of waste has expanded over the last few years.

47

Cell Line Authentication using Short Sequence Repeats

Darian R Tilton[1], Vanessa Cardenas[1], William K Thomas
[1]Hubbard Center for Genome Studies , UNH Durham
[2]Hubbard Center for Genome Studies, UNH Durham

State of the art genetic identification of humans and the authentication of human cell lines uses highly polymorphic Simple Sequences Repeats (SSRs) to provide unique DNA "fingerprints". These methods of identification are critical to forensic analysis and for keeping track of human cell lines in research. Misidentified cell lines are a major factor for limiting accuracy and reproducibility in research. In addition, misidentification of human forensic samples can have serious consequences. Current methods for SSR based genotyping are based on fragment sizes of polymerase chain reaction products and is constrained by the need to multiplex several loci with unique florescent tags. This method is costly, and can lead to misidentification due to variability across laboratories and the inexact communication of fragment sizes.

One possible solution to this problem is to develop a DNA sequence based approach that sizes SSR loci by counting the number of repeats in each allele, producing a "digital" ID that will be reproducible. This approach requires much smaller DNA fragments for identification and is likely to be more successful with damaged input DNA. The techniques involved in this research included primer design, DNA amplification, next gen sequencing, and bioinformatic analysis of SSR loci.

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Investigating the Efficiency of Aerosol Collection Methods

James F Haney, Hailey E Carter
Biology , UNH Durham

Aerosols from freshwater lakes with toxigenic cyanobacteria pose a potentially serious threat to humans and wildlife. Toxic aerosols are emitted by a wide range of lakes, but the mechanisms of cyanobacterial aerosolization are unknown. In order to further understand how to estimate exposure and health risks, it is necessary to first understand environmental factors that influence aerosol production. To investigate environmental drivers of aerosol production, The University of New Hampshire Center for Freshwater Biology uses a compact lake aerosol monitor (CLAM). While this method has produced significant results, the method itself had never been tested for efficiency.

This project tested the efficiency of the CLAM through a series of controlled experiments. The overall goal of this project was to determine the efficiency of the CLAM and modify the CLAM to increase efficiency. The CLAM works by pumping air from the surface of lakes through a filter and into a trap with distilled water that retains both aerosolized particles and water soluble toxins. Throughout this project, aerosol collections were run with various collection times, number of liquid traps and physical conditions. Instead of preforming these experiments over a natural lake ecosystem, they were performed in a controlled closed system using a flask with a known concentration of toxins. After testing the efficiency, the system was modified to improve efficiency and testing was repeated. These samples will now be processed and tested for toxin concentration using the ELISA method (enzyme-linked immunosorbent assay). Graphics of results will be produced using SigmaPlot and JMP.

The overall goal of this project is to determine the efficiency of the CLAM before and after modifications and estimate in prior studies what percentage of toxins were escaping undetected. Results of this study will help contribute to a risk assessment of cyanobacterial toxin inhalation by humans and wildlife by better understanding results of past studies and providing more accurate results in future studies on cyanobacterial aerosolization.

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Evaluating skin carotenoid levels via the Veggie Meter ® in college men and women

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It is recommended that adults consume 1.5-2 cups of fruit and 2-3 cups of vegetables daily, however only 9% of adults meet this recommendation. Diets rich in fruits and vegetables have been found to reduce the risk of chronic disease. Fruit and vegetable intake is routinely self-reported; this limits the confidence in the accuracy of data collection and the efficacy of intervention studies. Carotenoids are plant based compounds that are hypothesized to protect and promote health due to their antioxidant properties. Measuring skin carotenoids is a novel and non-invasive assessment, and may offer practical application to objectively assess the intake of fruit and vegetables. The purpose of this study is to evaluate skin carotenoid levels (Veggie Meter) in a sample of college adults (18-24 years of age). Students (n=395) were recruited from an introductory nutrition course in November and December of 2018. Students' carotenoid levels were assessed via index finger in triplicate. The scores ranged from 120-642; males had a mean score of 303.0±77.9 and females had a mean score of 288.5±90.0. Study findings demonstrate skin carotenoid assessment is a practical and simple tool to evaluate dietary behaviors in a large sample of young adults.

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Expression and Regulation of Cysteine Rich 61-Connective Tissue Growth Factor-Nephroblastoma Overexpressed 1 (CCN1) in Ovarian Adenocarcinoma (OVCAR8) and Human Granulosa Tumor (KGN) Cells

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Angiogenesis is the process of new blood vessel formation and is needed for tumor progression. There are a variety of polypeptide factors that mediate angiogenesis, including CCN1. Our studies on non-cancerous ovarian cells have shown that CCN1 expression is mediated through the protein kinase C (PKC) pathway. In the present study, our goal was to determine CCN1 expression by OVCAR-8 and KGN cells in response to phorbol 12-myristate 13-acetate (PMA), an activator of PKC. The OVCAR-8 and KGN cells were grown in the presence of fetal bovine serum (FBS) to expand the respective cultures for our experiments. Since CCN1 is induced by FBS, both cell types were serum-starved for 2 hrs prior to treatment with PMA for 2 hrs. Analysis for CCN1 expression was done via quantitative polymerase chain reaction. Our goal was to test a broad range of PMA concentrations, starting with 2.4nM, 0.24nM, 0.024nM, and 0.0024nM. In OVCAR-8 cells, except for the 2.4nM PMA, preliminary data showed that the other three concentrations appeared to increase CCN1 above the negative control (without FBS). In KGN cells, the 0.0024nM PMA, but not the 2.4nM PMA, appeared to increase CCN1 above the negative control. Moving forward, besides addition of more replicates, we plan to treat these cells with high concentrations of PMA (10nM and 100nM) to determine their effects on CCN1 expression.

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The Influence of Land Use on Wood Decomposition and Algae Growth

Danielle D Chancey, William H McDowell

Given the connection between streams and the surrounding terrestrial landscape, varying land uses can influence the physical and chemical characteristics within streams. These characteristics in turn, play a role in the rates of decay of woody material and algal growths. Algae acts as an energy source for the system, while wood decomposition releases nutrients and provides habitats. Three sites in the seacoast area were chosen based on differing land use: the Lamprey River, a large, suburban river; a small rural stream in Dowst Cate Forest: and Wednesday Hill Brook, a small suburban stream. Wood decomposition was tracked by decomposing wooden spoons over the course of four months. Algal growth was measured by deploying ceramic tiles and later analyzed for chlorophyll a. The forested site had the fastest wood decay rate, while the small suburban site had the slowest. With high stream flows, due to rain and snow fall, many materials and samples were lost downstream and only two months of data were collected for two sites. Further studies should be conducted over a longer time span to further explain the relationship between land use and algal growth and wood decomposition.

6

Sex Differences in Ultrasonic Vocalization Emission and Serotonin Dorsal Raphe Activation

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Since the 1990's, anxiety disorders are estimated to cost the United States a total societal burden of $42 billion and have increased in prevalence by 36% in the past 2 decades. Moreover, studies demonstrate that anxiety disorders are 50% more prevalent in women than men. Even so, the psychiatric response to such stressors varies widely from subject to subject based on these individual differences in resilience. Previous research has indicated that rats emitting 22 kHz ultrasonic vocalizations (USVs), thought to mimic coping responses in male models, predict these individual differences when exposed to an extreme stressor. Although research demonstrates the vast neurobiological differences between the male and female brains, it is still unknown whether these vocalizations can also predict resilience in the female rat model under the same circumstances. Therefore, we will be analyzing the emission of USVs in correlation with the results of a behavioral post-test as well as the levels of active serotonin in the dorsal raphe nucleus in female subjects. The purpose of this research is to validate the theory that USV emission predicts resilience in individuals following an inescapable stress in females as well as males, in order to work toward a better treatment for women affected by anxiety.

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Determining Self-Quenching Error for Fluorometric Pigment Analysis of Phycocyanin and Chlorophyll α Using Fresh and Frozen Samples

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Cyanobacteria are photosynthetic bacteria that occupy a wide range of ecosystems throughout the world. Many species of cyanobacteria secrete toxins that can have a negative effect on the health of terrestrial mammals, including humans. There becomes a need for a simple and cost-effective monitoring protocol for these toxins through the biomass of the cyanobacteria. Some studies suggest there is a correlation between the biomass of sample and the level of pigments, phycocyanin and chlorophyll. Self-quenching of a sample occurs when the concentration of the pigments surpasses the detectable range of values for the fluorometers. The extraction of these pigments is important in understanding these levels as an indicator of biomass because the pigments must be extracted to observe them in their entirety. This study sought to determine at what pigment levels self-quenching occur and how freezing and thawing a sample would affect these values. The fluorometers that were used in this study were the Amiscience FluoroQuik (FQ) and the Turner AquoFluor (T1). A dilution series was performed on a variety of samples to determine at which linearity does not occur indicating self-quenching. Using linear regression, the levels at which 5%, 10% and 20% quenching error were determined for all of the samples on both machines. The results showed quenching occurring at higher levels for the T1 than the FQ but showed a more drastic increase in PC following freezing for the FQ.

2

Obesity Mediates Leukemia Progression Through Ceramide Kinase and NADPH Oxidase

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Acute myeloid leukemia (AML) is a heterogeneous leukemia that causes the cloning of hematopoietic progenitor cells in the bone marrow, creating an accumulation of immature myeloid cells. Studies have shown that a possible risk factor of AML and many other cancers is obesity. Ceramide kinase (Cerk) is an enzyme whose activity produces ceramide-1-phosphate (C1P), a sphingolipid metabolite known to regulate inflammation, such as that caused by obesity. C1P serves to activate the NADPH oxidase which can play a role in cancer cells through redox regulation of proliferative and signaling pathways. This study evaluated ceramide kinase and NADPH oxidase in obese mice models with AML.

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Understanding the Future of Oyster Aquaculture in the Great Bay. Applications of the IPCC Anticipated Ocean Acidification Impacts

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Research conducted on the impact of ocean acidification in the Great Bay on *Crassostrea virginica*. Oyster aquaculture is in important part of the net economic fishery export totaling $219 million as of 2013. The Intergovernmental Panel on Climate Change has projected that ocean pH will range between 0.2-0.4 more acidic by 2100 (60-120% more acidic than pre-Industrial Revolution). In addition, Estuarine ecosystems are anticipated to see larger swings in water pH dependent on flooding, drought, and runoff from surrounding terrestrial environments. *C. virginica,* along with other calcium carbonate reliant organisms, are greatly impacted by change in pH within the environment and have been known to have impacted growth and survival when faced with lower pH. This research was aimed to understand the future survival and growth of *C. virginica* in future IPCC predicted ecosystem conditions for the Gulf of Maine.

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Devil's Club: the Alaskan Ethnobotanical Plant and the Opportunity for the Development of Foregut Cancer Therapeutics

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Foregut cancer is characterized by cancer of the gastrointestinal tract. Colorectal carcinoma (CRC) is a type of foregut cancer and is the third most commonly diagnosed cancer to occur in both men and women, affecting 1 in 22 men and 1 in 24 women in the United States in their lifetime. CRC occurs when polyps develop on the inner lining of the colon/rectum and begin to grow uncontrollably. Rates of CRC cases in young people (below the age of 50) have been increasing by 1.6% per year for unknown reasons. A second type of foregut cancer is pancreatic cancer. It is characterized by the development of abnormal pancreatic cells into cancerous tumors which, if not caught early, can metastasize and spread to other organs. Pancreatic cancer kills more people each year than breast cancer, and over 56,000 Americans are expected to be diagnosed with this disease in 2019. These devastating statistics dictate the clear necessity for the development of new chemotherapeutics for the treatment of foregut cancers. Devil's Club (*Oplopanax horridus*) is one of the most significant medicinal plants used throughout history among the indigenous people of Southeast Alaska and the coastal Pacific Northwest to treat upwards of 34 different conditions including cancer. Studies have shown the ability of DC extracts to decrease foregut cancer viability by inducing programmed cell death and suppressing proliferation. My experiment tested the hypothesis that DC, when extracted in different solvents, would decrease the viability of these two foregut cancers. MTS assays were performed to analyze the resulting cancer cell viabilities after extract treatments. Future projects may involve supplementing DC extract-treated drinking water to transgenic mice with foregut cancer.

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The Relationship Between Microbial Diversity and Aggregation of Soils Under Varying Levels of Tillage Treatments at Kingman Farm

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Aggregates are soil particles that bind together to form groups. These aggregates can range in size due to the chemical make-up of the soil or treatment that the soil has received, such as amount of tillage. It has been shown that a lower level of soil tillage in agricultural environments leads to greater macroaggregation (formation of larger particulate soil clumps) within that soil. While it has been observed that macroaggregates tend to contain more microbial biomass per unit of soil than microaggregates do, it is not as apparent how aggregate size affects microbial diversity. To investigate this, we collected soil from a tillage experiment at Kingman Farm and looked for a relationship between aggregate size and microbial diversity. Aggregates were classified into three size groups (<53um, 53-250um, and >250um) using mechanical sieving. DNA was extracted from fresh soil using the DNeasy Soil Extraction Kit and then quantified. We then ran PCR on this DNA to amplify the 16S region—a region of DNA that is highly conserved across a majority of bacteria. The product of this PCR was then sent to be sequenced. From these sequences, we were able to tell what species of bacteria were in this soil and what the relative abundance of these species was. I hypothesize soils with a greater abundance of large aggregate sizes will correlate with a more diverse microbial community because larger aggregate sizes allow for a greater retention of nutrients and water that are essential for microbial growth.

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Factors Influencing Seed Selection by Small Mammals in New England Forests

Rebecca J Rowe, Corina N Danielson

Small mammals in New England primarily consume seeds and nuts in the summer. Their selection process while foraging is influenced by many factors, such as seed availability, the density of nearby shrubs, and moon luminescence, and in turn, their selection can affect the composition of plant establishment in forests. To examine the primary factors behind small mammal feeding behavior, we used camera traps to record the activities and habits of deer mice (*Peromyscus maniculatus*), white-footed mice (*Peromyscus leucopus*), and southern red-backed voles (*Myodes gapperi*) while they were foraging at experimental seed trays in softwood and mixed forest stands. Seed trays contained American beech, eastern hemlock, and red maple tree seeds, all of which are native to our study site, the Bartlett Experimental Forest in the White Mountains. The data we've collected has provided insight into the variables driving foraging behavior in these rodent species and could have important implications for the relationship between small mammals and forest communities in New England.

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Green Sea Urchin Aquaculture

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Effective methods of *Strongylocentrotus droebachiensis,* green sea urchin, aquaculture has not yet been established. Demands for the roe, to make the sushi called uni, lead to a severe decline in the 1990s but in recent years the populations have evened out. However, this has been under close management and restrictive harvesting rules in the Gulf of Maine. These circumstances have generated interest regarding incorporation of the species into existing aquaculture sites, as *S. droebachiensis* roe remains more valuable than other varieties of urchin roe. Therefore, creation of reliable methods of urchin aquaculture could both assist the fishing industry in supplying commercial vendors as well as replenish local ecosystems.

This study assessed various aspects of green sea urchin aquaculture, centered around successful larval culture as well as diet optimization and behavioral components. Larval cultures were performed using wild, mature urchins. Growth and behavioral studies were performed on both wild urchins as well as urchins raised from culture in order to build a more complete understanding of the life history of *S. droebachiensis*. Diet studies included species of *Gracilaria, Saccharina,* and commercially available pellets. This study outlines many beginning factors of understanding the life history of *S. droebachiensis* to better incorporate it into aquaculture. However, more research is still necessary in order to fully understand all the requirements of the organism and its' behavior both in lab and in the field.

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Comparing Amino Acid Sample Recovery for Heated vs. Non-heated N_2 Reduction

(A 15N-Isotope Pool Dilution Method)

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The Grandy Lab is the first laboratory in the United States to adopt an amino acid (AA) pool dilution method to determine the gross rates of AA depolymerization and consumption within soils. These processes are critical in understanding the flux of nitrogen (N) between stable organic matter and biologically available mobile fractions of N. The lab is currently in the process of optimizing sample preparation steps to maximize recovery and processing time. Specifically, inconsistent recovery has been observed between soil extraction and gas chromatography–mass spectrometry (GCMS) analysis. We hypothesize loss is most likely associated with sample extract evaporation and derivatization steps. Two experiments were conducted to assess losses associated with these steps.

The first experiment assessed analyte loss during extract concentration. This technique applies a constant stream of nitrogen gas (with or without heat) to reduce the sample volume and concentrate the analyte. If AA recovery is related to length of time in the heated nitrogen dryer, then reducing drying time will result in increased recovery in the heated samples. To evaluate the correlation between evaporation rate and AA recovery, I controlled the amount of time the samples spent under the nitrogen dryer by consistently checking for completion of drying with a minimum amount of drying time allowed in one experiment and allowed two times the minimum amount of drying time allowed in a second experiment. My control set of samples was evaporated at room temperature under the nitrogen gas stream. Then I added heat to the drying block during the blow down process to increase the rate of evaporation. I controlled the height of the dryer needles, flow of nitrogen, and temperature of dryer block in both trials.

The second experiment assessed analyte loss during derivatization. Sample derivatization applies a reactive derivatizing agent to the sample in order to transform the analyte into a chemical compound that is amenable to GCMS analysis. This is an extremely exothermic reaction and can potentially lead to sample spatter and spray out of the container. If AA recovery is related to loss of solution from the vessel when a chemical reaction occurs during the blow down and derivatization steps, then using a vessel with greater volume will result in changes to AA recovery in the heated samples. To evaluate the correlation between solution loss and AA recovery, I used a 25ml conical vial during the blow down and derivatization steps to increase surface area and eliminate splash out during the application of nitrogen gas stream and the addition of reactive chemicals in derivatization.

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Investigating the Role of Protein Phosphatase 2A in the Salt Stress Response in *Arabidopsis thaliana*

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Protein Phosphatase 2A (PP2A) is a ubiquitous enzyme in eukaryotes that moderates a large array of cellular signaling processes. PP2A is composed of three subunits: catalytic C subunit, regulatory B subunit, and scaffolding/regulatory A subunit. In *Arabidopsis thaliana,* the A subunit has three isoforms-A1, A2, and A3-that are highly conserved at the protein level with at least 86% conserved amino acid sequences. In addition, all three isoforms are expressed in roots. Taken together, these observations indicate that the three A subunits may be functionally interchangeable. In comparison to wildtype seedlings, *A. thaliana* seedlings with a mutation in the *A1* gene have roots with obvious root cell file rotation that cause root twisting under conditions of moderate salt stress. The twisted root cells result in a characteristic root curling phenotype when seedlings are grown on vertical plates. In contrast, mutations in the *A2* and *A3* genes do not result in any observable root phenotype. We hypothesized that differences in expression may be responsible for mutant phenotype variation. To test this hypothesis, hybrid genes were constructed using promoters from one subunit and coding regions from a different subunit. The hybrid genes were transformed into *a1* mutant *Arabidopsis* for complementation tests. Preliminary results suggest that different promoter-coding region combinations do affect the ability of the transgene to complement the phenotype.

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The Effects of Calorie Restriction on the Development of Anxiety in Female Rodents

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Anorexia Nervosa is an eating disorder that affects over 30 million people in the United States, most of whom are women. Recent research indicates that anxiety, a separate mental disorder which disproportionately affects women, is frequently present before the development of an eating disorder. It is suspected that this correlation is due to the anxiolytic effects of caloric restriction, and that the self-starvation is reinforcing for those who are in the first phases of an eating disorder. Although females are especially vulnerable to both disorders, very few studies have been completed that specifically assess female reactivity to stress in relation to calorie restriction. We utilized female rodents in a traumatic stress paradigm in order to assess how calorie restriction affects their ability to cope with a stressor as well as its ability to induce stress resilience. Our findings indicate a stress-resilience effect as a result of calorie restriction when exposed to a traumatic stressor. This may indicate that positive reinforcement might play a role in the development of disordered eating as the reduction in calories allows for better coping with stress symptoms.

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Understanding Male College Athletes' Perceptions Related to the Purpose of Body Composition Assessment Using Air Displacement Plethysmography

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Background: A primary research aim was to explore how male college athletes' understanding of the purpose of measuring body composition compares to the actual clinical function. Additionally, what differences exist among sports in relation to athletes' perceptions.

Methods: A sample of 111 collegiate male athletes (Hockey, Basketball, Soccer, and Football) were invited to meet with the Sports Dietitian and undergo multiple body composition assessments. Between the first and second body composition assessment, athletes completed an 8-item questionnaire related to exercise and dietary habits since the initial assessment. The concluding item inquired what the athlete, "hoped to get out of the BOD POD assessment".

Results: Most common themed response (37.8%) indicated desire to lose fat, gain muscle/weight, and/or see 'better' results. Many of these responses reinforced misconceptions that leaner is always better and 'great' or 'successful' results were tied to decreases in body fat (BF). This was most common among Football (51%) and Soccer players (37.9%), despite 72% of Soccer having less than 10% BF (M=8.89% BF). The next most common themed response (33.3%) expressed interest in how body composition might have changed since initial assessment and eagerness to monitor results over time.

Conclusion: Despite efforts by the Sports Dietitian, majority of athletes' responses indicated incomplete understanding of the clinical purpose of conducting body composition assessment or expressed misconceptions related to the relationship between body composition and performance. Continued sport-specific education is needed to uncover other misconceptions and help athletes contextualize results to increase the likelihood of body acceptance and satisfaction.

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Effects of Claw Removal on Jonah Crabs (*Cancer borealis*)

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Jonah crabs (*Cancer borealis*) have been bycatch of the lobster fishery for at least 80 years and in the last 20 years landings, and total value of the fishery, have more than quadrupled. Current regulations allow removal of both of their claws before they are released. The three objectives of this project were to determine: 1) If using a tool to remove claws reduced mortality; 2) if claw removal reduced their mobility and; 3) impaired their ability to feed. Our results indicate that mechanical removal of claws reduced mortality from 50% to 10%, likely because this method resulted in smaller wounds. Surprisingly, crabs missing their claws are more active than they were prior to removal, perhaps indicating a flight response. Finally, feeding was possible without claws but they required more time to open hard-shelled prey and they used a prying instead of crushing strategy. Overall, claw removal can be lethal, but less so when the mechanical method is used. Additionally, sublethal effects such difficulty feeding, and changes in behavior, may further decrease survival. These data suggest that it would be worthwhile reassessing the practice of harvesting Jonah Crab claws, or at least modifying the technique to reduce mortality.

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The influence of foliar chemistry and stream nitrate levels on leaf decomposition

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Abstract:

Leaf litter is a liable energy source to freshwater streams. In fall, 30-42% of stream carbon pools are made up of leaf litter and this secondarily affects carbon fluxes through the microbial and aquatic food web. For these reasons, it is important to understand stream leaf decomposition and the microbial community as a link and catalyst to the larger network of our stream ecosystems. In previous studies by Wymore et al. 2016 and Wymore et al. 2017, time was determined to be the major factor in leaf decomposition as leaf chemistry changes throughout the process. Because bacterial community is affected by genotype- level foliar chemistry, the bacterial assemblages changed over time and varied across leaf species types. The results of these studies indicate bacterial communities form in patterns and bacterial colonies are not formed randomly. Another major finding was after two weeks in decomposition, bacterial communities converge as litter species consist of recalcitrant compounds. The results of these studies supplied mechanisms to be researched in detail.

Our focus is to further understand foliar chemistry and stream nitrate effects on leaf decomposition. We have multiple hypotheses in our study. First, we hypothesize a positive correlation between nitrate levels and leaf decomposition rate, as well as more recalcitrant leaf species to decompose at a slower rate. Secondly, we hypothesize leaf phytochemical convergence as time progresses based off previous scientific findings of bacterial species convergence.

Testing our hypotheses through a leaf litter bag study. Leaf litter bags were evenly filled with oak and maple leaves found locally. Two species, five streams, three harvests dates and four replicates gave us approximately 120 leaf litter bags. The bags were labeled, randomly tied to rebar and placed on stream beds in five streams across New Hampshire. At day 7, 14 and 28 the leaves were harvested from the water and frozen until analysis. In our analysis, we are performing the Ash Free Dry Mass (AFDM) technique to determine decomposition rate and measuring leaf chemistry through pyrolysis gas chromatography (Py- GC).

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Differences in Social Behavior of Chimpanzee Mothers Based on Sex of Offspring at Chimfunsi Wildlife Trust, Chingola, Zambia

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Chimpanzees (*Pan troglodytes*) are one of the most social species on the planet. They thrive being in close knit groups some as small as 3-4 chimpanzees, to some groups in the hundreds. Within those communities, chimpanzees work together to raise their young. Depending on specific rank and sex, some chimpanzees do better than others. The main objective of this study was to determine whether chimpanzee mothers socialized their sons more than daughters. This study was conducted at Chimfunshi Wildlife Orphanage in Chingola, Zambia over nine weeks. Data was collected with seventeen mother-offspring pairs (referred to as a dyad), but only fourteen were included in data analysis; there were seven male offspring and seven female offspring. Chimpanzees begin the weaning process around five years old, so to only chimpanzees four years and under were included. The data was collected by recording all dyad's interactions for five minutes through a focal follow and analyzed by looking at the amount of time of social play, number of social partners, and individuals the dyad interacted with throughout the day. It has been hypothesized that mothers with male offspring will spend a greater amount of time within the mixed group of adults, as social rank for males is very important. This study observed the amount of time mother and offspring pairs spend in; 1) a mixed group including adult males, 2) time spent with just mothers and offspring, and 3) time spent with mothers and female offspring, within their enclosures at Chimfunshi. The results from this study provide closer insight to how our closest relatives interact with one another and how they parent their offspring in such social troops.

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Harnessing the Power of Ecosystem Services to Save the Future of Coffee: A Bioeconomic Approach

Benjamin M Fehr, Shady S Atallah

Coffee is the most economically important tropical export crop. For some regions of the world, it provides the sole foundation of the economy. To meet global demands, coffee growers often turn to intensive, sun-grown systems to increase yields. Sun-grown coffee systems are heavily reliant on external inputs, and the removal of shade trees contributes to biodiversity loss in these already sensitive ecosystems. With rising global temperatures, coffee growers also face significant pest and disease pressures. Outbreaks of pests and diseases have significant impacts on yields, which in turn have far-reaching economic consequences for farmers. One possible solution, intercropping shade trees, is the subject of much debate. On one hand, shade trees provide yield-enhancing crop growth ecosystem services. These include increasing biodiversity, incorporating additional sources of revenue from timber and other products, and reducing the amount of inputs needed. On the other hand, excessive shade has been shown to depress yields, and in some cases, the microclimates created by shade trees may be beneficial to pest and disease outbreaks.

There has been a recent effort to create comprehensive models that encompass all the factors that go into these production systems. To study the complex system of pests in an agroecosystem, researchers use cellular automata and individual-based models. A bioeconomic model for coffee berry borer, a significant insect pest, developed by Atallah et al. (2018) provides a glimpse at how shade-grown production systems can be optimized for maximum economic and ecological benefits. Using data from coffee production in Columbia, they determined the optimal level of shading. We believe that this model can be easily adapted to assess other economically important pests, including coffee rust. This will ultimately lead to the development of more sustainable coffee production practices.

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Linking Activity of DNA Damage Response (DDR) Proteins to Temporal Map of Histone Modifications

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Epigenetic regulation plays a role in several critical cellular processes, including DNA damage and cell fate determination. One of the main mechanisms in epigenetic regulation is carried out through histone modification. Histone octamers associate with DNA forming structures called nucleosomes that control the access of various proteins to genomic DNA. The modification of these histone proteins can modulate the binding of nuclear proteins and affect the organization and structure of chromatin. DNA damage response (DDR) is the collective set of biochemical pathways include cell cycle checkpoints, DNA repair and damage tolerance. DNA repair primarily consists of two separate, but interconnected pathways, Homologous Recombination and Non-Homologous end joining. The primary repair pathway chosen is a function of the type and timing of the DNA damage. The repair of DNA damage is critical to cell health with unrepaired damage resulting in cell death or genetic mutation. The recruitment of the proteins responsible for repairing DNA breaks has been shown to be highly dependent on numerous histone modifications. The first goal of this study is to chart the temporal regulation of DNA damage response proteins and histone post translational modifications at various time points after damage induction in order to create a time map of the DNA damage response. The second is to link these histone modifications to likely interacting partners in the DNA damage response to elucidate the orchestration of chromatin remodeling pathways.

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Analysis of STAT3 and STAT5 Activity in Breast Cancer

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STATs are a family of transcription factors that regulate cell growth and differentiation. In normal mammary development, STAT5 is activated by prolactin to promote survival, terminal differentiation, and milk production. STAT3 is activated by leukemia inhibitory factor (LIF) to promote involution and remodeling to a pre-pregnancy state. In breast cancer, both STATs can be activated in the same tumor. Previous studies have found that activation of STAT5 showed a better prognosis, whereas activation of STAT3 showed a poorer prognosis. Importantly, when both STATs were active, the prognosis was better than when STAT3 was active solely suggesting that STAT5 modulates the activity of STAT3. Using Chromatin Immunoprecipitation, we have identified the binding sites of STAT3 and STAT5 in breast cancer and have found that they both bind to a subset of target sites. We are currently analyzing the gene expression of these target genes by activating STAT3 and STAT5 both separately and together. This would give us the data necessary to determine which genes were upregulated and downregulated by these STATs. Importantly, we will use this data to better understand the roles of STAT3 and STAT5 in breast cancer and how STAT5 exerts dominance over STAT3.

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Self-Pollination and Development of Organic Strawberries in New England

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Within the last 5 to 10 years, it seems as if everyone has become more aware of how their food is grown and the want for organic, locally grown food has increased exponentially. Strawberries are typically grown commercially in warmer states such as California and Florida. Here at the University of New Hampshire, research has been on-going for several years to produce a variety that is suitable to be grown organically in New England climates. Thousands of strawberry plants have been maintained at Woodman Farm and the Macfarlane Greenhouses. To produce the variety we want, plants have been bred and harvested for excellent fruit quality and disease resistance. Through the processes of self-pollination and cross-pollination, we aim to develop new varieties of strawberries that will be viable for growers in the region while keeping up with the ever increasing demand for high quality, locally grown produce.

At Woodman Farm, strawberries were harvested and collected to phenotype. From the phenotyping we did, we could determine which plants showed the best qualities so that we could select them for the traits we want. Before the season was over, we collected runners from the select plants we determined had the best traits to be later grown in the greenhouses.

In the Macfarlane Greenhouses, the runners that were collected earlier in the year were planted into plug trays and eventually transplanted into their own individual pots. When all the runners we wanted to prepare were set up, I began to self-pollinate the flowers. To do this, a flower is chosen from a plant and tagged with the plant name/number as well as the date it was bagged. A mesh bag is placed over the flower and sealed in order for the pollen to stay within the vicinity of that one flower. If the flower is self-compatible, it will successfully pollinate the flower and begin to form the achenes of the strawberry. In this report, I will go into depth in self-pollinating.

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Investigating GLI3 Interacting Proteins in Innate Immune Cells

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The Hedgehog (HH) signaling pathway is mediated by the GLI family of transcription factors.To date, 3 members have been described: GLI1-3. In response to HH stimulation, GLI1 and GLI2 positively regulate the pathway while GLI3 negativelyregulates HH signaling pathway. Our lab has identified a novel role for GLI3 in mediating inflammation via toll-like receptor (TLR) stimulation. In previous work, we have shown that GLI3 binds to the acetyl transferase protein p300 in cancer cells. The goal of this project is to determine if GLI3 can complex with p300 in monocytes and determine the biological significance of this interaction.

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Lasting Effects of White-Nose Syndrome: Wing Damage and Reproductive Status of Little Brown Bats (*Myotis lucifugus*)

Olivia P Fortuna, Rebecca J Rowe

White nose syndrome (WNS) is a disease caused by the accumulation of fungus (*Pseudogymnoascus destructans)* on the ears, nose and wings of numerous bat species in eastern North America during hibernation. This disease causes wing damage, necrosis and awakens bats during hibernacula, which depletes their fat reserves and typically kills them due to starvation. However, some bats are surviving WNS and returning to their summer habitats. While the immediate effects of the fungus have been studied extensively, the lasting effects have not. This study will examine how WNS is affecting the overall reproductive success of little brown bat populations by examining wing damage and looking for correlations with the reproductive status of female bats. The results of this study will provide a better understanding of how WNS is affecting North American bat population dynamics.

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Characterizing Expression of S-Acyl Transferase Genes in *Arabidopsis thaliana*

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Protein S-acyl transferases are found in all eukaryotic cells where they transfer lipid residues onto their substrate proteins. Lipidation can affect protein location, stability, or activity. In humans, dysfunctional PAT proteins are known to be associated with disorders including schizophrenia and Huntington's disease, but little is currently known about the function of PAT proteins in flowering plants. Further information about the expression patterns of *PAT* genes in the model plant *Arabidopsis thaliana* can provide clues about potential *PAT* gene transformations. I used transgenic plants that expressed *PAT* genes as N-terminal translational fusions with the β-glucuronidase (GUS) gene. Using histochemical GUS assays, the expression patterns of two of the *PAT* genes, *PAT3* and *PAT8*, were mapped at tissue and cellular levels in *Arabidopsis* throughout the life cycle. *PAT3-GUS* was expressed only in anthers and pollen, while *PAT8-GUS* was expressed throughout the life cycle of *Arabidopsis*, including root meristems, vascular tissue, true leaves, and flowers. Additional assays at various developmental timepoints are needed to complete GUS expression data sets.

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Abuscular Mycorrhizal Fungi Symbiosis in Crops Affected by Pesticide Seed Treatments

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In commercially important crops such as soybeans, pesticide seed treatments (PST) are often used to protect against insect pests and plant-pathogenic fungi that cause disease within the crop. These fungicides have also been found to diminish the positive symbiotic relationship between commercial crops and arbuscular mycorrhizal fungi (AMF), a beneficial fungus which colonizes roots and helps crops absorb nutrients such as nitrogen, phosphorus, and sulfur. If PST degrade AMF colonization rates, this may result in a negative feedback to crop productivity. In this study, we measured how PST applied to soybean seeds affected AMF colonization rates in a no-tillage corn-soybean crop rotation. The data generated from this study will be important because a disruption in AMF colonization may result in decreased crop production. Furthermore, a decrease in nutrient uptake by the crop could result in less efficient use of fertilizer and the potential for environmental pollution.

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Influence of Soil Salinity on Plant Community Distribution on Appledore Island, ME

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Coastal habitats have distinct plant communities, adapted to habitat-specific salt spray exposure. This study investigated the reliability of soil salinity and elevation to predict coastal habitat. 37 soil samples were collected from the rocky barren, gull lawn, and upland shrub habitats. The elevations of these sample sites were also recorded. Analysis of this data found that the rocky barrens and upland shrub soil salinities and elevations were significantly different. The data was split into northeast and southwest exposure groups, and we found that the northeast soil salinities and elevations had weaker trends and more variability than the southwest data. These results were consistent with scientific literature that suggests seasonal nor'easters might cause the inconsistency in the northeast data.

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Examination of Resting State Brain Oscillations in Participants with Multiple Concussions

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Brain oscillations are important for neural communication between different regions of the brain. My research study focuses on brain oscillations in the alpha (8-13 Hz), beta (14-25 Hz), and gamma (26-100 Hz) frequency bands. Neural oscillations can be measured with an electroencephalogram (EEG) while a person performs a task or while they are at rest. We recorded brain waves in participants with multiple concussions and from control participants without concussions while they were at rest (resting state) to determine whether concussions alter the communication between brain regions. Changes in communication during resting state would illustrate differences in how neural communication occurs in people with concussions and suggests that there may be changes during cognitive tasks. We collected eyes-open resting state data for four minutes and then broke the four minutes into four second epochs. Twenty-three participants were used for the control subjects (n = 14 female, n = 9 male). An additional twenty-three participants were used for the experimental group (n = 16 female, n = 7 male), which consisted of subjects with more than two major concussions in their past. The average age of each male and female group were recorded and was not different between groups. Time frequency decomposition was used to convert the EEG data into oscillations, which were then examined. We average three electrodes for each of the six regions of interest, taking both hemispheres into consideration. A 2 (group) x 6 (ROI region) ANOVA will be run three times in order to analyze alpha, beta, and gamma oscillations. From the analyses, we will be able to determine whether concussions change oscillatory power during resting state.

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Understanding the Role of Polyamines in Rice under Drought and Salt Stress

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Abiotic stresses are important constraints on crop yield. Paddy-grown rice is particularly susceptible to drought and salt stress, which have negative effects on carbon and nitrogen intake that limit plant growth and grain yield. Polyamines (PAs), mainly putrescine (Put), spermidine (Spd), and spermine (Spm), are important molecules in plant metabolism and have been implicated in abiotic stress responses, both as protectors of plants from stress and preparing the plant for tolerance of stress. This has led to genetic manipulation of PA metabolism aimed at improving drought and salt tolerance in rice and other crops. Prior to overexpressing PA biosynthetic genes, we have profiled the response of a commercial rice variety to drought and salt stress. We found that PAs may be involved in recovery from stress, but levels during stress appear to fluctuate widely. To minimize sampling errors, we also studied differences in PA contents among different parts of the long, morphologically heterogeneous rice leaf. The results show that under drought, Put is increased in the sheath and decreased in the lamina as compared to the control, suggesting that the plant prioritizes protection of the meristematic tissues by compatible solute accumulation. There were no differences in Spd or Spm under drought. Furthermore, PA levels were higher under moderate salt stress than severe stress. In all cases, the PA levels were significantly higher in the leaf blade than the sheath. This research will ultimately increase scientific understanding of abiotic stress tolerance for plant improvement.

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CRISPR Mediated Knockdown in the Hydra

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The hydra is a tractable cnidarian model organism that can provide insights into how simple behaviors are encoded by relatively simple nervous systems based on cues from the environment. Hydra reproduce sexually when food is limited but asexually through budding when food is present in environment. This poster describes our efforts to develop an animal husbandry protocol for generating large quantities of sexually derived hydra embryos for microinjection and experimentation with CRISPR. The goal of this project is to create a knockout hydra for the single cyclic nucleotide gated (CNG) ion channel in the hydra genome and to characterize the coarse effects on behavior.

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Detection of American Eel and River Herring in New Hampshire Rivers using eDNA: A Comparison of Metabarcoding and ddPCR

Jessica L Haskins, Alison W Watts

Environmental DNA (eDNA) is any DNA from an environmental sample such as water, soil, or air. DNA is shed by fish and other animals through scales, feces, eggs, etc. Due to the nature of the samples, the relatively low concentration of DNA in the samples can make it difficult to identify specific species without collecting very large sample volumes. Metabarcoding and digital droplet PCR (ddPCR) are two methods to identify species in the samples. Metabarcoding is amplification and sequencing of the DNA to identify a wide range of species. ddPCR is amplification and quantification of one particular species of interest. Comparing these two methods will provide a better understanding of their limits of detection. American eel and River herring are the focus of this study since NH Fish and Game and NH Sea Grant track their migration. If the use of these methods with eDNA are successful for the detection of fish movements and migrations, they could supplement or replace the traditional monitoring efforts currently deployed by New Hampshire Fish and Game.

Water samples collected in the Oyster and Lamprey rivers during the spring and summer of 2018 were extracted and analyzed. The two methods are compared to each other, and to fish counts conducted at the sites.

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Disentangling the Mechanisms of Toxin Sequestration in the Poison Frog, *Ranitomeya imitator*

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Aposematism is a biological mechanism in which an animal displays a certain pattern or coloration to warn predators that they are dangerous via things like spines, sharp teeth, and toxins. Aposematic organisms can be found in a wide variety of biomes and ecosystems, and most aposematic organisms contain a secondary defense that is chemical in nature (harboring toxins, for example). While aposematism is well-understood in a predator/prey relationship context, the processes by which those organisms actually obtain the secondary defense are largely unknown.

It is generally agreed upon that there are two potential explanations for the variation in toxin profiles: ecological (toxins constructed via components of diet), genetic factors (genes that produce proteins that help organisms build toxins), and microbiota (gut and skin bacteria aiding in the production of said toxins). While the first two have a fair amount of research and support behind them, the third has remained largely unexplored. It is likely that all three factors work in tandem to affect toxin acquisition among different organisms. The aim of this study would be to examine how these factors and their interplay contribute to the underlying, prevalent variation in chemical defenses in aposematic species. The model organisms of choice are 4 species of poison frogs in the genus Ranitomeya from 4 localities across Northern Peru in the departments of San Martin and Loreto.

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The Influence of Thalamic Manipulations on Cortical Activity in Rats Performing the DNMTP task

Anna D Hayes, Abigail R Sheridan, Kaitlyn S Howard, Robert G Mair, Miranda Jane Francoeur

The thalamus is a relay area of the brain in which neuronal signaling is distributed widely to areas like prefrontal cortex. Previously, the thalamus was thought to only passively relay motor and sensory signals. However, current research indicates that the thalamus also relays complex information needed for reward-guided decision making. In this study, we investigate the type of information thalamus is sending to prefrontal cortex (PFC) by recording from cortical neurons while thalamus is either permanently lesioned or temporarily inactivated. Long Evans rats were given unilateral thalamic lesions both pre and post learning with an implant inserted bilaterally into the PFC to record neuronal activity. The task the rats performed was delayed non-match to position or DNMTP Bilateral recordings allow us to compare the activity from the lesioned and non-lesioned hemisphere in one rat. In a different set of rats, thalamic connections to PFC were temporarily inhibited by using DREADDS. In both studies, we found response types in PFC related to movement, lever pressing actions, and reinforcement. Fewer cortical neurons responded to DNMTP events the hemisphere with a thalamic lesion. We also found examples of prefrontal neurons that lose activity with thalamic inhibition from DREADDs. Our research indicates that thalamus is important for neuronal responses to PFC which influence decision making. These findings are applicable to human studies because the connection between thalamus and PFC are important for higher order thinking such as decision making and not just isolated to the PFC.

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Modeling Gene Gain and Loss Across the Metazoan Tree: Are Sponges Degenerate?

Matthew D MacManes, Nhen Hunter

Apopulation's ability to adapt over generations is an incredible biological phenomenon. Genes can be lost or gained and lead to a clear genotypic or phenotypic change within a population. This process of evolution gives rise not only to new genes, but entirely new taxa. The traditional hypothesis of early animals (metazoans) on a phylogenetic tree presents sponges branching from the last common ancestor of all animals before comb jellies (ctenophores). This would imply that over time, there was primarily gene gain which led to the existence of ctenophores and other organisms in their present state. More recent studies have shown evidence that the opposite may be true. If ctenophores branched first, it would imply that there was extensive gene loss in sponges, resulting in the sponges' far simpler body plan. Both hypotheses have support, but with our research we will be able to provide a deeper look into the phylogenetic position of these early-branching metazoans. Understanding these early branching metazoans, in regards to their evolutionary life, is essential because their evolution gives us insight to our own human evolution. It is also imperative to comprehend where these genes and their functions originated in order to apply them to present day ideas.

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Perfluorinated Compound Regulation of Sphingolipid Metabolism in Acute Myeloid Leukemia

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The Seacoast region of New Hampshire has seen an emergence of cancer clusters, as well as environmental perfluorinated compound (PFC) contamination which may be linked to high health-risk potential. Sources of contamination include the Former Pease Air Force and the Coakley Landfill, where PFC levels in the drinking water are much greater than the current health advisory level. Blood serum of adults and children reported PFC levels 2 to 3 times higher on the base compared to the general public. Little evidence exists linking PFCs to health problems, but the emergence of cancer clusters, as well as PFC contamination emphasizes the need for research on possible biological links between these problems. Sphingolipids have also gained interest in research due to their role in cell death and proliferation, oncogenesis, and multidrug resistance. Ceramide, a pro-apoptotic sphingolipid, is known for its roles regulating cellular stress and death. Catabolism of ceramide leads to the ultimate formation of sphingosine-1-phosphate (S1P), a pro-survival lipid known for its roles in regulating cell survival, proliferation, and mitogenesis. Overall sphingolipid biology is significant due to its roles in cellular processes. In the context of PFC exposure, sphingolipid biology has yet to be investigated, but given the relation of sphingolipid metabolism to cellular regulation and fate, an understanding of PFC-mediated regulation of sphingolipid metabolism may have broad implications.

4

Plastic Use By Gender on The University of New Hampshire's campus

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Recently, there has been an educational push among American universities to recognize the substantial sustainable environmental impacts of plastic use and recycling on college campuses. Much of the literature regarding this subject suggests that student's plastic consumption and recycling habits are motivated by their attitudes on conservation. However, there is a lack of research analyzing how gender may affect plastic use and recycling behaviors. To better understand the factors that influence university student's plastic consumption and recycling habits based on gender, we plan to analyze the results of a survey conducted on the UNH campus in 2018. This research examines (1) environmental conservation attitudes effect on plastic purchasing decisions and (2) if gender has statistically significant recycling habits. Results indicate a significant relationship between gender preferences in certain consumption and recycling behaviors.

To date, we have received responses from 215 students on a 22 question survey addressing plastic awareness and expenditures. We found a *statistically significant* relationship between female and male responses. We are continuing to analyze the survey data to determine how these statistical significance effects plastic consumption choices and associated sustainability awareness. Understanding the factors that influence student plastic and recycling purchases and awareness, allows students and facility alike to increase sustainable practices on the University of New Hampshire's campus.

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Scaling Methane Emissions Using Vegetation Cover Type at Sallie's Fen

Madeline Ann Juffras, Ruth K Varner, Clarice Rachelle Perryman, Michael L Zampini

Wetlands are the largest natural source of methane to the atmosphere, yet there are still large uncertainties in the magnitude of these emissions due to the spatial and temporal heterogeneity of methane production and transport processes. One process by which methane can be emitted to the atmosphere is through plant-mediated transport - the diffusion of methane through plant aerenchyma. The objective of my project was to determine how methane emissions vary depending on the plant species composition at Sallie's Fen in Barrington, NH. Static flux chambers were used to measure methane emissions at six locations across the fen. Quadrat sampling was used to determine species composition. Aerial photography and a geographic information system in combination with transect quadrat sampling was used to create a vegetation map of the entire site. The combination of methane emission data and species composition allowed for scaling of emissions across the entirety of the fen. Overall, this project furthers our understanding of complex wetland ecosystems and its relation to methane, a radiatively important greenhouse gas.

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Developmental Pattern of Primary Cilia in the Mouse Adrenal Glands

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Primary cilia are non-motile, centriole-derived organelles found in neurons and many other vertebrate cells. Defects in primary cilia cause many diseases in humans including polycystic kidney diseases and various developmental disorders. ARL13B is a protein marker for astrocytic primary cilia, and it is involved in cell division and organogenesis. Type 3 adenylyl cyclase (AC3) is mostly expressed in neuronal primary cilia and mediates ciliary cAMP signaling. The adrenal glands are composed of three structures (capsule, cortex, and medulla), each with their own unique function. The medulla mediates the body's fight-or-flight response by releasing epinephrine from neuroendocrine cells into the bloodstream. We found that neuroendocrine chromaffin cells in the adrenal medulla represent a good model to study AC3 in neuronal primary cilia because they lack neurites that normally interfere with the signaling from the primary cilia. Through immunostaining primary cilia in mouse adrenal glands, we examined the changes that the adrenal gland structures undergo during mouse postnatal development. We used two common protein markers for primary cilia (AC3 and ARL13B) with different expression patterns and functions and compared them in the three layers of the adrenal gland. Our preliminary data shows that the expression pattern and morphology of primary cilia changes as the adrenal gland develops postnatally. This research helps reveal how primary cilia affect the adrenal gland's development, and additionally, can provide useful clues for the study of AC3 in the brain.

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“Not so Lice:” Developmental Sampling Methods of Sea Lice on UNH Caged Steelhead Trout (*Oncorhynchus mykiss*)

Nathaniel Alan Kinsman, Elizabeth A Fairchild

Commercial aquaculture is a highly dynamic industry created to efficiently raise fish and other aquatic life. The growing environment is closely monitored to ensure product quality and to minimize potential problems during cultivation. A critical ecosystem problem for salmonid farms is parasites, specifically sea lice, which can render the host fish unmarketable. Chemical treatments can damage local marine ecology and ultimately lead to chemical-resistant lice. A more environmentally friendly solution to control sea lice is through the use of cleaner fish which will consume the parasites. However, any new species introduced as a parasite control must be an effective control, cannot compete with the commercially grown fish, and must mature with the life-cycle of the sea lice. Therefore, knowing when and why sea lice outbreaks occur in certain environmental conditions is important. To understand how and when sea lice affect the steelhead trout (*Oncorhynchus mykiss*) at the UNH integrated multi-trophic aquaculture farm in New Castle, NH, sea lice sample collection methods were developed in fall 2018 and preliminary analysis on the number and distribution of two common species of sea lice, *Lepeophtheirus salmonis* and *Caligus elongatus,* were determined. Only *C. elongatus* appeared in low numbers during a three-month sampling period (October-December) on the trout at the farm. During this period, the average number of lice was ≤ 3 per sample date. Although the standard deviations for each sampling date had a relatively high variation (greater than one), indicating a high variance from the calculated mean, no differences were observed between the mean number of lice (ANOVA, $p>0.05$) over the three months. In addition, there were no differences in the ratio of male to female lice within each (ANOVA, $p>0.050$) and across all (two-way ANOVA, $p>0.05$) sampling periods. Future research should examine the occurrence of lice over the entire steelhead trout growing season (May-December), not just the colder months. The relationship between species of lice, their sex ratio, and the effect of water temperatures should also be studied at the farm to determine how these factors affect cage reared steelhead trout.

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Monitoring the Success of Restored New England Dune Systems: Results from Harborside Dunes, Seabrook, NH

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Coastal dune systems are dynamic and play fundamental ecological roles such as providing wildlife habitat and buffering the coastline from storms. However, the health and sustainability of dune systems is threatened by factors such as human use and storm surge. NH Sea Grant and UNH Extension, as part of the UNH Coastal Habitat Restoration Team, have been restoring coastal dune habitats along the NH and northern Massachusetts coasts since 2014. Efforts have included public forums to solicit feedback from community members, the creation of a Common Garden, a free resource of native dune plants for residents to replant dunes in front of their homes, a school-based program, and community-based revegetation and fencing efforts. To date over 200,000 stems of beachgrass (Ammophila bevilgulata) have been planted, in addition to other species, but a comprehensive monitoring effort has not been completed to evaluate the success of these efforts. The objective of this study was to design and implement a monitoring protocol to measure the success of dune restoration activities using data from the Harborside Dunes of Seabrook New Hampshire.

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Cyanobacteria and the Food Web of Norway Pond

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Cyanobacteria produce toxins in the environment that are contributing to neurological diseases in humans via bio-magnification through trophic levels. Norway pond was sampled in September 2018 to determine the amount of beta-methylamino-L-alanine (BMAA), a type of cyanobacteria toxin, in the lake. An EXO probe, an ELISA, and other limnilogical tools were used to collect data such as toxin concentration, depth, turbidity, pH, E7, and pigments to assess Norway pond. Zooplankton, phytoplankton, and size fractions within the lake were collected and BMAA levels were found for each. Norway pond was found to have an Oscillatoria producing bottom layer of cyanobacteria that coincided with a rising pH and increasing chlorophyll, indicating photosynthetic activity. Large numbers of Daphnia were counted throughout all depths of the lake, but the highest concentration was at the surface layers. Daphnia in Norway pond were large, averaging 1.2 mm and producing a predator to pan-fish ratio of 1.7, indicating a high level of piscivorous fish. There were no significant differences in BMAA levels among the various size fractions in Norway pond. A significant difference between phytoplankton and zooplankton toxin levels were found. The bio-magnification factor for Norway pond was 22, comparatively high to other lakes in New Hampshire. BMAA is bio-magnifying in Norway pond. This survey sought to gain a basic understanding of the biological patterns and characteristic of Norway pond. Future research should look at the concentration of toxins in Norway pond fish and make residents aware of the potential danger of consuming fish from this lake.

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A Developmental Study of Apoptotic Markers and Histamine Receptors in Cephalopod Statocysts

Samantha N Leef, David B Needle

Cephalopods navigate complex environments due in part to their statocysts. Statocysts, analogous to the vertebrate vestibular and auditory system, are encased in cartilage rather than bone making them more easily accessible, and a potential model for physiology and pathophysiology research. Age and anatomical dysfunctions are the reasons for many human auditory and vestibular malfunctions. Two of these causes are endolymph hydrops and aging. In people, high salt diets were thought to cause endolymph pressure changes resulting in Menière's disease and treated with diuretics. However, recent studies have illuminated the possibility of histamine receptors in the semicircular canal being the cause. Cephalopods have provided several models for studying vestibular dysfunction as well as a multitude of other peripheral and central nervous system aspects. The natural life stage of cephalopods results in immune suppression called senescence. Identifying developmental apoptotic changes, as well as finding histamine receptors could indicate the potential cause of senescence-related vestibular malfunctions in cephalopod senescence and offer potential insight into human patients' vestibular morbidity.

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Enabling Hydroponics; Evaluating Root Development using Synthetic & Aquaponic Nutrient Sources

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Plant roots play a vital role in the overall health and adaptability of plants to their environments. Hydroponic and integrated aquaponic systems are becoming more popular as sustainable alternatives for greenhouse production. By using a nutrient solution derived from an aquaponic system to fertilize plants grown in a hydroponic system (integrated aquaponics), hydroponic operations could be certified organic and therefore increase their sale markets. It is important to know how these nutrient solutions impact growth of plant roots. The objective of this research was to evaluate how organically derived and synthetic nutrient sources impact root development of greenhouse grown strawberries. Root growth was evaluated by measuring root length, diameter, branching and root index using the WinRhizo image analysis software. Overall no significant differences were observed between the two treatments over the 4-week collection period. When comparing week to week, strawberries grown in synthetic fertilizer averaged higher surface area, diameter, root tip number, and fresh and dry weight. With the knowledge gained from this initial study, more research is needed to further understand the differences between the root development of plants grown in synthetic fertilizer and organic aquaponic derived nutrient sources.

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Evaluation of a Rapid, Low-Cost Method for Measuring Oxalic Acid Content in Kiwiberries

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Like many fruits and vegetables, kiwiberries contain the compound oxalate or oxalic acid which can create an irritating sensation in the back of the throat and ultimately limit the number of berries consumers can eat. When eaten in excessive amounts, oxalates have also been implicated in the formation of kidney stones. The development of low-oxalate kiwiberry varieties is therefore essential to furthering the production and consumption of this emerging fruit crop. Breeding for low oxalate content requires variation in that trait among available germplasm, thus the necessary first step in this process is an accurate characterization of the oxalate content of existing cultivars. In this study, a rapid, low-cost method of evaluating oxalate content was tested to ascertain its suitability for such a screen. In this method, lactic acid is used to clarify thin slices of different kiwiberry varieties, allowing manual counting of oxalate crystals (number per gram of fruit) under a microscope. From the data gathered so far, the method appears to generate reproducible data; and very importantly, there appears to be significant variation in the oxalate concentrations among kiwiberry varieties. This is likely a trait that can be modified through breeding. Using this evaluation method, it may be possible to screen breeding lines, allowing the rapid culling of high-oxalate lines, thereby greatly increasing breeding efficiency.

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Effect of Selenium on the Expression of Cysteine Rich 61-Connective Tissue Growth Factor-Nephroblastoma Overexpressed 1 (CCN1) in Bovine Luteal Cells

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In the ovary, growth of the corpus luteum (CL) is characterized by rapid development of new vasculature or angiogenesis. This process requires polypeptide factors such as CCN1. We know that CCN1 is expressed by bovine luteal cells and it is upregulated by fetal bovine serum (FBS). Since FBS is a common supplement in culture media, its presence could confound our findings. Luckily, bovine luteal cells are cultured without FBS, but with insulin/transferrin/selenium (ITS). Insulin is a growth factor, while selenium is an essential trace element with antioxidant properties. In the present study, the goal is to determine the regulation of CCN1 by selenium. Luteal cells were obtained from 4-day-old (day 4; n=2) and 8-day-old (day 8; n=3) bovine CL and one million cells were seeded in 6-well plates containing Ham's F12 supplemented with ITS. Then, medium was removed and replaced with Ham's F12 alone, or supplemented with FBS, ITS, ITS+FBS, or selenium (5 or 100 ng/mL). Cells were treated for 2 hrs or 24 hrs. In day 4 luteal cells, preliminary results showed that selenium did not appear to have an effect on CCN1 expression after 2 hrs, but it appeared to have increased CCN1 after 24 hrs. Similarly, in day 8 luteal cells, selenium had no effect on CCN1 expression after 2 hrs, but 100 ng/mL selenium increased ($p<0.05$) CCN1 expression after 24 hrs. Additional studies will determine the effects of insulin and selenium+insulin on CCN1 expression.

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A Comparison of Pre- and Post-Operative Transfusion Treatments for the Prevention of Transfusion Transmitted Malaria in Local Ghanaian Hospitals

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As a blood-borne parasite, malaria may be transmitted via blood transfusions. Yet, national and international blood safety regulations in malaria-endemic developing countries focus on inhibiting the spread of viral infections, neglecting the spread of malaria. The few policies and procedures regarding the transmission of malaria by blood transfusions prescribed by the World Health Organization (WHO) fail to account for a hospital's location and funding. Furthermore, the policies struggle with identifying methods to prevent the spread of resistant strains of malaria.

In Ghana, National Health Service policies often contradict the broader international recommendations regarding transfusion-transmitted malaria (TTM). These conflicting policies challenge local hospitals in Ghana's malaria-endemic regions to develop their own approach to minimize the transmission of malaria consistent with the WHO guidelines. This descriptive study reviewed patient charts and interviewed lab technicians and ward clinicians to compare the policies and procedures used by a rural hospital and an urban hospital in Ghana. Results indicate that 50% of the lab technicians in the rural hospital test donors' blood for malarial parasites, while none in the urban hospital conduct this practice. Furthermore, both hospitals rarely prescribed anti-malarial drugs in the 24-hours following transfusions (Urban: 2.2%; Rural: 2.7%). These practices contravene international policies regarding safe blood handling protocol. Thus, there is an urgent need for concise, evidence-based blood safety guidelines in malaria-endemic countries and for inexpensive, quick blood screening techniques to allow for donor screenings.

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Creating a Combined Pedestrian-Vehicle Accident Reporting System: Analyzing Durham and UNH Police Departments' Accident Reports

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Purpose: This project was created to address pedestrian safety among the UNH-Durham community. Combining both Police Departments' pedestrian-vehicle accident reports creates a more accurate depiction of pedestrian-vehicle accidents. Analyzing this compilation of data can help identify possible patterns and trends leading to more effective and efficient solutions, creating a safer environment for both the students of UNH and Durham residents.

Methods: Gathering, combining and analyzing two Police Departments' annual pedestrian-vehicle accident reports using a new system in Microsoft Excel and GIS/UCAT.

Results: A combined single-system process which would be updated annually. This system consists of four components: an annually updated GIS/UCAT visual representation of the accidents, an annually updated Excel database of all past and present accident data, an annual accident report summary, and an instructional manual to assist this process and ensure consistency of data collection and reporting. An analysis of past and present data highlights specific locations for necessary improvements to increase pedestrian safety.

Conclusion: Combining datasets from both Police Departments leads to more accurate and detailed information for developing solutions to improve pedestrian safety.

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The Role of Nutritional Supplementation in Lessening the Negative Effects of the Biomedical Bleeding Process on the American Horseshoe Crab, *Limulus Polyphemus*

Brianna M Looney, Winsor H Watson

The American horseshoe crab, Limulus polyphemus, is important to the biomedical industry because its hemolymph is used to produce Limulus Amebocyte Lysate (LAL), which is used to test medical devices and vaccines for pathogenic gram-negative bacteria. Unfortunately, the bleeding procedure has a 10-30% mortality rate, as well as several sublethal impacts. The overall goal of this study were to determine if nutritional supplementation during the bleeding process could lessen the negative impacts. All the experiments were conducted in outdoor tanks and the UNH Jackson Estuarine Laboratory using animals collected in the Great Bay Estuary. Accelerometers were attached to 81 animals to monitor their activity and blood samples were repeatedly drawn to measure hemocyanin levels. A subset of the horseshoe crabs (36 animals) were fed different foods to determine if the supplements helped them recover from being bled. The results obtained demonstrated that animals that were fed had faster increases in their hemocyanin levels and overall activity than control animals. We hope that the findings from this experiment can be used to help make the horseshoe crab bleeding process safer and thus help maintain a healthy population of this important species.

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Biophysical Studies on an Antifreeze Protein from the Desert Beetle, *Anatolica polita*

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Antifreeze proteins (AFPs) are biological cryoprotectants, found in various organisms, which prevent ice crystal growth in fluids. This is achieved by lowering the freezing point of water without significantly affecting the melting point, a phenomenon known as thermal hysteresis activity (THA), and by inhibiting ice recrystallization. An antifreeze protein, *Ap*AFP752, was expressed in *Escherichia coli* strain BL21 (DE3) and purified using Fast Protein Liquid Chromatography (FPLC). The structure and dynamics of this antifreeze protein, *Ap*AFP752, were investigated by Nuclear Magnetic Resonance (NMR) spectroscopy. Functional characterization studies of *Ap*AFP752 are ongoing and involve various techniques including Differential Scanning Calorimetry (DSC).

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PDE1 and PDE4 As Potential Targets For Nematicide Development

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Every year, $80-100 billion of damage is done to crops in the agricultural industry by plant parasitic nematodes. In order to combat such drastic losses, action needs to be taken against these pests. However, current chemical controls (e.g., nematicides) with the greatest likelihood of treating this problem also have damaging effects on the environment and on the health of agricultural workers. But by looking at a specific family of proteins called phosphodiesterases (PDEs), we hypothesize that targeting nematode PDEs with specific inhibitors may control parasitic nematodes without harming other organisms. To test this idea, we have chosen to examine specific PDEs (PDE1 and PDE4) from *Caenorhabditis elegans* (a non-parasitic nematode easily cultured in the lab) to compare its pharmacological sensitivity with human PDE1 and PDE4. This work will evaluate whether inhibitors to the PDE1 and PDE4 families can discriminate human and *C. elegans* PDEs as a first step toward developing novel nematicides that target nematodes while lacking adverse effects on other organisms.

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Three-Dimensional Echocardiographic Analysis of the Equine Aortic Valve

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This research focused on 3D echocardiography of the aortic valve (AV) in horses. Aortic regurgitation (AR) can be a normal function of aging or a disease in younger horses, and symptoms range from no outward signs to decreased performance to sudden cardiac death. Standard AR diagnosis includes 2D echocardiography from the right side of the horse. Three-dimensional echocardiography (3DE) records a pyramid of tissue rather than a 2D plane, showing cardiac structures difficult to visualize in 2D methods, and can be more accurate. Images from 9 horses with normal AV's were analyzed and novel measurements taken, along with 14 horses that had varying degrees of AR. These images had been previously taken by veterinarians at the Royal (Dick) School of Veterinary Studies Equine Hospital, part of the University of Edinburgh in Scotland. New 3DE images from the left side of 9 normal horses were taken for comparison to right sided images. In normal valves, only the edges of the cusps were visible as the tissue is very thin. The cusps of the AV were thickened in horses with AR, with degree of thickening corresponding to AR severity. Left sided images were generally worse quality than right sided, but in some cases there was better visualization of the right and noncoronary cusps. 3DE could potentially be used as a standard for diagnosis of AR, specifically by looking at cusp thicknesses, and could more specifically diagnose which part of the valve is affected by disease.

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What Is Our Water Worth and What Does Our Water Cost?

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The goal of this Project was to gather and develop information regarding the worth and cost of water services and resources in New Hampshire in order to better understand the value of water to our state's economy and the real cost of maintaining clean and safe water for drinking, recreation and businesses.
We reviewed and summarized over one hundred reports, presentations, fact sheets and other relevant information. We performed an economic analysis on some forms of water-based recreation in New Hampshire, and provide more detailed information on costs and benefits associated with culvert upgrades. We reached out to experts and stakeholders to locate information that is not readily identified through internet searches, and we identified gaps and opportunities for future works.

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Bryde's Whale Call Structure and Seasonal Distribution in the Equatorial Pacific

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Bryde's whales (*Balaenoptera edni*) are part of the genus that includes blue, minke, fin and sei whales, yet Bryde's whales are the least studied genus member according to NOAA stock assessments. The population structure and seasonal distribution of Bryde's whale are currently unknown, and passive acoustic recordings offer an opportunity to provide new information about this elusive species. All members of this genus are known to produce vocalizations and mating songs. Previous work characterized seven distinct Bryde's whale calls in the Pacific Ocean (Be1-Be8; Be 7 was only seen in the Caribbean Sea). Multiple other baleen whale populations have recently been reported to have developed changes in their call and song tonal frequency. This has raised questions about the driving pressures. The blue whale has shown a steady decline in tonal frequency worldwide. The present study aimed to 1) assess seasonality and temporal distribution of the western equatorial Pacific population of Bryde's whales and 2) assess any changes in call structure over time. Acoustic data from the Comprehensive Nuclear-Test Ban Treaty Organization International Monitoring System (CTBTO IMS) at Wake Island (19°16'48" N X 166° 39'0" E) in 2007, 2010, and 2012 were analyzed. Calls found as part of this population's repertoire included Be1, Be2 and Be3. Fundamental frequency of Bryde's whale calls were assessed in Adobe Audition. Within each year selected calls were located using previously analyzed hourly presence data. Detection of the Be1, Be2, and Be3 calls were consistently present off Wake Island from August through October and used as a proxy for species seasonal presence. Results do not indicate that Bryde's whale song and call tonal frequency is decreasing or changing over the six years of this study.

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Agricultural Impacts on Microbial Composition and Decomposition Rates on Two Streams in New Hampshire

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Agriculture can disrupt surrounding ecosystems resulting in adverse effects, specifically in aquatic systems, due to the addition of excess nutrients running off into waterways. The purpose of this study is to understand the link between agriculture, microbial composition, and decomposition within aquatic ecosystems in New Hampshire. Two study sites were considered, one site dominated by agriculture with a low-lying stream adjacent to the agricultural crops, and the other being a forested control stream. Soil and sediment samples were taken from each site and analyzed for their microbial communities. DNA extractions and PCR were used to obtain and amplify the 16s rRNA region of the DNA and then the amplicons were sequenced at the Hubbard Center for Genome Studies. Following sequencing, the study sites will be compared using statistical analyses to understand how agriculture may alter the microbial communities that colonize the surrounding water way. If the aquatic system at the agriculture site mimics the microbial communities in the soil of the terrestrial environment than it can be assumed agriculture can alter microbial communities. Secondly, decomposition rates will be measured at both sites using maple leaves in a mesh bag. Each week for four weeks a litter bag will be removed and weighed to establish a decomposition rate at each site. I hypothesize that decomposition rates will be higher and microbial communities will simulate terrestrial microbes at the agriculture site. Microbes contribute to decomposition rates as they breakdown organic material and agriculture can alter the terrestrial microbiome resulting in run off from an agricultural plot to enter waterways. This run off carries microbes into an aquatic ecosystem where they can colonize the waterway which may affect the natural decomposition rate. This study aims to establish a link between agriculture, decomposition, and the microbiome that establishes in both the terrestrial and aquatic environment.

1

Effect of Aging on Sensorimotor Processing: An ERP and Response Time Investigation

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As people age, their performance on tasks requiring cognitive control is often slowed or declined compared to that of a younger population. Research using a variety of tasks such as simple reaction time, choice reaction time, and decision making has shown greater response times in healthy older adults compared with younger adults. While this has been firmly established, there has been little research on the neural mechanism that causes these changes. The purpose of this study is to analyze different stages of sensorimotor information processing in the brain to evaluate their contributions to aging-related behavioral slowing, using a stimulus response time paradigm. To better understand the neural mechanism that may cause these changes, this experiment is using electroencephalographic (EEG) event related potentials (ERPs) to evaluate specific stages of information processing. ERPs are extremely useful due to their ability to capture fast neuroelectric events from the millisecond time scale so that neural mechanisms preceding response production can be analyzed. Two groups', young (18-30 years old) and old (over 50 years old), EEG and EMG recordings during a reaction time paradigm including simple reaction time, choice reaction time, and choice reaction time dual tasks are recorded and analyzed to measure reaction time and movement preparation time to hopefully prove whether or not the functional reactivity of the motor cortex is reduced in older adults. This experiment is ongoing and therefore results have not been analyzed to this point.

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Characterization of the Protein S-acyl Transferase Mutant *pat4-4* in *Arabidopsis thaliana*

Estelle M Hrabak, Lily K Mooney

The palmitoyltransferase (PAT) family in eukaryotes catalyzes S-acylation (i.e., covalent attachment of 16-carbon fatty acids to cysteine residues in substrate proteins). Acylation can affect membrane localization, stability, or activity of these substrates. All PAT proteins contain a conserved active site (DHHC-CRD domain) and usually have four transmembrane domains. Our long-term goal is to characterize the functions of *PAT* genes in the model plant *Arabidopsis thaliana* using a reverse genetic approach. *pat4-4* is a mutant allele of *PAT4* created by insertional mutagenesis with a fragment of foreign DNA (T-DNA). The junctions between the genome and the T-DNA were sequenced to reveal that, in addition to the inserted T-DNA, there was a 50 bp deletion involving part of intron 3 and exon 4 that removes part of the third transmembrane domain. To determine the effect of the mutation on transcription, RNA isolated from seedlings, leaves, flowers, and siliques of wildtype plants and of *pat4-4* plants was reverse transcribed to cDNA. Expression of the wildtype *PAT4* gene was detected in all tissues tested, indicating that *PAT4* is expressed in seedlings, leaves, flowers and siliques but full-length cDNA was not detected in *pat4-4* plants. Publicly-available databases indicate that *PAT4* is expressed in pollen. Fertilization of wildtype plants with pollen from a *pat4-4* heterozygote showed no effect of the *pat4* mutation on pollen transmission.

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The Use of Mountain Laurel as Potential Travel Corridor Habitat for New England Cottontails

Ethan Parker Belair, Matthew D Morris, Steven S Roberge

The New England cottontail (*Sylvilagus transitionalis*) is a state endangered species in New Hampshire that requires dense shrub cover to avoid predation. Habitat fragmentation is one cause of its population decline. Forests that lack dense shrubs limit the cottontail's dispersal between core shrubland habitats. Mountain laurel (*Kalmia latifolia*) is a shade tolerant shrub found to be utilized by cottontails in forests and can potentially provide travel corridors between core habitats. We attempted to find patches of established mountain laurel in southern New Hampshire using remote sensing. With a multiband raster dataset, we created an unsupervised classification image that divided the area's forests into ten different clusters. However, the vegetative compositions of the clusters were unknown, so field plots were conducted to determine the abundance of mountain laurel in each cluster. The unsupervised scheme was moderately successful in identifying areas with different quantities of mountain laurel. Also, there was a positive correlation between basal area and mountain laurel abundance. This classification scheme could be used in other forests to find potential corridor habitat for cottontails, which could connect populations and improve gene flow and viability.

5

Targeting STAT3 with Atovaquone in Ovarian Cancer

Sarah R Walker, Kayli E Neil

Ovarian tumors can arise from inappropriate and uncontrollable growth of either stromal, germ, or epithelial cells. It has recently been found that the inappropriate activation of transcription factor 3 (STAT3) has been linked to the vigorous growth and survival of cancer. Therefore, there is a need to target the uncontrollable activation of STAT3. It's known that Atovaquone inhibits STAT3 by affecting GP130 expression in other tissues. We hypothesize that Atovaquone will inhibit STAT3 and kill ovarian cancer cells and are currently assessing the activity of Atovaquone in ovarian cancer.

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Quantitative Histone Modification Characterization of Endoderm Cells

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Histone modifications regulate genome organization and gene expression, thus play an essential role in cell fate and diseases such as cancer. These post-translational modifications can change depending on the cell differentiating process. Through this project, we will be investigating histone modifications on variations of the same stem cell line to see what role the modifications play in determining cell fate. The objective of this project is to see the difference in cell fate between endoderm, mesoderm, and neural progenitor cells; and from mass spectrometry data, we will be able to see the differences in histone modifications to answer the question of: what histone modifications and post translational modifications matter? Our hypothesis is if the differentiated cells will all have different morphologies from one another then they must have different histone modifications. We will answer our question by differentiating three different types of cells from an E14 cell line, and using a number of processes to extract proteins. These proteins will then be analyzed to see what modifications they have gone through. The significance of this project is to further the knowledge base surrounding stem cell growth and proliferation, as well as how different histone modifications can have effect on diseases.

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Soil Seed Bank Response Following Forest Conversion to Silvopasture and Open Pasture

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As food demands increase, we will require new food production practices and more agricultural land. Silvopasture is an agroforestry system that integrates forage production, tree products, and livestock. Converting some forested land to silvopasture could be a way to increase the agricultural land base in heavily-forested New England while still maintaining the ecosystem services that trees provide. However, such conversions could also lead to a shift in the plant community toward more weedy plant species, and little is known about how plant communities respond to the establishment of silvopastures from mature forest stands. We measured the soil seed bank in a recently established silvopasture, open pasture, and a mature forest (control) at the UNH Organic Dairy Research Farm. Soils were sampled along transects at 5 m intervals extending from the plot edge to the interior of each land use system. We then quantified the germinable seed bank in the UNH greenhouse. We assessed plant species diversity and density for each system and sample location, expecting that density and diversity would vary by system and that both would decline with increased distance from the plot edge. We observed little evidence that land use system or distance from the plot edge affected the seed bank community. These preliminary results suggest landowners may be able to establish silvopasture or open pasture from mature forest stands without rapid shifts in the soil seed bank community. Future studies could focus on the mechanisms driving seed bank dynamics in recently established silvopastures and the functional relationships between soil seed bank communities and forage productivity and quality.

8

Comparing the Effects of Serum Starvation on the Expression of Cysteine Rich 61-Connective Tissue Growth Factor-Nephroblastoma Overexpressed 1 (CCN1) in Bovine and Human Ovarian Granulosa Cells

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The ovarian follicle is a fluid-filled structure that houses the oocyte. Granulosa cells line the inner compartment, and they produce polypeptide factors, including CCN1. Angiogenesis, the building of new blood vessels, is mediated in part by CCN1. Since CCN1 is serum-inducible, studying it poses a problem, because cell culture media often contain fetal bovine serum (FBS). Thus, the lab protocols we use to examine the regulation of CCN1 typically include a 2-hr-long FBS starve period. In the present study, the effects of a 24-hr-long FBS starve period on CCN1 were investigated in bovine and human (HGrC1) granulosa cells. Bovine granulosa cells were obtained from follicles (<5mm) and seeded into T-25 flasks until 100% confluency. They were expanded by splitting cells into 6-well plates until 80-90% confluency was reached. HGrC1 cells were cultured in 6-well plates until 80-90% confluency. Following treatments, quantitative polymerase chain reaction was used to determine CCN1 expression. For bovine granulosa cells, compared to the absence of FBS, addition of FBS increased CCN1 by 2-fold and 3-fold, respectively, after a 2-hr or 24-hr-serum starve. In contrast, for human granulosa cells, compared to the absence of FBS, addition of FBS increased CCN1 by 8- and by 5-fold, respectively, after a 2-hr or 24-hr-serum starve. While both cell types responded to FBS, the magnitude of CCN1 increase varied between them, perhaps due to species differences.

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Maternal Aggression and Nestmate Interactions in a Facultatively Social Bee

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Eusocial species are known to be more ecologically dominant, but eusocial bees are rare in nature, with most bee species exhibiting solitary behavior. As major pollinators, bee activity is crucial for the maintenance of healthy ecosystems and human agriculture. Therefore, it is important to understand the mechanisms that lead to the evolution of eusocial species, such as the honeybee. The small carpenter bee, *Ceratina calcarata*, is subsocial (provides extended parental care), and thus represents an intermediate stage between social and solitary behavior. *Ceratina calcarata* mothers remain in the nest with their maturing brood and may produce a worker daughter to help care for their offspring. Parental care and maternal manipulation of brood have been suggested as possible mechanisms for the evolution of social behavior. Here, observation nests were used to establish behavioral profiles, based on foraging and provisioning behavior, and nestmate interactions, in an effort to compare both solitary and social nests in *C. calcarata*. This work aims to reveal the role that the mother plays in establishing a simple social nest.

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Does Basic Fibroblast Growth Factor (FGF2) Regulate the Expression of the Angiogenic Inducer (CCN1) in Bovine Luteal Cells?

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Angiogenesis, the building of a new blood vessel network from an existing one, is mediated by a variety of factors including Cysteine rich 61-Connective tissue growth factor-Nephroblastoma overexpressed 1 (CCN1) and basic fibroblast growth factor (FGF2). These factors are present in the bovine corpus luteum (CL), and both bind to heparin sulfate and glycosaminoglycans in the extracellular matrix. It has also been reported that CCN1 is upregulated by FGF in fibroblasts. Thus, for the present study, we asked- *Is CCN1 expression regulated by FGF2 in bovine luteal cells?* Bovine luteal cells from early and mid-cycle CL were seeded at approximately one million cells and cultured in six-well plates containing Ham's F12 + insulin/transferrin/selenium (ITS) for two days until about 60% to 80% confluency. Cells were then treated with FGF2 (1 or 5ng/mL) for 2 or 24 hours. Afterwards, total RNA was extracted followed by cDNA generation. Lastly, quantitative polymerase chain reactions (qPCR) were performed to analyze CCN1 messenger RNA levels. For early and mid-cycle cells, preliminary analysis revealed no effect on CCN1 expression after treatment with either concentration of FGF2 for 24 hours. A similar effect was observed for early cycle cells at 2 hours. However, it appears that treatment with 1ng/mL FGF2 in mid-cycle cells may increase CCN1 expression after 2 hours. Additional replicates are needed to confirm these findings.

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Quantification of Histone Modifications of Neural Progenitor Cells

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Histone modifications play an essential role in the regulation of gene transcription. Our ever growing knowledge of the "histone code" has contributed to the understanding of how histone modifications alter chromatin structure and regulate the establishment of different cell types.[1] The highly coordinated and dynamic nature of histone modifications allows for investigation into the role that they play in cell differentiation and the establishment of different cell lineages.[2] The transformation of pluripotent embryonic stem cells into definitive neural progenitor cells will allow for investigation and mapping of this cell line's unique histone modifications. Quantifying the histone modifications from this cell line will allow for comparison to modifications of other cell lineages to create a comprehensive modification map. From this information it is possible to determine which modifications are essential in the establishment of cell identity. This project will aim to determine how epigenetic states regulate the transformation of cell types and organize the genome for a cell-type specific transcription profile.

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The role of small reservoirs in reducing reactive N export via denitrification

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Reactive Nitrogen (N), which can harm ecosystem health, has been increasing in the biosphere, leading to higher N export to coastal ecosystems. Although man-made reservoirs have been cited as significant sources of greenhouse gases, they have also been shown to retain N, thus reducing N export. Because many dams are relics from hydropower, removal is becoming increasingly common. It is therefore crucial to understand the ecological impacts of man-made reservoirs. While previous studies have examined nutrient budgets and denitrification at inputs and outputs of large reservoirs, internal and small reservoir dynamics remain understudied. In this study, we measured inputs and outputs of NO_3 and N_2 at two small reservoirs and assessed reasons for changes with internal sampling. We hypothesized that denitrification is occurring more in reservoirs compared to channels due to lower dissolved oxygen. We found evidence of denitrification in all inputs and in one of the two reservoirs, but found evidence of N fixation in the other reservoir. Fixation occurred with low NO_3 concentrations and high algal growth, suggesting that NO_3 was being assimilated and used for growth, rather than denitrified. In this case, reservoirs may actually be a source of additional N. As dam removal decisions continue, the role of reservoirs in reactive N export should be carefully considered.

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Biological Applications of NMR Spectroscopy

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Protein Nuclear Magnetic Resonance (NMR) spectroscopy is a powerful tool to study protein structure, function, and dynamics. We have been using NMR spectroscopy to characterize protein structure, protein-ligand, and protein-protein interactions, on three different proteins: the inhibitory gamma subunit (Pgamma) of photoreceptor phosphodiesterase (PDE6), the polar organizing protein Z (PopZ), and the regulator of G protein signaling 8 (RGS8). Preliminary structure calculation for Pgamma and PopZ have been performed based on multidimensional NMR data. The effect of amino acid substitution on ligand binding affinity is being studied through comparison of wild type RGS8 versus the C160S mutant variant of RGS8 using titration experiments.

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The Effects of Methamphetamine on Histone Modifications.

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Epigenetics is the study of inheritable changes in phenotype without an alteration in the sequence of genomic DNA. Post-translational modifications (PTMs) on histones, major chromatin proteins, lead to alterations in the organization of nucleosomal arrays and the accessibility of transcriptional factors to DNA. Studies have shown that these changes play a role in many biological processes, affecting memory, cognition, aging, addiction, and neurodegenerative diseases. Methamphetamine (METH) is a highly addictive psychostimulant with both physical and social impacts. This drug's effects on the central nervous system are far greater than any amphetamine, causing the release and preventing the enzymatic breakdown of neurotransmitters such as dopamine, norepinephrine, and serotonin. Previous studies on a few selected histones have revealed changes in global histone modification levels in rodents upon METH exposure. This project will study the effects of METH on post-translational modifications on histones H3 and H4 in the striatum in an unbiased and systematic manner, with the rat as a model. The striatum is highly involved in drug addiction and produces enough proteins for in-depth biochemical analysis. We hypothesize that prolonged exposure to METH will lead to an altered epigenome and histone state in the striatum of the rat brain, and therefore a persistent change in behavior. This will be elucidated through the comparison of histone PTMs in the striatum tissue of saline- and METH-treated rats. The histone proteins will be extracted from the tissue, separated, and analyzed via mass spectrometry. These findings will further the current understanding of the impact of addictive drugs in epigenome remodeling, while also elucidating potential therapeutic targets for future studies.

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A Freshwater Lake on a Maritime Island: The First Limnological Assessment of Crystal Lake

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Crystal Lake, located on Appledore Island in the Gulf of Maine, is a small, shallow, freshwater lake. This study represents the first comprehensive limnological assessment of the physical, chemical and biological components of the lake. Changes in pH, dissolved oxygen, temperature, nutrient concentrations, plankton, and associated pigments were monitored for 14 weeks, from June to mid-September. The lake is considered eutrophic with elevated levels of nitrogen and phosphorus. The zooplankton community experienced a shift from one that was dominated by *Asplanchna*, a predatory rotifer, to one dominated primarily by grazers. The phytoplankton community shifted from one dominated by large green algae during the early summer to one that included colony-forming species of cyanobacteria. Increases in phycocyanin concentrations from 2.26 µg L-1 to 106.3 µg L-1 corresponded with the increase in cyanobacteria, including a late-season bloom of *Microcystis*. The cyanotoxin microcystin produced by these cyanobacteria was also found to be present with concentrations exceeding those found in other state-wide surveys in New Hampshire. Overall, results from this study highlight the importance of consistent, long-term monitoring of freshwater ecosystems. Within the Isles of Shoals, there is a clear need for more comprehensive study of the potential risks of exposure to wildlife that rely on Crystal Lake as an important freshwater resource.

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Evaluating the Efficiency of Glass Fiber Filters in Cyanotoxin Aerosol Collection

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Toxic aerosols released from lakes with cyanobacteria represent a potential threat to wildlife and humans. In the current aerosol collection system, glass fiber filters collect aerosolized particulate matter while Milli-Q water traps collect aerosolized dissolved toxins. However, the effect of the filters on the total amount of toxins measured is not well understood. To determine the effect of the filters, six flasks with lake water were tested over a six-hour period. Three flasks had both a Milli Q water trap to collect aerosolized dissolved toxins and a glass fiber filter to collect aerosolized particulate matter while three flasks had only a Milli Q water trap. The experiment was repeated four times with water from York Pond, Willand Pond, Crystal Lake, and Old Durham Reservoir. Toxins were tested in the lake water fractions, the Milli Q Traps, and the glass fiber filters. Toxin levels in the Milli-Q traps suggest that glass fiber filters may be increasing the total toxins collected in the traps. However, more experimentation is needed to confirm the trend and determine the mechanism.

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Finding Alternative Ways to Synthesize Precursors for Small Molecule Inhibitors of β-lactamase Enzymes

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Antibiotic-resistant bacteria have become a challenge for medical providers when treating bacterial infections. Many of these acquired resistance phenotypes are due to β-lactamase enzymes, which when present in bacteria, are responsible for hydrolyzing the four-membered ring in β-lactam antibiotics, rendering them inactive. *Staphylococcus aureus* is one of the many bacterial species that has acquired resistance to penicillin via β-lactamase activity. The resistant strain is better known as methicillin-resistant *Staphylococcus aureus* (MRSA). Various organic compounds were synthesized for the development of small molecule inhibitors of β-lactamase enzymes. The synthesized compounds were then analyzed via thin-layer chromatography (TLC) and nuclear magnetic resonance (NMR) spectroscopy. The goal of this research is to regain anti-microbial activity when using penicillin to treat *Staphylococcus aureus*. One of the many challenges that this research faced is synthesizing molecules efficiently and with clean reactions. Therefore, a literature review was conducted to find alternative ways in which precursors for inhibitors of β-lactamase enzymes could be synthesized more effectively and successfully.

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Transgenic *Arabidopsis thaliana:* The Synthesis of Human α-Galactosidase-A

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Enzyme replacement therapy has become a standard technique for many diseases including Fabry Disease. Fabry Disease is the result of a loss of function mutation in the human enzyme alpha-galactosidase A (hGLA). Without the ability to degrade a group of glycosphingolipids, they build up in the body and cause symptoms such as angiokeratomas, cardiomyopathy and early onset stroke. Therefore, the ability to effectively treat individuals with this disease can be life-saving. The current method of enzyme replacement therapy (ERT) utilizes synthetic, functional hGLA protein administered to patients intravenously. However, the current protocol uses animal cell cultures to synthesize hGLA, which is a very costly (the treatment cost is >$200K/year/patient). The goal of our research is to test the efficiency of producing hGLA in plants using *Arabidopsis thaliana* as a model bioreactor, and assess the functional properties of the enzyme thus produced. Two previous undergraduate students in our lab produced the transgenicArabidopsis plants that I am using. They had tested the plants for the presence of the gene. We then began by producing 5 generations of these plants. My next objective was to determine if the h*GLA*gene is being expressed to produce a functional enzyme. Further research will focus on the ability to purify the enzyme and compare its physiological properties with the currently available commercial protein.

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Developing *Galleria mellonella* as an infection model for virulent mutations in *Vibrio parahaemolyticus*

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Vibrio parahaemolyticus a bacterium found in marine and estuarine environments is the most common cause of seafood-borne bacterial gastroenteritis. *V. parahaemolyticus* has two type III secretion systems (T3SS) that deliver toxins into host cells. All strains harbor an ancestral T3SS1 that plays no role in human infection, whereas most human pathogenic strains have an acquired T3SS2 which is strongly linked to disease and is located in one of three known Vibrio Pathogenicity Islands (VPaI): VPaIα VPaIβ and VPaIγ. T3SS1 and VPaIα T3SS2 toxins are known whereas the toxins produced and delivered by T3SS2 from VPaIγ have not been identified. The goal of this project was to evaluate the utility of *Galleria mellonella* larvae (greater wax moth) for assessment of toxin production and delivery by T3SS1 and T3SS2. *G. mellonella* show similarities to the mammalian innate immune system and could provide visible differences in health related to the amount of toxin production and delivery by *V. parahaemolyticus*. To evaluate the utility of the model for quantifying effects of T3SS effectors, we generated mutations in T3SS1 and T3SS2 and determined their impact on animal health. Loss of T3SS1 and T3SS2 significantly reduced toxicity of *V. parahaemolyticus*. *G. mellonella* could be an invaluable tool for identification of specific toxins and other secretion systems that may play a role in human infection and disease.

3

Using Comparative Transcriptomics to Analyze Differences between Lung Cancer, Colorectal Cancer, Acute Myeloid Leukemia, and their Respective Healthy Controls.

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Lung cancer is the second most common cancer in both men and women and is the leading cause of cancer-related deaths. Colorectal cancer is the third most common cancer diagnosed in men and women and the fourth most common cause of cancer-related death. In contrast, acute myeloid leukemia is the most common leukemia in adults, can be triggered by prior chemotherapy, and is usually fatal. By using bioinformatics, differential gene expression analysis can be used to identify dysregulated cellular pathways that are crucial to cancer development and survival. Ultimately, this can be used to guide drug discovery efforts to develop better therapeutics to treat these deadly malignancies.

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Sympatric Evolution of *Vibrio fischeri* strain H905 to Potential Pathogenicity from a Mutualistic Lineage

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Vibrio fischeri is a symbiont of the Hawaiian bobtail squid, *Euprymna scolopes.* Although different strains of *V. fischeri* can colonize *E. scolopes*, some strains may live in a non-symbiotic state. Strain ES114 is the model organism for symbiosis whereas close relative H905 is a poor symbiont. Genomic comparison revealed strain H905 contains two mobile elements known as pathogenicity islands (PAIs) that are absent in ES114. This led to the hypothesis that H905 evolved to a non-symbiotic, potentially pathogenic niche. One PAI contains genes encoding an RTX-like toxin, which typically forms pores in eukaryote cell membranes, a hemolysin-like toxin that is cytotoxic to yeast, and a predicted toxin secretion system. The other PAI contains a type six secretion system (T6SS), which some symbiotic *V. fischeri* use to kill competitors. H905 does not kill ES114, but a distantly related symbiont strain, EM17, with the same T6SS toxin allele does kill ES114, implying either that there are differences in production or secretion of this toxin or there are other T6SS effectors. Next, we will test cytotoxicity to assess the pathogenic potential of wildtype H905 and PAI toxin knockouts against a human intestinal cell line and potential eukaryotic predators. Though H905 and ES114 inhabit the same environment, the poor symbiotic capacity and novel genome content of H905 indicate sympatric evolution to a potentially pathogenic niche.

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Recombinant Expression, Purification and Antimicrobial Activity of Mammalian Antimicrobial Peptides in *E. coli*

Subhash C Minocha, Kali Elizabeth Scott

Antibiotic resistance is a growing global health concern. As pathogens evolve and adapt to their environments, resistance to selective pressure arises naturally. Over decades of widespread antibiotic use in medicine and agriculture, the lethal dose for certain malicious pathogens continues to increase – and in some cases, pathogens have evolved beyond the known lethal dose of most antibiotics. Thus, there is a global need for alternative methods of treatment for diseases caused by microbial infections. With new research on the naturally-occurring antimicrobial peptides in our own body, there is hope to treat infections the way nature has been doing. Antimicrobial peptides (AMPs) are small proteins produced naturally by all life forms. These peptides are part of our innate immune system and have been demonstrated to kill a wide variety of bacteria not only within the host organism, but also have broader targets in related organisms. Unfortunately, their concentrations in the host are rather low. If natural mammalian AMP's can be produced in transgenic organisms such as bacteria or plants, they are likely to become an important new group of pharmaceutical compounds to replace or supplement traditional antibiotics. Our research is aimed at investigating the potential of a recombination DNA pathway to produce two Human Keratin 6 (K6A) and two horse AMPs, DEFA1 and eCATH1, in bacteria and eventually in plants. Our multimeric expression strategy generates a chain of six linked AMPs and we hypothesize this design to reduce the toxicity of the protein product to the host organism. Production of these mammalian AMPs in transgenic organisms such as *E. coli*will allow for clinically relevant quantities of the peptide to be synthesized in a cost-effective manner, thus, allowing for the advancement of research in clinical uses of antimicrobial peptides.

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Gene Dosage May Explain Phenotypic Differences Between Mutants in *Arabidopsis*

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Protein phosphatase 2A (PP2A) is an enzyme that removes phosphate groups from proteins and is involved in signal transduction pathways in plants and animals. As one of the most abundant phosphatases in eukaryotes, PP2A plays critical roles in responses to light and to multiple hormones and also regulates key enzymes of primary metabolism. The PP2A heterotrimer consists of one A subunit (scaffolding), one B subunit (regulatory), and one C subunit (catalytic). Five distinct isoforms of the C subunit of PP2A are encoded within the genome of the plant *Arabidopsis thaliana*. The C3 and C4 proteins are almost identical and both are expressed in roots, but *c3* and *c4* mutants respond differently to salt stress. Cells of *c4* mutant roots are twisted while the cells of *c3* mutant roots remain straight like wildtype roots. We hypothesized that variations in gene expression might account for the phenotypic differences between *c3* and *c4* mutants. A hybrid gene consisting of the *C4* promoter driving the expression of the *C3* gene (*C4::C3*) was constructed and transformed into *c4* mutants. This transgene tests whether the *C3* coding sequence, when expressed from the *C4* promoter, can complement loss of the *C4* gene. Some of the transformants had straight roots. Genotyping of the transformants is in progress to see if straight roots correlates with presence of the transgene.

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Analysis of Phytoestrogens in Legumes through HPLC

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Phytoestrogens are components that are naturally occurring in forages and legumes, and that have been associated with both beneficial and detrimental health effects on humans and animals. Within the phytoestrogen family, major groups are: isoflavones, prenylflavonoids, coumestans, and lignans. In this work, isoflavones and coumestans are going to be the focus. To analyze these phytoestrogens, a high-performance liquid chromatography (HPLC) will be used. We will be analyzing these phytoestrogens found in soybeans, alfalfa, white clover, and red clover. First, a custom-made hydroponics system will be designed to grow these plants, which will allow collecting clean roots for analysis. Then, extraction procedures for different plant tissues and parameters for HPLC analysis will be optimized. This study is ongoing, with the ultimate goal of analyzing both plants and foods containing phytoestrogens, that can result in being consumed by animals and humans.

67

Effects of Dams on Water Quality

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With over 800,00 dams in the world, rivers are being strongly altered. With the construction of dams, biodiversity and river quality is affected. Dams have a significant impact on stream water quality including; temperature, dissolved oxygen and specific conductance. We quantified the effects of dams by measuring specific conductance, dissolved oxygen and temperature at three different dams (Mill Pond, College Woods, and Exeter River) in coastal New Hampshire. Measurements were made just upstream and downstream of the dam. We hypothesized that each variable would increase below the dam because with temperature going through the dam would give it more energy, ultimately making it hotter. With dissolved oxygen, going over the dam will mix more oxygen into the water. Lastly, with specific conductance more energy will be put into the water, allowing energy to flow in and out of the water more easily. Measurements indicate that there was little to no significant change for any of the three characteristics. This suggests that there is no different in stream water quality upstream and downstream of dams.

100

The Impact of Ocean Acidification on the Olfactory Abilities of *Homarus americanus* During Prey Acquisition

Winsor H Watson, Nathaniel N Spada

Olfaction in some aquatic species, like sharks and crayfish, has been shown to be impaired by acidification. Because olfaction is a key sense required in prey acquisition there is concern that this could lead to population declines. The goal of this project was to determine if ocean acidification influenced the ability of the American lobster, *Homarus americanus,* to locate food or bait. The natural pH of the Gulf of Maine ranges between 7.9-8.1, and ocean acidification estimates suggest that the pH of the ocean may decrease to as low as 7.5. To test the impact on olfaction of the American lobster, two systems were set up; a control tank with natural pH levels and an experimental system where CO_2 was added to lower the pH to 7.5. Individual lobsters were put into each system and provided with a shelter. A small piece of herring, which is used for bait in lobster traps, was put in small canisters that were then were placed inside each tank and a time lapse camera was used to record the time it took the lobster to find the cannister and the handling time. Then a week later the experiment was repeated, but the lobsters were placed in the opposite tanks. Our preliminary data indicate that acidification lowers the olfactory abilities of lobsters but does not completely block it. These results suggest that we should be concerned that ocean acidification could impact the ability of lobsters to find natural prey and be attracted to lobster traps.

63

Effect of Plant Cultivar on Efficacy of Biochemical Inducers for Suppression of Plant Diseases

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A major challenge in sustainable agriculture is development of non-toxic alternatives to traditional pesticides. Biochemical pesticides are naturally occurring substances which control pests through induction of natural plant defense mechanisms. Several studies have reported on the ability of biochemical pesticides to reduce disease on multiple crops. It is documented however, that plant genotypes respond differently to biochemical pesticides. The objective of this research was to evaluate the effect of plant cultivar on biochemical pesticide efficacy to suppress disease using apple and cucumber. Three experiments were conducted to evaluate Regalia®, Lifegard™, Actigard®, Pipecolonic Acid, and Hexanoic Acid. A foliar spray of these inducers was tested on four cucumber cultivars for suppression of Powdery mildew in a RCBD with 5 replicates. Foliar spray and drench applications were tested in suppression of *Erwinia amylovora* on four apple scion/rootstock combinations with 5 replicate trees per treatment. A significant effect of cultivar on suppression of powdery mildew was observed on cucumber. However, the efficacy of inducer to suppress fire blight symptoms was not affected by apple cultivar. Actigard® significantly suppressed powdery mildew on three of the four cucumber cultivars. More replications are needed to determine the effect of cultivar in both systems on biochemical pesticide efficacy.

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Effect of Feeding Strategy on Striped Bass Growth Cultured in Recirculating Systems

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Striped bass are a commercial and recreationally important species that have been widely cultured as a food and gamefish for decades. Recent expansion of this industry necessitates the need for detailed feeding protocols at different life-stages. Altering feeding methods such as ration size and frequency of delivery has proven effective for improving feed efficiency in many species within commercial aquaculture. The present study was performed in two separate trials to evaluate feeding strategies with juvenile striped bass in indoor recirculating systems by manipulating frequency and ration size to maximize growth performance.

72

Evolutionary Genomic Insights on Novel Trait Evolution in Hagfish

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Hagfish are a group of jawless fishes that broke off from the rest of fish early in the evolution of vertebrates. As such, hagfish are quite distinct in comparison to other fish. Novel to the hagfish are the slime glands which run along the sides of the fish and secrete sticky slime in response to predation attempts. Slime glands are a unique evolutionary trait that have developed only in hagfish, so understanding the evolution of these glands may elucidate something about how novel structures arise. Additionally, this study aims to discover if hagfish possess the *T1R* taste receptor gene. The *T1R* gene appears in many animals, including invertebrates, but has been lost in the closely related lampreys, so it is unknown if hagfish possess the gene. Results will be obtained by extracting RNA from slime glands and sensory barbels and converting the RNA into DNA for sequencing. Genes found in the processed DNA will be compared to a database of genes to uncover the function of the genes. With these results, the evolutionary history of slime glands and the possession or lack of the *T1R* receptor in hagfish can be determined.

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Gdf1 Regulates Sphingolipid Metabolism in Acute Myeloid Leukemia

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Acute myeloid leukemia (AML) is a hematological cancer with a very low 5-year survival rate compared to most other cancers. AML is characterized by the uncontrollable growth and lack of differentiation of hematopoietic stem cells. Irrepressible proliferation of said stem cells monopolizes nutrients and prevents the growth of normal blood cells that the body needs to survive. Although treatment is available, it is limited. Sphingolipids are essential cell signaling molecules that regulate cell survival as well as cell death. Pro-apoptotic ceramide levels are less than normal in cancer cells due to atypical upregulation of ceramide neutralization enzymes. The growth differentiation factor 1 (Gdf1) protein activates TGF beta receptors in the cell, recruiting SMAD transcription factors that regulate stem cell development. Preliminary research has shown that treatment of AML cells with decitabine, a chemotherapeutic commonly used to treat myelodysplastic syndromes, results in the upregulation of *Gdf1*, suggesting that *Gdf1* is under epigenetic control. Additionally, prior studies have shown that abnormal downregulation of *Gdf1* expression may be correlated with an increase in the expression of ceramide neutralization enzymes, suggesting an inverse relationship. This study evaluated the direct effects of recombinant *Gdf1* expression on sphingolipid metabolism and AML.

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Winter Tick Parasitism of Moose: Influence on Adult Cow Productivity and Winter Calf Mortality

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Moose (*Alces alces*) in New Hampshire have experienced slow population decline in the last decade. The principal cause is from the effects of the winter tick (*Dermacentor albipictus*) that has caused epizootics (>50% mortality of 10 month-old calves in March-April) and reduced productivity of yearling and adult cows. As part of a larger research effort to investigate the impact of winter ticks, we measured birthrates of 35 radio-collared adult cows and summer calf survival in northern New Hampshire. We also measured tick loads on hides collected from 10-month old calves dying in March-April. Productivity measurements required field monitoring from mid-May through July using radio-telemetry techniques to stalk and directly observe the study animals. Tick loads were measured by complete counts of 50% of each hide (n = 9). The calving rate was 60% which was lower than the range in 2014-2017 (73%-78%). Calf survival rate to July 1 was 66%, slightly lower than that measured in 2017, but within the 5-year range (64%-93%). As in past years, neonatal mortality was concentrated in the first week of life, after which, survival was >90% until March-April. The average tick load measured on hides of deceased calves was 35,691 (range =17,412-49,414). This range was similar to that measured in past years and is sufficient to induce mortality from acute anemia associated with concentrated massive blood loss and protein imbalance. Our data corroborate the individual and population impact of winter ticks on moose.

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White-Nose Syndrome: Analysis of the Microbiome in infected and non-infected *Eptesicus fuscus*

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Over the past decade, several bat species living in the Northeastern United States have suffered a dramatic decline in populations due to White-Nose Syndrome, a fungal infection caused by *Pseudogymnoascus destructans*. However, the susceptibility to infection is largely unknown. My research project focuses on *Eptesicus fuscus*, commonly known as the big brown bat. I will focus on exploring the microbiome of infected and non-infected *E. fuscus* bats found in 10 different states between 2011 and 2016. Specifically, I will be comparing the bacterial species detected in pairs of infected and non-infected bats found in the same cave. From this comparison I hope to discover if a difference in microbiome content affects the infection rates in *E. fuscus*.

81

How Surrounding Landscape Composition Effects Avian Diversity within Shrubland Habitat Patches

Michael C Thompson, Matthew David Tarr

Shrubby transmission line rights-of-way (ROW) and clear cuts provide important habitat for numerous species of songbirds that require shrubby habitat for nesting. In recent years this habitat has been declining and increasing work is being done to protect these shrublands. These habitat patches are incredibly important to a wide variety of both shrubland-obligate bird species and, non-shrubland birds that occupy neighboring habitat types. As a result, these surrounding habitats may influence bird abundance and diversity within shrubland habitat patches. With our human population expanding and development increasing, it is important that landscape composition surrounding shrubland patches be considered when creating and conserving shrublands. However, the distance at which the surrounding landscape effects avian diversity within shrublands is still unknown. My research used two years (2017-2018) of shrubland bird banding data collected in shrubby ROW and clearcuts in southern NH and ME to determine how landscape composition around shrublands influences bird diversity within these patches. ArcGIS was used to build four landscape buffers (100m, 250m, 500m and 1000m) around each shrubland and I quantified the proportion of each buffer composed of 13 predominant habitat types. We are using our bird banding and landscape composition data to develop predictive models that identify the habitats and landscape buffer distance that best predict bird diversity and abundance in shrublands. This research will not only help land managers be better informed when making recommendations for implementing new shrubland cuts but also when deciding how to manage surrounding habitats. Landowners that don't have shrubland patches on their property could still impact these important habitats far more than we realize.

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Greenhouse gas ebullition in streams of varying watershed land use and sediment composition

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Wetlands, lakes, and streams are significant contributors to global carbon (C) and nitrogen (N) cycles, and major sources of greenhouse gases (GHGs). Although previous studies in streams primarily focused on diffusion fluxes, my study quantified ebullitive (bubble) emissions, which may also be important. I compared two streams of differing dominant land use and sediment composition in the watersheds of the Plum Island Ecosystems-LTER (PIE-LTER). I installed twelve inverted funnel style bubble traps at each of the two study sites to capture gas from ebullition. I also collected gas bubbles via intentional physical disturbance of the channel beds to calculate GHG concentrations in the bubbles and flux rates of CO_2, CH_4, and N_2O. I also characterized sediment composition of each stream using organic content and particle size analyses. My findings indicate significant methane flux rates via ebullition in these urban and forested streams (0.01-13.77 mmol C/day) and high concentrations of methane in gas bubbles (1-53% CH_4) that are similar to findings of previous ebullition studies in wetland streams in other regions (Crawford et. al, 2014). Therefore, my findings suggest that GHG emissions via ebullition need to be considered not only in wetlands and lakes, but also in rivers and streams. Although I found no significant correlation in the measured bubble rates and sediment composition, my data suggest that major disturbances, such as storm flow events, or rapid air pressure or temperature changes are more likely to cause ebullition, suggesting short-term temporal variability may be important. Further research may explore other mechanisms leading to significant ebullition rates and greenhouse gas fluxes from streams.

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Dynamic Causal Modeling of the Speech Network in Stroke-Induced Apraxia of Speech

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Apraxia of speech (AOS) is a motor speech disorder caused by the inability to effectively translate kinematic parameters required for speech production (McNeil et al., 1997). In adults, it is typically caused by a left hemisphere stroke, though a progressive form exists as well. Little is known about the underlying neuropathology of the disorder. Three key regions of interest are hypothesized to be associated with apraxia: the bilateral inferior frontal gyrus (IFG), premotor cortex (PM), and anterior insula (aINS). Previous work quantified resting state functional MRI network functional connectivity strengths between these regions and found that AOS was defined by reduced connectivity strength between left and right PM cortices as well as negative connectivity between left PM and right aINS. In order to enhance our understanding a primary network underlying AOS, the resting state fMRI data from 31 human subjects with history of left hemispheric stroke (15 with AOS, 16 non-AOS) was further modeled here. This investigation used a Bayesian-based modeling approach, dynamic causal modeling (DCM), to determine the causal relations among the previously mapped regions. In support of our hypothesis, findings indicate that the PM, not the IFG, is the node responsible for driving connectivity strength and direction. These data support involvement of the regions of interest previously described (bilateral PM and aINS) and further define the nature of that relationship, more specifically informing a neurobiological model of AOS that may fuel future investigations and treatment methods and/or outcomes.

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Use of the Plasma Free AA Dose-Response Technique to Quantify Bioavailability of Rumen-Protected Histidine

Nancy L Whitehouse, Bailey B Veilleux, Andre Fonseca De Brito

Rumen-protected (RP) Met, Lys, and His have been added to diets for optimizing milk protein synthesis and reduce N excretion to the environment in lactating dairy cows. Therefore, it is critical to accurately estimate the relative bioavailability (RBV) of RPAA supplements. The plasma free AA dose-response technique has been used to determine RB of RP-Met and RP-Lys, but not RP-His. Our objective was to determine the RBV of a prototype RP-His supplement (Ajinomoto Co., Inc, Japan) using the plasma AA dose-response method. Six multiparous Holstein cows fitted with ruminal cannulas were used in a 6 × 6 Latin square design with 7 d experimental periods. The basal diet consisted (DM basis) of 31% corn silage, 20.4% haylage, and 48.6% concentrate. The diet was 16.4% CP, 177 g/d MP, and 3.5 Mcal/d NE_L. Treatments were abomasal infusions of His at 0, 8, 16 and 24 g/d, and 20.2 and 33.6 g/d of RP-His (42% His in the prototype). Blood samples were collected at 2, 4, 6, and 8 h after the morning feeding in the last 3 d and composited by day. Plasma AA was quantified using ultra performance liquid chromatography tandem mass spectrometry. Data were analyzed with the MIXED and PROC REG procedures of SAS. Both DMI and milk yield were not affected by treatments. Plasma His concentration linearly increased from 49.1 to 79.2 μ*M* in response to incremental amounts of His infused in the abomasum. Feeding RP-His also elevated the concentration of plasma His in a linear manner (49.1 to 66.8 μ*M*). Plasma carnosine concentration showed linear responses to both abomasal infusion of His (14.4 to 16.2 μ*M*) and RP-His supplementation (14.4 to 16.2 μ*M*). Treatments did not significantly change the concentrations of other plasma AA. The slopes from regressing plasma concentration of His (%TAA minus His) on incremental amounts of abomasally infused His or RP-His averaged 0.044 and 0.021, respectively. The RBV of the prototype RP-His tested averaged 48 ± 3.2% (0.021 divided by 0.044 times 100). Our data suggests that approximately 48% of His in RP-His was absorbed in the small intestine when using the plasma free AA dose-response technique.

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Bioinformatic Analysis of Staphylococcus pseudintermedius Genomes, an Important Bacterial Pathogen in Pet Animals

Sean M Vigeant, Cheryl Marie P Andam

Staphylococcus pseudintermedius is the most common bacterial pathogen involved in ear, skin, and postoperative infections in cats and dogs. Although it does not commonly infect humans, methicillin resistant strains have been isolated from animals. Unlike the more well-studied human pathogen Staphylococcus aureus, the diversity and genome structure of S. pseudintermedius is poorly understood. My project aims to investigate the genomes of 141 genomes strains of S. pseudintermedius from the National Center Biotechnology Information (NCBI) and elucidate the phylogenetic relationships, pan-genome structure and evolutionary history of this species. Using bioinformatics software, all available genomes from the NCBI database were analyzed to determine core and accessory genomes among that population. Prokka and Roary will be used to annotate the genomes and determine core and accessory genes. FastGEAR will be used to determine the highways of recombination between strains. Using R, rhierBAPS will organize the genomes into clusters of similar strains to determine the presence of subspecies. PopPUNK will define each strain based on core and accessory gene distance distribution. RaxML will be used to determine evolutionary lineages among the genomes, and this data will be visualized using the iTOL server. These results will provide important insights into host adaptation, pathogenicity and emergence of antibiotic resistance in this important animal pathogen, which can have important consequences to human health.

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Occurrence of Blood Parasites in Raptors, Waterfowl, and Seabirds Admitted for Wildlife Rehabilitation in the Northeast, United States

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Altered disease dynamics are among the biosphere's responses to global climate change. Many species, including hosts and vectors of disease, will expand their ranges, which can result in exposure of wildlife to novel pathogens. Parasites can become pathogenic, causing disease and mortality of their hosts, and in extreme cases may result in wildlife population declines. There is surprisingly little recent research about the occurrence of wildlife blood parasites in the Northeast, which is undergoing change faster than many other regions of North America. To help establish a baseline, we investigated the prevalence of blood parasites, from the order Haemosporidia, in three groups of avian hosts commonly admitted to the Center for Wildlife (Cape Neddick, Maine) for rehabilitation. By microscopy of blood smears, taken from a total of 170 individuals, belonging to 19 bird species, we determined both occurrence and intensity of parasitemia of three Haemosporidian genera. We tested for differences in occurrence and parasitemia based on species group (raptor, waterfowl, seabird), sex (male, female), life stage (adult, subadult), and migratory status (migratory, non-migratory), as well as a suite of ecological traits and habitat associations. These data provide a much-needed baseline for future research, and our findings contribute to an emerging understanding of the prevalence of Haemosporidian blood parasites in wild birds of the Northeast.

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Effect of STAT3 Inhibition on Ovarian Cancer Mesothelial Clearance Ability

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Ovarian cancer is widely diagnosed in late stages where the five-year survivability is low. Of those diagnosed, the majority of ovarian cancers are epithelial. The metastatic pathway of epithelial cancer is conserved in the cancer. It involves the cancer cells dissociating from the primary tumor site into the abdominal cavity. Once free of the primary tumor, the cancer cells that survive aggregate into a floating mass called a spheroid. The spheroid then binds to the mesothelial cells that line the abdominal wall and begins to invade. This transition is called mesothelial clearance. As ovarian cancers need to first pass the mesothelial layer to metastasize, mesothelial clearance is a good model of metastatic ability. Studies have shown that signal transducer and activator of transcription 3 (STAT3) leads to a decrease in metastatic ovarian cancer cells though it is not known if this is through decreased mesothelial clearance. The goal of my research was to explore this gap in knowledge. The mesothelial clearance of spheroids was modeled with an LP-9 plated monolayer, onto which ovarian cancer spheroids with reduced STAT3 expression were added. The invasion of the monolayer was monitored for 24 hours and my data supports that inhibiting STAT3 results in a decreased mesothelial clearance ability of the spheroid. This suggests that targeting STAT3 may be useful to prevent or treat metastatic ovarian cancer.

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Designing a Biofilter to Remove Ammonia from a Commercial Scale Composting Facility

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Composting provides an environmentally friendly alternative to landfill disposal for processing organic waste material. Aerated static pile composting is a method of composting that pulls air through the compost to promote microbial activity, generating usable heat energy while also minimizing surface and groundwater contamination. While limiting some environmental impacts, this process still produces exhaust vapors with pollutants like ammonia that can impair local air quality. One potential solution to the problem of ammonia emissions is a simple woodchip and finished compost biofilter. These biofilters are cost efficient and easily installed. Biofilters work by removing NH3 as the exhaust vapors pass through it. Available literature on this process explores biofilters in lab-scale settings with low concentrations and does not consider commercial-scale facilities and higher gas concentrations. More research is needed to address the efficiency of biofilters at high concentrations, and the ideal ratio and size for effective NH3 removal.

The presentation will address construction, sampling methods, and NH3 removal results for two different organic biofilters. The biofilters are located at the UNH heat recovery compost facility at the UNH organic dairy research farm in Lee NH.

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Characterizing STAT3 Activity in Cisplatin-sensitive and -resistant Ovarian Cancer Cells

Brittnee L Wirth, Sarah R Walker

Ovarian cancer cell metastasis and migration often promotes the formation of malignancies in the peritoneum that are resistant to standard chemotherapies, and thus it is necessary to develop novel therapies to treat these malignancies. STAT3, a signal transducer and activator of transcription, is involved in normal cell proliferation and motility and regulates many genes, including SOCS3, BCL6, POLD4, and DEC1. Bioinformatic data from cisplatin resistant cells suggested that cisplatin-resistant ovarian cancer cells demonstrate enhanced STAT3 activity. Therefore, we wanted to determine the role of STAT3 in cisplatin resistance. Initial RT-qPCR data for OVCAR8 cisplatin-sensitive and -resistant cells demonstrated a difference in the expression of several STAT3 target genes, suggesting that STAT3 was enhanced in cisplatin resistant cells. We thus hypothesized that reducing STAT3 activity would sensitize cisplatin-resistant cells to the drug, decreasing their viability. Knockdown of STAT3 in this experiment was achieved with two constructs of siRNA targeting STAT3. We found increased apoptosis in cisplatin-resistant cells with STAT3 knockdown compared to cisplatin-sensitive cells. We are currently assessing the effects of STAT3 inhibition by siRNA and STAT3 inhibitors on sensitizing resistant cells to cisplatin. Understanding the role of STAT3 in cisplatin resistance may provide us with a new method to prevent chemotherapy resistance.

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The Role of Chitosan in Improving Plant Iron Deficiency Chlorosis

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Soybeans are a staple food in agriculture that contain significant amounts of Iron (Fe), an essential nutrient to plant and human health. The manipulation of nutritional content in agricultural products could enhance plant health and agricultural productivity. Growth efficiency is hindered by low Fe, causing Fe deficiency chlorosis (IDC), a state induced by ineffective absorption of Fe from the soil environment. A combatant to IDC to increase absorption of Fe would be beneficial in increasing crop yield, and food nutritional value for human consumption. Supplementation with chitosan, a derivative of chitin, has been seen to improve plant growth. Preliminary data suggests chitosan can improve IDC status in soybean plants. To study the role of chitosan improving IDC, soybean plants were grown in hydroponics under Fe sufficient and deficient conditions, with or without chitosan supplementation. Plant growth, internode length, and chlorophyll content were measured in plants grown for two weeks in hydroponics, and the role of chitosan supplementation in improving Fe status was assessed.

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Exploring the Potential of Marine Actinobacteria as Source of Novel Antibiotics

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New antibiotics are critically needed as resistance to our existing arsenal of drugs is growing. An important source of drugs or drug precursors with broad pharmaceutical application, including serving as the most effective antibiotics, are natural products produced by environmental microbes. The phylum Actinobacteria constitutes one of the largest and most diverse phyla, and are known to inhabit a wide range of ecological niches. They are well known for their ability to produce numerous bioactive compounds against a variety of human diseases, such as infectious diseases and cancer. This project seeks to address the urgent need to explore previously unrecognized sources of antibiotics in nature. Under the mentorship and supervision of Dr. Cheryl Andam (Assistant Professor, MCBS/COLSA), I propose to investigate the potential of Actinobacteria collected from marine samples to inhibit the growth of bacterial pathogens.

82

Impact of Nitrogen Inputs on Plant Composition at a New Hampshire Fen

Ruth K Varner, Michael L Zampini

Wetlands provide important ecosystem services to the environment. Along with hosting a wide range of species diversity, wetlands act as a natural filter and aid in nutrient cycling for the ecosystem as a whole. Wetlands help control flooding by acting like a sponge, retaining excess water and nutrients and effectively regulating water levels and purity. Nutrient like nitrogen in the form of nitrate (NO_3^-), nitrogen dioxide (NO_2), and total dissolved nitrogen (TDN) can lead to soil acidification, pollution, and N_2O emissions into the atmosphere. Increased nitrogen can also affect species composition in wetland ecosystems. Understanding influence of nitrogen inputs on the health and vegetation composition of wetlands is important for maintaining these environments.

The objective of this project was to study the change in species composition and below ground dissolved nitrogen at Sallie's Fen, a wetland located in Barrington, NH. This site has been the location of wetland research for over 30 years. Using previously collected datasets this project compared the concentration of dissolved nitrogen species from the past to samples collected and analyzed in summer 2018. Aerial photographs of Sallie's Fen and plant species composition surveys have been taken in the past to assess the vegetation cover in Sallie's Fen. In summer 2018, we completed another survey of vegetation composition across Sallie's Fen. This research aimed to aggregate these datasets (past and present) to (1) examine the changes in vegetation species composition over time and (2) correlate these changes to porewater nitrogen concentrations A k-means cluster analysis was used to group vegetation into categories and create vegetation maps. Porewater nitrogen data was compared to wetland plant species spatial distribution. We expect that the alder tree species (*Alnus spp.*), which has been observed expanding across the eastern side of Sallie's Fen, may be influenced by belowground available N. Nitrogen also promotes the growth of tree species such as Alder species increase water uptake and can begin a transition from wetland ecosystem to a tree dominated community.