RHODE ISLAND SUMMER RESEARCH SYMPOSIUM

2026

Friday, July 31, 2026

UNIVERSITY OF RHODE ISLAND

BEAUPRE CENTER FOR CHEMICAL & FORENSIC SCIENCES
FASCITELLI CENTER FOR ADVANCED ENGINEERING
PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY

Sponsored by

RHODE ISLAND INBRE
Biomedical Research Excellence

RI NEST
Rhode Island Network for Excellence in Science and Technology

RI-INBRE & RI NEST

2026 Rhode Island Summer Research Symposium

8:00 – 9:00 AM	**CHECK-IN & CONTINENTAL BREAKFAST** • BEAUPRE CENTER FOR CHEMICAL & FORENSIC SCIENCES **POSTER SET-UP** • FASCITELLI CENTER FOR ADVANCED ENGINEERING • PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY
9:00 – 9:30 AM	**WELCOMING REMARKS** • BEAUPRE CENTER FOR CHEMICAL & FORENSIC SCIENCES DR. MARC B. PARLANGE • PRESIDENT, UNIVERSITY OF RHODE ISLAND DR. KELLI J. ARMSTRONG • PRESIDENT, SALVE REGINA UNIVERSITY
9:30 – 11:00 AM	**POSTER SESSION A** • FASCITELLI CENTER FOR ADVANCED ENGINEERING • PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY
11:00 AM - 12:30 PM	**POSTER SESSION B** • FASCITELLI CENTER FOR ADVANCED ENGINEERING • PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY

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POSTER PRESENTATION SCHEDULE

*** PLEASE NOTE: Posters are to be set up prior to the welcoming remarks and should remain up until 12:30 PM. Posters are to be presented according to the schedule below.*

Session	Presentation Times
A	9:30 – 11:00
B	11:00 – 12:30

Poster numbers	Location
1-30 (A & B)	Fascitelli Center for Advanced Engineering, 1st Floor (FCAE – Toray)
31-56 (A & B)	Fascitelli Center for Advanced Engineering, Ground Floor (FCAE – Lower Level)
57-86 (A & B)	Paramaz Avedisian '54 Hall, College of Pharmacy (Avedisian)

NOTE: an Author Index is located at the end of this document

POSTER SESSION A

9:30 – 11:00 AM

Fascitelli Center for Advanced Engineering, 1st Floor
A-1 to A-30

Fascitelli Center for Advanced Engineering, Ground Floor
A-31 to A-56

Paramaz Avedisian ’54 Hall, College of Pharmacy
A-57 to A-86

AI-Assisted Design and Experimental Validation of 3D-Printed Terahertz Fiber Sensors for Biomedical Sensing Toward Early Cancer Detection

Matthew Doolittle[1], Cooper Thomas[2], Lukas Huffman[1], Andrew Fournier[1] & Ahmet Akosman[1]

[1]School of Engineering, Roger Williams University, Bristol, RI
[2]Physics, Brown University, Providence, RI

Terahertz (THz) technology has emerged as a promising platform for non-invasive, label-free sensing with potential applications in chemical analysis, biomedical diagnostics, and security. The development of low-loss waveguides capable of efficiently transmitting THz radiation remains a challenge for these sensing applications. In this project, hollow-core negative-curvature fibers are designed for THz sensing because they provide low propagation loss, strong light-matter interaction, and improved electromagnetic confinement. The proposed fiber sensors are designed and fabricated using resin-based stereolithography (SLA) 3D printing, providing a low-cost and accessible alternative to conventional fiber manufacturing techniques while enabling rapid prototyping. The fiber sensors are experimentally characterized using terahertz time-domain spectroscopy (THz-TDS) to evaluate their performance for sensing liquid analytes. The experiments focus on the implementation of the fabricated sensors, including the development of a cap that minimizes leakage, a low-loss cover, and a self-aligning optical stage to ensure THz beam centering. Experimental reference liquids include isopropyl alcohol (C_3H_8O) and ethyl alcohol (C_2H_6O), to establish baseline optical characteristics and a better understanding of the interaction between THz radiation and the fabricated sensors. The experimental results reveal that the low-loss THz transmission spectra shift with liquids in the core, confirming the sensor performance over wavelength intervals above 0.5 THz. Finite-element simulations are performed to validate the sensing spectrum in the experiments. The simulated optical characteristics are further analyzed using MATLAB-based machine learning models to predict fiber performance. The optimized sensor geometries exhibit reduced confinement loss and predict sensitivities approaching 98%, with correlation coefficients (R) exceeding 0.95 across the sensing spectral interval. The combination of experimental characterization, numerical modeling, and machine learning optimization provides a comprehensive framework for designing future THz biomedical fiber sensors. Studies of representative blood constituents, having refractive indices comparable to those of the reference chemical analytes, predict similar sensing performance in the proposed fibers. The results obtained from the chemical analytes establish the foundation for the experimental investigations of the blood constituents in the fiber sensors. This work demonstrates a framework for developing THz fiber sensors by combining additive manufacturing, terahertz spectroscopy, electromagnetic modeling, and machine learning, providing a pathway toward biomedical applications such as blood analysis and early cancer detection.

This work was supported by RI-INBRE

Characterizing Plastic and Non-Plastic Litter on Rhode Island, USA Beaches

Sabrina DiNovi[1], Sarah M. Davis[1], MC Cicenia[2], Andrew J. Davies[1,2] & Coleen C. Suckling[1]

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[2]Graduate School of Oceanography, University of Rhode Island, Narragansett, RI

Microplastics (MPs, <5mm) are a classification of pollutants pervasive in the environment. Although larger plastics (macroplastics, >20 mm) can accumulate in the environment, they eventually fragment into MPs, making cleanup increasingly difficult.This research examined whether identifiable plastic products could be used to trace sources of plastic pollution on Rhode Island (RI), USA beaches to assess the need for waste management strategies to reduce plastic litter that contributes to the formation of MPs. Identifiable plastic items may provide insight into whether litter originates from local beach use or is transported to shore by coastal processes before fragmenting into secondary MPs. Plastic litter was surveyed on 4 different beaches in RI spanning a north-to-south gradient. Litter was first categorized using protocols developed by the Surfrider Foundation, then further categorized as identifiable (can be traced back to their original product) or non-identifiable (unmarked plastic litter that cannot be traced back), and recorded both by total number of pieces and by mass. Preliminary data shows that identifiable plastics were found at all 4 beaches, with identifiable plastics representing an average of 17% of the total litter mass at the 3 more northern beaches. At the southernmost beach surveyed identifiable plastic accounted for 82% of the collected litter mass. The increased amount of identifiable plastic litter at the southernmost site suggests that this beach may be an important source of plastic beach pollution, however, more research needs to be done across beaches along the coast of Narragansett Bay to better understand plastic distribution in the bay. Plastic waste was additionally categorized into 5 groups for source comparisons (Tobacco, Food, Straws, Bottles, and other). Across all 4 beaches, the two highest categories of collected trash were food waste and tobacco waste products. This is important when discussing potential management strategies for beach litter as well as potential policies that could be implemented to help combat the spread of MPs found in our environment. By understanding where this litter comes from, we can be more accurate in how we enforce these potential policies and management strategies, and prevent the spread of MPs at the source.

This work was supported by SIMCoast

Ingestion and Accumulation of Microplastics in the Ribbed Mussel (*Geukensia demissa*)

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[1]College of the Environment and Life Sciences, University of Rhode Island, Kingston, RI
[2]Graduate School of Oceanography, University of Rhode Island, Kingston, RI

Microplastics (MPs, <5mm) are persistent pollutants that are increasingly present in marine and coastal ecosystems. Due to their small size, MPs can be ingested by filter-feeding organisms such as ribbed mussels (Geukensia demissa). As mussels filter large volumes of surrounding water, they can accumulate MPs from the water column and potentially transfer these particles through coastal food webs when consumed by other organisms. This study aimed to quantify and compare the abundance and composition of MPs in ribbed mussels collected along a north-south coastal gradient within Narragansett Bay, Rhode Island, USA, spanning the highly urbanized northern estuary to the less developed southern estuary. Fifteen ribbed mussels were collected from each of the four sampling locations, for a total of 60 mussels. Mussels were dissected and tissues analyzed using Laser Direct Infrared Spectroscopy (LDIR) for MP composition. MP abundance was also normalized to wet tissue weight and reported as MPs per gram of wet weight. Preliminary results demonstrated variation in MP abundance among the four sampling sites, with concentrations ranging from 72 - 520 MPs per individual and 3.9 - 35.5 MPs per gram wet weight. Site 1 (Bold Point Park, Providence RI) exhibited the greatest overall MP abundance. While Site 3 (Wickford Harbor, Wickford RI) had the lowest concentrations, indicating spatial variation in MP contamination across the sites and suggesting a potential influence of urbanization on MP contamination. Overall, the results suggest that ribbed mussels from different coastal locations are potentially exposed to varying levels of MPs which is reflected in their tissue concentrations. These findings provide a foundation for future studies investigating the factors contributing to site-specific MP accumulation, and the potential ecological effects of MP exposure on ribbed mussels and the organisms that consume them.

This work was supported by SIMCoast

Designing Molecular Gene Probes Using Bioinformatics and Molecular Tools to Detect the 'Presence' of *Pseudo-nitzschia delicatissima*

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Harmful Algal blooms (HAB) are caused by microscopic organisms that produce toxins which pose significant risks to marine ecosystems, public health and fisheries. Several species within the genus *Pseudo-nitzschia* are associated with HAB's, and they produce the neurotoxin domoic acid (DA) which accumulates in shellfish and causes Amnesic Shellfish Poisoning (ASP). In 2017 *Pseudo-nitzschia delicatissima*, a known DA producer, contributed to shellfish harvesting closures in Narragansett Bay, Rhode Island, and the recall of tons of shellfish due to the presence of DA. Current detection methods are slow, costly and require lab equipment. A cost-effective, portable, electrochemical genosensor could improve parasite detection. This study analyzed the large subunit rRNA gene of *Pseudo-nitzschia delicatissima* to select four short, unique DNA sequences. The four identified regions were amplified using PCR and analyzed by gel electrophoresis to determine a suitable gene probe in an electrochemical genosensor. These findings provide the foundation for developing an electrochemical genosensor that is capable of rapidly detecting *P. delicatissima* in the water. This tool could support earlier monitoring of harmful algal blooms, helping protect Rhode Island's coastal water, shellfish industry and public health.

This work was supported by the Mark Gould Fellowship RWU

Gaining Insight into Perspectives on Microplastics Pollution Through Summer Camp Curriculum at Camp Woonasquatucket

Elizabeth Turbi[1], Judith LaRose[2] & Daniel Hewins[1]

[1]Biology, Rhode Island College, Providence, RI
[2]Environmental Studies, Anthropology, Rhode Island College, Providence, RI

Plastic pollution is an emerging field of research as macro-, micro-, and nanoscale plastic particles (MNPs) are increasingly recognized as ubiquitous and pervasive across scales, from cells and tissues to ecosystems and watersheds. This environmental issue impacts riparian ecosystems and the health and well-being of the human populations that call them home. Despite the scale of this issue, regional insight into community perceptions, challenges, and understanding of plastic pollution is limited. Mitigation and prevention of such pollution will likely require community buy-in and support, suggesting that community engagement and involvement are essential to the success of these strategies. To engage youth in our region and promote meaningful change, we worked with students at Camp Woonasquatucket, providing a unique perspective into how children think about plastic pollution. The camp is held three times each summer and serves 12 children, age 7 – 13, per cohort. Our goal was to develop and deliver a curriculum that increased campers' understanding of plastic pollution, how it interacts with and impacts the environment, and strategies to reduce the plastic pollution generated in our daily lives. The curriculum introduced campers to the concept and sources of MNPs, how they enter and their impact the Woonasquatucket River Watershed. Through hands-on activities, campers developed a deeper understanding of plastic pollution and its environmental consequences. Our work promoted environmental awareness, fostered critical thinking, and inspired campers to develop strategies for reducing plastic waste and protect local waterways. Two activities stood out as particularly effective. A hands-on sorting activity reinforced the distinction between primary and secondary source plastics, with campers successfully classifying common plastic items and applying this knowledge during subsequent activities. In contrast, an activity estimating the time required for common plastics, such as fishing line and plastic water bottles, to degrade into MNPs revealed that campers consistently underestimated their persistence in the environment, highlighting a common misconception about plastic pollution. As a result of this work, we developed modular lessons that can be used in future summer camps and incorporated into educational programs offered by the Woonasquatucket River Watershed Council throughout the year, promoting community-centered environmental education for children across our region.

This work was supported by SIMCoast & RI NEST

Effects of Wind Speed and Direction on Microplastic Deposition in Narragansett Bay

Paola Pamias-Nieves, Gianna Wesling, Cassie Allen, Logan Szenda & Lillian Jeznach

Engineering, Roger Williams University, Bristol, RI

Microplastic pollution is an increasing environmental concern due to the persistence and widespread distribution of plastic particles in land, aquatic, and atmospheric environments. In Rhode Island, where densely populated areas and roadways are located alongside coastal waters, major atmospheric sources include sea spray and road traffic. However, baseline data for atmospheric microplastic deposition are currently unavailable. The objective of this study was to establish an initial deposition baseline for the Narragansett Bay region and assess how wind speed and direction influence microplastic flux. Atmospheric deposition samples were collected by deploying a custom deposition sampler on the Roger Williams University campus for one to two days during periods with no forecasted rainfall. The sampler was approximately 95 meters from Route 136 and 320 meters from Mount Hope Bay, allowing for the collection of both traffic and aquatic microplastic sources. Samples were visually analyzed using a compound microscope, blue light, and Nile Red staining. Suspected microplastics were categorized as fibers, fragments, or beads, and visual analysis was verified by using a hot needle test. The microplastic flux of each sample was calculated by dividing the total microplastic particle count by the sampler surface area and the deployment time. To date, microplastics have been identified in all 21 atmospheric deposition samples collected at Roger Williams, with a total of 589 particles. Fibers account for approximately 89% of all particles, and fragments account for the remaining 11%. Preliminary analysis indicates that lower wind speeds were generally associated with higher microplastic fluxes, suggesting that calmer atmospheric conditions promote particle settling. Microplastic fluxes were approximately 59% higher when wind speeds were below average (8.5 mph). While 64% of samples were collected during westerly/southwesterly winds, no consistent pattern was observed with wind direction. These findings demonstrate that atmospheric microplastics are consistently present in the Narragansett Bay region and that wind speed plays an important role in deposition. Establishing this baseline supports future monitoring efforts and provides a foundation for understanding microplastic transport dynamics in coastal environments.

This work was supported by SIMCoast

Ready for Recovery: Preparing Coastal Communities for Extreme Weather Through Education and Outreach

Amber Lopes, Ava Lesiak, Amanda Solano & Anabela Maia

Biology, Rhode Island College, Providence, RI

Climate change is increasing the rate of extreme weather events for coastal low lying communities. The most common occurrence for these areas is flooding, hence the goal of this coastal resilience funded project (www.3crs.org) is to help communities better prepare for these events and recover more smoothly. Scientific information like sensor data and models on coastal hazards/extreme weather events are often indigestible for a public audience. By making critical information accessible we can put the tools for preparedness in the hands of community members. We created a glossary of common terms from the material created by the coastal resilience team, as well as an explanatory note for legal disclaimers for real time storm impact modeling through Coastal Hazards Analysis Modeling and Prediction (CHAMP). This will set the tone for the expectations associated with the responsible and appropriate use of the resources created and funded by this project. We also developed a lesson on how sensors installed by this project work and how the information collected in an open access dashboard can be easily used. The video lesson and worksheet on sensors was curated for middle school students, sixth to seventh grade, to help encourage young scientists to explore how and why flood sensors are used in their local coastline. Fostering understanding of the science behind highly technical products, these activities geared towards young learners encourage students to participate and engage with real world applications of classroom material. Two additional deliverables, a maze and a word search, were designed to offer low stress activities that make use of the information and some common terms for the coastal resilience program to boost interaction between program coordinators and the public. By offering tangible educational resources after community meetings, programs, or workshops, citizens will be able to take the content home with a better understanding of the tools and resources near them. Promoting responsible engagement with the resources for students, citizens, agencies, and legislative bodies ensures communities can be better prepared for coastal hazards/extreme weather and exhibit resilience in recovery.

This work was supported by 3CRS

Fishing Through Microplastics: The Impact of Microplastics on Black Sea Bass

Elizabeth Shepard, Suleimen Seitkarim, Nailea Estrada, Cassandra DeBlois & Anabela Maia

Biology, Rhode Island College, North Providence, RI

Microplastics are classified as plastic particles ranging in size from 1µm to 5mm and have slowly been increasing in concentration in marine environments over the past decades. Microplastics pose a threat to marine organisms, impacting physiology, and serving as a substrate for microorganisms . These pollutants are also transported throughout the trophic food web and can potentially pose a threat to human health. The black sea bass (*Centropristis striata*) is a finfish found along the North Atlantic coast that opportunistically feeds on a variety of prey and utilizes estuaries as nursery habitats. Investigating black sea bass digestive systems will not only assess the ingestion of microplastics by this species but will also help assess microplastics loads from their prey and the environment. During the month of May, representing the rainy season in Rhode Island, a total of 10 black sea bass were caught in collaboration with the Marine Fisheries Division of the Rhode Island Department of Environmental Management using otter trawl and pots from different regions of Narragansett Bay. Black sea bass collected from the lower part of the Bay are expected to have lower loads of microplastic due to lower anthropogenic pressures. Fish were dissected and stomach, intestine, and muscle samples were collected and weighed. These tissue samples underwent dehydration and digestion with 9.5% potassium hydroxide. These samples were then filtered and stained with Nile Red solution and observed under the microscope with UV light for microplastics. The microplastics were then picked, identified, and photographed. Microplastics were retrieved from the stomach of multiple black sea bass. Along with the microplastics, their natural prey was also found in the stomach such as amphipods, as well as different species of fish such as hake, highlighting their opportunistic diet. As plastic use becomes more prevalent and more plastics end up in landfills, breakdown of these items leads to higher microplastics loads in the environment. This poses a potential risk of physiological impacts on marine organisms and a potential danger to the trophic levels as microplastics can be transferred from prey to their predator. Assessing the prevalence in these organisms during different seasons and areas of the Narragansett Bay is a first step to determine the risk for the ecosystem and human health.

This work was supported by RI NEST and SIMCoast

Skates Have Microplastics Too!

Suleimen Seitkarim, Elizabeth Shepard, Nailea Estrada, Cassandra DeBlois & Anabela Maia

Biology, Rhode Island College, North Providence, RI

The harmful effects of microplastics – plastics ranging in size from 1 µm to 5 mm - have attracted global interest due to their pervasive nature and long residence time in ecosystems. These include colon and intestine cellular changes, chronic inflammation, and disrupted reproductive hormones. While current studies outline their presence in Narragansett Bay, Rhode Island, their concentration in different parts of the digestive system – stomach and valvular intestine - of little skate (*Leucoraja erinacea*) is unknown. The little skate population in Narragansett Bay has increased in the last 25 years. They are a small benthic skate species along the Atlantic coast, found everywhere from North Carolina to Nova Scotia, living on sandy/muddy seafloor in shallow-to-shelf waters. They eat worms, small crustaceans, and occasional small fish; they are eaten by dogfish, larger skates and rays, cod and seals. Our goal is to assess microplastic load in the stomach, valvular intestine and muscle of little skate individuals collected from different locations in Narragansett Bay. We expect specimens from the northern parts of the Bay to have higher concentrations of microplastics due to the increased pollution closer to higher populated areas; we also expect more microplastics to be in the stomach and valvular intestine since after chemical and mechanical digestion, microplastics in the muscles are expected to be too small – in the nanoplastic range - to be detected. A total of 15 skates were collected on the 13th and 15th of May from the Lower Bay using a trawl. For each individual, the stomach and the valvular intestine were dissected in a clean room. The stomach was also opened to visually assess prey items. Samples were then dehydrated at 60°C for 2 days, and then digested with 9.5% potassium hydroxide. We then fully neutralize the sample with 1M Citric acid and filtered the samples using a 100µm sieve and then a 5.0µm polycarbonate filter. The samples were stained with a Nile Red in hexane solution for easy identification of microplastics under a microscope with ultraviolet light. Samples were inspected for number, type and size of microplastics. We found 6.6 particles/g of dry weight in the stomach and valvular intestine of skates and 5.3 particles/g of dry weight in muscles. We also found that content in the skates' tissues correlated well with microplastic content in the water grab samples. As little skate occupy a mid-trophic position, linking benthic invertebrates to larger predators, these findings suggest microplastic contamination is present throughout the food web - both in the organisms they consume and in those that consume them.

This work was supported by RI NEST and SIMCoast

Exploring Aerial Environmental DNA Methods for Invasive Species Detection

Anthony Aldana Mendez & Jeffrey Markert

Biology, Providence College, Rhode Island

Rhode Island has been affected by many invasive species through the years. Even though these species cause a huge impact on our local ecosystems, there are very few ways of eradicating these invaders and even fewer methods for early detection. My goal with this project is to expand on the recently found tools for airborne environmental DNA and find a reliable way of detecting terrestrial species in the wild. Finding better detection methods can save many ecosystems and economic burdens. To do this, we took a comparative approach, comparing different sample sizes of two different materials to determine the effectiveness and reliability of each. Currently, we have sampled only for lantern flies, Lycorma delicatula, in two different locations. The initial location was the Providence College campus, and the second was Grills Preserve, Westerly. At Providence College, we were able to observe the nymphs emerging, while at Grills Preserve there was no sighting of the insect. We left the different materials hanging approximately 50cm down from trees. We initially started with an embroidery ring with 13cm in diameter and set it out as a filter-like system using electrostatic dust cloth and dry dusting cloths for 3 days. Then we experimented with strips of these materials for easier handling to extract the DNA, and we found that it provided similar results quantitatively but with the benefit of easier handling and setup efficiency. Using qPCR to gather eDNA collection readings, we found that using the electrostatic paper strips was more effective than the dry dusting cloths, showing faster detection of eDNA in the extraction samples, fewer procedural complications, and reduced sample processing time.

Mortality Salience, Delay Discounting, and Environmental Risk Perceptions

Anthony Ramos, Delaney Ryan, Emily Achin, Katherine Lacassse & Vincent Medina

Psychology, Rhode Island College, Providence, RI

Awareness of one's mortality (thoughts of one's own death) increases existential anxiety. Reminding people of their own inevitable death (mortality salience) frequently leads them to think about other future events and therefore become more future-oriented. Future thinking can affect a broad range of cognitive decision-making processes with implications for many real-world topics such as finances and environmental pollution. Research question: How does mortality salience influence financial decision-making and environmental risk perceptions about microplastic pollution? We recruited 165 American participants to complete an online experiment via Prolific. They first responded to a writing prompt. They were randomly assigned to either write about their future death (mortality salience condition) or the experience of dental pain (control condition). Afterwards they all completed the Monetary Choice Questionnaire, in which they responded to 27 questions where they indicated their preference either a smaller-sooner reward vs. larger-later reward (e.g., Would you prefer $55 today or $75 in 61 days?). They then responded to questions about their concern about microplastics, beliefs about plastics' impact on future, personal use of plastics, and demographics (age, state of residence, perceived SES). T-tests were conducted, but no significant differences were found between the experimental conditions (p's > .07). Exploratory analyses revealed that participants who are struggling to pay their monthly expenses prefer getting immediate financial rewards over larger-later pay outs, regardless of experimental condition. Future work can aim to identify other ways of motivating future-oriented behaviors, which can help to promote better financial decision-making and environmental actions such as supporting innovative sustainability technology.

This work was supported by RI NEST and SIMCoast

Effects of Energetic Stress on the Development of Gonads in the Purple Sea Urchin (*Strongylocentrotus purpuratus*)

Shakina Tanjong & Carla Narvaez

Biology, Rhode Island College, Providence, RI

Sea urchin gonads serve a dual function as both primary reproductive organs and nutrient storage sites. Nutritive phagocytes (NPs) accumulate nutrients from food and store them within the gonads; during gametogenesis, these reserves are reabsorbed to support the development of germ cells (GCs). As gametes mature, gonad composition shifts progressively through six distinguishable reproductive stages (I–VI). *Strongylocentrotus purpuratus* commonly inhabits zones in which macroalgae has been depleted and thus experience prolonged periods of food limitation. In addition to nutritional stress, sea urchins commonly lose tube feett to predation or exposure to challenging hydrodynamic forces. Because tube feet are essential for attachment, locomotion, and food acquisition, their regeneration may further increase energetic demands. As a result, *S. purpuratus* is often under energetic stress driven by reduced energy intake and increased energetic expenditure from tube feet regeneration. Despite the ecological importance of these stressors, their combined effects on reproductive investment remain poorly understood. We hypothesized that reduced energy intake and increased energy expenditure would each independently impair gonad development, with the combination of both stressors producing the greatest reduction in gonad index and the most pronounced delay in reproductive staging. In this six-month study, purple sea urchins were exposed to a 2 × 2 factorial experiment consisting of two energy intake treatment (starved, fed once monthly vs fed, fed ad-libitum serving as control) and two energy expenditure treatments (amputated tube feet, inducing regeneration vs or non-amputated tube feet, serving as control). At the experiment end, gonads were dissected and weighed to calculate the gonad index, then processed for histological analysis by fixing, sectioning, and staining with hematoxylin and eosin (H&E). Histological analyses included identifying the reproductive stage, estimating acinus size, and calculating the relative abundance of NPs and GCs within individual acini. Preliminary results suggest altered gonad development in response to energetic stress, highlighting the sensitivity of sea urchin reproductive investment to concurrent energetic challenges in variable coastal environments.

This work was supported by RI-INBRE

Spatial Distribution of Adhesive Granules in Sea Urchin *Strongylocentrotus purpuratus* Tube Feet Discs

Noah Furtado[1], Madison Silvia[2], Gary Wessel[2] & Carla Narvaez Diaz[1]

[1]Biology, Rhode Island College, Providence, RI
[2]Molecular Biology, Cell Biology, and Biochemistry, Brown University, Providence, RI

Echinoderms, such as sea urchins, possess external structures known as tube feet (or podia) that allow them to attach strongly, but temporarily to a substratum. Hundreds of tube feet work in coordination for critical functions such as fleeing predators, manipulating food, and withstanding challenging hydrodynamic forces. Each tube foot consists of a flexible proximal stem, and an adhesive distal disc. Within the disc, specialized adhesive and de-adhesive secretory cells release adhesive and de-adhesive granules that allow for reversible chemical adhesion: adhesive granules bind the disc to the substratum, while de-adhesive granules break that bond, leaving a "footprint" of adhesive material behind. The adhesive secretion contains glycoproteins bearing the sugar N-acetylglucosamine (GlcNAc), and in-situ hybridization on *Paracentrotus lividus* has shown adhesive cells arranged in ring-shaped patterns around the middle area of the discs. However, the spatial distribution of adhesive cells in *Strongylocentrotus purpuratus*, a species with a particularly high adhesive force, is unknown. In this study, we aim to 1) validate wheat germ agglutinin (WGA), a GlcNAc-binding lectin, as a tool for visualizing adhesive cells and secretion in discs and footprints, and 2) map the spatial distribution of the adhesive granules of *S. purpuratus* discs. Tube feet (n = 10) were isolated from a live urchin and fixed overnight in 4% paraformaldehyde (PFA) with three fluorescent labels (WGA, DAPI, Phalloidin). Footprints were collected by allowing urchins to strongly attach or walk on a glass surface. All samples were examined via confocal microscopy. Results demonstrate that WGA labeling was successful in both discs and footprints, and footprints from strong attachment showed a stronger WGA signal than those from walking, suggesting different amounts of adhesive granules release depending on adhesive behavior. Adhesive cell spatial distribution of *S. purpuratus* differed markedly from *P. lividus*, concentrating both at the center and around its perimeter. This study advances our understanding of comparative anatomy in sea urchin adhesion systems across species and suggests that adhesive cell organization may vary with species-specific differences in attachment strength.

This work was supported by RI-INBRE

Linking Rhode Island Local Food Supply and Consumer Demand: Integrating Spatial Food Flow Mapping with Consumers Demand Survey

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Rhode Island's local food system plays a vital role in supporting farmers, strengthening communities, and shaping statewide food policy yet little is known about how local supply and consumer demand align. This research project brings together three complementary efforts: a statewide local food consumer survey, local food producer interviews, and a spatial food flow map of local food production and where it's retailed which will help identify mismatches, market gaps, and strategic opportunities. The Rhode Island Department of Environmental Management (RI DEM) has redesigned the "RI Grown" local food label with the goal of increasing consumer recognition of locally produced food and strengthening farm-to-market connections. While the state has robust datasets on agricultural production, there is currently no integrated analysis linking what and where local food is produced and retailed with consumer purchasing preferences for locally branded products.

Consumer survey

The online consumer survey is currently being piloted with the statewide distribution scheduled for the first week of August. This survey includes detailed questions on preferred purchase outlets, RI Grown label awareness, along with discrete choice modeling that will allow for willingness to pay (WTP) estimation to be calculated to quantify market value for locally labeled products.

Producer survey

To assess awareness, adoption, and perceived benefits of the RI Grown label, interviews of local food producers have been conducted. Data collected will be used to create a producer adoption profile detailing the findings and will provide RI DEM with actionable, data-driven recommendations for targeted marketing, outreach, and infrastructure investments.

Spatial map

This project will deliver the first iteration of an integrated Rhode Island local food system map linking farm-level production and distribution data with consumer demand for local food products. Together, these components will create a comprehensive, policy-relevant picture of how agricultural products move across the state and how local markets function. By actively engaging RI DEM as a collaborative partner in applying the results, this project ensures that findings will directly inform the evaluation and strategic development of the RI Grown label, support the growth of local farm-to-market connections, and strengthen the long-term sustainability of the state's agricultural economy and food system.

This work was supported by RI NEST

CCRI Science Art Mentorship Program

The 2026 Science Art Mentorship Program at Community College of Rhode Island (CCRI) offers a unique interdisciplinary experience, blending scientific research with studio art. Students from both Biology and Art Studio backgrounds are invited to apply. Participants engage in workshops at leading research laboratories, where they learn techniques for capturing, manipulating, and displaying images essential to scientific inquiry. These techniques include illustration, microscope photography, video, 3D imaging, and the creation of physical 3D models. Based on these workshops, students apply a design process to create original art and design work for public exhibition. Students are encouraged to experiment, pursue their creative concepts, and produce personally meaningful projects. Guidance and mentorship will be provided by faculty from CCRI's Art and Biology departments, along with special guests. We are grateful to the Wessel Lab and Tingle Lab at Brown University for partnering with us and welcoming us into their labs.

The program exhibition will be on view from **September 1st – 30th at CCRI's Flanagan Campus Art Gallery in Lincoln Rhode Island**. There will be an opening reception on Friday September 11th from 4:00 - 7:00pm. The posters here at SuRS offer a glimpse into the work that will be on exhibit.

51 Summers - Aaron Ames

this is homage to my hometown's beauty that i hope the tourists never find

Sea Urchin! - Gale Cabral

This program gave me the opportunity to study and observe purple sea urchins up close and personal. I was enchanted by these creatures and wanted to recreate that experience for the audience. To take something so small and detailed and scale it up to really appreciate and highlight how cool and intricate they are!

Poem of the Common Dandelion - Elwood Crosby

In my paintings, it is important to me to feel like I do my muse justice. I strive to tell its story and show its beauty and hidden magic that can only be seen when you allow yourself to get close enough to see a whole new perspective.

This is a piece that embodies a perspective that goes against what we are told to believe about the dandelion plant. It works as an educational, symbolic and eye-opening piece that critiques the unnecessary treatment weed killer companies enforce on such beneficial herbs. The collage style of the painting part is a stylistic choice to make it feel more natural and authentic. The plastic interactive covering is very geometric with clean color and shapes to mimic the corporate design of common weed killing ads. The imagery of the target on the dandelion is a reference to a real commercial for Kiwicare weed weapon. I wanted to feature this to show how strangely violent these commercials can be. In contrast, I made the painting softer; and wrote a loving poem that integrates facts about the dandelion, rather than a facts sheet like I originally intended, to give more life and feeling to the painting. The poem consists of three parts, one that talks about the medicinal uses of the plant, the second is about its impact on the environment, and the third is talking about the cultural symbolism for the queer community, which is right next to a subtle transgender flag that appears in the sky background and a shimmer of rainbow. The hanging string and paper leaves of this piece that peak out from under the plastic ad, is a representation of the strong resilient spirit of the dandelion.
Thank you for taking time to look at a weed in the light they deserve. (o゜▽゜)o☆ <3

Hidden Beauties - Samantha Kukulka

I've made an animation to help bring appreciation for things we see in everyday life, showing the viewer a closer look into microscopic views of pollen, leaf skeletons, a cross section of a leaf vein, and a pinecone. In this modern age of technology it's clear that our deteriorating attention spans are becoming an obstacle for us to stop and admire the amazing beauty that nature has to offer. This is what inspired me to showcase these hidden beauties that many don't even think about.

Little Hidden Things - Rook Zoglio

I love a good surprise. And I find that if I approach the mundane day to day with a sense of curiosity, I see them everywhere. A cool bug. An interesting rock. A particularly fluffy cloud. With my work, I've attempted to showcase that when I focus on gentleness and patience, the world becomes a place full of little hidden things to discover.

Additional works will be displayed during Session B

Sunburned Plastic: The Effect of UV Radiation on Plastics

Abigail Bratsos, Christian Falcon, Kayla Riley, Marcus Raposo & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

The widespread production, use, and disposal of single-use plastics have resulted in extensive contamination of marine environments. Microplastics, generated through the weathering and fragmentation of larger plastic debris, are of particular concern because of their persistence, accumulation in sediments, and potential impacts on aquatic organisms. Ultraviolet (UV) radiation is a primary driver of plastic weathering, altering polymer chemistry through photo-oxidation and increasing susceptibility to fragmentation. This study investigated the effects of UV-induced weathering on common consumer plastics and developed an analytical framework for identifying weathered polymers using complementary spectroscopic, microscopic, and surface characterization techniques. Pristine polymer standards and environmentally weathered plastics were characterized using Fourier-transform infrared (FTIR) spectroscopy to identify polymer composition and monitor chemical degradation. Surface morphology was examined with a Keyence digital microscope, while elemental composition was evaluated by laser-induced breakdown spectroscopy (LIBS). Laboratory weathering experiments exposed consumer plastics and polymer standards to UV radiation under controlled conditions. Selected samples were further characterized by Raman spectroscopy, and changes in surface hydrophobicity were quantified using static water contact angle measurements. UV exposure initiated polymer bond scission generated free radicals that reacted with atmospheric oxygen to form oxygen-containing functional groups. These photo-oxidative reactions promoted chain scission, and in some polymers cross-linking, resulting in altered surface chemistry, reduced hydrophobicity, increased brittleness, and enhanced fragmentation. FTIR spectra showed pronounced changes in the C–H stretching (~3000 cm^{-1}) and fingerprint (1500–600 cm^{-1}) regions, consistent with polymer degradation and oxidation. Contact angle measurements demonstrated increased surface hydrophilicity following UV exposure, while digital microscopy revealed greater surface roughness, cracking, and pitting characteristic of advanced weathering. These findings demonstrate that UV-driven photo-oxidation fundamentally alters the chemical composition, morphology, and surface properties of plastics, accelerating their transformation into persistent microplastics. The integrated use of FTIR, Raman spectroscopy, LIBS, digital microscopy, and contact angle analysis provides a robust framework for characterizing polymer weathering, improving identification of environmentally aged plastics, and advancing understanding of microplastic formation and persistence in marine ecosystems.

This work was supported by SIMCoast

A Wrack of Our Own Making: The Characteristics and Impacts of Plastics Entangled in Macroalgae

Marcus Raposo, Abigail Bratsos, Christian Falcon, Kayla Riley & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

The widespread use and environmental persistence of single-use plastics in recent decades has resulted in extensive contamination of coastal ecosystems. Microplastics are of particular concern because they accumulate in sediments and biota, posing potential risks to ecosystems and human health. Macroalgal wracks are an ecologically important component of shoreline ecosystems, providing habitat, supporting nutrient cycling and contributing to RI's Blue Economy. However, the interactions between algal wracks and plastic debris remain poorly understood. This research investigated the abundance, composition and physical interactions of plastic debris associated with algal wracks on Brayton Point Beach of the tidal Taunton River. Four intertidal shoreline transects, including two wrack-line transects, were surveyed. Macroplastics were collected, weighed and identified by polymer type using Fourier-transform infrared and Raman spectroscopies. The surface morphologies of plastics fused with algal tissue were characterized using Keyence digital microscopy. Using laser-induced breakdown spectroscopy and static water contact angle measurements, changes in elemental composition and hydrophobicity were evaluated. Spectral techniques identified polyethylene, polypropylene and polystyrene accounted for approximately 78%, 18% and 3% of the recovered plastic mass, respectively. Wrack-line transects contained substantially greater quantities of plastic debris (>140 g per transect) than adjacent wrack-free transects (8-44 g), demonstrating that algal wracks function as efficient entanglement sinks for floating plastics. Plastics fused to algal tissue exhibited localized alterations in surface chemistry, with 5–10% differences in relative carbon, oxygen and hydrogen composition compared with adjacent non-fused surfaces. Three-dimensional surface contour profiling showed increased roughness on algal-fused regions, while contact angle measurements indicated a decrease in hydrophobicity ranging from 28-45%, following attachment. Laboratory $ZnCl_2$ density separations recovered microplastic standard from macroalgal samples, though residual organic material was also retained, suggesting physical entrapment or adsorption within the algal matrix. These findings demonstrate that tidal algal wracks both concentrate plastic debris and promote physical and chemical modification of plastic surfaces through attachment and prolonged environmental exposure. Such interactions may promote fragmentation and contaminant adsorption and increase the environmental persistence and bioavailability of plastics. Continued investigation of algal wracks within Mount Hope Bay will improve understanding of its role as both a reservoir and transport pathway for plastic pollution in coastal ecosystems.

This work was supported by SIMCoast

Pollinators of Maleberry (*Lyonia ligustrina*) in the Rhode Island Great Swamp

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Maleberry (*Lyonia ligustrina*), is an ericaceous shrub species native to the Eastern United States. It has a wide range, spanning the East Coast from Maine south to Florida and west to Texas. It is particularly abundant in New England forests. While maleberry is known to host a specialist blunt-horned bee (*Melitta melittoides*), its general pollinator composition has not been intensively studied. To identify pollinators of maleberry, surveys were conducted in the Great Swamp Management Area in Kingston, Rhode Island throughout the bloom period in June and July 2026. We established nine 20 meter transects along the forest edge. We randomly selected three transects on each survey day and walked them for 10 minutes, netting every floral visitor encountered. Weather and density data was also collected for each transect during each survey. We also completed four visual surveys each day, observing floral visitors and their movement between flowers in a 1 m^2 area for 10 minutes. Bumblebees were the most prevalent pollinators in our surveys, and a varying number of beetles, flies, small bees, and ants were also caught. Further research includes an assessment of pollen foraging fidelity by analyzing the pollen species on the collected specimens.

This work was supported by RI NEST

Design and Development of a Deep-Sea Hydrophone with Tethered Fiber-Optic Communication to an UAV

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In deep-sea applications, real-time data from in situ sensors is constrained by the distance data can travel over standard copper tethers (e.g. ethernet cables) before the signal is lost due to resistance. Fiber optic cables allow for reliable high-bandwidth data transmission over a longer distance, enabling real-time communication to the deepest parts of the ocean. Traditionally, fiber optic cables for deep-sea applications are situated within heavy-duty steel reinforced umbilicals requiring large cumbersome winches. A patented fiber optic microtether developed between URI and Nautilus Defense has changed this standard, allowing for small lightweight winches and reels to be used for underwater communication, including from aerial drone (UAV) platforms. In this project, we developed a size-optimized fiber optic tethered hydrophone payload to be used for passive acoustic monitoring (PAM) via a UAV.

The payload features a small hydrophone, Data Acquisition (DAQ) microcontroller, Raspberry Pi 4b microcomputer, and an ethernet to fiber converter, all contained in a 3D resin-printed pressure housing designed to withstand a depth of 1500 meters in seawater. The payload is connected to a fiber optic microtether, which is linked to the drone's telemetry system. Data received by the hydrophone is sent to shore over a drone radio link, then processed into a real-time spectrogram viewer. A future iteration of the hydrophone payload will feature a DAQ microcontroller with native ethernet capabilities, removing the need for an onboard Raspberry Pi and simplifying the overall design. All this work has been done in collaboration with Juice Robotics, a URI-affiliated blue-tech startup company, in preparation for a field demonstration at the end of August 2026.

This work was supported by RI NEST

Developing an Optical Microscopy Method to Detect Microplastics in Environmental Samples

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Microplastics often result from the breakdown of plastic waste in the environment. Their presence in food and drinking water as well as air and soil raises concerns about their impact on the environment and human health. Despite this need to identify microplastics in environmental samples, current analytical techniques (i.e. FTIR and Raman spectroscopy) are limited by their cost, accessibility, and low sensitivity. This study aims to develop a method to identify microplastics based on particle dynamics and light scattering patterns detected on an optical microscope. Microplastic spheres with diameters 0.5 µm, 1 µm, and 2 µm composed of either polymethyl methacrylate or polystyrene were diluted in water and prepared on glass slides. Videos of the samples were taken on a microscope at 100X magnification and analyzed using differential dynamic microscopy (DDM) algorithms. Difference images were computed between all frames separated by the same time delay. The Fourier transform and radial average of this image results in the image structure function, which is analytically fit to extract three important parameters: A(q), B(q), and $\tau_D(q)$. The amplitude gives insight into the scattering properties of the material and is used to determine a relationship with polymer chemistry. This research demonstrates how microplastics can be characterized using accessible equipment, hopefully leading to rapid detection and identification of microplastics in real-world environmental samples.

This work was supported by URI Plastics REU

Investigation of DNA-SWCNTs as a Near-Infrared Fluorescence Sensor for HDPE Microplastic Detection

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Microplastics are a rapidly emerging environmental contaminant with potential impacts on ecosystems and human health. Despite increasing concern over microplastic pollution, reliable methods for detecting and characterizing microplastics remain under development. DNA-functionalized single-walled carbon nanotube (SWCNT) sensors show promise for microplastic detection, but their responses to varying concentrations of high-density polyethylene (HDPE) microplastics, one of the most common plastic pollutants, are not fully understood. In this study, we evaluated the responses of GT_6- and GTT_4-functionalized SWCNT sensors following exposure to HDPE microplastics. HDPE dilute suspensions at concentrations of 0.1 mg/L, 1 mg/L, and 10 mg/L were prepared and combined with 5 mg/L GT_6- and GTT_4-functionalized SWCNT sensors. Near-infrared fluorescence and UV-Vis absorbance measurements were collected at 0, 1, 4, and 24 hours across multiple experimental replicates. Preliminary analysis demonstrated concentration-dependent variation in fluorescence spectra, indicating distinct sensor responses across different HDPE microplastic concentrations. Increased fluorescence peak intensity was also observed after 24 hours of incubation compared to earlier time points, suggesting that sensor responses are influenced by both microplastic concentration and incubation time. These findings demonstrate the sensitivity of DNA-functionalized SWCNT sensors to varying HDPE microplastic concentrations while highlighting the importance of incubation time in fluorescence-based detection. This work supports the continued development of fluorescence-based sensing methods for environmental microplastic detection. Future work will expand this sensing platform to additional microplastic types and environmental conditions, further advancing fluorescence-based approaches for monitoring microplastic pollution.

This work was supported by URI Plastics REU

Microfluidic Particles as Larval Diet: Development of Alginate Hydrogel Spheres

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Larval fish rely on a small live prey diet of copepods, rotifers, and artemia until they are large enough to eat complex pelleted feeds. Live diets provide nutrients at a size that larval fish can consume while also remaining active in the water column allowing for minimized food waste. However, live diets are challenging to scale due to high demand for skilled labor, space, and other hatchery constraints. Existing larval microdiets have several drawbacks as a replacement to live feeds, such as movement and waste. Current larval microdiets do not move easily through the water column like live prey, floating on the surface or sinking quickly. This leads to increased waste that can decrease water quality and therefore affect the fragile health of larval fish. Developing a diet that is small enough for consumption, contains all necessary nutrients, enzyme activity, and remains in the water column could replace or better augment live feeds and improve the success and consistency of larval production.

Alginate is a polysaccharide extracted from brown seaweed that forms hydrogels. Sodium alginate exposed to calcium chloride creates a permeable gel exterior with a liquid interior. Alginate hydrogels can encapsulate oils, nutrients, and compounds while the size, shape, and buoyancy can be customized based on formation methods. Microfluidics provide precise control over small volume of liquids, providing a method of development for specialized particles as a larval feed. This project customized a centrifugal microfluidic alginate hydrogel method to assess the capability of microparticles as a supplemental feed based on size, nutrient content, and water column behavior.

Centrifugal microfluidic conditions and alginate solutions were varied to observe changes in particle formation. Ground fish feed, liquid enrichment, fish oil, and algal cells were incorporated to mimic diet components. Dye was added to test the permeability and potential limitations in compound retention. The produced particles were analyzed microscopically for size, shape, and consistency. Buoyancy was tested in lightly aerated water to observe whether the particles sank, floated, or remained in the water column.

Alginate hydrogels were successfully produced to include potential diet ingredients and move within the water column. Particle buoyancy and size are not consistent, and there are current limitations to compound incorporation and retention. This study demonstrates the potential of hydrogels as a larval diet and future work will build on the results to produce a microparticle fabrication process with optimal size, buoyancy, and nutrients to replace live feeds.

This work was supported by the RWU Blue Fellows Program

Reproductive Development of *M. mercenaria* Populations Across Rhode Island

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Monitoring the reproductive status and development of wild M. mercenaria is vital to detecting significant changes in populations. In RI, declines in wild clams have been seen through decreased landings over the past few decades. Our investigation looked at asynchronous reproductive development and spawning between male and female clams from different populations in RI as a potential contributing factor. While usually normal and strategic, any more widening in the timing gap between male and female gonadal development could easily weaken struggling populations. Here, 30 *M. mercenaria* specimens were collected from Greenwich Bay, Providence River, Bristol Harbor, and Block Island. Shell volume was measured before removal of the visceral mass. The weight of the visceral mass, which contains the gonad, was measured. Visceral mass index (VMI) was calculated as the ratio of said weight to the shell volume. VMI is more sensitive than the frequently used condition index since it specifically targets the reproductive organ rather than the entirety of soft tissue. The visceral mass was then processed for histology, followed by grading of the reproductive stages: (1) Resting described empty follicles surrounded by much connective tissue, (2) Early Development described follicles with gametes forming on the walls, (3) Late Development described follicles with gametes moving to the center and follicles beginning to fill, (4) Ripe described enlarged follicles packed with gametes and minimal connective tissue. T-tests were used to analyze differences between males and females within a location and ANOVA tests were used to analyze differences of males or females between locations. There were no significant differences in the VMI between males and females at any of the 4 locations. However, there were significant differences in the VMI of males and females between all locations. There were significant differences in the reproductive grade between males and females at each location. There was also a significant difference in the reproductive grade of females between each location, but not for males. The consistent, abnormally large timing gap seen in reproductive maturation of males and females, despite similar VMI, may lead to failed fertilization and contribute to population decline. However, much larger sample sizes, more locations, and many more collection points during different seasons are needed to conclude if a growing asynchrony is indeed a contributing factor to the declining populations of *M. mercenaria* in RI.

This work was supported by the RWU Blue Fellows Program

Microbiome Dynamics of Reduced Winter Dormancy in the Temperate Coral *Astrangia poculata*

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Astrangia poculata, a temperate coral found along the U.S. East Coast undergoes a period of dormancy termed quiescence during winter months in the northernmost portion of its range in Narragansett Bay. Previous research demonstrates that the microbiome of these *A. poculata* populations exhibits predictable shuffling around quiescence, likely triggered by temperatures reaching and sustaining below 5°C. *A. poculata*'s microbiome resembles that of a diseased tropical coral during quiescence and reassembles into a predictable microbiome composition as it re-emerges into an active state after dormancy. These studies have identified taxa that initiate post-quiescence microbiome re-assembly– microbes that may drive coral microbiome re-assembly, therefore guiding our understanding of tropical coral recovery from disturbances. Due to recent winter warming events in 2023-2025, the threshold surface seawater temperature correlated with quiescence was rarely reached or sustained. In 2023-2024, little to no quiescence was observed in the Narragansett Bay A. poculata population. In this study, *A. poculata* colonies were collected, and high-throughput 16S rRNA gene sequencing was used to characterize microbiome dynamics in low-quiescent colonies from this winter warming period. Microbiomes were compared with colonies collected in prior years– populations that exhibited quiescence.

Microbiome diversity (richness) and composition significantly differed across months in the low-quiescence winter. Compositional differences were driven by eight bacterial families: Endozoicomomadaceae, Flavobacteriaceae, Fokiniaceae, Terasakiellaceae, Rubritaleaceae, Pirellulaceae, Stappiaceae, and Bacteria (unknown). Comparative analysis with previously published microbiomes from *A. poculata* colonies that underwent quiescence suggests that the seasonal microbiome shifts in the 2023-2024 A. poculata samples lacked the signature of re-emergence from quiescence, including spikes in specific taxa identified as pioneer species for post-disturbance recolonization of *A. poculata*, and a loss of seasonal changes in beta-dispersion. Ongoing work includes generation of new models of host-microbial interactions in non-quiescent corals. Characterizing the response of the *A. poculata* microbiome and holobiont to winter warming provides insight into the impact of climate change on the *A. poculata* microbiome, and, broadly, on host-microbe interactions, informing monitoring and management for coastal ecosystems.

This work was supported by RI NEST

Resident and Transitory Behavior in Juvenile Sand Tiger Sharks Using Acoustic Telemetry

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Sand tiger sharks (*Carcharias Taurus*) are globally classified as a critically endangered species. Their slow and complex reproductive cycle makes them vulnerable to population decline, and their coastal distribution overlaps with active commercial fisheries, increasing the risk to incidental capture. This study used acoustic telemetry to examine the movement patterns of resident and transitory juvenile sand tiger sharks and identify habitats important for conservation. Between 2024 and 2025, acoustic detections from 12 tagged juvenile sharks were analyzed. Detection data were condensed and mapped in QGIS, and the maximum number of detections at each receiver was calculated for each individual. Distance from each receiver to the nearest inlet and shark swimming speed were also quantified. Juvenile sand tiger sharks exhibited residency in Delaware Bay (NJ), Smith Point (NY), and Nantucket Sound (MA). Swimming speeds differed significantly between resident and transitory behaviors (t-test: $p < 0.05$). Residency may reflect areas of high prey abundance or refuge from predation, whereas transitory behavior may be associated with seasonal migrations and shifts in preferred thermal habitat. Distance to nearest inlet did not influence the number of detections at acoustic receivers (Regression: $p = 0.35$), and future research will examine which estuarine characteristics influence variation in site fidelity. These findings identified areas of high juvenile site fidelity and habitats where enhanced conservation efforts may be warranted.

This work was supported by RI NEST

Mercury Contamination in Stocked Rainbow Trout Relative to Species in Upper Melville Pond, Portsmouth, Rhode Island

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Mercury (Hg) is a widespread contaminant in aquatic ecosystems that bioaccumulates in fish tissues and biomagnifies through food webs, posing risks to wildlife and human consumers. Stocked rainbow trout are regularly introduced into Rhode Island freshwater systems for recreational harvest and consumption, making it important to evaluate Hg accumulation following stocking. This study examined total Hg concentrations in stocked rainbow trout relative to wild bluegill and largemouth bass from Upper Melville Pond, Portsmouth, RI. Objectives were to compare species-specific Hg concentrations, evaluate Hg levels relative to U.S. FDA/EPA consumption screening values, and assess relationships between Hg concentration and body length in largemouth bass and time since stocking in rainbow trout. Trout from the Lafayette Fish Hatchery were stocked on May 4, 2026 (t = 0), and all three species were collected from May 21 to June 29 using electrofishing and rod-and-reel sampling. Muscle tissue was freeze-dried, homogenized, and analyzed for total Hg using automated atomic absorption spectrometry. Total Hg concentrations differed significantly among species, increasing from rainbow trout (mean = 0.02 ppm, n = 99) to bluegill (0.09 ppm, n = 25) and largemouth bass (0.26 ppm, n = 20), with all pairwise comparisons significant. Rainbow trout and bluegill were classified as “Best Choice” fish for consumption (3 servings/week). In contrast, Hg concentrations in largemouth bass increased significantly with total length. Legal-size bass (>30.5 cm) were classified as a “Good Choice” (1 serving/week), with predicted Hg concentrations exceeding the “Avoid” threshold at 51.1 cm (20 inches). Mercury concentrations in rainbow trout also increased significantly during the eight-week post-stocking period, demonstrating measurable short-term Hg accumulation following release into Upper Melville Pond. These species differences reflect trophic transfer of Hg, with largemouth bass occupying the highest trophic position in the system. Low initial Hg concentrations in stocked trout indicate minimal contamination prior to release, whereas subsequent increases reflect environmental uptake after introduction. These findings emphasize the importance of species- and size-specific fish consumption advisories for recreational anglers and contribute to ongoing collaborative research with the Rhode Island Department of Health and the U.S. Environmental Protection Agency evaluating contaminant exposure in stocked and wild fish populations.

This work was supported by the RI Department of Health

The Role of Particle-Particle Collisions on the Generation of Secondary Microplastics

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Microplastics are a growing concern for the environment and human health; they are found in the arctic ocean, the human blood stream, and freshwater systems across the globe. Despite their pervasiveness, little is known about the mechanisms by which microplastics break into smaller, secondary microplastics. To minimize the production of secondary microplastics, the role of different environmental and physical factors in their formation must be understood. Our research investigates how shear forces and particle-particle collisions affect the generation of secondary microplastics over time. We aim to standardize a methodology for sampling and quantifying secondary microplastics generated in simulated environments. We conducted two experiments using glitter as our primary microplastic to evaluate reproducibility, the effect of the water matrix (water vs. simulated wastewater), and the effect of primary particle concentration. To simulate a collision environment, the glitter solutions were stirred continuously in mixing jars over 9- and 14-day periods for experiments 1 and 2 respectively. Specimens were collected daily to analyze the generated secondary microplastics. The secondary microplastics were collected on a 1.2 µm filter. An area of approximately 1 mm2 was imaged using optical microscopy. The images were processed through ImageJ to get a total particle count and area for each sample.

Results show that in both MilliQ and wastewater environments the average particle count and total area coverage increased over the sampling period. Additionally, sampling within the same jar had a lower average standard deviation than sampling between jars. Findings suggest that particle-particle collisions contribute to the generation of secondary microplastics. Measuring particle counts and total area coverage were reliable methods for the quantification of secondary microplastics, while weight was less reliable. Our research provides a methodology to standardized sampling and quantification procedures, allowing for consistency in future research into the factors affecting secondary microplastic generation.

This work was supported by URI Plastics REU

Magnetically Responsive Shape Memory Composites for 4D Printing

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Shape memory polymers (SMPs) recover a programmed geometry in response to a temperature change. This study investigates the development and characterization of polylactic acid (PLA) matrix composites containing iron oxide (FeO) particles. By using magnetic FeO, heating can be triggered by remote alternating magnetic fields (AMF), driving a change in part shape. This composite material has potential applications in 4D printing and remotely actuated systems in space. The use of AMF actuation eliminates the need for gears, motors, and other mechanical components while also facilitating system redundancy.

Composite filaments containing varying FeO weight percentages were produced through microcompounding and extrusion, and shape memory performance was evaluated. Recovery angle measurements were utilized to quantify shape recovery behavior and determine if FeO amount influenced the recovery percentage. Thermal characterization included manual determination of the glass transition temperature (Tg) through differential scanning calorimetry (DSC), while mechanical performance was evaluated using stress-strain analysis to assess the effects of FeO loading on mechanical properties. In addition to conventional thermal activation, alternating magnetic field (AMF) heating was investigated to trigger remote composite actuation. Approximate temperature over time was measured using an infrared (IR) camera to quantify heating behavior. Vibrating sample magnetometry (VSM) was employed to determine the magnetic properties of the composites and estimate the actual FeO content within fabricated samples. At the same time, X-ray microscopy was used to characterize the FeO particle distribution and dispersion throughout the ideal 15 wt% FeO filament.

Preliminary findings indicate that lower FeO concentrations produce insufficient heating under AMF exposure to achieve activation. Alternatively, higher FeO loadings, ranging from 50–80 wt%, activate efficiently under AMF, but are not malleable enough to be used in 3D printing or prototypes. Results from the combined thermal, mechanical, magnetic, and microstructural analyses identified 15 wt% FeO as the optimal composition, providing sufficient AMF-induced heating while maintaining flexibility and optimal AMF shape memory activation. The implementation of these materials may enable the development of lightweight, remotely deployable structures and smart components for aerospace and other advanced manufacturing applications.

This work was supported by NASA RI Space Grant

Synthesis and Characterization of Iron α -Diimine Complexes and Exploration of Applications in Electrocatalytic Reactions

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A major contributor to global climate change is the rising level of CO_2 in the atmosphere due to the combustion of fossil fuels. Potential solutions to this problem include reduction of CO_2 to more useful organic compounds and the replacement of fossil fuels with hydrogen, a clean fuel source, which requires the development of new methods of hydrogen production, via reduction of protons. The most effective catalysts for these reduction reactions contain expensive platinum group metals. Research in the Carroll Lab focuses on developing electrocatalysts for these reactions utilizing cheaper 3d transition metals bound to redox active ligands, which may enable the two-electron transfer processes necessary to facilitate these catalytic reactions. We synthesized a series of iron tricarbonyl complexes containing α-diimine (DAB) ligands with varying imine and backbone substituents. These complexes were characterized using several analytical techniques including ^{1}H and ^{13}C NMR spectroscopy, cyclic voltammetry (CV), IR spectroscopy, and single crystal X-ray diffraction. Based on crystallographic data these complexes also are best described as containing a Fe(I) center bound to a radical anionic DAB ligand. CV data shows that each complex exhibits two or three reductions at potentials that vary in accordance with the electron donating abilities of the DAB ligand substituents. Research has focused on the activity of $Fe(^{F5Ph}DAB^{Me})(CO)_3$ as an electrocatalyst for proton reduction because it contains the least electron-rich metal center based on carbonyl stretching frequencies and exhibits a reversible reduction. In the presence of excess acid, the current of this reduction wave increases, which is indicative of proton reduction catalysis. To identify potential catalytic intermediates, reaction of the complex with a reducing agent and acid was explored. Addition of lithium triethylborohydride, a strong reducing agent, causes the CO stretching frequencies to decrease from 2047 and 1975 cm^{-1} to 1939 and 1867 cm^{-1}, suggesting that the complex has been reduced. Addition of triflic acid to this reduced product results in an increase in CO stretching frequencies to 2074 and 2027 cm^{-1}, which suggests that protonation occurred. In the future, we aim to optimize the electrocatalytic hydrogen production reaction, structurally characterize intermediates in the catalytic cycle, and explore reactivity with carbon dioxide.

This work was supported by a Providence College Walsh Summer Research Fellowship

Comparison of *Mya arenaria* Habitat Characteristics at Two Locations in the Great Salt Pond of Block Island, RI

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Soft-shell clam (*Mya arenaria*) populations in New England have been in decline due to the combined effects of warming temperatures and the introduction of European green crabs (*Carcinus maenas*) in the 1950s, which have decimated soft-shell clams in their overlapping habitats. Notably, in the Great Salt Pond (GSP) on Block Island, Rhode Island, there are areas where soft-shell clams have more success growing to adulthood. In Cormorant Cove, clams have been observed to grow with relative ease, while at Andy's Way, they are only able to grow to adult sizes when protected by predator exclusion nets, which were first used at the site in 2023. The goal of this study was to determine if there were habitat differences between Cormorant Cove and Andy's Way that might explain the differential survival of soft-shell clams between the two sites, as predation does not affect both sites evenly. Sediment samples of equal volumes were collected in 2025 (Andy's Way n = 6; Cormorant Cove n = 4), which were weighed to obtain bulk density. In-Situ Aqua TROLL 800 water sensors were deployed in the Spring of 2026 (March 19th through May 29th), which collected data on temperature, pH, and chlorophyll fluorescence for the water at both Andy's Way and Cormorant Cove. The distribution of bulk densities in the sediment did not significantly differ between the two test sites. However, temperature, pH, and chlorophyll-a fluorescence of the water varied significantly between the two sites. Temperatures were less extreme during the test period at Cormorant Cove, but they rose above maximum ideal values for clam growth (20°C) ten times at Andy's Way. This discrepancy between locations could be contributing to uneven soft-shell clam success by hindering growth or causing stress to the clams, making them more vulnerable to predation by the European green crab. Knowing what constitutes habitat conditions at each site and how they compare to optimal conditions for clam growth will inform which locations are ideal to place predator exclusion nets and attempt restoration in the GSP.

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Establishing Goal-Oriented Pollinator Gardens in Southeastern New England

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Bees and butterflies are vital to local communities, supporting ecosystem services such as food webs, decomposition, and pollination. Insect pollinator populations, however, are declining. One of the major factors causing this decline is habitat fragmentation due to urbanization. To help protect these insects, many communities have turned to pollinator gardens. As of 2024, more than one million gardens had been planted across the United States. These gardens aim to provide essential floral resources for bees and connect fragmented habitats. However, many of these gardens are left unmonitored, so their long-term effectiveness remains unknown. Our research aims to evaluate the long-term impacts of pollinator gardens by establishing clear goals. This summer, we prepared the ground for six 10’ x 15’ pollinator patches throughout the town of Swansea, Massachusetts. This fall, these patches will be planted according to the Somerville Pollinator Protection Plan and are expected to attract two target species: *Bombus griseocollis* (brown-belted bumble bees) and *Danaus plexippus* (monarch butterflies).
We are conducting mark-recapture surveys in order to estimate the local population size of each target species and how those populations change once pollinator gardens are installed. Over the duration of this longitudinal study, we predict that activity of the target species will increase as the gardens mature and provide more floral resources. Furthermore, as additional pollinator gardens are established throughout the area, we expect the target species to travel between gardens, creating a pollination corridor to connect otherwise fragmented pieces of land.

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Microwave-Assisted Synthesis and Characterization of Multifunctional Nanomaterials

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Heusler alloys, intermetallic compounds with the formula X_2YZ, show promise in their tendency to produce a split density of states, exhibiting both metallic and semiconductor properties depending on their spin orientation. This behavior can theoretically form spin polarized materials, which have the potential to produce next-generation spintronic devices. This experiment used a microwave reactor to create $〚Fe〛_2PtGe$ nanoparticle cores, with a quantum dot (QD) shell to create multifunctional materials. Direct QD shelling was done in situ with a two-part injection method but had limited results originally due to quenching of the QDs from the core. To mitigate this issue, subsequent runs were done with a double shelling method utilizing an intermediate MgO shell. Particles were examined via XRD, XRF, UV-Vis, and TEM to analyze their structural and optical properties. The produced cores were ~9.7 ± 2.6 nm and showed a disordered fcc-Pt XRD pattern when unshelled but exhibited an fcc-$〚Fe〛_3Pt$ pattern following the addition of the MgO shell. Shelling success was further confirmed by an increase in particle size from the TEM along with elemental analysis in XRF.

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Hypoxia Plus Heavy Metals Alters Growth in *Tetrahymena pyriformis*

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Freshwater environments are under stress from human activities including industrial pollution, run off and climate change. Water temperatures are rising as a result of climate change, lowering dissolved oxygen levels, while more and more metal pollutants are being found in freshwater everywhere. Our current understanding of the long-term effects these combinations could have on aquatic organisms and human health is limited. The EPA which tracks all types of conditions found across ecosystems has tracked many significant increases in temperature in freshwater streams, rising to an average 1.2°F greater than what it used to be, and 2.2°F in some places. *Tetrahymena pyriformis* is a ciliate found in nearly all freshwater environments and serves as an ideal model for toxicological studies. The goal of this project was to examine *Tetrahymena*'s response to the combination of hypoxia and toxicant exposure, specifically to represent conditions similar to those seen in freshwater environments as temperature and metal pollutants increase. Hypoxia conditions were mimicked by sealing culture tubes and growing in a static chamber to keep oxygen availability minimized. Normoxia was mimicked by leaving the culture tube cap loose and shaking to maximize oxygen availability. Cells were exposed to common heavy metals ($4x10^{-4}$ mM Cadmium, 0.3mM Copper, or 100mM Zinc) in hypoxic or normoxic conditions. Cell growth rate, cell size and expression of metallothionein (MT1) were measured after exposure. Growth rates were lower with hypoxia than normoxia, and cells exposed to zinc and hypoxia had a significantly lower growth rate compared with hypoxia alone. Cells exposed to hypoxia for 24h were significantly smaller than the cells in normoxia conditions. Zinc exposure alone, under normoxia conditions, resulted in significantly smaller cells. Exposure to metals increased MT1 gene expression, but there were no significant differences between hypoxia and normoxia. Collectively this demonstrates that hypoxia alters cell growth and may exacerbate metal toxicity. By studying *Tetrahymena pyriformis* under these conditions, we can learn more about the what the future of freshwater organisms could look like as climate change and global pollution continues to worsen, shedding light on a topic, where previously little was known.

This work was supported by RI-INBRE

Phagocytosis of Microplastics in *Tetrahymena pyriformis*

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Plastic pollution of aquatic environments is a growing environmental concern. Larger plastic waste is broken down over time into small and smaller fragments. Microplastics are common contaminants found in all environments and are considered a significant threat to organisms that consume them. *Tetrahymena pyriformis* is a ciliated protist found in most freshwater ecosystems. When hungry *Tetrahymena* encounters food, they use their cilia to sweep material into their buccal cavity. As the receiving vacuole fills with food and extracellular fluid, it pinches off becoming a food vacuole within the cell. *Tetrahymena* commonly consume small particles, yeast, bacteria, and other small molecules. The goal of this project was to determine whether *Tetrahymena* would phagocytose microplastics, and if other stressors would influence the rate of phagocytosis. *Tetrahymena* were grown in proteose peptone media. During log phase of growth, cells were exposed to 1% India Ink or 1% 1-5µm fluorescent microspheres. Samples were collected every 5 minutes for 30 minutes and fixed with 3% glutaraldehyde at each timepoint. Fixed cells were wet mounted, and the number of food vacuoles in 20 cells was counted under the microscope. *Tetrahymena* showed increase vacuole formation over time with India ink, and a steady rate of phagocytosis. *Tetrahymena* did phagocytose the microplastics, but at a lower rate of phagocytosis compared to India Ink. We also observed more microplastics per vacuole than India Ink particles, and higher aggregation of microplastics outside of the individual cells. These findings suggest that *Tetrahymena* will ingest microplastics in the aquatic environment and may represent a first step to microplastics entering the food chain. Future work will examine if other stressors influence the rate of microplastic phagocytosis to better understand this phenomenon.

This work was supported by RI NEST and SIMCoast

Feedback Structure May Impact Link Between Performance and Metacognitive Confidence Differently in ADHD and no-ADHD Groups

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Background: ADHD is often characterized by impulsivity and attentional deficits, both of which are often linked to impairments in internal time estimation mechanisms. In this project we aimed to identify how exactly timing deficits affect impulsivity-related learning deficits in those with ADHD, specifically with respect to the link between performance accuracy, metacognitive confidence, and feedback structure.

Methods: We ran two experiments: Experiment 1 included 161 online (Prolific) participants doing a time estimation task, and Experiment 2 included 16 participants doing the time estimation task, using a Tobii Eyetracker in the lab. The task required participants to estimate three durations (short – 3 seconds, medium – 5 seconds, and long – 10 seconds) and periodically rate their self-confidence and how well they believe they are performing. The ASRS.v1.1 scale was utilized to determine the severity of the ADHD symptoms, as well as a brief anxiety and impulsivity scale.

Results: Analysis has shown that the ADHD group made more timing errors overall than the noADHD group, in all three conditions; furthermore their errors tended toward under- rather than overestimation of durations. Self-confidence when completing the task was not different among the groups, while the ADHD group showed a correlation between higher self confidence and more errors. Gaze analysis showed differences in how ADHD and no-ADHD participants modulate their gaze and visual attention.

Discussion: Our findings indicate that there is a link between performance and metacognitive confidence, and the mechanisms behind this link may function differently in ADHD. Further work is needed to fully characterize how feedback structure may mitigate ADHD-related deficits in the confidence-performance link.

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Using AI Assistants Changes Cognitive Problem-Solving Profile and Physiological Responses to Stress

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Background: Within the rapidly developing world of Artificial Intelligence (AI) it is critical to understand how its use within problem solving tasks impacts our cognitive mechanisms and our mental health. The study evaluated how the choice to engage with generative AI related to task effort and engagement, creativity, and stress, as measured by heart rate and HRV.

Methods: We investigated how generative AI tools such as ChatGPT influence cognitive load, creativity, and physiological responses during creative generation tasks. 23 Providence College students completed a task that required them to create 8 short, narrative stories with varying emotional valence. They completed their task on a computer; their gaze was recorded via Tobii eye-tracker and their heart rate was measured through an arm band. Participant responses were later assessed using the Linguistic Inquiry and Word Count (LIWC) software tool.

Results: We found that the use of AI tools for narrative assistance changes cognitive load and physiological responses to stress. In the participants who chose to use AI to help with the task in various ways, active engagement with their narrative task with the aid of AI led to a decrease in cognitive load. Analyzing various dimensions from the LIWC scale revealed that the group that did not use AI had a higher level of use of causal words, implying that responses that aren't written by a generative artificial intelligence have a deeper explanation of their text. Heart rate patterns also showed differences between the two groups, with those who chose to use AI showing higher entropy and higher zero-crossing rates in their HRV dynamics, suggesting lower task engagement.

Discussion: Our findings indicate that use of genAI in creative problem solving may shift cognition from a focus on exploratory knowledge search and lateral thinking to a cognitive de-load as they focus on contextualizing and prompt-calibration. More work is needed to explore the potential benefits and costs of such cognitive changes.

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Three Passive Mechanisms Allow the Caudofemoralis Longus to Serve Terrestrial and Aquatic Locomotion in the American Alligator

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Animals that move across multiple environments often rely on the same muscles to perform mechanically distinct roles. The American alligator (*Alligator mississippiensis*) exemplifies this, transitioning between terrestrial walking and aquatic tail-powered swimming using the same hindlimb musculature. The caudofemoralis longus (CFL) spans from the tail to the thigh and knee, making it a powerful actuator for leg retraction and tail flexion, yet without a switching mechanism it risks causing the tail to flex during walking or the leg to paddle during swimming. We hypothesize that the transversus perinei (TP), which wraps around part of the CFL, behaves as mechanical clutch, redirecting CFL forces based on limb posture. Testing and manipulating specimens with and without the sling, we found that it is necessary for appropriate CFL force transmission across locomotor modes. The TP and posture stabilize the hip by pointing muscle forces into the anterior hip socket during tail-based swimming, while knee and ankle posture keeps the auxiliary tendon taut, preserving the force chain from leg to hip. This force chain locks the leg into place as the tail flexes for propulsion, enabling the alligator to swim without actively stabilizing the hindlimb. Two supporting passive mechanisms were also found; a fat pad separating the CFL from the ilio-ischio-caudalis (IIC), allowing each to contract independently so the alligator can paddle its legs and bend its tail out of sync during slow maneuvering behaviors, and skeletal geometry seating the femoral head more deeply into the acetabulum during fast swimming for passive joint stabilization. Together, these mechanisms form a clutch-like system enabling one of the alligator's largest muscles to serve radically different locomotor roles.

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Do Genome Editing Tools Effect Transformation Efficiency in *Sorghum bicolor*?

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Genome editing in sorghum is constrained by two major bottlenecks: transformation efficiency and limited genome editing throughput. In many systems effective genome editing depends on efficient vector delivery, stable integration of genome editing cassettes and regeneration of edited cells to plants. *Agrobacterium*-mediated transformation of sorghum remains restricted by limited transformation efficiencies, typically relies on immature embryos, limiting scalability and accessibility. CRISPR-Cas based genome editing tools including Cas9 for generating knockouts, and more precise approaches using base and prime editing have been used to successfully create mutant lines. Here, we compare the transformation efficiencies with performance of three major editing strategies, Cas9 knockout systems, cytosine base editors, and prime editors, while evaluating how editing architecture may influence overall transformation frequency outcomes. Extending a conceptual framework in which transformation success is determined by delivery, integration, and regeneration efficiencies, we describe editing success as the combined relationship between transformation efficiency (Te) and editing efficacy (Ee), together determining the number of regenerated T0 plants carrying heritable edits. Across all experiments in this study, Trex2-Cas9 knockout systems provided the most robust balance of Te and Ee, enabling consistent recovery of edited plants with indels. Transformation vectors with base editing functions, was associated with increased recovery of edited events. In contrast, prime editing showed inherently low Ee and lacked tolerance for reductions in Te, and incorporation of additional processing elements such as Csy4 did not alleviate these constraints. Overall, these results reveal that editing system architecture may influence both regeneration and heritable editing outcomes in sorghum, and highlight the need for optimized prime editing strategies that minimize complexity while preserving efficiency.

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Serotonin Transport and Ethanol-Associated Feeding in *Drosophila melanogaster*

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Serotonin is a key neuromodulator that regulates many behaviors, including mood, sleep, appetite, and cognition. Serotonin levels at the synapse are controlled in part by the serotonin transporter (SERT), which is also a target of several treatments for neuropsychiatric disorders. However, serotonin's effects are complex and often depend on the behavior and context being studied. Here, we investigated how the *Drosophila* serotonin transporter (dSERT) relates to ethanol-associated preference and feeding behavior. We compared dSERT16 loss-of-function mutants with w1118 controls when flies could choose between sucrose and ethanol. We hypothesized that dSERT16 flies would differ from controls in licking, feeding-event number, or ethanol preference. Using the Fly Liquid-food Interaction Counter (FLIC), we continuously recorded feeding from 36 chambers, with 18 chambers per genotype for five days. Each chamber contained sucrose and 15% ethanol. We compared transformed licks by food source, feeding-event number, total licks over time, and event preference using mixed ANOVA and Welch tests. In an exploratory food-specific comparison, dSERT16 flies produced fewer transformed ethanol licks than controls (6.94 vs. 8.40; Welch $p = 0.016$), while sucrose licks did not differ (8.00 vs. 8.63; $p = 0.522$). The genotype × food interaction was not significant ($p = 0.336$), and feeding-event number did not differ by genotype ($p = 0.591$). Across genotypes, flies made more feeding events at sucrose than at ethanol (food effect $p = 0.001$). Total licks and event preference over time also showed no significant genotype effects ($p = 0.132$ and $p = 0.129$, respectively). These preliminary results suggest that disrupting serotonin transport may influence ethanol-associated licking without producing a broad change in feeding or ethanol preference. Future work will test additional cohorts and examine lick duration, bout structure, and locomotor activity. Separating intake, feeding-event frequency, and preference may help identify behavioral effects that are missed by total consumption alone.

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Characterizing Serotonin Levels in the Brain of the *Drosophila* Serotonin Transporter Mutant (dSERT)

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Serotonin is a highly conserved neuromodulator that shapes a range of behaviors across nearly all animal phyla. The serotonin transporter (SERT) clears serotonin from the synaptic cleft through reuptake and is the main target of widely prescribed antidepressants (SSRIs). *Drosophila melanogaster* serves as a model system for studying SERT function, as a set of roughly 80-100 serotonergic neurons broadly innervates the central brain and can be visualized in whole-mount preparations. How the loss of long-term SERT function affects serotonin levels in the brain, however, remains poorly understood. Here, we asked whether serotonin levels differ between loss-of-function dSERT mutants and controls. To investigate this, we performed whole-mount immunohistochemistry on dissected adult brains from dSERT mutant flies (1-4 days old) and their corresponding w1118 genetic controls. Brains were labeled with a rat anti-serotonin primary antibody and a fluorescent (AF488) secondary antibody and mounted in glycerol-based medium for fluorescence imaging, after which serotonin immunoreactivity were compared across genotypes. Serotonergic cell counts and innervation patterns were also analyzed. We predict that dSERT mutant brains will show altered serotonin levels relative to controls, and accompanying differences in the distribution or projection patterns of serotonergic neurons. By characterizing serotonin in dSERT mutants, this work will clarify whether the loss of serotonin reuptake alters serotonergic signaling in the adult brain, potentially linking neuromodulatory function with the memory- and reward-related behaviors it mediates.

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Studying the Relationship Between Cellular Respiration and Mutated Clock Gene Expression Patterns

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Drosophila have circadian rhythms which are daily biological rhythms synchronized by an internal clock. The internal fly clock is made of an oscillating gene-protein feedback loop found in central pacemaker cells in the brain which sets endocrine, locomotor, and metabolic rhythms to the 24-hour Earth day. The central clock signals to peripheral clocks, setting rhythms that can be studied in research. Mutations to these clock genes disrupts the oscillator, resulting in rhythm changes. In this project, we will study how flies' circadian rhythms and cell respiration in the brain changes with mutations to the clock genes. In the future, we will aim to visualize where these clock genes are most present in the brain. By measuring oxygen consumption in the brain at different times of day, we can plot the flies' metabolic circadian cycle. This data will then allow us to evaluate how alterations in clock function alter brain metabolism. The use of locomotion monitors and the Agilent Seahorse HS XF Mini Analyzer will allow up to plot the cycle of the molecular clock and the rhythm of activity against fly brain cellular activity in normal and mutated flies.

This work was supported by Providence College

Investigating the Substrate Specificity of Azo Bond Reduction in the Human Gut Microbiome

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The human gut microbiome can metabolize drugs, which can either cause unintended side effects or be used to activate drugs in the large intestine. An individual's variable microbial composition, coupled with our limited understanding of the enzyme function and specificity, complicates predictions of therapeutic outcomes. One well-studied family of enzymes, azoreductases, is known to reduce azo bonds (a nitrogen-nitrogen double bond), which are found in drugs and food dyes. Azo dyes can also be reduced nonenzymatically by hydrogen sulfide, a bacterial metabolite produced during sulfate and cysteine metabolism. Previous studies suggest that azoreductases reduce the quinone-like tautomer of azo compounds, requiring a para-substituent capable of donating electron density through resonance for complete reduction to the corresponding aniline products. To test this mechanism, this study investigates how the electronic properties of azo compounds influence their susceptibility to reduction by the gut-abundant azoreductase, R5RX41. We synthesized a library of 39 structurally diverse azobenzene compounds spanning a range of electron-withdrawing and electron-donating substituents. Of these, the reduction potential of 30 was measured to characterize its abiotic redox behavior, with ongoing efforts to characterize anaerobic reduction by sulfide. The measured reduction potentials ranged from -0.823 V to -0.591 V among the phenylazophenol derivatives, from -0.988 V to -0.566 V for the sulfonic acid derivatives, and from -0.726 to -0.431 for the benzoic acid derivatives, highlighting clear electronic effects on reduction behavior. Concurrently, enzymatic reduction rates for multiple compounds have also been measured to evaluate whether substrate specificity is governed by the proposed mechanism. Preliminary correlation with Hammett σ_R constants showed no linear relationship ($R^2 = 0.002$, slope = 0.08) for one set of compounds and a moderate negative linear relationship for another set of compounds ($R^2 = 0.1$, slope = -0.4), consistent with the proposed mechanism. These findings broaden our understanding of microbial azoreduction, helping to develop safer therapeutics for treating diseases of the large intestine and supporting future personalized medicine efforts.

This work was supported by Providence College

Abundant and Ubiquitous Drug- and Dye-Modifying Azoreductase Activity in the Human Gut Microbiome

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The human gut microbiome is composed of trillions of microorganisms that produce enzymes that can metabolize various types of xenobiotics we consume. Understanding the mechanisms and rates of these enzymes can improve health outcomes and treatment for various gut diseases, including colitis and cancer. One of the most prototypical examples of gut bacterial drug metabolism is by a family of enzymes known as azoreductases (AzoRs), which can reduce the nitrogen-nitrogen double bond found in certain xenobiotics. However, research on these proteins has primarily focused on those from model organisms, such as *E. coli*, while not characterizing those most commonly found in the human gut microbiome. Using a bioinformatic analysis of this family, we identified candidate azoreductases that are found in most individuals and in high abundance. We screened multiple of these AzoRs for solubility and activity. We then determined the kinetic parameters of those active enzymes by monitoring changes in absorbance over time, analyzing the reduction of various dyes and drugs. We kinetically characterized an AzoR from Alistipes sp. CHKCI003, with 4 xenobiotics. The food dyes amaranth and indigo carmine, the pH indicator ethyl red, and a quinone-like molecule, phenol blue. Indigo carmine exhibited the greatest catalytic efficiency with ACAzoR (kcat/KM value of 4 x 105 $M^{-1}s^{-1}$), but similar efficiencies with phenol blue and ethyl red (kcat/KM of 2.1 x 105 $M^{-1}s^{-1}$ and 2.9 x 105 $M^{-1}s^{-1}$, respectively) and amaranth was the least catalytically efficient with our enzyme (kcat/KM of 1.1 x 104 $M^{-1}s^{-1}$). We have obtained a soluble and active AzoR from Bacteroides ovatus that we are currently working to kinetically characterize, it appears to reduce 8 xenobiotics. We are also pursuing the AzoR from *Clostridium symbiosum*, representing the last set of commonly found AzoRs from the human gut. They have proven difficult to characterize because they are membrane-bound proteins, and we have not yet been able to obtain soluble protein to begin in vitro characterization. Currently, we are working on genetic knockouts in *E. coli* W3100 so that, in the future, we can characterize the membrane-bound proteins in vivo. Characterizing these abundant and ubiquitous AzoRs can enable us to predict how their orthologs will react, while focusing on the most abundant and ubiquitous gut microbial proteins provides insight into reactions occurring in most people, which has the potential to aid personalized medicine.

This work was supported by Providence College

Influence of Fluctuating Salinity on Marine Bacteria from Mt. Hope Bay

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Climate change is an increasing threat to organisms that depend on stable environmental conditions to survive, particularly in marine ecosystems where bacteria play essential roles in ecological processes such as nutrient cycling. Estuaries such as Mt. Hope Bay, which contains a mix of saltwater from the ocean and freshwater from the Taunton River, may be especially vulnerable to these changes. As sea levels rise and saltwater floods into freshwater environments, salinity patterns may shift, making it crucial to understand how bacteria adapt to different environments and how much change they can tolerate. In this study, bacteria were collected from the sediment of Mt. Hope Bay using a Van Veen grab, strains were isolated and identified by Sanger sequencing, and salinity growth tests were performed to determine salt tolerance. Four bacterial genera were isolated and identified: *Guptibacillus*, *Priestia*, *Bacillus*, and *Rossellomorea*. Salt tolerance tests were performed on each genus of bacteria ranging from 0-8% to determine their salinity tolerance, and it was shown that the isolated bacteria can grow more in environments with lower salinity levels compared to higher salt environments. Some of the isolated bacteria tolerated high-salinity conditions with reduced growth, while others failed to grow. Sea level rise causes an influx of higher-salinity water into estuarine environments, increasing overall salinity (Baird, 2020) and potentially decreasing populations of bacteria, like *Rossellomorea*, that are less tolerant of high-salinity environments. Estuaries also experience natural changes in salinity due to the input of freshwater, making it important to understand both the upper and lower salinity levels these bacteria can tolerate. Studying salinity tolerance in marine bacteria can further our understanding of how these organisms will respond to rising sea levels in coastal environments and how changes in bacterial communities may affect marine ecosystems.

This work was supported by RI NEST

Screening Oxidative Stress Proteins for Hyper Kinetic Stability

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Even though there have been major recent advances in protein structure design, protein kinetic stability is still an understudied topic. Model proteins, such as superoxide dismutase 1 (SOD1), have been documented to be hyper kinetically stable, presumably due to their interactions with unstable molecules, like reactive oxygen species (ROS). When the amount of ROS exceeds the amount of antioxidants in the cell, this reactiveness can lead to interactions with a cell's components causing irreversible damage that leads to several diseases. We have constructed a protein database of ~300 hyper stable, SDS-resistant proteins. Of this database, more than 12% work with ROS. This experiment aimed to analyze whether this characteristic of hyper stability is present throughout additional oxidative stress proteins. To explore this, we performed Boiled/Unboiled gel electrophoresis. In this method, the same protein is exposed to sodium dodecyl sulfate (SDS) in two different environments, one is kept on ice and the other is put under extreme heat for a specific amount of time. Non-kinetically stable proteins fold and unfold regularly, leading to irreversible SDS trapping in either environment. In the resulting gel, this will appear as two lanes with similar protein migration. However, hyper kinetically stable proteins do not unfold under the environmental stress of SDS alone, they require extra energy, like heat, to unfold. This will appear as two lanes with vastly different protein migrations. We found evidence that contradicted previous claims that hyper stability is a crucial adaptation for proteins that work with the unstable ROS molecules. SOD2 and peroxiredoxin 5 (PRDX5) were found to be non-kinetically stable. There is a need to explore the evolutionary, structural, and environmental differences between these proteins to investigate why some are kinetically stable while others are not, even though they have the same function. Gaining a deeper understanding of protein stability, especially in the context of oxidative stress proteins, may lead to a better insight into their related diseases and treatments.

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Comparative Characterization of Markers Brain Injury in Woodpeckers and Songbirds

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Repetitive cranial impacts and mild traumatic brain injuries (mTBI) in mammals induce neurodegenerative pathologies, notably cell death and the formation of neurofibrillary tangles (NFTs). While adult headbutting mammals, such as musk oxen, exhibit extensive hyperphosphorylated tau accumulations (a marker of tau pathogenicity), our preliminary data in wild-caught woodpeckers reveal a surprising absence of these aggregates. This contrast challenges earlier findings based on museum woodpecker specimens and suggests unique neuroprotective adaptations. Accordingly, we hypothesized that woodpeckers demonstrate few tau aggregates and degenerating neurons in mTBI-vulnerable regions compared to non-drumming birds. To test this, we evaluated brain trauma markers across avian species with varying impact ecologies. We compared drumming woodpeckers (Downy Woodpecker, Red-bellied Woodpecker, and Northern Flicker) to niche-matched, non-drumming songbirds (White-breasted Nuthatch and Tufted Titmouse), alongside chickens. Unilaterally injured Zebra Finch puncture model along with PS19 tauogenic mice served as positive controls for cell death and NFTs, respectively. Histological assessments utilized PathoGreen, Thioflavin-S, and Gallyas staining to detect degeneration, fibrillar aggregates, and NFTs, respectively. Our findings were complemented by anterior pallium transcriptomics to identify differential gene expression of transcripts and pathways linked to cellular damage and stress responses. Overall, both woodpeckers and songbirds exhibited a negligible presence of NFTs compared to PS19 mice. Furthermore, while we observed sparse cell death in these wild-caught birds, it was minimal compared to the extensive damage seen in the injured Zebra Finches. By contrasting these findings with those of impact-adapted mammals, our work highlights the profound evolutionary heterogeneity of brain trauma resilience and underscores to possibility for novel physiological mechanisms for trauma mitigation.

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Characteristics of Deleted Loop Regions in zPol θ to Confirm Critical Functional Homology Between zPol θ and hPol θ

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The DNA polymerase theta (Pol θ) plays an essential role in the repair of DNA damage such as double strand breaks via translesion synthesis and theta-mediated endjoining. Specific DNA damages targeted by Pol θ include a-basic, 8-oxoG, thymine-Glycol, cyclobutane pyrimidine dimers, etc [1]. Within the structure of human Pol θ (hPol θ) are three specific loop regions that are key for this specific DNA repair mechanism, where loop regions 1, 2, and 3 are located in the subdomains thumb (DNA binding), fingers (nucleotide binding), and palm (catalytic site) domains respectively. Initial functional studies suggest that *Danio rerio* or zebrafish Pol θ (zPol θ) is like human Pol θ, and a structural analysis using AlphaFold suggests a similar structure. Despite zPol θ and hPol θ sharing homology in structure and sub-domain/full-length amino acid sequences, the loop regions vary in amino acid sequences. However, zPol θ and hPol θ share biochemical characteristics even though the essential loop regions differ in amino acid sequences between zPol θ and hPol θ. To confirm that the loops in zPol θ are functionally as important as human (and to verify AlphaFold structure prediction), we generated deleted loop regions into the pSUMO zPol θ vector. Furthermore, deleted constructs were expressed in *E. coli* and assayed for DNA repair activity. Initial observations suggest that there is a significant reduction in DNA repair activity in Delta 2 and 3, especially in bypassing specific DNA damage, compared to human Pol θ wild type. This reduction in activity aligns with human delta constructs suggesting that these loops are equally important for translesion synthesis in zebrafish as well as confirms the AlphaFold predicted model of zPol θ. Many hypothesize that carcinogenesis is enhanced by Pol θ due to the error prone nature of the necessary mechanism Pol θ uses for repairing double-strand breaks, such as theta-mediated endjoining and translesion synthesis, as well as the abnormal behavior of Pol θ in cancer cells. The similarity of dependence on loop regions for both zPol θ and hPol θ presents the possibility of utilizing zebrafish as a model organism for studying the abnormal behavior of Pol θ in cancer.

This work was supported by RI-INBRE

Building a Library of Platinum Anticancer Agents to Overcome Chemoresistance

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Multidrug resistance (MDR) remains a formidable challenge in cancer treatment. Overexpression of efflux pump transporters is associated with the resistance to a wide spectrum of chemotherapeutics, yet effective clinical strategies to overcome MDR are still limited. To mitigate this urgent issue, we have built a library of platinum-containing anticancer agents by attaching conventional anticancer drugs to a platinum pharmacophore. Our preliminary in vitro studies show that these drug conjugates not only retain the anticancer activity of the parent drugs but also effectively kill MDR cancer cells.

This work was supported by RI-INBRE

Myror of ÖLand: Natural History and Environmental Biology of Ants from Sweden to New England

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Biodiversity and natural history forms the foundation of ecology and evolutionary biology. Last year a new ant species was identified in North America, *Myrmica rugulosa*. *Myrmica rugulosa* is a species of myrmicine ant typically found in Northern and Central Europe, having an especially high density in Sweden and Belgium. As a relatively cryptic ant, despite its abundance in Europe, little is known about this ant in its native range and even less about its behavior and ecology in its introduced range. Building on this discovery of a new invasive ant species in New England, I traveled to Öland, Sweden to find and document its behavior and natural history in its native environment. This project allowed us to survey for ants species in *M. rugulosa*'s native habitat. Using a variety of collection methods, we collected and preserved 70 ants from over 15 species that can be compared to the *Myrmica rugulosa* specimens. In this poster, we highlight a range of different ant species we collected, photographed, and identified from different surveying locations across the island Öland, off the coast of mainland Sweden.

This work was supported by the Center for Engaged Learning at Providence College

Association Between Sodium-Glucose Cotransporter-2 Inhibitor Use and Gout Prevalence Among U.S. Adults with Diabetes: A Population-Based Cross-Sectional Study

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Background: Previous studies have suggested that sodium-glucose cotransporter-2 inhibitors (SGLT2i) may reduce the risk of gout flares and all-cause mortality among patients with gout and type 2 diabetes mellitus (T2DM) compared with glucagon-like peptide-1 receptor agonists (GLP-1 RA) and dipeptidyl peptidase-4 inhibitors (DPP-4i). However, these findings have been inconsistent and may not be generalizable to the U.S. population.

Objective: To evaluate the association between SGLT-2i use and the prevalence of gout among U.S. adults with diabetes using data from the National Health and Nutrition Examination Survey (NHANES).
Methods: A population-based cross-sectional study was conducted using NHANES data collected from 2017-2020. Adults who self-reported a physician diagnosis of diabetes were eligible for inclusion. Participants without documented ICD-10-CM diagnostic codes were excluded. Exposure was defined as current use of an SGLT2i, GLP-1 RA, or DPP-4i based on generic medication names and drug codes. Gout was identified using ICD-10-CM codes M10.9 (gout, unspecified), M10.9P (prevent gout), or M1A (chronic gout).

The association between SGLT2i use and gout prevalence was evaluated using odds ratios (ORs). Multivariable logistical regression and 5:1 propensity score matching was performed to adjust for potential confounding. Adjusted odds ratios (aORs) and 95% confidence intervals (CIs) were estimated. Statistical significance was defined as a two-sided p-value < 0.05. All analyses were performed using SAS version 9.4.

Results: Among 1,339 eligible participants, 74 were receiving SGLT2i therapy and 1,265 patients were not. Following 5:1 propensity score matching, 67 SGLT2i users were matched to 335 controls, achieving excellent covariate balance (largest standardized mean difference < 0.05).
In the unadjusted analysis, SGLT2i use was not significantly associated with gout prevalence (OR: 0.280, 95% CI, 0.038-2.050). Multivariable logistic regression adjusting for age, body mass index, sex, alcohol use, kidney disease, and serum uric acid likewise demonstrated no statistically significant association (aOR: 0.370, 95% CI, 0.049-2.784). Similarly, propensity score-matched analysis showed no significant association between SGLT2i use and gout prevalence compared with non-use (OR: 0.445, 95% CI, 0.056-3.156).

Conclusion: SGLT2i use was not significantly associated with gout prevalence among U.S. adults with diabetes in the nationally representative

This work was supported by RI-INBRE

Benchmarking Computational Deconvolution Methods for Rare Cell Detection

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The ability to detect rare cell types within tissue samples is a critical aspect of being able to understand cancer progression. One cost-effective way to estimate cell type proportions is by using computational deconvolution methods. However, the accuracy of these methods in identifying cells with low proportions is very inconsistent. We set-out to evaluate existing deconvolution methods on a unique set of pediatric liquid biopsy samples to identify different performance benchmarks with the long-term goal of developing an optimized deconvolution machine learning tool for detecting rare cell types in cancer liquid biopsy samples. For benchmarking of current computational methods on rare cells, we generated pseudo bulk data from single cell liquid biopsy data with known cell proportions focused on low proportion cell type presences and applied MuSiC, ReDeconv, and DWLS. To evaluate the performance of cell detection on each method we calculated three statistical metrics with respect to ground truth: Pearson's correlation, RSME, and mAD. Clear performance variation emerged across methods. MuSiC was able to achieve the highest correlation, as high as 0.96, as rare cells were spiked-in to the pseudo bulk datasets. In contrast, ReDeconv demonstrated a decrease in correlation as more rare cells were spiked-in. Significantly, a vulnerability was shared as each existing method struggled to make predictions at 0%. Our results not only revealed the gaps in current deconvolution methods but confirmed our choice to use MuSiC as our benchmark for developing our own optimized tool.

This work was supported by RI-INBRE

Investigating the Role of STIM1 in Sea Urchin Embryonic Development

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Stromal interaction molecule 1 (STIM1) is a transmembrane Ca^{2+} sensor protein located in the endoplasmic reticulum (ER). When STIM1 detects Ca^{2+} depletion in the ER, it oligomerizes and activates to replenish Ca^{2+} through transmembrane Orai channels at the membrane. The STIM pathway is an important regulator of cell migration and mediates the Epithelial to Mesenchymal Transition (EMT). The role of STIM1 has been extensively explored in certain tissues and cell lines; however, understanding of its role in early embryogenesis remains somewhat limited. In this study, we used *S. purpuratus* sea urchin embryos as a model system to investigate the expression patterns and functions of STIM1. Immunofluorescence followed by confocal microscopy was used to determine the localization of STIM1 across developmental stages, which showed enrichment in the cortex and tubulin in 16-cell-stage embryos. In the blastula stage STIM1 was observed in the spindles and asters. To test the roles of STIM1, we knocked down STIM1 using a morpholino antisense oligonucleotide (STIM1 MO), which slowed cell cycle progression at the 16-cell stage and, at higher doses, caused embryonic lethality by the blastula stage. These phenotypes were rescued by STIM1 mRNA introduction. This indicates that the observed phenotypes were due to the STIM1 knockdown. Overall, these observations suggest that STIM1 plays a critical role in early embryogenesis of the sea urchin.

This work was supported by RI-INBRE

Essential Tremors

Joseph Campione, Peter Chim, William Johnston, Jack Phillips, Brian White & Marwan Abdelatti

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Assessing tremors is a difficult process because no direct diagnostic test exists. Clinicians rely on subjective rating scales scored during brief office visits, which capture only a narrow snapshot of a fluctuating symptom. This problem matters when distinguishing essential tremor (ET) from Parkinson's disease (PD), since early presentations often look similar, and clinicians frequently misclassify them. Yet, the conditions require different treatments and carry different prognoses. Wearable inertial sensors in consumer smartwatches offer continuous, objective measurement, but large-scale validation remains limited. Existing efforts also treat ET as a secondary class, leaving it largely unstudied. We developed an automated pipeline to classify tremor using the PD Smartwatch dataset (PADS). This is one of the largest public efforts containing bilateral sensor recordings from standardized movement tasks. Exploratory analyses such as PCA and t-SNE revealed substantial overlap between natural movement and tremor-related motion, which limits the utility of single-sensor approaches. Guided by this finding, we trained deep sequence models including BiLSTM and TCN. These models distinguish Parkinson's patients from healthy controls, and non-Parkinsonian tremor disorders from healthy controls. Our approach achieved [89%/.91auc], improving by [13%] over the original PADS study classifiers. We used explainability methods like SHAP, saliency, and attention maps. These tools confirmed that model decisions track physiological tremor features rather than artifacts. They also identified which tasks and signal features carry the most diagnostic information. Our next phase deploys a multi-modal sensor rig, where EMG and fingertip tactile sensing separate true tremor from task movement. We will collect an essential tremor-enriched dataset locally using our highest-value tasks to enable direct tremor discrimination.

This work was supported by RI-INBRE

This presentation has been withdrawn

Synthesis and Metal Complexation of Schiff Base Ligand Library for G-Quadruplex Binding Studies

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In many cancers, cells undergo uncontrolled proliferation through the enzyme telomerase and maintain telomere length, allowing them to divide indefinitely and drive tumor growth. Guanine quadruplexes (G4s) are structures that form in G4-rich regions such as telomeres, using Hoogsteen base pairing to form three-dimensional structures with varying geometries and unique metal-binding properties. G4s have been found to play important roles in protecting telomeres, regulating gene expression, and inhibiting telomerase access to telomeric DNA. These G4 structures can also be stabilized with organic ligand-based metal complexes, which are attractive due to their unique electronic, geometric, and even catalytic properties. These specialized binders are promising in future cancer-related research, as their modulated structures make them ideal for increasing selectivity towards G4s associated with oncogene promoters and telomeres. This study focused on the synthesis, collection, and analysis of a series of organic ligands and their metal complex counterparts. By varying the diamine component of these ligands, complementing a parallel study on aldehyde variation, Cho Lab has synthesized a combined library of ten organic ligands to date, calculated their yields, and characterized them using both IR and NMR spectroscopy. The group also generated a series of Ni(II)-based metal complexes and set up crystallization trials for future X-ray crystallographic analysis.

This work was supported by RI-INBRE

Biochemical Protein Workflow for Future Combinatorial Biosynthesis of Novel Siderophores

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Siderophores are iron-chelating natural products produced by microbes that play essential roles in microbial host survival. By utilizing these remarkable iron-chelating abilities within microorganisms such as bacteria, we can scavenge Fe(III) to be used in combinatorial biosynthesis for bioremediation, as this sequestration may reduce toxic levels of heavy metals present in wastewater and contaminated soils. Our research in Cho Lab aims to ultimately mix and match proteins responsible for synthesizing siderophores in the hopes of synthesizing these novel metal-chelating compounds.

As a new research lab at Providence College, we have worked to establish our own lab space and protocols, as well as laid out the foundations for our future goals and directions. Throughout summer research, Cho Lab has completed many of the vital goals of our new lab, including expressing and purifying desired proteins, analyzing the proteins with various techniques, and implementing our own standard operating procedures. As proof of concept, we successfully carried out the full workflow — transformation, expression of His-tagged protein, purification via Ni-NTA affinity column chromatography, and protein quantification via SDS-PAGE — using two known acyl carrier proteins as practice substrates. With this workflow validated, we are now positioned to apply it to carrier proteins actually involved in siderophore production.

Future work will include building a library of amino acid sequences of various carrier proteins from different microorganisms producing siderophore, running multiple sequence alignments, performing sequence-level analysis on Sfp-compatibility, isolating these carrier proteins, and conducting in vitro activation of these carrier proteins using Sfp.

This work was supported by a Walsh Student Research Fellowship

Reproducible Fluorescent Labeling of *Clostridium novyi*-NonToxic Spores with Preserved Spore Viability

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Clostridium novyi-NT is a spore-forming bacteria with strong potential for development as a cancer therapeutic modality through the application of engineering biology principles. However, the structure of its spore coat and how the spore interacts with different environmental conditions remains poorly understood. This knowledge gap limits the development of effective fluorescent imaging techniques – particularly for in vivo applications. Reliable staining of *Clostridium novyi*-NT spores is critical for pre-clinical characterization and further therapeutic advancements. However, most commercially available fluorescent staining protocols are intended for eukaryotic cells and are poorly suited for bacterial sores due to their complex, multilayered structure, which can limit dye penetration. Here, previously published methods were optimized to stain *C. novyi*-NT spores with carboxyfluorescein succinimidyl ester (CFSE) with adjustments to dye concentration, incubation conditions, and methodological parameters to ensure consistent fluorescence while preserving spore integrity and germination capacity. Preservation of these capacities directly impacts therapeutic efficacy and are therefore anti-cancer activities. Through development of a low cost, accessible, and reproducible methodology, this approach enables consistent detection and visualization of *C. novyi*-NT spores and provides a framework adaptable to alternative fluorophores and related spore-forming systems. Ultimately, this undergraduate research project developing alternative C. novyi-NT detection modalities will expand downstream experimental applications and facilitate clinical translation, including therapeutic strategies for metastatic pancreatic cancer and other solid tumors.

This work was supported by RI-INBRE and URI College of Pharmacy

Optimizing CRISPR Associated Transposons (CASTS) to Limit Virulence of *Vibrio* Pathogens within Aquaculture and Human Microbiomes

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Vibrio parahaemolyticus is an aquatic pathogen that accumulates in oysters and causes food-borne illnesses such as gastroenteritis in humans, as well as Acute Hepatopancreatic Necrosis Disease, which threatens shrimp aquaculture. The current and previous practices for managing Vibriosis in aquaculture are limited to probiotic and antibiotic treatments but may result in antibiotic resistance and have varying results. To address this issue, this project explores the possibility of using microbiome editing, an emerging technique of selectively targeting bacteria in a site-and species-specific manner within mixed microbial communities, to control *Vibrio* abundance. This project takes the first step towards this goal by optimizing a new class of genome editing tools, called CRISPR-associated transposons (CASTS) for editing within *V. parahaemolyticus*. The goal of this project is to optimize two distinct plasmid features that may affect editing efficiency and accuracy: 1) the promoter strength driving the CASTs and 2) CAST source bacteria (e.g., *Vibrio* (VchCAST) or *Pseudoalteromonas* (PtrCAST)). To accomplish this goal, new plasmid parts were developed using Gibson assembly, plasmid parts were combined and guides were cloned using Golden Gate assembly, and the fully assembled plasmids were conjugated into *V. parahaemolyticus*, using an editing efficiency assay to compare the plasmid structures. In total, four new plasmid structures were generated, each with a non-target and safe site guide, resulting in seven total plasmids constructed and confirmed for this project. We observed that pLac resulted in a higher editing efficiency under these conditions compared to J23119. Additionally we saw that VchCAST resulted in higher integration than PtrCAST within our experiment. These findings are important because they lay the foundation for a new intervention in aquaculture that has the potential to improve food quality and quantity within aquaculture hatcheries while also improving food safety and protecting consumer health.

This work was supported by RI-INBRE

Amidated Tung Oil for Sustainable Wood Coatings

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The growing demand for sustainable materials has increased interest in renewable alternatives to petroleum-derived wood sealants. Conventional petroleum-based coatings rely on finite fossil resources and often release volatile organic compounds (VOCs), which contribute to air pollution and pose potential health risks. Consequently, renewable plant-derived materials have emerged as promising environmentally friendly alternatives. Tung oil (*Vernicia fordii*) is a naturally obtained drying oil that has been used as a wood finish that forms a durable, protective layer on the wood. Although tung oil is renewable and biodegradable, its slow curing rate, characteristic odor and potential safety concerns leaves room for further optimization. This project investigates whether tung oil can be chemically modified through amidation and the removal of characteristic ester backbone to produce a bio-based product for the development of improved, environmentally- friendly wood sealants. Filtered tung oil was subjected to a one-pot amidation reaction using a diamine reagent and basic catalyst under controlled heating conditions. Following amidation, the reaction was purified through a series of filtrations and extractions using pentane and dichloromethane (DCM) with aqueous and brine washes before product isolation. The resulting product was then characterized using FT-IR, and 1H-NMR to monitor the conversion of ester groups into amide groups allowing for the evaluation of reaction success. 1H-NMR and FT-IR analysis demonstrated the disappearance of the ester group accompanied by the appearance of amide moiety. Although additional purification steps may be necessary to remove reaction impurities, the collected spectroscopic data indicated that amidation of tung oil was successfully accomplished. Successful conversion of tung oil represents an important step towards the development of renewable, plant-based coating materials that may provide environmentally sustainable alternatives to conventional synthetic wood sealant. Future work will investigate how amidation influences properties such as odor, wood penetration, and overall sealing performance.

This work was supported by RI-INBRE

Evaluating the Antimicrobial Activity of Durlobactam Against Carbapenem-Resistant Enterobacterales

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Antimicrobial resistance is an urgent public health threat with more than 2.8 million associated infections in the US per year. Carbapenem-resistant Enterobacterales (CRE) that produce metallo-β-lactamases (MBLs) represent a particularly dangerous group of bacteria resistant to nearly all antibiotics, including drugs often considered to be the last resort. With limited treatment options available and documented resistance to these options rising, we aimed to study durlobactam's antimicrobial properties to determine whether it could serve as an additional treatment option for clinicians against CRE.

Minimum inhibitory concentrations (MIC) of durlobactam were initially determined against 12 MBL producing *E. coli* isolates in duplicate using broth microdilution. Bacterial colony counts were standardized to 6 log10 CFU/mL in 96-well plates, which were then inoculated in a series of decreasing durlobactam concentrations and incubated overnight. Five isolates (AR#0137, AR#0151, AR#0162, AR#1055, AR#1035) were then selected for pharmacodynamic evaluation using static 24-hour time-kill assays (TKAs) in triplicate, simulating clinical durlobactam concentrations (fCavg,ss: 17.6 µg/mL). CFU/mL of each isolate was sampled at 0-, 4-, 8-, and 24-hour time points to monitor bacterial activity. A quantitative evaluation was performed to determine whether the action was bactericidal (> 3 log10 CFU/mL reduction from the initial inoculum), bacteriostatic (<3 log10 CFU/mL reduction from the initial inoculum), or if regrowth was observed at 24 hours. Bacterial colony counts were compared at all time points by two-way analysis of variance using Tukey's post-hoc test. A p-value of ≤ 0.05 was considered significant.

The most frequent MIC observed for the various *E. coli* isolates was 0.25 µg/mL, with a few at 2-4 µg/mL. Isolate AR#0149 demonstrated a particularly high MIC at 64-128 µg/mL. Each isolate that progressed to TKA testing demonstrated significant bactericidal activity between the starting inoculum and the 8-hour mark ($p < 0.05$). Regrowth was observed at the 24-hour mark and did not result in any significant difference from the starting inoculum for AR#0137 ($p = 0.77$), AR#1055 ($p = 0.56$), and AR#1035 ($p = 0.25$). Statistically significant sustained bactericidal kill was observed for AR#0151 ($p < 0.001$) and AR#0162 ($p < 0.001$).

Durlobactam demonstrated significant antimicrobial activity against the selected *E. coli*. Determining the effectiveness of durlobactam against specific isolates requires a holistic consideration of all relevant durlobactam resistance genes and recorded MICs. Further testing should assess possible genetic mutations in these resistance mechanisms to isolate the specific drivers of durlobactam's antimicrobial properties.

This work was supported by RI-INBRE

Mechanism of O^6-Methylguanine Oxidative Demethylation by FTO-Mediated Repair and Its Implications for Disease

Luke Tomosieski, Jian Ma, Roy Chen, Evans Boateng & Deyu Li

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Maintenance of genomic integrity is essential for cellular survival, and DNA repair pathways protect against endogenous and exogenous damage that can lead to mutagenesis, cancer, and other diseases. O^6-methylguanine (O^6mG) is a highly mutagenic DNA lesion generated by endogenous and exogenous methylating agents, which disrupts normal base pairing and promotes G to A transition mutations. Members of the AlkB family of Fe(II)/2-oxoglutarate-dependent dioxygenases repair alkylated nucleic acids through oxidative demethylation, directly restoring damaged bases without excision. While bacterial AlkB and its human homologs ALKBH2 and ALKBH3 are established DNA repair enzymes, the Fat Mass and Obesity-Associated (FTO) protein has emerged primarily as an RNA demethylase that regulates N^6-methyladenosine (m^6A)-mediated gene expression and influences obesity, type 2 diabetes, cardiovascular disease, and cancer. Here, we examined FTO activity toward O6mG. The results demonstrate that FTO catalyzes the oxidative removal of the methyl group from O6mG, representing the first example of an oxygen-linked methyl group being processed by a 2OG/Fe(II)-dependent nucleic acid dealkylase. This work establishes a foundation for exploring previously unrecognized DNA repair functions of FTO and their potential implications for genome maintenance and human disease.

This work was supported by RI-INBRE

Investigation of Possible Synthetic Pathways of Boron-Based Metal Catalysts

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Traditional organometallic catalysts have played an essential role in modern synthesis by enabling bond formation through cross-coupling and C-H activation reactions. As such, the organic ligands which scaffold the central metal of a given catalyst are a critical component of their design. Typically, these complexes are based around a Lewis-acidic transition metal center and a ligand framework, which acts as a nonmetal Lewis base. State-of-the-art ligands often consist of expensive organophosphorus architectures. In this project, it is hypothesized that a boron-based ligand, as opposed to phosphorus, may provide novel and cheaper catalyst alternatives. Since boron compounds are often Lewis-acidic, coupling such a compound with a Lewis basic metal would provide an innovative approach to catalysis and potentially lead to increased reactivity for both the boron moiety and the Lewis basic metal in a cooperative catalytic mechanism. A multistep synthetic route was adapted from established literature to produce chlorinated bis(pentafluorophenyl)borane as the proposed borane moiety. Isolation of the expected product was confirmed through 1H NMR spectroscopy, as the spectra lacked the peak associated with the borane starting material. Following this reaction, 6-methyl-2,2’-bipyridine was then reacted with n-butyllithium (n-BuLi) to undergo direct lithiation to prepare for the installation of the boron moiety. Once lithiation was complete, bis(pentaflourophenyl)chloroborane was added to synthesize the ligand. Subsequent NMR spectra taken of this crude material lacked peaks associated with methyl protons of 6-methyl-2,2’-bipyridine after lithiation, suggesting that the target ligand was formed. Going forward, the target ligand will undergo complexation with late transition metals like gold and zinc, as well as base metals like iron. Once complexed, these catalysts will be tested for viability in the dehydrogenation of liquid organic hydrogen carriers.

This work was supported by RI-INBRE

Targeting Quiescent and *E. coli* for Preventing Recurrent Urinary Tract Infections

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Around 11 million urinary tract infections occur yearly; twenty-seven percent of the patients experience recurrence within twelve months despite antibiotic treatment. Uropathogenic *Escherichia coli* (UPEC) is the leading cause of urinary tract infections (UTIs) and clinical isolate CFT073 can enter a metabolite-dependent, non-proliferative state termed quiescence. During infection, cells have high levels of antibiotic tolerance and form quiescent intracellular reservoirs, contributing to recurrent disease following antibiotic treatment. At a low inoculation density in glucose minimal media, UPEC enters quiescence, and can be reversed by metabolites such as succinate, lysine, and methionine, as well as peptidoglycan-derived peptides, indicating a role for metabolic and cell wall signals in resuscitation. This study aims to analyze the mechanisms of dormancy reversing molecules using proliferants. A mini-tn5 transposon mutagenesis screen in CFT073 identified genes required for resuscitation. Mutants were screened for the ability to respond to signals following the quiescent state. Genome sequencing mapped transposon insertion sites and identified genes involved. Characterizing these mutants will clarify molecular pathways promoting resuscitation from antibiotic-tolerant states.

This work was supported by RI-INBRE

Synthesis of Peptides to Combat Quiescent *E. coli* for the Prevention of Recurrent Urinary Tract Infections

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There are approximately 11 million urinary tract infections (UTIs) reported each year and twenty-seven percent of the patients who are treated with antibiotics experience a recurrence of the infection within twelve months. These infections are predominantly caused by uropathogenic *E. coli* (UPEC) in the urinary tract, bladder, and sometimes kidneys. One of the underlying causes of recurrence is the ability of UPEC to enter a dormant, quiescent state within the epithelial cells of the bladder. This state allows the bacteria to survive antibiotic treatment and continue growth after treatment. It was recently discovered that certain peptidoglycan (PG) stem peptides, specifically tetra- and pentapeptides, can prevent or reverse the quiescent state in UPEC. The goal of this research is to synthesize various peptides using the manual solid phase synthesis method to determine the molecular characteristics required to reverse quiescence. These studies will enhance the understanding of the quiescent state in UPEC, the ability of certain peptides to reverse this quiescent state and potentially lead to an approach for treatment of recurrent UTIs.

This work was supported by RI-INBRE

Medicines from the Sea: Antimicrobial Potential of a Rhode Island Shipworm Symbiont

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Antibiotic-resistant pathogens present a critical threat to global health, driving the urgent need for novel antimicrobial compounds. Marine environments are promising sources of complex natural products, and animal-microbe symbioses are particularly promising for the discovery of new chemical scaffolds. *Teredinibacter turnerae* is an intracellular endosymbiont of the wood-eating bivalves shipworms and is a prolific producer of secondary metabolites. However, no shipworm symbionts from Rhode Island have been investigated for their potential to produce natural products. This study investigates a local strain of *Teredinibacter* and how altering growth conditions affects the production of secondary metabolites in culture. Strain RIS005.S.0a.02 was isolated from the gill homogenate of a shipworm extracted from a wood sample collected in Mt. Hope Bay. The strain was grown in liquid media for four days utilizing three distinct carbon sources: cellulose, glucose, or sucrose. Following incubation, cultures were harvested and extracted for bioactivity assays and comparative HPLC analysis. Antimicrobial activity was assayed via agar well diffusion on Lysogeny Broth (LB) plates inoculated with either *Staphylococcus aureus* or *Pseudomonas aeruginosa*. Modest but reproducible zones of inhibition were observed in extracts from cultures fed with sucrose and glucose, but not cellulose. HPLC analysis revealed distinct chromatographic profiles between the extracts, suggesting that the carbon source directly influences the metabolic profile of *T. turnerae*. These findings indicate that T. turnerae RIS005.S.0a.02 produces secondary metabolites with antibiotic activity against clinically relevant pathogens, and modulates their production based on nutritive input.

This work was supported by RI-INBRE

Nanostructured Immunosensor Array Based on Poly-Horseradish Peroxidase (HRP) for Rapid Simultaneous Electrochemical Detection of Cancer Biomarker Proteins

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Early diagnosis of cutaneous T-cell lymphoma (CTCL) remains challenging because its clinical manifestations often resemble benign inflammatory skin disorders. Herein, we report a simple rapid 10 minutes multiplexed electrochemical immunosensor for the simultaneous detection of the CTCL-associated cytokine biomarkers interleukin-6 (IL-6) and interleukin-22 (IL-22) in diluted serum samples. The immunosensor employs a nanostructured eight-electrode screen-printed array modified with glutathione-functionalized gold nanoparticles (AuNP-GSH) to enhance antibody immobilization and signal sensitivity. Capture antibodies were covalently immobilized using EDC/NHS coupling chemistry, while target biomarkers were detected through a sandwich immunoassay incorporating poly(horseradish peroxidase)-labeled secondary antibodies. Enzymatic reduction of hydrogen peroxide in the presence of hydroquinone generated an amplified electrochemical signal that was quantified using a multichannel potentiostat. The multiplexed immunosensor exhibited a detection limit of 50 pg mL^{-1} and a linear dynamic range of 50–1000 pg mL^{-1} for the simultaneous determination of both IL-6 and IL-22 in diluted serum. This immunosensor strategy demonstrates strong potential for point-of-care (POC) cancer diagnostics, facilitating early CTCL detection, disease monitoring, and personalized therapeutic management.

This work was supported by RI-INBRE

Investigating the Role of Intracellular Zinc Mobilization on Neurogenesis

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Zinc (Zn) is an essential trace element that serves as a cofactor for hundreds of enzymes and plays critical roles in brain development, including neurogenesis, neuronal migration, and differentiation. Disruptions in Zn homeostasis during development impair DNA, RNA, and protein synthesis, contributing to neurodevelopmental abnormalities and increasing susceptibility to neurodegenerative disease. Despite the importance of Zn in neural development, the molecular mechanisms linking intracellular Zn trafficking to neurogenesis remain poorly understood. We recently identified the first vertebrate Zn metallochaperone family, termed Zn-Regulated GTPase Metalloprotein Activator 1 (ZNG1), which facilitates intracellular Zn delivery to Zn-dependent metalloproteins. Using biochemical and protein interaction analyses, we demonstrated that ZNG1 binds Zn and promotes the activity of specific client metalloproteins through targeted Zn transfer. Notably, several ZNG1-interacting proteins are enriched in developing neural tissues and have established functions in neurodevelopment, suggesting that ZNG1-mediated Zn trafficking may contribute to neural homeostasis and differentiation. To investigate the role of ZNG1 in neurogenesis, we examined neurogenesis and cellular responses to Zn stress in wild-type (WT) and Zng1-deficient Neuro2a (N2a) neuroblastoma cells. Cells were exposed to the Zn chelator TPEN or $ZnCl_2$ to model Zn-deficient and Zn-excess conditions, respectively, and cell viability was assessed using MTT assays. We observed that TPEN treatment reduced cell viability in both WT and Zng1-deficient cells, indicating that Zn deficiency broadly impairs N2a cell growth. Exposure to $ZnCl_2$ similarly decreased viability in both genotypes, consistent with the known cytotoxic effects of elevated Zn concentrations. However, Zng1-deficient cells exhibited increased sensitivity to both Zn deficiency and Zn excess compared with WT cells, suggesting that ZNG1 functions to buffer intracellular Zn fluctuations and maintain Zn homeostasis under stress conditions. Together, these findings support a protective role for ZNG1 in regulating cellular Zn homeostasis and suggest that ZNG1-mediated Zn trafficking contributes to neuronal health. Ongoing analyses will determine how loss of ZNG1 alters neurodevelopmental gene expression and neuronal differentiation, providing new insight into the mechanisms linking intracellular Zn regulation to neurogenesis and neurological disease.

This work was supported by RI-INBRE

Spot the Difference: Temperature-Sensitive Melanophore Phenotypes in Adult Oberon Mutant Zebrafish

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Hermansky-Pudlak Syndrome (HPS) is a rare autosomal recessive disorder driven by defects in the biogenesis and trafficking of lysosome-related organelles (LROs). Unlike standard lysosomes primarily used for waste degradation, LROs are cell-specific and help cells perform specialized tasks like pigmentation, immunity, and blood clotting. HPS is characterized by oculocutaneous albinism, bleeding diatheses, and pulmonary fibrosis because of these defects. Zebrafish (*Danio rerio*) serve as an ideal model for HPS due to their conserved intracellular trafficking pathways, high fecundity, and easily quantifiable skin pigmentation patterns that mimic human melanocyte defects. The oberon zebrafish mutant, which exhibits a disrupted adult pigment pattern, provides a unique platform to study LRO development. Because physiological stressors can alter metabolic kinetics and gene expression, this study investigated whether varying temperature exposures induced a temperature-sensitive adult phenotype in oberon mutants. We raised cohorts of wild-type and oberon mutant zebrafish from embryonic stages through adulthood under two distinct thermal conditions: a cool condition of 24°C and a warm condition of 32°C. Adult zebrafish were evaluated for variations in stripe formation, melanophore density, and overall melanin pigmentation. Our preliminary results showed distinct morphological differences between the two temperature cohorts with zebrafish raised at 32°C developing fewer and less pigmented melanophores than the lower-temperature cohort, suggesting that thermal stress modulates the penetrance of the oberon genetic mutation. This study highlights the utility of the oberon line in modeling HPS pathologies and demonstrates how environmental factors interact with LRO biogenesis machinery, offering deeper insights into the phenotypic variability observed in human HPS patients.

This work was supported by RI-INBRE

Investigating Molecular Mechanisms of Cilia Regrowth in *C. elegans*

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Sensory neurons rely on specialized structures called cilia to transduce environmental stimuli. Olfactory cilia located in the nasal cavity are directly exposed to the external environment and are therefore particularly vulnerable to injury and infection. Disruption of olfactory cilia morphology can lead to anosmia, or loss of the sense of smell. Despite the clear importance of cilia integrity for olfaction, the molecular mechanisms that drive cilia regrowth and restore sensory function are not well understood. To investigate how cilia regenerate following damage, we are utilizing the nematode *Caenorhabditis elegans* as a genetically tractable model organism. We have developed a genetic mutant background that enables inducible truncation of *C. elegans* olfactory cilia followed by rapid regrowth. Using this system, we have previously conducted a forward genetic screen to identify mutants with specific disruptions in cilia regrowth and not initial ciliogenesis, using neuronal uptake of a lipophilic dye as a readout. We are now using green fluorescent protein (GFP) to visualize olfactory cilia in targeted neurons, and we are precisely quantifying cilia regrowth to identify the most promising regulators of regeneration. From the highest-priority candidate mutants exhibiting the most robust regrowth defects, we are expanding worm populations and isolating genomic DNA for whole-genome sequencing to identify causal mutations. Given the strong conservation of cilia genes across species, this work has the potential to uncover fundamental and conserved molecular regulators of cilia regeneration that may ultimately inform therapeutic strategies aimed at restoring cilia structure following damage or in diseases associated with ciliary dysfunction.

This work was supported by RI-INBRE

Effects of Inflammatory Challenge on HA-1 and HA-2 Innate Immune Cell Development in *Ciona intestinalis*

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Innate immune cells function as the first line of defense against foreign pathogens. Infection is known to activate the immune system, yet this challenge during development can adversely alter innate immune cell composition. Understanding the molecular underpinnings of this problem is challenging in vertebrate models. The invertebrate chordate *Ciona intestinalis*, our most closely related invertebrate relative, serves as an excellent model organism for certain embryonic immune- focused research due to its rapid development, simplified genome, full array of molecular tools, and absence of an adaptive immune system. We aim to understand how inflammatory challenge during embryogenesis influences innate immune system development. In *Ciona*, embryonic progenitor cells differentiate into many distinct cell states, including hyaline amoebocytes (HA) cells. Some HA cells are thought to function as phagocytes that engulf and eliminate foreign pathogens. This project focuses on two forms of HA cell, HA-1 and HA-2 cells. Unpublished data showed the timing of emergence and abundance HA-3 cells were affected by pathogen exposure. Therefore, we wanted to test whether HA-1 and HA-2 cells are similarly affected. To develop HA-1 and HA-2 tracing tools, we first investigated genes highly-expressed exclusively in those cell types. We then amplified putative enhancer-promoter regions and cloned them into GFP reporter plasmids, which were electroporated into fertilized *Ciona eggs*. We are currently using successful reporters for inflammatory challenge experiments. After embryos develop into larvae and attach to dishes at the start of metamorphosis, we are exposing them to bacterial (LPS) or fungal (zymosan) inflammatory molecules. We are quantifying the number and emergence of HA-1 and HA-2 cells and comparing them with untreated controls to determine whether exposure alters the abundance of these cell states. We are currently collecting and analyzing the data. In addition, we are also testing a hypothesis proposed in a recent single-cell RNA sequencing analysis of *Ciona* blood cell states: that HA-1 cells are the developmental precursors to HA-2 cells. To test this, we are using a two-color co-electroporation strategy. The results of these research projects will contribute to a broader understanding of the role that infection plays during development and how it influences innate immune cell specification and differentiation.

This work was supported by RI-INBRE

Childhood Trauma as a Moderator of the Relationship Between Ethnic Identity and Perceived Everyday Discrimination in Adults with PTSD and Alcohol Use Disorder

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Introduction

Discrimination harms physical and mental health (Williams et al., 1997). Ethnic identity, a person's sense of belonging to their ethnic group (Phinney & Ong, 2007), is linked to how individuals perceive or respond to discrimination in everyday life (Romero & Roberts, 2003). Similarly, childhood trauma is linked to increased discrimination in adulthood (Wang & Wang, 2025) and may increase discrimination's impact on mental health (Kwon et al., 2023). However, to our knowledge, no research has assessed whether childhood trauma strengthens this link. This study examined whether childhood trauma moderated the relationship between ethnic identity and discrimination. We hypothesized that discrimination would have a stronger negative impact on mental health among individuals with more severe childhood trauma.

Methods

Participants were 152 community adults (Mage = 45.88, SD = 10.44; 57.2% male) who reported a history of trauma and were regular drinkers. Participants completed self-report measures assessing perceived everyday discrimination (Everyday Discrimination Scale; Williams et al., 1997), ethnic identity (Multigroup Ethnic Identity Measure–Revised; Phinney & Ong, 2007), and childhood trauma history (Childhood Trauma Questionnaire; Bernstein et al., 1998).

Results

Moderation analysis was conducted using Hayes' (2022) PROCESS macro (Model 1).The overall model was significant, $R^2 = .24$, $F(3, 115) = 12.17$, $p < .001$, accounting for 24% of the variance in perceived discrimination. Ethnic identity was significantly associated with perceived discrimination (b = -3.16, SE = 1.13, t = -2.81, p = .006, CI [14.9, 19.7]). Childhood trauma was also significantly associated with perceived discrimination, (b = 0.32, SE = 0.06, t = 5.27, p < .001, CI [0.20, 0.44]). Contrary to our hypotheses, the interaction between ethnic identity and childhood trauma was not significant, (b = -0.03, SE = 0.05, t = -0.67, p = .502, CI [- 0.13, 0.07]).

Discussion

Although our findings did not confirm our hypothesis, ethnic identity and childhood trauma were each independently associated with perceived discrimination. Notably, stronger ethnic identity was associated with lower, rather than higher, perceived discrimination, potentially reflecting a protective or buffering role in this clinical population. A limitation of this study is that our findings may not generalize to non-clinical populations, given that the sample consisted of adults with co-occurring PTSD and AUD.

This work was supported by RI-INBRE

Medial Prefrontal Cortex Ensembles Bias Action Selection During Motivational Conflict

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To ensure survival in complex environments, organisms require a central nervous system capable of flexibly facilitating action planning and guiding decision-making processes to pursue the most optimal course of action. While neural circuits that drive survival behaviors (e.g., food seeking) under a singular need (e.g., hunger) are highly conserved and well-characterized, the mechanisms by which the brain resolves action selection in response to conflicting motivations (e.g., hunger and threat avoidance) are not fully understood. Behavioral phenotypes observed in contexts where animals face multiple concurrent needs are coordinated through integrating and weighing of cues related to the most pressing need. The medial prefrontal cortex (mPFC) plays a pivotal role in preferencing actions, and our lab's previous works demonstrates that two competing stimuli – environmental threat and food – are represented by activity in largely separable mPFC ensembles in hungry mice. How might the mPFC accomplish this resolution of needs? In our study, we used awake-behaving mouse models to evaluate the capacity of these ensembles to influence behavior in contexts in which the two motivations oppose one another. We employed the targeted recombination in active populations (FosTRAP) model and chemogenetic tools involving designer receptors exclusively activated by designer drugs (DREADDs) to inhibit independent subsets of mPFC neurons that respond to either the predator odor trimethylthiazoline (TMT) or the presence of food following food-deprivation. Once the DREADDs were expressed, both cohorts of mice were subjected to a series of counterbalanced behavioral assays in which they received an intraperitoneal (i.p.) injection of either the DREADD receptor ligand clozapine-N-oxide (CNO) to silence their specific (i.e., TMT- or food-responsive) neuronal ensembles or vehicle as a control. Most notable of these tests is our predator odor assay, in which hungry mice enter a two-chambered apparatus with food secured directly adjacent to the predator odor. We found that inhibiting TMT-responsive mPFC ensembles significantly increased food consumption. The inhibition of food-responsive ensembles is still in progress, but thus far displays the inverse result, decreasing food consumption. Inhibiting activity in both ensembles did not impact locomotion in an open field, and neither ensemble influenced food consumption in the absence of predator odor. These findings suggest that mPFC ensembles demonstrate the capacity to bias an animal's behavior toward one need at the expense of another in contexts where motivations directly compete.

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Hypothalamic Hunger Neurons Drive Food Consumption in the Presence of Visual and Olfactory Threat

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The ability to process and make decisions regarding variable environmental and internal information is a critical aspect of animal survival. In order to better understand how the brain makes decisions when faced with competing survival motivations, we investigated how hunger-sensing neural circuits can influence the consumption of food when it is only available in the presence of an environmental threat. Agouti-related peptide (AgRP) neurons located in the arcuate nucleus of the hypothalamus are a critical component of hunger sensing and regulation. We optogenetically activated AgRP neurons in mice during behavioral tests utilizing the light-sensitive ion channel channelrhodopsin (ChR2) with a fiber optic implanted above the arcuate nucleus. Increasing stimulation frequencies of AgRP neurons between 0-20 Hz led to a gradual increase in food consumption in a threat-free chamber. A predator odor assay where food was only available adjacent to the predator odor trimethylthiazoline (TMT) was then utilized to assess how AgRP stimulation affected food consumption in the presence of an olfactory environmental threat. Only the highest levels of stimulation, 10 and 20 Hz, showed an effect in increasing food consumption in the presence of TMT. Similar results were seen in the presence of visual threat in the looming stimulus assay, where food was only available under a rapidly enlarging disc presented on an overhead monitor. Only the maximum stimulation frequency, 20 Hz, drove an increase in food consumption. We also found that prestimulation of AgRP neurons during a 10-minute acclimation period preceding the looming assay showed an increase in overall food consumption, compared to trials without prestimulation. This data suggests that while AgRP neurons do play a role in the regulation of competing hunger and survival motivations, only the highest activation of these hunger neurons can significantly overpower innate survival instincts to avoid environmental threats.

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Comparative Morphology and Mechanics of the Coracomandibularis Muscle, and Its Effects on Jaw Opening

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This research investigates the musculoskeletal morphology and mechanics associated with jaw depression in three shark species, a high-powered suction feeder, *Chiloscyllium plagiosum*, intermediate-powered suction feeder, *Squalus acanthias*, and a low-powered suction feeder, *Mustelus canis*. The goal of this research is to better understand how the morphology of the jaw depressor may vary across the levels of suction feeding performance exhibited by the study species. Results show a significant decrease in muscle fiber length, and increase in muscle cross-sectional area and maximum force in the high-powered suction feeder. The muscles in the intermediate and low-powered suction feeding species are similar. Both species have long muscle fibers, and small cross-sections and maximum forces, compared to the high-powered suction feeding species. All species did not differ in leverage. Our results suggest that the jaw opener is designed to maximize force output over short distances in high-powered suction feeders, rather than fast movements over long distances, as in the intermediate and low-powered suction feeders. They also suggest that these differences are not influenced by mechanical leverage. The short, large and forceful muscle may be well suited for the *C. plagiosum*, which has a small maximum gape relative to the other species and has to open its mouth against high suction pressures. In contrast, the longer muscles of *S. acanthias* and *M. canis* may promote fast jaw opening and wide gapes that would facilitate their ability to capture or seize larger prey than *C. plagiosum*, but at the cost of reduced suction ability.

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The Complexly Divided Jaw Muscles of Cartilaginous Fishes Lift Mechanical Constraints Associated with Large Joint Angle Changes

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In Chondrichthyes (cartilaginous fishes), the adductor mandibulae complex (AMC) is primarily formed by two muscles with multiple divisions, the preorbitalis (PO) and quadratomandibularis (QM) responsible for jaw protrusion and closure during feeding, respectively. The architecture of these muscle divisions varies greatly across cartilaginous fishes and can contain many complex subdivisions. The degree of complexity seems counterintuitive given the relative simplicity of the movements they actuate. Furthermore, the AMC is not well understood, mechanically. In the case of spiny dogfish (*Squalus acanthias*) descriptions and visualizations of AMC architecture have varied widely across scientific literature. Despite this, it is commonly used as a model for comparative anatomy instruction. This study aims to provide a revised understanding of AMC structure and function in *S. acanthias*, through anatomical investigation, biomechanical analysis, and digital imaging. Our results reveal the actual architecture of the AMC, which includes previously undescribed muscle divisions and a unique tendinous insertion. Preliminary assessment of leverage mechanics revealed that the divisions of the AMC in *S. acanthias* have varying force transfer characteristics, the preorbitalis (PO) demonstrates high force transfer efficiency at maximum gape, while the QM divisions (ventral, anterior, posterior, and superior) become more effective near full jaw closure. Furthermore, the superior division of the QM (QMS) can only actuate movement of the upper jaw. This variation allows for relatively stable total bite force across the full range of gape. The complex designs of the AMC in Chondrichthyes may have been key adaptations that lifted the muscle constraints exhibited at joints that undergo relatively large changes in angle. Thus, allowing for larger gapes and consumption of larger prey items. We plan to do more in depth comparative work to see how the AMC varies with feeding strategy.

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Investigating the Role of Uropathogenic *Escherichia coli* Hemolysin Genes in Quiescence

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Uropathogenic *Escherichia coli* (UPEC) is the leading cause of urinary tract infections (UTIs) which affect 50-60% of women at least once during their lifetime. Of this population, about a quarter of patients will experience a recurrent UTI (rUTI) even after antibiotic treatment. UPEC cells are able to enter a dormant, quiescent state in which the cells are metabolically inactive and consequently highly antibiotic tolerant. It is predicted that quiescent UPEC contributes to rUTIs by remaining viable in the host after antibiotic treatment and later resuming growth when conditions are favorable. Despite its prevalence, the genetic mechanisms that regulate bacterial quiescence are not fully understood. Previously, a miniTn5 transposon mutagenesis screen was performed to identify genes important for quiescence. This screen identified hemolysin genes *hlyA* and *hlyB* as important for entry into a quiescent state.The objective of this study is to determine the role of the hemolysin genes, which encode known virulence factors, in regulating bacterial quiescence in the UPEC model strain CFT073. UPEC hemolysin genes are part of a fourgene operon including the acyltransferase hlyC, the alpha-hemolysin hlyA, the ABC-transporter hlyB, and a membrane fusion protein hlyD. Upon deletion of the whole operon, the wild-type phenotype was restored. It is predicted that in the absence of hlyA and hlyB, HlyD may accumulate and cause membrane stress. To investigate this, microscopy of wild-type CFT073 and hemolysin mutant strains was performed using a lipophilic membrane dye. The cells displayed an altered cell shape, potentially indicative of membrane disruption. To further confirm this, growth curve analyses were conducted to compare the growth characteristics of wild-type and mutant strains in high and no salt conditions. These experiments will help determine the role of hemolysin genes and the effects of membrane perturbation in bacterial quiescence. The results of this study will improve our understanding of the genetic mechanisms regulating bacterial quiescence and may identify genetic factors that can reduce recurrent urinary tract infections.

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Student Status Moderates the Association Between Employment Status and Annual Healthcare Checkups Among Young Adults

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Background: Young adults are among the least likely age groups to receive recommended preventive healthcare. Employment and educational demands may each influence healthcare utilization, but little is known about how these factors interact to affect receipt of preventive healthcare. The purpose of this study was to examine whether student status moderates the association between employment status and receipt of an annual healthcare checkup among young adults.

Methods: Data from 1,008 participants in the 2024 Rhode Island Young Adult Survey were analyzed using multivariable logistic regression to examine receipt of an annual healthcare checkup, including an interaction between employment status and student status while adjusting for demographic, socioeconomic, insurance, and mental health characteristics.

Results: Student status significantly moderated the association between employment status and receipt of an annual healthcare checkup (full-time employment x student status: $p=0.042$). Among students, the adjusted probability of receiving an annual healthcare checkup was substantially lower for those employed full-time (59.1%) than for those employed part-time (73.6%) or unemployed (77.1%). In contrast, among nonstudents, adjusted probabilities were similar regardless of employment status (69.5% full-time, 64.6% part-time, and 71.0% unemployed).

Conclusion: Full-time employment was associated with a lower likelihood of receiving an annual healthcare checkup among students but not among nonstudents, suggesting that interventions to improve preventive healthcare access should address the competing academic and employment demands faced by working college students.

This work was supported by RI-INBRE

Joint Associations of Psychosocial Resources with Mental Health Outcomes in Young Adults

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Background: Emotional support (ES) and subjective social status (SSS) have each been independently associated with better mental health, but little is known about whether they interact to influence mental health outcomes in young adults. This study examined whether ES moderates the association between SSS and depressive symptoms, suicidal ideation, and insomnia.

Methods: Data were drawn from the 2024 Rhode Island Young Adult Survey (RIYAS), a cross-sectional web-based survey of 1,008 young adults aged 18–25. Depressive symptoms were assessed using the CES-D10, suicide ideation was assessed with a single yes/no question, and insomnia was assessed with the ISI-7. ES was measured on the 5-point Likert scale with a single question, and SSS was measured with the 10-rung MacArthur Scale of Subjective Social Status. Separate multivariable logistic regression models adjusted for age, sex/gender, and race/ethnicity estimated the main effects of ES and SSS and their interaction for each outcome. Adjusted predicted probabilities were plotted across levels of ES at representative values of SSS.

Results: Greater ES and higher SSS were each independently associated with lower odds of depressive symptoms, suicide ideation, and insomnia (all $p \leq .003$). Significant ES × SSS interactions emerged for all three outcomes (depression: aOR = 0.91, 95% CI 0.84–0.98; suicide ideation: aOR = 0.89, 95% CI 0.82–0.98; insomnia: aOR = 0.89, 95% CI 0.81–0.97), indicating that the protective association between SSS and mental health strengthened as ES increased. Among young adults reporting little or no emotional support, higher subjective social status was associated with minimal reductions in risk.

Conclusion: These findings suggest that emotional support strengthens the protective association between subjective social status and mental health, indicating that these psychosocial resources operate synergistically rather than independently. Higher subjective social status alone may not translate into better mental health outcomes in the absence of adequate emotional support. Efforts to improve young adult mental health should address these psychosocial resources conjointly rather than in isolation.

This work was supported by RI-INBRE

Contributions of Extracellular Traps to Vascular Pathologies in CAA Model rTg-DI

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Background/Methods:
Cerebral amyloid angiopathy (CAA) is a cerebral small vessel disease and Alzheimer's disease related disorder driven by amyloid-β (Aβ) deposition in cerebral vessel walls, leading to blood-brain barrier disruption, microbleeds, vessel occlusions, pronounced perivascular neuroinflammation, and cognitive decline. It has been previously demonstrated that the rTg-DI transgenic rodent model of capillary CAA, featuring the Dutch and Iowa Aβ familial mutations, recapitulates human CAA pathology including age dependent global vascular Aβ deposition, pronounced neuroinflammation, cerebral microbleeds and thrombotic occlusions, and cognitive decline. Proteomic analysis indicated neutrophil extracellular traps (NETs) pathology associated with regions of vascular damage, microbleeds and vessel occlusions within the rTg-DI model. Extracellular traps (ETs) are an innate immune response involving web-like structures composed of exocytosed nucleic acid, histones, and proteases purposed to trap and destroy microbes and pathogens, but can promote thrombotic occlusion, and vascular damage during sterile inflammation, and could potentially contribute to CAA pathology progression. It has been reported that in addition to neutrophils, microglia can also produce ETs (MiETs). Here, using archival rTg-DI tissue, we investigated the presence of NETs and MiETs in the rTg-DI model, a timeline of NET involvement, and cannabidiol (CBD) as a potential treatment for CAA, given its reported anti-inflammatory and antioxidant effects.

Results:
We show age-dependent increases in neutrophil extravasation and presence of citrullinated histone 3 (H3Cit), a specific NET marker, coinciding with CAA progression in the rTg-DI model. Furthermore, these markers displayed colocalization in major areas of pathology, and within occluded vessels and microbleeds. Trap formation was captured via immunolabeling of nuclear and granular trap components, and measuring relative signal intensity and signal coverage area. Immunolabeling revealed microglia co-localizing in areas with occluded cerebral vessels and microhemorrhages in rTg-DI rat brains, however because of the pronounced neuroinflammatory response it was not possible to discern whether microglia co-localization with ET markers was specific to indicate presence of MiETs. CBD treatments did not result in significant reduction in CAA related inflammation in the rTg-DI model. These results support a model whereby vascular Aβ fibril deposition recruits neutrophil extravasation and NET production, contributing to CAA pathology progression.

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Self-Amplifying RNA for Cerebral Amyloid Angiopathy Treatment

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Cerebral amyloid angiopathy (CAA) is a disorder characterized by the deposition of amyloid within the walls of cerebral blood vessels, leading to cerebral microbleeds, hemorrhagic stroke, and cognitive decline. Currently, there are no disease-modifying interventions for CAA. Irisin, an exercise-induced peptide secreted by skeletal muscle, has been shown to disrupt amyloid formation, promote neurogenesis, enhance synaptic plasticity, reduce neuroinflammation, and improve cognitive function in several models of neurodegenerative disease. However, the impact of irisin on CAA is unknown. The emerging mRNA-lipid nanoparticle (LNP) technology provides a versatile method to produce irisin in the body; however, protein expression by mRNA is often limited in durability. The objective of this study was to evaluate a novel self-amplifying RNA (saRNA) LNP as a platform for irisin expression in muscle and brain-derived cells. We hypothesized that saRNA-loaded LNPs would produce higher and more sustained protein expression than conventional mRNA-loaded LNPs. Irisin-mCherry saRNA and mRNA were synthesized by in vitro transcription and formulated into LNPs. Mouse myoblasts, human glioblastoma cells, and rat primary astrocytes were transfected with the RNA-loaded LNPs, and transfection efficiency was assessed by measuring mCherry expression. LNPs successfully transfected all three cell types, and saRNA produced greater protein expression than mRNA. These findings demonstrate the potential of saRNA-LNPs as an efficient platform for irisin delivery and support further investigation of this approach as a potential therapeutic strategy for CAA.

This work was supported by RI-INBRE

Virtual Reality Environment for Experimental Drone-Human Robot Interaction

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Human-Robot Interaction (HRI) is a promising field with vast application and research potential. Mobile robots and robotic manipulators have been thoroughly studied, but the implementation and experimentation of HRI on unmanned aerial vehicles (UAVs) remain largely underexplored due to safety concerns.

The objective of this research is to develop a controlled simulation environment using the Robot Operating System (ROS) and virtual reality (VR) to facilitate safe human-drone interaction studies. In the proposed setup, a human subject wearing a VR headset will interact with a simulated hovering drone while a physical robotic arm will provide haptic feedback and measure the corresponding haptic forces. This setup requires communication between the VR environment, the simulated drone, and the robotic arm to ensure synchronized interaction. By creating a controlled and safe testing environment, this approach enables analysis of human-UAV interaction dynamics and supports the future development of real HRI-capable drones.

Gazebo simulates a virtual ROS-enabled drone that calculates flight trajectory using an implemented admittance controller and particle filter. Gazebo's physics engine completes the calculations and runs headless throughout the experiment. The simulated drone includes full attitude control and realistic flight dynamics, allowing it to tilt, rotate, and respond to external forces in a manner consistent with an actual aerial vehicle. To visualize, Unity collects all pose information from Gazebo and replicates it in its own environment which is projected to the VR headset for human immersion.. Within Unity, Meta's SDK packages are used for hand tracking and users can view their hands in VR. A payload calibrator is used to account for the end effector, whose weight influences the arm's taring. The payload's mass, the difference in center-of-mass alignment, and orientation are taken into account. The payload calibrator's completion permitted the arm to replicate the drone's motion through velocity imitation. The joints move within an enveloped workspace, restricting motion to a boundary to prevent injury and damage.

In the future, the project will focus on refinement to establish the consistency and safety needed to begin human-drone interaction trials with real participants.

This work was supported by RI-INBRE

Characterizing Microglial Distribution Around Tau Pathology in Alzheimer's Disease

Zorayda Gutierrez

Objectives: Alzheimer's disease (AD) is a progressive neurodegenerative disorder that affects certain brain regions and neuronal populations more than others. Pyramidal neurons in layers 3 and 5 of association areas in the neocortex, such as the dorsolateral prefrontal cortex (DLPFC), show early degeneration and accumulation of tau pathology in AD. However, other neocortical brain regions, such as the primary visual cortex (V1), are relatively resistant. Microglia are the resident immune cells of the central nervous system that respond to injury and disease and could affect the progression of AD through their interaction with tau pathology. Here, we classify neurons with and without tau pathology and investigate the spatial relationship between microglia and tau pathology within neurons to better understand regional vulnerability in AD.

Methods: Highly multiplexed immunofluorescence (MxIF) images from DLPFC and V1 postmortem human brain specimens were analyzed in QuPath. The specimen cohort included control (n=5), mild cognitive impairment (MCI, n=4), and Alzheimer's disease (AD, n=3) cases and was characterized by Clinical Dementia Rating (CDR), Thal stage (amyloid-β pathology), and Braak stage (tau pathology). Neurons with and without tau pathology were identified and classified, and a custom QuPath script was used to generate concentric rings around microglia. These rings provide a framework for measuring the spatial relationship between microglia and nearby neurons with and without tau pathology.

Results and Conclusion: Classification of neurons by their tau burden and development of the concentric ring-based analysis pipeline have been completed. Ongoing work will classify microglia based on their proximity to neurons with and without tau pathology to determine whether microglial distribution differs between the AD, MCI, and control groups. Understanding these spatial relationships may help explain why some brain regions are more vulnerable to AD than others and provide insight into the role of microglia in AD progression.

This work was supported by RI-INBRE

POSTER SESSION B

11:00 AM – 12:30 PM

Fascitelli Center for Advanced Engineering, 1st Floor
B-1 to B-30

Fascitelli Center for Advanced Engineering, Ground Floor
B-31 to B-56

Paramaz Avedisian ’54 Hall, College of Pharmacy
B-57 to B-86

Terahertz Spectroscopic Investigation of Biodegradable Microplastic Contaminated Liquids

Andrew Fournier[1], Lukas Huffman[1], Matthew Doolittle[1], Cooper Thomas[2] & Ahmet Akosman[1]

[1]Engineering, Roger Williams University, Bristol, RI
[2]Physics, Brown University, Providence, RI

Microplastic contamination has become an increasing environmental concern, which necessitates the development of rapid and non-destructive detection techniques for identifying microplastics in liquid samples. In this project, we investigate the changes in the refractive index of pure and microplastic-contaminated liquids, including deionized water and isopropyl alcohol (IPA). Samples containing known concentrations of microplastics are analyzed to determine whether concentration-dependent refractive index variations can be detected. The refractive index serves as a quantitative optical parameter that can reveal changes in the dielectric response of the liquid resulting from the presence of suspended microplastics. Terahertz time-domain spectroscopy (THz-TDS), which is particularly attractive for liquid characterization because it is label-free, non-ionizing, and sensitive to subtle changes in dielectric properties, is employed to characterize the optical properties of the liquid samples. The interaction between terahertz radiation and microplastic suspensions depends on the effective dielectric properties of the mixture, which vary with particle concentration, particle morphology, and the surrounding liquid medium. Quantifying these effects is essential for assessing the feasibility of terahertz spectroscopy as a practical environmental sensing tool. The acquired time-domain signals are processed using a MATLAB-based optimization algorithm to extract the refractive index spectra, allowing quantitative comparison between the pure and contaminated samples. The experimental results showed good agreement with theoretical predictions obtained using the transfer matrix method calculations. The extracted refractive index data provide a basis for the characterization of different microplastic suspensions due to their unique terahertz optical properties. As a complementary analysis, the same suspensions are characterized using a custom-built visible spectroscopy system, in order to compare the impact of microplastic concentration on optical scattering when the wavelength of the probe optical signal is significantly shorter. Since water strongly absorbs terahertz radiation, comparing multiple optical path lengths allows the identification of an optimal balance between terahertz transmission and analyte interaction, maximizing measurement sensitivity while maintaining a strong signal-to-noise ratio, as well as providing a better control of multi-reflection oscillations within the sample. Together, these spectroscopic methods will establish baseline optical characteristics of microplastic-contaminated liquids and provide a foundation for future terahertz-based environmental sensing technologies capable of rapid and label-free detection of microplastic pollution.

This work was supported by RI NEST

Validating Methods for Assessing Microplastic Ingestion in Arctic Zooplankton

Sienna Hepworth[1], Cecilia Gelfman[2], Robert Campbell[2], Brice Loose[2] & Alessandra D'Angelo[2]

[1]Environmental Sciences, University of Redlands, Redlands, CA
[2]Graduate School of Oceanography, University of Rhode Island, Narragansett, RI

Microplastic pollution has become a growing concern in Arctic marine ecosystems, where zooplankton forms the foundation of food webs and may serve as vectors for microplastic transfer to higher trophic levels. Accurate assessment of microplastic ingestion requires standardized methods that reliably isolate and identify synthetic particles while minimizing contamination. This study validated and customized a recently developed digestion protocol for assessing microplastic ingestion across zooplankton taxa, evaluating its performance on environmental samples and determining whether digestion efficiency varied among taxonomic groups. Individual organisms were identified, counted, and fixed prior to chemical digestion. The resulting digests were filtered to isolate suspected microplastic particles, which were analyzed using Raman microscopy and OpenSpecy spectral matching to identify polymer composition and distinguish synthetic materials from natural debris. Quality assurance measures, including procedural blanks and contamination control protocols, were implemented throughout sample processing and analysis. Digestion efficiency varied among zooplankton genera, requiring minor protocol customization; however, all taxa were sufficiently cleared to enable reliable microscopic examination and particle recovery. Analyses identified mineral particles, residual organic material, and confirmed microplastics within the samples. Fragments were more abundant than fibers, and particles ≤50 µm represented the dominant size class for both morphologies. Black and blue were the most common fiber colors, whereas fragments were predominantly black, blue, and orange. The validated workflow establishes a reproducible method for detecting and identifying microplastics in taxonomically diverse Arctic zooplankton, providing a reliable foundation for future monitoring efforts and improving our understanding of microplastic pollution in Arctic marine ecosystems.

This work was supported by URI Plastics REU

Microplastics in Narragansett Bay Food Webs: Variation Across Trophic Positions as Observed in Ribbed Mussels (*Geukensia demissa*) and Bufflehead Ducks (*Bucephala albeola*)

Corinne Ruddy[1], Sarah Davis[1], MC Cicenia[2], Andrew Davies[2], Scott McWilliams[1] & Coleen Suckling[1]

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The continuous and rapid increase in global plastic production has led to the widespread accumulation of plastic litter in aquatic environments, making plastic pollution one of the most pressing environmental challenges of this century. As larger plastics degrade into particles that are smaller than 5mm, known as microplastics (MPs), they become ubiquitous in marine environments and can be detected in marine organisms across multiple trophic levels. However, the fate and transport of MPs within coastal food webs remains poorly understood, especially with MPs < 100µm. To examine how MP abundance and characteristics compare across trophic positions in a coastal food web, this study observed the size, shape, and polymer composition of MPs in ribbed mussels (*Geukensia demissa*) and bufflehead duck (*Bucephala albeola*) tissues using Laser Direct Infrared (LDIR) spectroscopy. Ribbed mussels were collected from four different shoreline locations in Narragansett Bay, Rhode Island and whole soft tissues were analyzed for MPs. Digestive tissues from hunter-harvested bufflehead ducks were isolated into the esophagus, gizzard, small intestine, and large intestine. Preliminary results show that MPs were detected in both ribbed mussels and bufflehead ducks. Particle polymer types were similar between the two organisms, while MP concentrations differed. Particle concentrations varied among duck digestive tissues, with the anterior gastrointestinal tract containing the greatest number of particles. Comparisons between mussels and duck digestive tissues provide insight into how microplastics are distributed across trophic positions, while changes in concentration through the digestive tract suggest that the birds were collected while material was moving through their digestive systems, or that MPs were being broken down in the gizzard into pieces too small for the LDIR to detect. This research improves the understanding of how MPs interact with coastal ecosystems and supports future studies on their biological effects and long-term environmental consequences.

This work was supported by URI Plastics REU

Development of an Electrochemical Genosensor for the Detection of *Pseudo-nitzschia delicatissima*

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[4]Engineering, Roger Williams University, Rhode Island

Amnesic Shellfish Poisoning (ASP) is a potentially fatal neurological syndrome, caused by the consumption of shellfish contaminated with domoic acid (DA). This neurotoxin is produced by several members of the genus *Pseudo-nitzschia*, which inhabit algal blooms worldwide. A local DA-producing species, *Pseudo-nitzschia delicatissima*, has been associated with shellfish harvesting closures in the Narragansett Bay area in 2017, and has caused the recall of more than 5 tons of shellfish in New England. Due to its harmful effect on humans, it is important to be aware of *Pseudo-nitzschia* spp. presence. To address the need for rapid species identification, this research focuses on developing an electrochemical genosensor that utilizes DNA hybridization within the D1-D3 region of the LSU rRNA gene for species-specific detection of *P. delicatissima*. The probe DNA was immobilized on gold nanoparticle-plated screen printed gold electrodes (SPGE), followed by the intercalation of methylene blue (MB) which was utilized as a redox indicator. Optimization of electrochemical parameters and hybridization conditions provided insight into the development of a genosensor which differentiates complementary and non-complementary target DNA. This work establishes a foundation for DNA-based detection of *P. delicatissima*.

This work was supported by RI NEST

Public Perceptions of Microplastic Pollution in Narragansett Bay: Everyday Relevance, Information Sources, and Consumer Behavior

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[1]Geography, McGill University, Montréal, Québec
[2]Marine Affairs, University of Rhode Island, Kingston, RI

Microplastics have infiltrated nearly every corner of the Earth, from glacial ice to deep sea trenches, and have been found inside plants, animals, food and drink, and even the human body. Despite this ubiquity, there has been minimal research on public awareness of microplastics, especially when it comes to individual perceptions of risk and responsibility for this pollution. This study aims to determine the relevance of microplastic pollution in the everyday lives of the public, including how often people are thinking and talking about, encountering information on, and experiencing the effects of microplastics, as well as what aspects of the issue are most prevalent. We evaluate consumer habits and individual behaviors to reduce microplastic pollution, and determine whether a correlation exists between plastic consumption habits and everyday relevance. Finally, we assess the sources of information that inform public perceptions of microplastic pollution, and whether these sources correlate with behavioral changes and everyday relevance. Intercept surveys were conducted with coastal recreators, visitors, and recreational fishermen (n=183) at coastal access points and public rights of way across Narragansett Bay, Rhode Island. The most relevant topics that participants reported thinking and talking about were impacts to human health, with many referring to the presence of microplastics in the human body, followed by impacts to nature and the environment. This study revealed a significant positive correlation between average everyday relevance and several individual behaviors to reduce microplastic pollution, namely purchasing products with recyclable packaging ($p=.001$) and purchasing non-plastic alternatives ($p=.001$). Social media and newspapers were the most common sources of information on microplastics ($n=70$ and $n= 42$, respectively), each associated with high levels of behavior change related to plastic use (74.3% and 73.8%, respectively). These findings provide insight into the salience of microplastic pollution among coastal recreators, visitors, and recreational fishermen, and how everyday relevance and information sources inform public opinion and consumer behavior to reduce plastic use and pollution. The results of this study may be used to enhance the effectiveness of public communications on microplastic pollution, and to increase the accessibility and impact of pollution reducing behaviors.

This work was supported by URI Plastics REU

Anthropogenic and Environmental Factors Influencing Microplastic Concentrations in Rhode Island Rivers

Cassie Allen, Logan Szenda, Gianna Wesling, Paola Pamias-Nieves & Lillian Jeznach

Engineering, Roger Williams University, Bristol, RI

Microplastic pollution across the state of Rhode Island in the Narragansett Bay is a growing concern due to the high degree of urbanization within the state and the importance of the marine environment to the economy. This study investigates anthropogenic and environmental factors that may impact microplastic concentrations in three major rivers in Rhode Island that drain to the Narragansett Bay - the Blackstone River, the Woonasquatucket River, and the Pawtuxet River. These rivers were selected based on their industrial history, sampling accessibility, and the presence of both wastewater treatment plants and USGS stream gages. Sampling was performed across 9 different sample sites either by wading or from a bridge using a flow through trawl method with a phytoplankton net (330 µm). Three samples were collected per site and digested using a 1M KOH solution at 40°C for 24 hours. Samples were filtered through a 1.6 µm glass fiber filter and stained with Red Nile Dye for 30 minutes. To analyze the samples, visual analysis was performed under a microscope to determine microplastic concentrations, with some samples additionally tested using the hot needle test for confirmation of microplastic identification. In this study, microplastic concentrations were compared to land use, river flow rates, and season (wet/dry). Microplastic concentrations were found to be higher with lower river flow rates. The Woonasquatucket and Pawtuxet rivers were found to have higher concentrations of microplastics during the wet season compared to the dryer season. In contrast, the Blackstone River had higher concentrations during the dry season. Microplastic concentrations were found to have weak correlations with percent of urban land and percent of forest land in the respective watershed areas. However, more data must be collected in order to fully assess trends in land use and microplastic concentrations. Ultimately, this data will help to understand the distributions of freshwater microplastics in the state of Rhode Island, how they are transported throughout the environment, and their contributions to the Narragansett Bay.

This work was supported by SIMCoast

Beaches in Your Backyard - Mapping Our Coastal Communities' Flooding

Ava Lesiak, Amber Lopes, Amanda Solano & Anabela Maia

Biology, Rhode Island College, Providence, RI

Communities along the Rhode Island and Maine coasts have a long-standing history in fishing, shipping, and waterfront tourism. These activities bring in millions of dollars in revenue each year along with thousands in jobs. These coastlines are impacted by erosion, rising sea levels, flooding and storms of increased frequency and strength. These impacts have eroded the shorelines and affected ports, public and private infrastructure. Creating education materials featuring local impacts of coastal flooding will give in-depth access to information, resources and a deeper understanding of how to protect their assets. We developed a 3D map in ArcGIS Pro to show potential flooding and impacts on infrastructure in a coastal community in Bath, Maine, one of the four case study communities on our coastal resilience grant – Community-driven Coastal Climate Research & Solutions, www.3crs.org. In collaboration with other teams on the project, we are also developing an ArcGIS Storymap board to show information relevant to communities in all four of the project locations – Port of Providence and Galilee in Rhode Island and Bath and Rockland in Maine. This information includes flood risk, perceptions of climate hazards collected during interviews and other relevant resources identified by the communities, for example transportation and accessibility. We have developed interactive maps which also allow access to models such as Coastal Hazards Analysis Modeling and Prediction (CHAMP) and Rhode Island MyCoast already available for Rhode Island communities. Education about impacts of coastal flooding provides communities with the information needed to develop more effective evacuation plans for storms, prepares communities to be more resilient and empowers communities to seek support from their municipal leaders. Seeing current and potential future coastal flooding effects can help identify which infrastructure and populations are most vulnerable. It could impact decisions in new construction locations, decisions about housing, and identifying priorities in public funding.

This work was supported by 3CRS

Investigating Microplastics in Scup from Narragansett Bay

Melany Sotomayor, Suleimen Seitkarim, Elizabeth Shepard, Nailea Estrada, Cassandra P. DeBlois & Anabela Maia

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Awareness about microplastics has been increasing as more studies find health implications for ecosystems and human health. Microplastics are also of growing concern for aquatic life in oceans, lakes, and other bodies of water over the last few decades. Microplastics can negatively affect aquatic organisms by interfering with feeding and digestion among other processes, which can negatively affect nutrient intake and cause irritation to the digestive tract. As more microplastics enter aquatic food webs, they can also negatively affect human health through the consumption of seafood. As part of the Narragansett Bay ecosystem, scup (*Stenotomus chrysops*) are benthic fish with a diet of primarily organisms on or near the sea floor such as amphipods, arthropods, shrimp, and other benthic prey. Scup may ingest microplastics accidentally as their prey may have either consumed these particles previously or have come into contact with them in the water. We hypothesized that scup collected from upper Narragansett Bay would have higher concentrations of microplastics than the lower bay because of more urbanization, meaning more people are living and working around the area which is likely to cause higher microplastics pollution. A total of 20 scup were collected in May 2026 from two stations in Narragansett Bay and were frozen until analysis. Fish were partially thawed before dissection to reduce the risk of puncturing the digestive system and to ease the dissection process. Before dissection, we measured total length, fork length and standard length and weighed each individual. After the stomach, intestine, and muscle tissue from the dorsal region were removed, each sample was weighed separately, dehydrated, and weighed again. Afterwards, these samples went through chemical digestion and filtration to collect any possible microplastics. Filtered samples were stained with Nile red solution and observed under microscopes with ultraviolet light to identify any microplastics which were then picked, identified, and photographed. Microplastics were found in abundant amounts in the stomach contents of several scup. The stomach contents included arthropods, shrimp, and needle fish. The high loads of microplastics found in the scup highlight the need for further assessment of microplastics in Narragansett Bay.

This work was supported by RI NEST and SIMCoast

AI-Driven Spectroscopy of Microplastic Aging: A Standardized Pipeline

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[2]Mechanical, Industrial and Systems Engineering, University of Rhode Island, Kingston, RI

Microplastics undergo chemical and structural changes as they weather in the environment, making polymer identification increasingly difficult using traditional spectroscopic techniques. Raman and Fourier Transform Infrared (FTIR) spectroscopy provide molecular "fingerprints" for polymer identification, but inconsistent data preprocessing and proprietary instrument file formats reduce reproducibility and limit the development of machine learning tools. This project developed SpectraReady, a standardized, open-source spectroscopy-to-artificial intelligence (AI) platform that improves the accessibility, reproducibility, and scalability of microplastic spectral analysis.

SpectraReady provides standardized Raman and FTIR preprocessing workflows based on literature-supported best practices, including baseline correction, smoothing, normalization, and spectral formatting. These workflows were validated using OpenSpecy, an open-source spectral reference database and identification tool, across three polymer types (polypropylene (PP), polyethylene terephthalate (PET), and polystyrene (PS)) in both pristine pellet and post-consumer product forms (PET bottles, PS plates, and PP cups). Across more than 200 Raman and FTIR spectra, every sample was correctly identified, with confidence scores exceeding 84%, and only two samples scored below 90%, demonstrating that the standardized preprocessing workflow preserves accurate polymer identification. SpectraReady also converts vendor-specific post-processed spectroscopy files into OpenSpecy-compatible formats and convolutional neural network (CNN)-ready datasets. The platform provides batch analysis of OpenSpecy polymer identification results and access to Raman CNN prediction models under development.

By removing barriers imposed by proprietary instrument software, SpectraReady enables consistent, scalable dataset generation for AI-driven polymer identification. This pipeline is actively training Raman CNN polymer prediction models, first on pristine microplastics and next on samples weathered under ultraviolet radiation, deionized water, and artificial seawater. This work lays the foundation for future AI models capable of identifying both polymer type and degree of environmental degradation directly from spectroscopic data.

This work was supported by URI Plastics REU

Evaluating the Detection of Allelic Variation in Atlantic Killifish with Environmental DNA

Matthew Sullivan & Jeffrey Markert

Biology, Providence College, Providence, RI

New Bedford Harbor is a federal Superfund site whose sediments are heavily contaminated with polychlorinated biphenyls (PCBs). As a result, the Atlantic killifish (*Fundulus heteroclitus*) populations living in the area evolved reduced sensitivity to PCB toxicity that is associated with heritable changes in the aryl hydrocarbon receptor (AHR) signaling pathway, which regulates responses to certain foreign chemicals. Researchers typically estimate the allele frequencies of these populations by collecting tissue samples for DNA extraction and genotyping, however, measuring allele frequencies with environmental DNA from water samples may be a less invasive and more efficient alternative. The objective of this research was to evaluate whether allele specific assays can detect two variable AHR1 alleles present in eDNA from environmental water samples, and whether their amounts can be used to estimate allele frequencies. The environmental water samples were collected from various sites in Rhode Island and from an EPA tank with fish from New Bedford Harbor, filtered (or concentrated) through Sterivex filters with a peristaltic pump, their DNA was extracted and target regions of the AHR1 gene were amplified with traditional PCR and then reamplified with allele specific qPCR probes. All the environmental samples detected trace amounts of F. heteroclitus DNA, but none were able to detect the target AHR1 genes. Control qPCR assays for the environmental samples detected general presence of killifish DNA although they did not detect either AHR1 allele. Only the sample from the EPA tank showed the AHR1 alleles, while having substantially higher amounts of killifish DNA present. This research shows that specific allele detection through eDNA derived from water samples may be viable in relatively high concentrations of DNA, but it is not good enough [yet?] to estimate allele frequencies.

This work was supported by SNEC

Mapping Sea Level Induced Inundation of at Risk Health Care Facilities in Vanuatu Using Geospatial Analysis and Digital Surface Modelling

Victoria Ortiz

Earth, Environmental & Planetary Sciences, Brown University, Providence, RI

Global mean sea level rise (MSLR) is projected to increase (5-10cm) globally within the next 20 to 25 years, which is and will continue to negatively impact islands and coastal communities in the Pacific Islands all of whom are extremely susceptible to the impacts of such increases. These effects include increased risk of climate disasters, large amounts of biodiversity loss and infrastructural damage and displacement. Alongside this are the effects of the lack of financial means to combat the disastrous impacts of increasing SLR on developing or poor countries. One such impact being infrastructural damage to health care facilities, including dispensaries, treatment centers, and hospitals, and as a result impacting the health and access to care for residents. This analysis evaluates Vanuatu, an archipelago of islands in the South Pacific, and the effect of various sea level rise (SLR) scenarios on the healthcare facilities there using ArcGIS. This study investigated how (1) Inundation rates of current and predicted SLR are affecting and inundating health care facilities in Vanuatu (2) Excess medical waste from the island's largest hospital and landfill and its contribution to microplastic and bioplastic accumulation. To conduct this research, I used Copernicus' digital elevation model (DEM)s in ArcGIS to map the topography of Vanuatu. Using health care facility coordinates, I intersected their location with the SLR scenarios to evaluate at what point they become inundated. I also used tide gauge data to more accurately evaluate local fluctuations on tide and SLR. Furthermore, data collected also shows the predicted rates of natural disaster and how likely they are to impact both Central Vila Hospital and the Bouffa Waste Site, and how that therefore is contributing to microplastic waste on the island. The research provides a geospatial assessment on the vulnerability of Vanuatu's health care facilities as projected sea levels and tides continue to rise, as well as how the secondary and tertiary impacts of SLR on the microplastic accumulation and waste on the island.

This work was supported by SIMCoast

Microplastic Contamination in Rhode Island Coastal Waters and Flounders *Paralichthys dentatus* and *Pseudopleuronectes americanus*

Alexander da Silva, Cassandra DeBlois, Suleimen Seitkarim, Elizabeth Shepard, Anabela Resendes de Maia & Carla Narvaez

Biology, Rhode Island College, North Providence, RI

Plastics have become essential in our lives, but improper disposal and degradation from natural and man-made processes have made microplastics and anthropogenic fibers prevalent in all ecosystems. Rainfall and runoff carry these contaminants into aquatic ecosystems, where they are consumed by marine animals, potentially affecting both marine and human health. However, few studies have determined the amount and type of microplastics and anthropogenic fibers present in edible marine organisms. This is particularly important for fish, which represent 17% of the world's meat consumption. In this project, we determined the presence and identity of microplastics and anthropogenic fibers in summer and winter flounders (*Paralichthys dentatus* and *Pseudopleuronectes americanus*) and water samples collected off the coast of Rhode Island in mid-May. Fish were dissected in a clean, nearly plastic-free laboratory to minimize the contamination from outside microplastics and fibers. Stomach, intestine, and muscle were analyzed. Samples were placed into glass jars, dried, digested using potassium hydroxide, and neutralized using citric acid. Fish and water samples were then processed by vacuum filtration and stained them with Nile Red to separate the liquid from the plastics and fibers and to highlight them under UV and Royal Blue light. Particles believed to be plastic or anthropogenic fibers were hand-picked under the microscope and mounted on double-sided tape. Samples will be analyzed to determine plastic type and abundance using Raman microscopy and Laser Direct Infrared (LDIR) imaging. Microplastics and anthropogenic fibers were detected in all sample types, including the stomach, intestine, muscle, and water. These findings suggest that microplastic contamination is widespread in flounder species commercially available for consumption. Continued monitoring of plastic pollution, paired with efforts to reduce waste, may help mitigate the ecological and human health impact of these contaminants.

This work was supported by SIMCoast

Arbacia punctulata Immunological Response to Thermal Stress

Susan Rosario[1], Mackayla Garzaro[2] & Carla Narvaez Diaz[1]

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Thermal stress in marine invertebrates induces physiological and developmental changes, such as reduced organismal performance and metabolic functions, that can impact population dynamics. Echinoderms, including sea urchins, possess an immune system comprised of coelomocytes, free-floating cells present in the coelomic fluid that respond to environmental stress such as thermal stressors and pollution-driven bacterial exposure. The sea urchin *Arbacia punctulata* is a warm-affinity species whose northern range ends in the cold waters of Cape Cod (MA). In this study, we evaluated the effects of warm (20°C) and cold (4°C) thermal stress on *A. punctulata* immune response and food consumption rate over seven days, followed by a two-day post recovery period. Given this species' affinity for warmer waters, we predicted that cold water temperature would pose a more pronounced physiological challenge than warm temperatures. Eighteen *A. punctulata* individuals were used, with six urchins assigned per treatment group (warm, control, and cold). Each urchin was housed individually in a glass jar with ~ 3 g of turf algae. Coelomic fluid (0.2 mL) was extracted via the peristomal membrane using a 1 mL syringe with a 26-gauge needle. We assessed four types of coelomocytes: phagocytes, red cells, colorless spherule cells, and vibratile cells using a hemocytometer under light microscopy. Urchins and their remaining turf were weighed after each coelomic fluid sampling day. Preliminary results show that water temperatures influence the relative proportion of coelomocytes and food consumption rate across treatment groups, suggesting that thermal extremes at either end of *A. punctulata*'s range may affect its immune competence and resilience to environmental stress.

This work was supported by RI-INBRE

North Woods Field Guide: Illustrating Ecology Through Deep Mapping

Ellie Lin[1], Stephanie West-Puckett[2] & Madison Jones[2,3]

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[2]Professional and Public Writing, University of Rhode Island, Kingston, RI
[3]Natural Resources Science, University of Rhode Island, Kingston, RI

Made up of over 200 acres of wetland and forested habitat over historic farm land, URI's North Woods are an outdoor classroom for hands-on communal learning. The North Woods Field Guide tells the story of this ecosystem through deep mapping, combining science, traditional ecological knowledge, creative writing, and art. The project is modeled after the Cascadia Field Guide (2023), in which visuals, research, and stories come together as a holistic depiction of an ecosystem.

This project has included multiple community-based events focused on inclusive, place-based making. We have hosted an annual Write-out in partnership with the National Writing Project, a Peeper Hike with wetland specialist Professor Michelle Peach, and most recently, an art and writing workshop. In this workshop, I led students to engage creatively through field notes, poetry, sketches, and writing. Outside of a formal classroom context, their subjective experience became an integral part of the field guide. Each workshop aims to raise awareness about human disturbance and encourage environmental stewardship for habitats and neighborhoods across Rhode Island.

In collaboration with researchers at URI, I also developed scientific illustrations to highlight native species, habitats, geological, and historical features of the North Woods. I began with primary research in interviews, getting to know students and professors through their work and personal experiences. As an illustrator, building a personal connection is the basis for my research. I use the process of developing sketches from field observations, photos, and conversations into detailed illustrations to answer questions like how can science make people feel? How can visuals make people curious and resonate with their local environment?

Alongside student consultants Brissia Rodriguez and Calder Puckett in the Digital Writing and Research Studio, I designed the look of the field guide for publication in print and digital formats. Our editorial process was driven by hands-on drafting and experimentation to capture the North Woods as an interconnected space, organized by fluid relationships between organisms and habitats rather than chapters. We aim to create reciprocity where users can partake in an ecology through their own field notes and stories.

Over subsequent volumes, the North Woods Field Guide will become an archive of the ways humans are impacting and being shaped by this space. The field guide, as a collaborative project between researchers, artists, and writers of all backgrounds, demonstrates how an interdisciplinary community-based approach is integral to ecology and conservation.

This work was supported by RI NEST

CCRI Science Art Mentorship Program

The 2026 Science Art Mentorship Program at Community College of Rhode Island (CCRI) offers a unique interdisciplinary experience, blending scientific research with studio art. Students from both Biology and Art Studio backgrounds are invited to apply. Participants engage in workshops at leading research laboratories, where they learn techniques for capturing, manipulating, and displaying images essential to scientific inquiry. These techniques include illustration, microscope photography, video, 3D imaging, and the creation of physical 3D models. Based on these workshops, students apply a design process to create original art and design work for public exhibition. Students are encouraged to experiment, pursue their creative concepts, and produce personally meaningful projects. Guidance and mentorship are provided by faculty from CCRI's Art and Biology departments, along with special guests. We are grateful to the Wessel Lab and Tingle Lab at Brown University for partnering with us and welcoming us into their labs.

The program exhibition will be on view from **September 1st – 30th at CCRI's Flanagan Campus Art Gallery in Lincoln Rhode Island**. There will be an opening reception on Friday September 11th from 4:00 - 7:00pm. The posters here at SuRS offer a glimpse into the work that will be on exhibit.

Many Hands - Emily Houle

I am so honored to be part of this experience, it has truly been so transformative.

My heart is so full,
now I just want to figure out how to share this feeling!

I'm not sure if I'll be successful yet
but I am so excited to keep trying!

Return to the Universe - Grace Bautista Dygert

My piece is representative of my personal life conviction. I believe that my purpose as a human being is to experience life, process such stimuli to the fullest, and express my perceptions of such experiences.

The focus of this piece is that of a woman whose body is failing her. Her body holds no more physical energy, yet there is so much more left to be done. The amount of creative potential and possibilities within her surpass the limited physical energy that her body holds, creative energy bursting at the seams of her body that cannot keep up with such a powerful life force. Instead of keeping it all inside, in a final and powerful effort, she streamlines this creative energy and potential out of her body, back out into the universe.

Cartwheel - Bradyn Guilmette

The intricacies of movement have been historically difficult to perceive. This is a prototype for potential expression of motion. Each curve represents a point on a body tracked through a motion using 3d software, then recreated using a series of suspended wires. The final product intends to deliver a way to observe motion delivered in such a way to appear vague and complicated, even if the motion is simple.

Hidden Perspectives - Avery Porter

Explore the beauty that exists at every scale of life. Inspired by the connection between art and science, this work encourages you to look beyond a first glance and discover that ordinary objects can contain extraordinary details. This is your reminder that curiosity and a closer look can reveal remarkable beauty throughout the natural world.

The Resilience of Fiber Art Through Human Evolution - Zoe Walsh

Fiber art is one of the oldest forms of human creation, something that can be found in societies throughout the world and time. Beads have been a close companion of fiber crafts for nearly the same amount of time that the art form has existed. The evolution of how humans have created threads to weave and materials to hallow out for artistic, cultural, and ceremonial purposes is a fact of life that I feel is severely overlooked. You cannot blame the average person for not knowing the intricacies of fiber art, just as you cannot blame non-scientists for not understanding the complicated mechanisms that make up the world around us. Since the Industrial Revolution, science has exploded with advancements while numerous art forms have been sharply declining. Being so closely connected to the beginning of the end for many ancient, hand-crafted art forms by living in the birthplace of America's Industrial awakening, is bittersweet.

Fiber art, more specifically beading, is the medium I took up for CCRI's 2026 Science Art Mentorship. Physical artwork I feel has a very lasting effect on people, especially if they get to handle it. Getting to personally interact with some of Brown University's Wessel Lab specimens inspired me not only to create, but also to appreciate the beauty of these marvelous, underappreciated creatures. Oceanic life like sea urchins and starfish are simplified by the fact that they cannot make sounds or move very freely. Just like the forgotten ways in which we used to create all fabrics, jewelry, and decorations, these seemingly simple creatures are overlooked and undervalued.

Moved by the gorgeous, natural patterning on the starfish I observed, I turned their very being into my art. Creating a pattern, collecting the materials, and harnessing the power of my own two hands, I shall have replicated these starfishes' intricacies, one bead at a time. Through a weaving technique that has existed for thousands of years, the peyote stitch, I developed a deeper appreciation for the sea life that inspired me, but also a newfound connection to my heritage and the generational skills that have been preserved by those before me and, hopefully, those after me.

Additional works will be displayed during Session A

Metals Meeting Microplastics - a Fatal Attraction

Christian Falcon, Abigail Bratsos, Marcus Raposo & Kayla Riley

Chemistry, Roger Williams University, Rhode Island

Plastics and heavy metals are commonly co-contaminants found in estuarine environments with their transport and transformation depending on environmental characteristics such as salinity, suspended sediments, and organic matter dynamics. Mechanically weathered plastics readily adsorb heavy metals, acting as vectors that transport contaminants from brackish waters and into marine ecosystems. Simultaneously, metal accumulation accelerates physiochemical degradation at the surface of polymers, promoting fragmentation into microplastics and moreover into nanoplastics. These coupled processes were studied by comparing laboratory-weathered plastics with environmentally weathered plastics from a local estuary.

Common polymer types were identified using Raman and Fourier Transform Infrared (FTIR) spectroscopy. Elemental compositions and metal distributions were characterized using X-Ray Fluorescence (XRF) spectroscopy, Laser Induced Breakdown spectroscopy (LIBS), and Inductively Coupled Plasma Optical Emission spectroscopy (ICP-OES) after acid digestion (HCl 1M) to quantify bioavailable metal concentrations. Controlled ultraviolet (UV) irradiation, mechanical abrasion, and metal adsorption techniques simulated environmental weathering allowing for direct comparison to environmental samples.

Mechanical and photo-oxidative weathering disrupted the hydrophobic polymer surface and exposed oxygen-containing functional groups, increasing the plastics' affinity for transition metals. Metal-enriched plastics exhibited enhanced photo-oxidative degradation, generating more reactive oxygen species that promote polymer chain scission and lead to increased surface embrittlement, further accelerating the fragmentation of plastics into smaller micro and nanoparticles. Relative to laboratory-treated samples, naturally weathered plastics exhibited greater structural deterioration, surface oxidation, and metal loadings.

Spatial analyses indicated that heavy metal adsorption and polymer degradation increased with salinity gradients and sediment interactions, reflecting the importance of physiochemical weathering in estuaries. These findings suggest that estuaries function as dynamic biogeochemical reactors, where interactions between microplastics, heavy metals, neuston, and other particulates accelerate polymer degradation and contaminant transport. Metal-enriched micro and nanoplastics increase the mobility and bioavailability of these contaminants, enhancing ecological exposure and trophic transfer within aquatic food webs. Supplementing controlled laboratory experiments with field observations provides a more comprehensive understanding of the mechanisms that govern microplastic deterioration, heavy metal cycling, and the fate of contaminants in coastal ecosystems.

This work was supported by SIMCoast

Influence of Sediment Adhesion and Surface Weathering on the Spectroscopic Characterization of Microplastics

Kayla Riley, Abigail Bratsos, Christian Falcon, Marcus Raposo & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

The rapid increase in plastic production and disposal, particularly of single-use products, has made microplastics one of the most pervasive contaminants in marine environments. Once introduced into coastal systems, microplastics accumulate in sediments, undergo physical and photochemical weathering, and fragment into progressively smaller particles. Sediment adhesion alters particle density, transport, degradation, and surface chemistry while increasing the capacity of microplastics to adsorb metals and other contaminants. Understanding these interactions is critical to predicting the environmental fate of microplastics.

This study investigated the effects of sediment adhesion, mechanical abrasion, and ultraviolet (UV)-induced weathering on the surface chemistry and spectroscopic characterization of 3 common polymer types. Pristine polymers were identified using Fourier-transform infrared (FTIR) and Raman spectroscopy, while surface elemental composition was characterized by X-ray fluorescence (XRF) and laser-induced breakdown spectroscopy (LIBS). Surface and subsurface sediments collected from Mount Hope Bay (RI) were oven-dried, ground to a fine powder, and applied to polymer surfaces to simulate environmentally relevant sediment adhesion. Following XRF and LIBS analyses, samples were rinsed with deionized water and reanalyzed to evaluate the persistence of sediment-associated species and spectral changes. Additional polymer samples were mechanically abraded using sandpaper and emery cloth to compare artificial roughening with natural sediment weathering. Separate polymer sets were exposed to ultraviolet radiation (Hg lamp) before sediment application to simulate photo-oxidative aging. Surface morphology was evaluated using three-dimensional optical microscopy, color contour mapping, and static water contact angle measurements.

Sediment adhesion produced measurable changes in the spectroscopic signatures of all polymers. XRF detected increased abundances of Fe, Si, Ca, and Ti after sediment application, while LIBS revealed corresponding changes in elemental emission spectra. UV-weathered polymers retained significantly more sediment and exhibited greater spectroscopic and elemental changes than pristine materials, indicating that photo-oxidative aging enhances sediment attachment. Emery cloth produced surface morphologies most similar to naturally weathered plastics.

These findings demonstrate that sediment adhesion and environmental weathering significantly alter the surface chemistry and spectroscopic characteristics of microplastics. Accounting for mineral coatings and weathering processes is essential for accurate polymer identification and for developing realistic laboratory simulations of environmentally aged plastics.

This work was supported by SIMCoast

Changes in Rhode Island Salt Marsh Accretion Rates and Organic Matter Contents Relative to Sea Level Rise over a Forty Year Period

Lilah Saunders

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Healthy salt marshes, which provide flood protection, habitat, and sequester carbon, are believed to grow at a pace equal to or greater than sea level rise. In order to investigate how salt marshes react to increasing rates of sea level rise, we recreated a study conducted on sediment cores collected in 1983 from five salt marshes in Narragansett Bay, RI. We revisited the same salt marshes, and collected cores in triplicate using a 1-m gouge auger. Following the 1983 study's methods, accretion rates were analyzed using excess Pb-210 and downcore sediment parameters, including organic matter contents and dry bulk densities. We determined that all sites aside from the Southernmost and Northernmost have lowered accretion rates when compared to 1983 values, but only three out of seven cores are actually failing to keep up with modern day rates of sea level rise. Accretion rates were calculated using the constant initial concentration model, but in order to get a more comprehensive picture of how marshes have changed over the last ~40 years, further calculations using the constant rate of supply model are necessary.

This work was supported by RI NEST

Characterizing Particles Emitted During Stages of a Plastic Paver Recycling Process

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The recycling of plastic waste into construction materials has garnered notable attention in recent years as a potential solution to the global plastic pollution crisis. One such manufacturing method begins with the collection of plastic waste, which is shredded and mixed with sand. This mixture is extruded, molded, and cooled. Afterward, CNC machining is used an additional stage to further refine the molded shape. Throughout this recycling process, particles are emitted; however, the potential health consequences of exposure to these particles are not well understood. Particulates with specific morphologies are strongly associated with longitudinal adverse respiratory effects. Therefore, prolonged exposure to these emissions poses significant occupational health and safety concerns for machine operators. This study investigates the morphology distributions and elemental compositions of particles emitted during specific stages of the manufacturing process for plastic-sand pavers with a 30:70 plastic-to-sand ratio. Two compositions of pavers are investigated in this study, and the plastic waste used in each paver was sourced from either HDPE kitchen waste or HDPE ghost fishing gear. During shredding, extrusion, and CNC machining, particle emissions were collected onto a polycarbonate filter-paper with 0.2 µm-diameter pores . Scanning Electron Microscopy (SEM) and Energy Dispersive X-Ray Spectroscopy (EDX) were used for the imaging and elemental analysis of particles. To extract particle morphology information, SEM images were analyzed using a semi-automated workflow in MATLAB. EDX analysis found particles commonly-composed of carbon, nitrogen, iron, oxygen, silicon, magnesium, aluminum, potassium, and/or chlorine across paver compositions and manufacturing processes. Results from SEM analysis revealed micro- and nano-sized particles. For each composition and manufacturing stage, features were extracted from thousands of particles, which revealed major axis lengths that ranged between 60 nm to 50 µm. Particle circularity values ranged between 0.5 and 0.7, whereas eccentricity values ranged from 0.6 to 0.8, suggesting particles have a predominantly elliptical morphology across compositions. Solidity values, a proxy for angularity, landed between 0.7 and 0.9, which indicates particles are mildly angular. Euler numbers closer to 1 were found across compositions and manufacturing stages, demonstrating that particles are generally solid with few holes. Despite the benefits of recycling plastic waste into construction materials to tackle global plastic pollution, it is important to investigate the potential health risks associated with particles exhibiting specific morphological features, which can vary across manufacturing processes.

This work was supported by URI Plastics REU

Recycle HDPE Plastic Paver Design

Tianyu Zhang[1], Korryn Narvaez[2], Sirri Neba Nforsoh[3], Rhea Panat[4], Vinka Oyanedel-Craver[3], Jennifer Bissonnette[5] & Jessica Smith[5]

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Plastic waste, particularly high-density polyethylene (HDPE), presents a growing environmental challenge while creating opportunities for sustainable material innovation. This project integrates material engineering, computational design, and aesthetic exploration to develop landscape pavers composed of 30% recycled HDPE and 70% sand. Beyond improving material performance, the research investigates how geometric design can enhance functionality, sustainability, and user experience. Inspired by the molecular structure of HDPE, a modular paver geometry was developed through abstraction and recombination to create a permeable paving system with improved replaceability and a distinctive visual identity. Surface textures and color variations derived from different recycled HDPE sources further expand the aesthetic potential of the material. Prototype pavers fabricated from recycled kitchen waste and discarded fishing gear were evaluated through compressive strength, water absorption, surface friction, abrasion, and UV weathering tests. Both material compositions achieved compressive strengths exceeding 30 MPa, demonstrating performance comparable to conventional paving materials. By combining sustainable materials with computational design, this research demonstrates how recycled plastic waste can be transformed into durable, customizable, and visually expressive landscape infrastructure that supports circular material use while reducing environmental impact.

This work was supported by RI NEST

Standardizing Small-Scale PLA Bioplastic Composting

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Plastic pollution is an international problem due to its growing environmental, health, and waste management impacts. Bioplastics offer a promising solution, as they are made from biomass sources and can degrade into naturally occurring compounds. Polylactic Acid (PLA) is a widely used bioplastic, with applications in packaging, 3D printing, and medicine. However, it has only been degraded in industrial composting facilities, limiting its end-of-life options. If disposed of improperly, PLA will persist similarly to petroleum-based plastics. Industrial composting requires temperatures between 50-60 °C and soil moisture of 50-60%. The present study aimed to recreate these conditions on a smaller scale using a commercial kitchen composter (Reencle). A 30-day procedure was developed to biodegrade pure PLA, and PLA embedded with a bacterial additive, to evaluate its effects on degradation. A food waste diet was formulated with the ideal C:N ratio (30:1) and weight (700 g), consisting of fruit, vegetable, and coffee-ground waste. For the first 15 days, all food waste was added on day 1. During days 16-30, the mixture was added gradually (10% of the total diet every other day). Temperature, moisture, pH, oxygen depletion, and organic solids were monitored to assess microbial activity and compost quality. To evaluate PLA degradation, weight loss, chemical bond analysis (FTIR), and surface characterization (SEM) tests were performed. The results showed that the compost temperature was kept between 40-50 °C, while moisture fluctuated considerably between 25% and 70%, requiring periodic addition of water to maintain the ideal value. More acidic pH values were recorded initially as organic acids were formed from the degradation of food waste, neutralizing over time, and eventually reaching the optimal range for microorganisms (6-8). Oxygen consumption tests showed more uniform activity when food was added periodically (days 16-30). Although changes in chemical bonding, opacity, and surface microcracks were observed from the previously mentioned analyses, no significant weight loss was detected during the 30 days, suggesting that these changes were likely due to hydrolysis (the first step of PLA biodegradation) rather than microbial assimilation. Visual changes were slightly greater in modified PLA than the pure sample, suggesting increased biodegradability due to the bacterial additive. In conclusion, the conditions created were not comparable to industrial composting and were insufficient to significantly degrade the PLA samples. PLA biodegradation depends on many factors, and the relationship between compost quality and polymer degradation is complex, warranting further studies using different parameters.

This work was supported by URI Plastics REU

Using Metabarcoding to Build Planktonic Foodwebs on the Northeast Shelf

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DNA metabarcoding is a powerful tool for determining community richness in a given biological sample. Characterizing the diet of zooplankton, which are critical in linking lower and higher trophic levels, can be difficult as traditional morphological identification is often limited by prey digestion. Our long-term aim is to resolve zooplankton food webs on the Northeast Shelf using DNA metabarcoding. To evaluate the suitability of this approach, we first analyzed a range of planktonic organisms (crustaceans, cnidarians, and salps, (n=8)), by extracting DNA and amplifying the highly conserved 18S V4 rDNA region. We recovered diverse prey communities across all taxa. Prey communities in salps exhibited high species richness, consistent with filter feeding. Salp-associated sequences were detected in all organisms examined despite not generally being recognized as a major prey resource for these taxa. Host-associated sequences dominated all samples, particularly crustaceans, reducing the relative abundance of prey-associated sequences and motivating methodological optimization. We evaluated whether incorporating mechanical lysis through bead beating prior to DNA extraction would improve prey-associated sequence recovery. Because mysid shrimp are abundant on the Northeast Shelf and link trophic levels, they were selected for further methodological optimization to support future long-term dietary studies. Individual mysids (*Neomysis americana*, n=10) were processed using either a standard extraction protocol (n=5) or a modified protocol incorporating bead beating (n=5). Bead-beating did not substantially reduce the proportion of host-associated sequences or increase species richness, indicating little benefit for this workflow. Prey composition was consistent with previous studies of mysid diets, with diatoms dominating most samples. Parasite-associated sequences were also abundant, particularly Hematodinium, a parasitic dinoflagellate responsible for “bitter crab disease”. Our results highlight the utility of metabarcoding for zooplankton diet studies, and lays the groundwork for detailed planktonic foodwebs.

This work was supported by RI NEST

Growth Response of Newly Described Suspected DDA Involving *Leptocylindrus hargravesii* to Light, Temperature, and Added Nitrogen Conditions

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Biologically available nitrogen is a major regulator of marine primary productivity in the ocean. In nitrogen-poor environments, nitrogen-fixing microbes known as diazotrophs provide the ecosystem with a significant source of bioavailable nitrogen. Diatom-diazotroph associations (DDAs) are one such group of diazotrophs, where a diazotrophic symbiont provides fixed nitrogen to a diatom host. The diatom *Leptocylindrus hargravesii* has not previously been acknowledged as a DDA, however, two strains maintained in our laboratory have exhibited growth in medium without added nitrogen (N-deplete medium) for over a year. This growth capability suggests the possibility of a diazotrophic symbiont, or another alternative nitrogen acquisition strategy. The physiological responses of these cultures to supplemental dissolved inorganic nitrogen (DIN) and environmental conditions have not yet been characterized. Here we investigate the effects of temperature, light intensity, and supplemental DIN on *L. hargravesii* growth, as measured by daily fluorescence readings, with the goal of better understanding their environmental niche. Our results have shown that growth rate varies with both temperature and light. Preliminary data indicates a maximum growth rate at ~28˚C ($\mu \approx 2.1$), with reduced growth rates at the thermal extremes of this experiment (16°C, 32°C). Growth increased across the range of light intensities tested, though the compensation irradiance and complete saturation point were not captured. Both strains exhibited similar trends across environmental treatments. This data provides an insight into the ecological niche of *L. hargravesii* and establishes a baseline for predicting responses to changing ocean temperatures. Growth rates did not differ significantly among nitrate, ammonium, and nitrogen-deplete treatments, however, variance was much higher for cultures treated with DIN. Because these cultures had already been maintained for months in nitrogen-deplete conditions, this finding suggests that the externally supplied DIN did not measurably stimulate growth beyond the capacity of internal nitrogen fixation. This data provides foundational physiological characterization of a suspected DDA involving *L. hargravesii* and can further inform our understanding of diazotroph distributions and global ocean nitrogen cycling.

Investigation of the Probiotic Potential of *Pseudoalteromonas rubra* in Aquaculture: Copepod Systems

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Copepods are microscopic crustaceans that play an essential role in aquatic ecosystems; they are primary consumers, consuming primary producers and serving as a food source for a variety of primary consumers, and they contribute to nutrient cycling. *Parvocalanus crassirostris* is a small pelagic calanoid copepod commonly cultured as a food source for marine larval fish. Although some microbes associated with copepods can be beneficial to the host animal, some are pathogenic. One common bacterial pathogenic genus across marine ecosystems is *Vibrio*. Some species in this genus can cause rapid mortality among a variety of marine organisms, including mass mortality events in aquaculture systems, thereby significantly affecting production rates and economic returns in the industry. *Pseudoalteromonas rubra* is a gram-negative red bacterium, an isolate of which was cultured in 2022 from crustose coralline algae (CCA) in tanks containing *Astrangia poculata* in RWU's Wet Lab. *Pseudoalteromonas rubra* is known to produce the prodiginines, which have antimicrobial, antibacterial, and apoptotic properties that effectively kill several species of *Vibrio*. The goal of this study was to characterize the impact of the putative probiotic *P. rubra* on the microbiome of *P. crassirostris* cultures. Replicate 3L cultures of *P. crassirostris* were prepared and dosed as either control, *P. rubra* (105 cells/mL), or INVE SanoLife Probiotics, and fed daily with microalgae. The study was maintained over seven days. Copepods and seawater samples were taken at five time points throughout the time series and preserved for 16S rRNA amplicon sequencing and for probe-based microscopy (FISH). Growth and health of the cultured copepod populations were also monitored and recorded via daily counts of the different life stages present. There was no significant difference in the abundances between treatments. Sequencing and microscopy results will be further analyzed in Fall 2026 to determine how the microbial communities respond to *P.rubra* treatment, and where specific microbes of interest are localized in the cultures. Combining microbiology with aquaculture, this project investigated the potential for *P. rubra* as an effective anti-*Vibrio* treatment for copepod culture in aquaculture and aquarium settings. Although we have yet to analyze the samples to determine how *P. rubra* exposure impacted the microbiome of the treated copepod cultures and whether it decreased *Vibrio* counts in the cultures, current results are encouraging: *P. rubra* did not negatively affect copepod culture performance, giving it strong potential as a probiotic for aquaculture systems.

This work was supported by the RWU Blue Fellows Program

Desiccation Sensitivity in Mutated sod1 *D. melanogaster* Is Driven by Dysregulated Fatty Acid Metabolism

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Amyotrophic Lateral Sclerosis (ALS) is a cell non-autonomous neurodegenerative disease characterized by progressive loss of motor neurons and paralysis. Over 150 distinct mutations in superoxide dismutase 1 (*sod1*), a gene involved in the elimination of toxic superoxide radicals, have been linked to ALS. Previously, the Stilwell lab showed that *dsod1*^{H71Y} and *dsod1*$^{-/-}$ mutants are dehydration sensitive and have reduced water content. The molecular basis for desiccation sensitivity is unknown. Here, we show that mutant *sod1* dehydration phenotypes can be suppressed by mutations in *cyp4G1*. The CYP4G1 protein is predominantly expressed in oenocytes, a cell type responsible for the biosynthesis of very long chain fatty acids (VLCFA) necessary to produce cuticular hydrocarbons. Furthermore, we show that mutant *sod1* alleles have a dramatic reduction in triglyceride content and reduced lipid droplet size in fat body tissue where neutral lipids are stored. Together, these data show that mutations in sod1 as associated with reduced triglyceride content likely leading to a reduction in VLCFAs. The mechanism by which sod1 impacts fatty acid metabolism is currently under investigation. Although the *Drosophila* desiccation sensitive phenotype is difficult to explain in the context of human ALS, recent work has shown that dysregulated fatty acid metabolism is present as a presymptomatic stage in human disease progression.

This work was supported by RI NEST

Spatial and Temporal Patterns in Elasmobranch Abundance Around Block Island, RI

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Elasmobranch community structure around Block Island was examined using baited remote underwater video systems (BRUVs), a non-invasive tool assessing spatiotemporal patterns in species occurrence, abundance, and diversity. BRUVs were deployed at five sites in Block Island Sound from June-October during 2021-2025 (n = 179 deployments), with each deployment treated as an independent sample. Twelve elasmobranch species were observed, including five sharks (Great White, Sand Tiger, Sandbar, Smooth Dogfish, and Spiny Dogfish) and seven batoids (Barndoor Skate, Clearnose Skate, Little Skate, Winter Skate, Bullnose Eagle Stingray, Cownose Stingray, and Roughtail Stingray). Batoid community composition showed limited spatial variation (site: $p = 0.13$), but significant temporal variation among years ($p < 0.001$) and months ($p < 0.05$). Skate abundance was highest during cooler months (May, June, and October), whereas ray abundance increased during warmer months (July and August), consistent with seasonal shifts in distribution. In contrast, shark community structure remained relatively consistent across sites, years, and months ($p = 0.10$-0.62). Smooth Dogfish were the most frequently observed shark species and occurred across a broad temperature range (10.9-24.6 °C), with highest occurrences in warmer water ($\bar{x} = 20.3 \pm 2.6$). Large-bodied sharks were also associated with warmer conditions (16.0-24.6 °C, $\bar{x} = 20.8 \pm 2.0$ °C). Although depth was not a significant predictor across all elasmobranch species, the intermediate-depth Site A, which is surrounded by deeper water, supported the greatest species richness. These findings demonstrate species-specific habitat use and likely reflect temporal shifts associated with environmental conditions, migration, and prey availability. Continued BRUVs monitoring provides a valuable non-invasive approach for detecting changes in species occurrence, biodiversity, and community structure within Northwest Atlantic coastal waters.

This work was supported by the RWU Blue Fellows Program

Role of Secondary Microplastics Formation on *S. epidermidis* Viability and Growth

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Although human skin represents one of the body's best barriers against external contaminants, recent studies have discovered that micro- and nano particles have potential for penetrating unbroken human skin. Furthermore, these particles can act as vessels for diseases, toxicants, and other forms of contaminants harmful to the body. *Staphylococcus epidermidis*, a member of the human skin and mucosal microbiota, can be appreciated as both beneficial and detrimental to human skin. In effect, this strain of bacteria both maintains immune cell responses and has potential for contributing to skin cell damage. Secondary microplastics, a byproduct of primary microplastic damage, is an emerging contaminant following plastic exposure to UV radiation, collision-collision forces, chemical weathering, and other pressures. In this study, *S. epidermidis* viability is determined when grown alongside varying concentrations of secondary microplastics generated by collision-collision forces. To do this, blue glitter underwent flocculation jar tester simulations, filtration, dehydration, then addition to *S. epidermidis* bacteria culturing. Considering the opportunistic nature of *S. epidermidis* regarding biofilm formation, it is hypothesized that the bacterium will favor secondary microplastic conditions in comparison to the absence of plastics. Results showed that following low-level and high-level exposure to secondary microplastics, bacterial growth curves exhibited little change in viability between plastic and no plastic presence. During high level exposure, however, *S. epidermidis* increased biofilm formation, indicating phenotypic changes that can affect their behavior and virulence. These results represent useful information for understanding the potential mechanisms that allow micro- and nano particles entry through the human skin barrier and their effects on human microbiomes.

This work was supported by URI Plastics REU

Low-Power Valves for Robotic Planetary Exploration

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Hydraulic actuation of components using water as the operating fluid encounter issues in microgravity environments such as biofouling and clogging. Hydraulic actuation is often controlled through solenoid valves which have the convenience of being actuated electrically, allowing for easy automation. However, they have the drawback of being mostly manufactured with high density materials and requiring continuous current application to maintain either their open or closed state.

We propose the design of a low-power, bistable valve by leveraging a magnetic silicone composite flexure which utilizes iron oxide microparticles. Through the use of a NdFeB magnet driven by a servo motor, rotating magnetic fields toggle the valve's operational state without the need to continuously apply an electric current. The magnetic silicone composite in contact with the operating fluid provides several additional functionalities. In particular, ultraviolet exposure has been shown to induce photothermally mediated cytotoxic heating for biofilm dispersal, while the magnetic actuation of the flexure component provides an anticlogging mechanism through mechanical activation. This bistable valve design provides a lightweight, low-power, and multifunctional approach that can be beneficial for fluid control systems used in future space exploration.

This work was supported by NASA Rhode Island Space Grant

Synthesis and Characterization of Magnetic Nanoparticles for Utilization in Hydrogels

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Iron oxide magnetic nanoparticles (MNPs) are highly biocompatible, and thus they can be used to provide magnetic functionality in biomedical applications. The magnetic properties of the MNPs allow for targeted delivery and actuation on the tumor cells, and elevated temperatures achieved under alternating magnetic field (AMF) actuation can trigger an immune response. This study investigates the synthesis of magnetic nanoparticles through the high-temperature polyol and thermal decomposition methods, with potential applications in targeted immunocellular death in tumors. A novel synthesis of magnetic nanoflowers with different coatings was attempted, motivated by their reported high heating ability under AMF actuation. In this project, the influence of synthesis conditions on MNP magnetic properties and morphology were investigated. The high-temperature polyol method employs a Fe(III) organometallic precursor and triethylene glycol (TREG) as a solvent, capping agent and reducing agent, and reacting at temperatures at 250°C in a self-pressurized vessel. The thermal decomposition method employs a Fe(III) organometallic precursor dissolved in a high-boiling-point TREG solvent with a capping agent reacted at 250°C under an inert atmosphere. The effect of the capping agent (triethylene glycol vs polyacrylic acid (PAA)) and reaction time and temperature was also evaluated. The synthesized particles were characterized using dynamic magnetic susceptometry, hyperthermia and transmission electron microscopy (TEM). Our findings suggest that adding PAA is critical for synthesizing nanoflowers, which show promise for enhanced heating capabilities under AMF. This systematic study also confirms that particle morphology is consistent with existing literature and indicates potential for stability within alginate matrices. Future research will investigate the loading efficiency of these MNPs into tetrazine- and norbornene-crosslinked alginate hydrogels, as well as their controlled release capabilities under a magnetic field for targeted therapeutics.

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Diversity of Southern New England's Rocky Intertidal Zone

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Intertidal zones are highly biologically diverse ecosystems that occur where the ocean meets the land. These zones are categorized into four divisions (spray zone, high intertidal zone, middle intertidal zone, and low intertidal zone) with distinct characteristics and ecological differences, causing vertical zonation of different plants and animals. Unfortunately, these ecosystems face high levels of negative anthropogenic impacts due to their close proximity to human activity. These negative anthropogenic impacts include rock-flipping, trampling, displacement of mobile species, artificial structures (sea walls), invasive species, sediment deposits, pollution, harvesting, and global climate change.. In addition, most of the species that live in the rocky intertidal cannot readily migrate to other regions as ocean temperatures change and consequently shift the biogeographic ranges that are inhabitable by species. Therefore, a changing environment, particularly when water temperature increases, leaves species ill-suited for their habitat, decreasing their fitness and potentially leading to extinction. The goal of this study is to continue to conduct long-term monitoring of rocky intertidal sites in Rhode Island at Kings Beach, Fort Wetherill State Park, and Beavertail State Park to better understand how human presence at these sites might change the distribution and abundance of common intertidal species. This was done by capturing photographs of the species in three of the four divisions (high, middle, and low intertidal zones) using PVC pipe quadrats to create photo plots. Following this, the data were used to compare species composition between 2025 and 2026 at the King’s Beach site using principal coordinates analysis and permutational analysis of variance (PERMANOVA). The findings, unsurprisingly, showed that there was extreme variation in species composition between zones but little variation between years. Furthermore, zonation, which is created by the varying tidal height, has a much stronger influence on community composition than year-to-year variation, though it is important to note that these results come after one year of monitoring. Continuing to build this dataset will help predict long-term trajectories of intertidal environments to protect coastal resources in areas with elevated human activity.

This work was supported by the Southeastern New England Educational and Charitable Foundation

How Far Can City Bees Travel for Food?

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Bees, just like humans, need balanced diets to perform their best. To balance their nutrient intake, bees must visit different patches of flowers, where they collect protein-rich pollen and carbohydrate-rich nectar. For many bees, different types of flowers, or food courses, are required to obtain this balance. Thus, city bees must travel across urban areas to access green spaces for resources. However, some bee species may struggle to reach these green spaces depending on distances and structures, such as roads, that may be blocking their paths. Fragmented habitats could limit the diversity of pollen and flowering plants for foraging bees and other pollinators.

Our research uses mark-recapture surveys to compare the traveling capacities of two different species (larger *Bombus griseocollis* and smaller *Agapostemon virescens*) and track their movement across gardens located on the urban Providence College campus. The campus contains five pollinator gardens separated by at least 75 meters. We expect that larger *B. griseocollis* will travel between all gardens, as they can move distances up to 5 km. However, smaller *A. virescens* may be limited to just one or two gardens since they have shorter average foraging ranges. This information can be used to plan pollinator gardens in urban areas that will account for the minimum distances needed for smaller native bees to travel between them.

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Synthesis Analysis of Sm Based Magnetic Nanoparticles

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Samarium (Sm) based magnetic materials are high-performance magnets that can withstand environmental extremes beyond what $Nd_2Fe_{14}B$ can handle. Despite this, Sm based magnets require additional modification to hold up to the standards set by Nd based magnets. This work looked to generate Sm-based nanoparticles to study both their individual characteristics as well as what happens when they are modified using a core@shell approach. Microwave heating was used to achieve the required high temperature and pressure conditions needed to incorporate the Sm into the systems, while working on a rapid time scale that is conducive to nanoparticle synthesis. XRD, XRF, and TEM, were performed on the products to analyze their structural properties, which showed 5-10 nm particles with an amorphous crystal structure. While a pure product has yet to be generated, XRF has confirmed the presence of Sm in the target ratio 1:5 / 2:17 Sm:TM ratio (TM = Fe or Co) as well as an observable increase in magnetic behavior when the reaction proceeds as intended. Post annealing of the Sm-Fe was done @700°C to try to achieve the target hexagonal crystal structure, however the structure was predominately Fe_3O_4 with an additional unidentified phase.

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Tetrahymena pyriformis Does Not Exhibit Dose Response to Combinations of Common Heavy Metal Pollutants

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Heavy metals are common aquatic pollutants, often leached into waterways from industrial activity. Exposure to heavy metals is associated with pronounced oxidative stress and systemic toxicity, even in acute doses. *Tetrahymena pyriformis*, a ciliated protist found in most bodies of fresh water, is a common toxicology model system. This study analyzed gene expression following 1-hour exposures to different combinations of copper (Cu), cadmium (Cd), and zinc (Zn). Our experiment quantified the expression of genes encoding metal-sequestering proteins metallothionein (MT1, MT2), and active transport proteins Zip6 and HM1. The purpose of this study was to identify differences in *T. pyriformis* gene expression when exposed to environments contaminated with multiple metals versus a single heavy metal. We compared equal concentrations of metals, as well as low concentrations of cadmium with highly concentrated zinc and copper. Each exposure included four treatment groups: a control (no heavy metals), single-metal exposures at a selected concentration, and a combined-metal exposure. Cells were exposed during log phase, RNA was isolated, and quantitative PCR was used to measure gene expression. 18s was used as a normalizing gene. Although there was numerical variation between treatments, sample groups did not exhibit significant differences in gene expression for any of the genes analyzed. These results suggest that *T. pyriformis*' toxic response may not necessarily be related to the concentration of heavy metals in the environment. Our observations promote additional questions as to how aquatic microbes regulate heavy metal toxicity in the wild.

This work was supported by RI-INBRE

Temperature Stress Alters Heavy Metal Response in *Tetrahymena pyriformis*

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Human activities are impacting freshwater environments resulting in an average of 1.2– 2.2°F increase in water temperature. Increasing temperatures in the freshwater environment may cause organisms to respond differently to contaminant exposure, though it is not currently well studied. In addition, human activity increases levels of industrial contaminants in freshwater environments, including heavy metals. *Tetrahymena pyriformis* is a ciliated protist found in nearly all freshwater ecosystems and often used in toxicology research. In this study we exposed *T. pyriformis* to varying concentrations of cadmium (0.4µM, 4.0µM, 40µM), copper (3µM, 30µM, 300µM), and zinc (3.5mM, 35mM, 100mM) for 1 hour at both 27°C and 35°C to measure differing metal response with temperature stress. Following exposure, we measured expression of genes involved in metal homeostasis including metallothionein (MT1 & MT2) and metal transport genes (ZIP6 & HM1). Cells were exposed in log growth phase; RNA isolated, and quantitative PCR was used to amplify the genes of interest. Temperature stress alone resulted in significantly decreased expression of HM1 and Zip6. Copper exposures at 27°C resulted in increased expression of HM1 at lower concentrations (3µM) and increased expression of MT1 at higher concentrations (300µM). Cells exposed to 300µM Cu at 35°C showed a significant increase in expression of both MT1 & MT2. Cells exposed to 40µM cadmium at 35°C showed increased expression in both MT1 & MT2, which was higher than cadmium alone. Both HM1 & Zip6 expression was increased with 0.4µM Cd at 35°C, compared to control or cadmium alone. Little to no change in gene expression was observed after zinc exposure, regardless of temperature. This study illustrates that *T. pyriformis* exhibits unique patterns of gene expression after exposure to different heavy metals and increased temperature. Higher temperatures may exacerbate heavy metal stress, resulting in increased metal uptake. While *T. pyriformis* is widely used in toxicological studies, there is limited research combining heavy metal exposure with temperature stress. We expect these combinations to become more common, and understanding the impact on aquatic organisms may allow us to mitigate broader environmental impacts.

This work was supported by RI-INBRE

Predicting the Impact of Early and Midlife Lifestyle Factors on Dementia Risk Using Retrospective Study and Machine Learning Approaches

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Background This project addresses a fundamental gap in dementia prevention science: the decades-long lag between modifiable lifestyle exposures and measurable cognitive outcomes. Leaps in big data and computing technology now allow access to reliable data insights retrospectively, by applying machine learning to extract multimodal signatures predictive of cognitive resilience and neuropsychiatric vulnerability.

Methods We propose here building a multidimensional lifestyle profile of AD using a mix of (a) machine learning approaches, including Exploratory Factor Analysis and Canonical Correlation Analyses on large open AD datasets and (b) cognitive modeling to predict and test the potential role of lifestyle factors in specific AD-related mechanisms. This framework will build on previous research findings on lifestyle choices in your 30's and 40's that may shape cognitive functions related to dementia decades later. We later plan to have AD patients and their caregivers complete a survey, examining their lifestyle choices in early life to determine some of the driving factors of AD. Through systematic literature review and analysis of existing research findings, we've compiled a list of lifestyle factors and choices that hold analytical weight worth including in our developing study.

Results Here, we present preliminary results from examining a subset of clinical and demographic data from the National Alzheimer's Coordinating Center (NACC), and a proposed cognitive model linking factors from that data to verbal processing and memory in AD.

Implications This project may contribute both to novel signal discovery and on setting up a methodological pipeline for streamlining big-data pattern search in AD to understand and ultimately intervene on the modifiable lifestyle determinants of cognitive aging.

This work was supported by the Calabria Cognitive Health and Aging project

Terahertz Fourier Ptychographic Imaging for Biomedical Samples

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Imaging with Terahertz (THz), electromagnetic radiation with wavelengths between the infrared and microwave regions, shows promise for biomedical applications due to its noninvasive, nondestructive nature and sensitivity to biomolecules. Among THz modalities, continuous-wave (CW) THz imaging systems are particularly attractive because of their compactness, lower cost, and stability. However, with CW THz Imaging, the long wavelength and limited availability of optics in the THz region can restrict spatial resolution. To address this challenge, we implement a computational imaging technique, THz Fourier Ptychography, which uses an acquired set of full-field images at various illumination angles to reconstruct an image with both a wide field of view and high resolution. The designed system employs a configurable source array to control the illumination angle in a low-cost, stable setup, eliminating the need for motorized components. Here, images were simulated with 20dB of additive Gaussian noise with angular illumination from the theoretical physical source array, and a Fourier ptychography reconstruction algorithm utilizing quasi-Newton's method with Tikhonov regularization was applied. The reconstruction resulted in a ~20% improvement in resolution with a 4.6mm field of view, obtaining a synthesized numerical aperture of 0.354 from a physical numerical aperture of 0.293. This work computationally demonstrates THz Fourier Ptychography for resolution enhancement with a wide field of view in a compact, cost-effective system to enable future biomedical applications.

This work was supported by RI-INBRE

CritterBender: Multi-Axial Tool for Comparative Biometrics and Physiology

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Organisms move in myriad ways to survive. Trees sway with the wind to keep from snapping and animals flex their muscles and bend their joints to perform incredible athletic feats. A central goal of the fields of biomechanics and physiology has been to measure the material and physiological properties of these structures. However, measuring these properties is a longstanding problem for several reasons. Firstly, the complex and variable shapes of organisms necessitate a variety of expensive equipment fitted with aftermarket customizations that are typically limited. Secondly, organismal motions are often complex, dynamic, and multi-dimensional. Finally, many biomechanical and physiological techniques often destroy tissue, thereby limiting the number of samples taken within a given specimen. We developed a multi-axial platform that measures passive material properties and active muscle mechanics in intact specimens across taxa, with rapid non-destructive mounting that preserves tissue viability across trials. Using sonomicrometry, we confirm that measured muscle strain strongly correlates with commanded strain, validating that the apparatus controls muscle fiber behavior as intended. Using dynamic work loops–a form of active muscle mechanics–we also tested the muscle pair as a coordinated bilateral unit, simulating the activation pattern of in vivo swimming. We designed custom fitted parts that allow the same motor-sensor unit to bend an organism along the three primary axes of rotation. Finally, we measured the passive mechanical properties of an alligator tail and ankle to demonstrate cross-taxa capabilities, as well as the ability to test both multiarticular spines and monoarticular appendages. We collected promising data of muscle force, power and kinetics which legitimately validate the mechanical claims of the CritterBender method.

This work was supported by RI-INBRE

Analysis of Parameters for Improved Morphogenic-Regulator-Meditated-Transformation Using Immature Embryo Explants in *Sorghum bicolor*

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Reliable *Agrobacterium*-mediated transformation of *Sorghum bicolor* remains constrained by genotype specificity and the need for immature embryos (IEs). Lee and Wang (2023) conceptualized framing transformation as $T = V(C_d \times C_i \times C_r)$, where C_d is DNA delivery efficiency, C_i is stable integration and selectable marker expression, C_r is regeneration competence, and V captures experiment-to-experiment variables, we systematically tested parameters predicted to act on terms C_d and C_r. Standard IE workflows established a baseline for somatic embryogenesis and regeneration. To increase C_d, we evaluated *Agrobacterium* strains and ternary *vir*-helper vectors, which improved attachment and transient expression of visual marker. To raise the frequency of stable integrative events progressing to regeneration (C_r), we compared developmental regulators (DRs) BBM-WUS2 and GRF-GIF delivered altruistically or on the T-DNA integrating cassette respectively. BBM-WUS2 accelerated embryogenic induction on the scutellar epidermis, presumably resulting from more transformed cells forming somatic embryos compared to the standard transformation, generating dense; rapidly advancing multi-stage embryogenesis. GRF-GIF increased transformation frequencies while markedly shortening the callus phase, consistent with increased apical dome organization. Presumably this is causing more transformed tissues of the callus to be developing towards regeneration much faster than compared to standard transformation. Media composition modulated *Cr* by supplementing different combinations of exogenous plant hormones. Wu and Kumar media regimes were compared, although both had good early responses for callus formation Kumar wasn't able to regenerate plants as often as the Wu media from GRF-GIF mediated transformations. Across experiments, standard protocols yielded low-copy, heritable insertions but remained efficiency-limited, while the combined optimization of DR strategy, ternary delivery, and stage-matched media improved overall T and the throughput of regenerated events.

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The Effects of Chronic Stress on Alcohol Tolerance in *Drosophila*

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Chronic stress is a major public health challenge associated with significant physical and mental health consequences, including cardiovascular disease, depression, anxiety, and alcohol use disorders. Despite its significant health burden, the mechanism underlying chronic stress remains incomplete. *Drosophila melanogaster* provide a powerful genetic model for investigating the impact of chronic stress on health and alcohol sensitivity. Evidence suggests that inhibiting serotonin transporters protects against the effect of chronic stress in *Drosophila*, including a decreased lifespan (Knapp et al. 2022). However, it remains unclear whether serotonin and its regulation modulate sensitivity to alcohol intoxication, specifically in the context of chronic stress. In this study, we use a novel loss-of-function dSERT mutant to investigate the role of the serotonin transporters in modulating alcohol sensitivity in a chronic stress model. Specifically, we compare alcohol sensitivity after exposure to chronic stress in flies lacking serotonin transporters (dSERT) versus control w^{1118} flies. To induce chronic stress, experimental w^{1118} and dSERT flies were exposed to dead flies of the same genotype for 2 days, then flipped into vials with fresh dead flies, which were killed 2-3 days prior via starvation. After 4 days of exposure, living flies were transferred to testing vials for a 90-minute sedation assay in which they were exposed to 50% ethanol. The number of sedated flies, as defined by inability to right themselves or prolonged immobility, was recorded at 5-minute intervals. We hypothesized that dSERT mutants would show less sensitivity to alcohol compared to genetic controls and be less sensitive to chronic stress. Preliminary data suggest dSERT mutants are less sensitive to alcohol-induced sedation compared to genetic controls. Although these differences were not significant, flies exposed to dead conspecifics exhibited a trend towards increased sensitivity to alcohol-induced sedation in both genotypes. These findings suggest that chronic stress may influence behavioral responses to alcohol, although additional experiments are needed to further evaluate this effect. Future work will continue to investigate the impact of chronic stress on alcohol sensitivity and investigate the role of serotonin signaling in modulating this response. In addition, experiments will examine the effects of chronic stress on survival following ethanol toxicity to better understand how stress influences organismal lifespan, overall health, resilience to alcohol exposure, and susceptibility to alcohol-induced toxicity. Together, these studies will provide a more comprehensive understanding of the interactions between chronic stress, serotonin signaling, and alcohol responses.

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I See Dead Flies: Effects of Chronic Stress in Drinking in *Drosophila*

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Chronic stress is a persistent state of physical or emotional strain that results in the dysregulated activation of the neuroendocrine system and can negatively affect mental and physical health. Prolonged exposure to chronic stress can increase the likelihood of developing substance use disorders, including alcohol use disorders (AUD). Serotonin and serotonin transporters are thought to play an important role in the relationship between chronic stress and AUD, however, the relationship is complex and not well understood. Here we investigate the role of serotonin transporters in the response to chronic stress and its impact on alcohol-related feeding behaviors in *Drosophila melanogaster*. We hypothesize that chronic stress will result in the development of preference for ethanol over sucrose, but disrupting serotonin regulation will be protective against this effect. To model chronic stress, the novel loss-of-function mutant, dSERT, and their genetic controls (w^{1118}) were chronically exposed to dead conspecific flies for five days. Sucrose and alcohol feeding behaviors were measured using Fly Liquid-Food Interaction Counter (FLIC), an automated system for continuous monitoring of Drosophila feeding and tasting behaviors, on the fifth day (Ro et al. 2014). Specifically, flies were given unlimited access to two wells, containing either 5% sucrose or 15% ethanol in 5% sucrose for three hours. We calculated preference indices for dSERT and w^{1118} flies in both stressed and non-stressed conditions and tracked preference over time. Preliminary results demonstrated preference for ethanol within the three-hour assay was not achieved as preference indices for all groups were negative. Interesting, though not significant, flies exposed to dead flies interacted with sucrose more than unexposed flies. Future research aims to continue investigating how chronic stress alters alcohol and sucrose feeding behavior and employ an extended assay to determine if flies eventually develop alcohol preference.

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Wheel-Running as a Window into the PTEN-KO Neurological Clock

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The phosphatase and tensin homolog protein (PTEN) is a critical regulator of the PI3K/AKT/mTOR signaling pathway, which governs cellular growth and metabolic balance. Mutations in the *PTEN* gene are strongly linked to macrocephaly and Autism Spectrum Disorder (ASD) in humans. While PTEN deficiency is known to cause neuronal hypertrophy and metabolic stress, its impact on the endogenous circadian clock, the internal timing system that regulates daily physiological cycles, remains poorly understood. Proper circadian function is vital for metabolic homeostasis, which may be dysregulated in PTEN-deficient models. In this poster, we compare *PTEN* conditional knockout mice with CRE controls to test whether PTEN-related cerebellar dysfunction alters entrainment to a light-dark cycle, free-running period in constant conditions, and food-anticipatory activity in age-matched animals between approximately 179 and 181 days. Together, these studies aim to clarify how Purkinje cell metabolic abnormalities influence circadian timing and the cerebellum's role in anticipating daily feeding.

This work was supported by Providence College

Screening Azobenzene Derivatives to Determine Effects of Electronics on Azoreductase Mechanism

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Azo compounds constitute more than two thirds of all dyes synthesized for food, drug, and cosmetic purposes. Most synthetic azo dyes are not reduced until they encounter the human gut microbiome, which contains trillions of microbes that are able to modify both biotic and xenobiotic compounds using millions of different metabolic enzymes. The identity and relative abundance of bacteria in every human gut microbiome vary greatly between individuals and change over time, which further complicates how an individual may respond to a given therapy. Azoreductases (AzoRs) are a family of enzymes which reduce the azo double bond between two nitrogen atoms. Our group is working to synthesize 41 synthetic azobenzene compounds. By doing so, we can learn more about our gut microbiome and what is responsible for metabolizing these azo compounds found in our everyday diet.

First, we used UV-Vis spectroscopy to observe changes in concentration over time to identify a candidate azoreductase enzyme capable of reducing our library of synthetic azo compounds. After testing with 14 different dyes, we identified a Firmicute (now Bacillota) AzoR identified from metagenomic data with the UniProt ID R5RX41, that is capable of reducing each type of azo structure we intend to study. Next, we conducted kinetics testing with R5RX41 and twelve azo dyes, and we are analyzing how changes in the relative donating and withdrawing character affects these relative rates. We have found that small changes in electronic substituents can greatly vary the rate that the AzoR can reduce our synthetic compounds, with K_{cat}/K_M values ranging from 7.4×10^2 $M^{-1}s^{-1}$ to 2.7×10^5 $M^{-1}s^{-1}$. By studying the mechanism in which azo compounds are reduced by enzymes in the gut microbiome, we can begin to model what metabolites will be formed in these reactions. This will further allow us to understand the role of azo compounds in gut health and the impact these compounds have on the human body.

This work was supported by Department of Chemistry and Biochemistry at Providence College

How Is Savoring Related to Multidimensional Sleep Health and Does the Correlation Differ Among Varying Ages?

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Sleep health is a multidimensional conceptualization of the sleep-wake cycle, looking to measure more than just the absence of sleep disorders. Dimensions that make up multidimensional sleep health (MDSH) include sleep duration, sleep efficiency, timing of sleep within the day, regularity of sleep timing, alertness, and satisfaction or quality of sleep (Buysse, 2014). Because of its multidimensional nature, there are many factors that can impact sleep health, including the practice of savoring behaviors. Savoring is a type of positive repetitive thought that has been associated with lower levels of sleep-related impairment (Tighe et al., 2022). However, little literature examines the relationship between savoring and MDSH. Our research seeks to address this gap by investigating how engagement in savoring is related to MDSH in an adult sample, and whether this relationship differs across adulthood. Participants (N=437) aged 18-82 years completed study questionnaires online at one time point. Methods used to measure study variables included the Savoring Beliefs Inventory (Bryant, 2010) and the Ru-SATED Questionnaire v4.0 (Buysse, 2016). In addition, sociodemographic and savoring questionnaires were designed by the researchers for use in this study. SPSS was used for data analysis. Descriptive statistics included frequency counts, means, and standard deviations; to test research questions, regression analyses were used. The sample was majority women, White, and non-Hispanic or Latino. Most participants reported engaging in savoring at least sometimes. Compared to nearly three-quarters of the sample who endorsed savoring during the daytime at least some days, slightly more than half endorsed savoring before sleep. Higher overall savoring beliefs ($B = 0.79$, $p < .001$), reminiscing ($B = 0.48$, $p = .006$), savoring the moment ($B = 0.88$, $p < .001$), and anticipation ($B = 0.50$, $p = .004$) were each associated with higher MDSH scores. Age did not significantly predict MDSH ($p > 0.05$) and the interactions between age and savoring scales were not significant (p-values > 0.05). Our findings suggest that savoring is positively associated with MDSH and associations of MDSH and savoring behaviors are similar across ages. Future studies should investigate relationships between savoring and MDSH more objectively by using wearable technologies such as actigraphy devices. Future research could also expand this work by using daily measures, manipulating savoring behaviors in an experimental way, and by diversifying the racial, ethnic, and socioeconomic populations they investigate.

This work was supported by RI-INBRE

Comparison of the Kinetic Stability and Structure of Superoxide Dismutase Variants

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Mutations in the *SOD1* gene are observed in up to 20% of Familial Amyotrophic Lateral Sclerosis (FALS) cases, and are considered responsible for disease occurrence. Mutations impacting the structure and stability of SOD1, as we see in FALS, causes the protein to unfold, forming toxic aggregates that accumulate in motor neurons. In its non-mutated state, SOD1 can be characterized as being kinetically hyperstable, which means that there is a high energetic barrier preventing the protein from transitioning from a folded to an unfolded state. Many of the known mutations causing FALS have destabilizing effects. This led us to investigate the role of kinetic stability of SOD1 variants, and how this ties to unfolding into toxic aggregates. The aim of this research is to quantify the rate that SOD1 unfolds, and examine how sequence variations impact protein structures and kinetic stability. In order to quantify kinetic stability, we utilize a method known as SDS-Trapping of Proteins (S-TraP). This method takes advantage of sodium dodecyl sulfate's (SDS's) ability to probe protein unfolding. We also add heat to the system to allow the sample to overcome the kinetic energetic barrier which typically prevents unfolding. This allows us to observe over time how the protein unfolds. We confirmed the high kinetic stability of both bovine and human SOD1 protein through a boiled/unboiled assay. We have also begun to quantify the kinetic stability of bovine SOD1 at varying temperatures, so we can theoretically determine the rate of unfolding under native conditions. Through literature, we have identified human SOD1 variants which cause FALS that may have significant effects on kinetic stability. We predicted protein structures using Alphafold and modeled them in Pymol to explore structural variations. Future studies will quantify the kinetic stability of these specific variants. We believe the kinetic stability of SOD plays an important role in disease occurrence and progression, so analysis of kinetic stability with regards to sequential variations will give us a deeper understanding of FALS as a whole.

This work was supported by RI-INBRE

Building LC/MS Workflows for Protein Stability Measurements

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Protein stability dictates the biological function and activity necessary for human health. Thus, understanding protein stability is fundamental to drug development including safety, shelf stability, and efficacy. Traditional biophysical methods of protein stability analysis are typically low throughput while requiring relatively large quantities of purified proteins, often hundreds of micrograms or more. These current methods produce individual measurements of stability rather than allowing for multiplexed analysis across many proteins. Liquid chromatography mass spectrometry (LC/MS) based approaches would allow for the collection of larger datasets with greater scalability and lower sample requirements. We aim to build workflows that include protease multiple reaction monitoring (MRM) methods, to generate larger datasets with consistently collected, quantifiable stability measurements. To develop this method, stability tests were performed by treating protein samples with proteinase K (PK), and comparing against untreated controls. Both PK and control samples were digested in trypsin, and filtered for LC/MS analysis. We wrote python CoLab notebooks to process this data, which were capable of reading chromatograms and mass spectra, matching data to in silico digests, and quantifying MRM transitions. In the future, we will further develop our LC/MS workflow by applying it to a wider variety of proteins, altering stability conditions and timepoints, and multiplexing. The generated data could be used in machine learning and enabling more accurate predictions of protein stability changes, expanding on the overall accessibility of stability knowledge. These predictive models may aid in the development of new protein therapeutics and medical developments.

This work was supported by RI-INBRE

Breast Cancer-Derived POLQ Variant E2370K Bypasses DNA Damage Induced by Chemotherapeutics

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Pol Theta (POLQ) plays a crucial role in DNA repair and is an error-prone enzyme, resulting in about 2.4 incorrect nucleotide insertions per 1000 bases. Its error-prone nature results in mutations that potentially cause genomic instability. In past studies, upregulation of Pol Theta has been found to be connected to breast cancer with poor clinical outcomes in patients. It has also been demonstrated that patients deficient in tumor suppressor genes such as *BRCA* experience increased genomic instability due to inefficient Pol Theta repair, which becomes the dominant pathway for double-strand breaks. To better understand the mechanistic link between Pol Theta-mediated repair and cancer, we've identified a *POLQ* variant from the cBIO portal in a patient diagnosed with stage II invasive breast carcinoma that metastasized to the bones and chest walls despite previous cancer treatment. Although the patient did not have a *BRCA* mutation, a *POLQ* mutation, E2370K, was identified. We hypothesize that the E2370K mutation may further reduce DNA repair, increasing genomic instability and cancer progression in this patient. E2370K was expressed and purified from *E. coli* to assess its DNA repair activity, including its ability to bypass 8-oxo-G and Cisplatin damage. A *POLQ*-knockdown MCF-7 breast cancer cell line was generated via CRISPR to introduce that mutation and evaluate repair with Cisplatin. Preliminary results show that Pol Theta E2370K can bypass damaged DNA despite common breast cancer therapy, indicating that mutated patients might develop chemoresistance and worse clinical outcomes.

This work was supported by RI-INBRE

Generation of Y239C Full-Length DNA Polymerase Theta to Understand Possible Linkages to Melanoma Cancer Development

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DNA damage, including double-strand breaks (DSBs), must be efficiently repaired to preserve genomic stability and prevent the development of cancer. The Family A DNA Polymerase Theta (Pol Theta, encoded by *POLQ*) is a replicative and repair enzyme that facilitates repair of DSBs through an error-prone alternate pathway known as microhomology-mediated end joining (MMEJ). We have identified an acral melanoma tumor sample from a patient in the Yale SPORE database with the Y239C missense mutation. Predictive software SIFT and PolyPhen-2 algorithms predict this substitution to be damaging to the function of the enzyme. Previous studies have explored truncated Pol Theta function through *E. coli* expression studies but have missed the coordinated function between the complex domains including the helicase, polymerase and disordered. Therefore, we will express and purify full-length in eukaryotic insect cells. We hypothesize that the Y239C variation located within the helicase domain of Pol Theta may affect the helicase structure, the MMEJ activity, and/or the helicase activity, such as its role in strand annealing of DNA templates for subsequent processing by the polymerase domain of Pol Theta. According to Alphafold predictions, there is a disruption in the alpha-helices conformation in the helicase domain. Using biochemical methods, we will characterize the functional effects of the full-length Pol Theta Y239C mutation including the ability of the variant to bind DNA, perform MMEJ, and its fidelity of function. If our hypothesis is correct, this change in amino acids may promote genomic instability, support cancer progression, and contribute to resistance to cancer treatment.

This work was supported by RI-INBRE

A Role for FA Proteins in Reproductive Aging and Serotonin-Dependent Egg Laying in *C. elegans*

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Fanconi Anemia (FA) is a rare genetic disorder affecting approximately 1 in 160,000 births and is caused by mutations in one of the twenty-three (FA) genes. While FA is associated with bone marrow failure, cancer predisposition, and congenital abnormalities, in recent years many patients have also exhibited neurological symptoms including developmental delay, ataxia, cognitive impairment, and seizures. This new manifestation has been termed Fanconi Anemia Neuroinflammatory Syndrome (FANS). Little is known about the molecular mechanisms underlying FANS and how FA proteins contribute to nervous system development and function.

In order to understand the molecular etiology of FANS, we have turned to model organism *Caenorhabditis elegans*, with its short life cycle, transparent body, well-characterized nervous system, and fully sequenced and annotated genome. Furthermore, many proteins of the FA pathway are evolutionarily conserved in these animals.

The objective of this study was to determine whether the *C. elegans* FA orthologs *fnci-1* and *fcd-2* contribute to reproductive aging and serotonin regulation of egg laying, which depends on proper neuromuscular function. To evaluate reproductive fitness, brood size assays were performed by transferring L4 larvae to fresh NGM plates every 24 hours until reproduction ceased, and progeny produced each day were counted. Egg-laying assays were conducted by transferring young adult worms to 96-well plates containing M9 buffer as a control, serotonin to directly stimulate vulval muscle contraction by bypassing the hermaphrodite-specific neurons (HSNs), or fluoxetine to enhance serotonin signaling by inhibiting serotonin reuptake. After one hour, the number of eggs laid was recorded. Wild-type animals were compared with *fnci-1* and *fcd-2* mutant strains and the respective complemented strains. Both *fnci-1* and *fcd-2* mutants exhibited a reduction in brood size compared with wild-type animals, indicating accelerated reproductive aging, a phenotype that was rescued in the complemented animals. Mutant worms also displayed impaired egg laying in response to both serotonin and fluoxetine, while the complemented strains restored wild-type egg laying levels. Because serotonin directly activates the egg laying muscles, this suggests that loss of *fnci-1* or *fcd-2* disrupts aspects of the egg laying circuit, consistent with impaired vulval muscle or neuromuscular function. Together, these results suggest a role for FA proteins in regulating reproductive aging and neuromuscular signaling, highlighting the value of *C. elegans* as a model for studying the neurological aspects of Fanconi Anemia.

This work was supported by RI-INBRE

Association of Glucagon-Like Peptide-1 Receptor Agonists Use with Psychological Outcomes Among Type 2 Diabetes Patients: A Target Trial Emulation

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Background: Glucagon-like peptide-1 receptor agonists (GLP-1 RAs) are widely prescribed for type 2 diabetes mellitus (T2DM), yet concerns have emerged regarding potential psychological effects. Evidence from real-world settings remains inconsistent.

Objectives: To evaluate the association between initiation of GLP-1 RAs and psychological outcomes compared with dipeptidyl peptidase-4 inhibitors (DPP-4i) and sodium–glucose cotransporter-2 inhibitors (SGLT2i) among patients with T2DM.

Methods: A target trial emulation was conducted using a U.S. administrative claims database to compare risk of psychological events among patients initiating GLP-1 RAs versus DPP-4i or SGLT2i. The primary outcome was a composite of major depressive disorder, anxiety disorder, and suicide attempt or ideation. Propensity score fine stratification was applied to balance covariates, and Cox proportional hazards models with robust sandwich variance estimators were used to estimate adjusted hazard ratios. Sensitivity and subgroup analyses were performed.

Results: A total of 8,143 patients were included, of whom 3,638 were treated with GLP-1 RAs, 2,115 with DPP-4i, and 2,390 with SGLT2i. GLP-1 RAs initiation compared with DPP-4i or SGLT2i was associated with a higher risk of any psychological event (HR: 1.49; 95% CI 1.29-1.71), as well as major depressive disorder (HR:1.59; 95% CI 1.31-1.94) and anxiety (HR:1.56; 95% CI 1.32-1.86). In agent-specific analyses, dulaglutide and liraglutide were associated with elevated hazards of major depressive disorder and anxiety; exenatide with major depressive disorder and suicide attempt or ideation; and semaglutide with anxiety.

Conclusions: GLP-1 RA initiation was associated with higher hazards of psychological disorders compared with alternative antidiabetic therapies. These findings highlight the importance of monitoring psychological outcomes following treatment initiation, although results should be interpreted in light of the potential for residual confounding. Further research is warranted to clarify causality and identify patients at greatest risk.

This work was supported by RI-INBRE

Early-Life Antibiotic Exposure and Risk of Neurodevelopmental Disorders: A Systematic Review and Meta-Analysis

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Background and Objectives: Early-life antibiotic exposure is common during the first two years of life, a critical period for brain and immune development. Growing evidence suggests that antibiotic exposure during this developmental window may have long-term neurodevelopmental consequences. However, findings from epidemiologic studies have been inconsistent, with some reporting an increased risk of neurodevelopmental disorders (NDDs) and others demonstrating attenuated or null associations after adjusting for potential confounders. This systematic review and meta-analysis aimed to evaluate the association between early-life antibiotic exposure and the subsequent risk of NDDs in children.

Methods: A systematic search of PubMed, Embase, the Cochrane Library, and Google Scholar was conducted independently by two reviewers to identify observational studies published between January 2000 and June 2026, that evaluated the association between early-life antibiotic exposure and NDD risk in children. The methodological quality of eligible studies was assessed using the Newcastle–Ottawa Scale. A random-effects meta-analysis was performed to estimate the pooled odds ratios (ORs) with corresponding 95% confidence intervals (CI). Sensitivity and subgroup analyses were conducted to explore sources of heterogeneity, including study design, duration of antibiotic exposure, number of antibiotic treatment courses and adjustment for key confounding variables.

Results: Eighteen studies comprising 13,070,162 participants met the inclusion criteria and were judged to be at low risk of bias. Overall, early-life antibiotic exposure was found to be associated with a higher risk of attention-deficit/hyperactivity disorder (ADHD) (OR = 1.20, 95% CI: 1.12–1.29, I2 = 98%), autism spectrum disorder (ASD) (OR = 1.11, 95% CI: 1.02–1.20, I2 = 96%), and intellectual disability (ID) (OR = 1.19, 95% CI: 1.12–1.27, I2 = 19%). However, sensitivity analyses restricted to sibling-matched cohort studies, as well as subgroup analyses stratified by duration of antibiotic exposure and number of antibiotic treatment courses, demonstrated no statistically significant association between early-life antibiotic exposure and the risk of these NDDs.

Conclusions: Early-life antibiotic exposure was associated with a higher risk of ADHD, ASD and ID in pooled analyses. However, the absence of significant associations in sibling-matched analyses suggests that these findings may be partially explained by shared genetic and familial environmental factors rather than a direct causal relationship. Additional well-designed studies incorporating sibling-comparison methodologies and genetic information are needed to clarify the nature of these associations and inform evidence-based clinical decision-making.

This work was supported by RI-INBRE

Benchmarking Deconvolution Tools: BisqueRNA, CIBERSORT, CIBERSORTx, and DeconRNASeq to Identify the Optimal Predictor of Circulating Tumor Cells in Medulloblastoma Patients

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Identification of cell types in a tissue, by both variety and quantity, provides many insights into an individual's health. In cancer, the cellular make-up of a tumor can help predict prognosis, however, tumor cells often have the capability to break off from the mass enter the blood stream and enter other tissue sites in a body. The focus of our research is to use liquid biopsy of blood to assist in determining prognosis of a cancer patients from the types and states of cells in the blood along with detection of circulating tumor cells (CTCs). Deconvolution tools make predictions of the quantity and variety of cells from RNA data thus are a cost-effective application to liquid biopsy for detection of CTCs in blood. However, deconvolution tools vary in their accuracy in prediction of rare cells that show up in small quantities such as CTCs. We set out to identify the most accurate deconvolution tool for low proportion cells using pseudo-bulk generated data. 10 healthy pediatric patients' blood draws were used to simulate bulk data in biologically restricted proportions. Each pseudobulk sample contained varying amounts of the twenty different cell types annotated from the pediatric blood processed through a liquid biopsy microfluidics device along with a sequential spike in of 0-100 vascular endothelial cells. The creation of this dataset allowed us to test four deconvolution tools (BisqueRNA, CIBERSORT, CIBERSORTx, DeconRNASeq) and unbiasedly compare their predictions. Our results also suggest that CIBERSORTx Fractions was the best at predicting rare cells (anytime the percentage of a cell type was equal to or less than 0.03% of a sample) when provided with a signature matrix generated via a gene-based t-test between cell types. However, despite having the highest correlation score when predicting rare cells among the deconvolution tools tested, CIBERSORTx Fractions had a correlation score of 0.52, while bisqueRNA was the most accurate at predicting overall cell proportions. These results will lay the foundation for creating our own deconvolution tool SparCell to accurately predict rare CTCs.

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Development of Gene Signature Matrices for Deconvolution of Heterogeneous Cell Populations

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Liquid biopsy is a minimally invasive approach for monitoring disease through the detection of differing cellular states or rare circulating cells in blood. In pediatric brain cancer, identifying these low frequency cell populations presents significant challenges due to their scarcity and the complexity of blood, which contains a diverse mixture of immune cell types. While single cell RNA sequencing (scRNA-seq) provides high resolution characterization of individual cells, it is costly, time intensive, and rare cells may be misclassified as cell labeling occurs through clustering algorithms as they often comprise less than 0.03% of the total sample. Therefore, computational approaches are needed to improve both cell type identification and downstream analysis. Our lab is developing a computational pipeline for liquid biopsy analysis in pediatric brain cancer by integrating optimized cell type deconvolution with rare cell detection. To establish reliable reference RNA-based profiles for deconvolution, we generated gene signature matrices from a unique liquid biopsy based healthy pediatric blood scRNA-seq dataset. We evaluated the effects of gene selection (t-tests, truncated nuclear normalization principle component analysis and feature importance weighting) and data normalization on signature matrix performance using heatmap visualizations and linear discriminant analysis (LDA). Log-normalized expression data consistently achieved the highest LDA accuracy compared with raw count and variance stabilizing transformation (VST) normalization, which demonstrates its importance for generating robust deconvolution reference matrices. Future work will integrate these optimized gene signature matrices into a custom deconvolution tool to account for the low tumor content in pediatric liquid biopsies. This approach aims to improve the identification of circulating tumor cells and potential biomarkers, enabling more accurate monitoring of disease progression and therapeutic response in pediatric brain cancer patients.

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In Solution Characterization of Biomolecular Corona Formation on DNA-SWCNTs

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The intracellular processing of nanomaterials in biological systems is governed less by their shape or surface alone and more by the biomolecular corona that forms upon exposure to proteins, lipids, and other biomolecules. This corona's composition is driven by molecular interactions like charge and hydrophobicity, not just by the amount of each molecule present. These factors affect how stable the nanoparticles are, how they interact with cells, and what happens to them inside the cell. Still, we do not fully understand how the biomolecular corona formation impacts the nanoparticle identity and downstream intracellular fate. Single-walled carbon nanotubes (SWCNTs) serve as great nanoparticle systems due to their excellent optical and tunable physicochemical properties. In this project, we examine how varying the protein concentration in the solution affects the properties of DNA-functionalized SWCNTs. This helps us learn how the corona might change their fluorescence and how cells recognize them. DNA-SWCNTs are a good choice for this research because of their stable near-infrared (NIR) photoluminescence, enabling tracking in live cells without fluorescent labeling. We exposed DNA-SWCNTs to DMEM with different amounts of fetal bovine serum (FBS): 0%, 0.5%, 1%, 2%, 5%, or 10%. We used UV-Vis spectroscopy to evaluate how changes in protein availability affected DNA-SWCNT absorbance. For zeta potential measurements using DLS, we removed the DNA-SWCNTs from the FBS-containing media using Amicon filters. These measurements allowed us to evaluate whether changing protein availability altered the effective surface charge of the DNA-SWCNT complexes. Early results showed that the zeta potential became less negative as FBS concentration increased, especially at 5% and 10%, suggesting that the surface charge of the DNA-SWCNT complexes changed after serum exposure. UV-Vis absorbance also changed between the different conditions and exposure times, but these changes did not follow a clear pattern as FBS concentration increased. In the future, we will study how these serum-induced changes affect how cells take up the nanoparticles, how they move inside cells, how stable their fluorescence is, and what happens to them in the end. The goal is to better understand how the biomolecular corona affects DNA-SWCNTs and to help design SWCNT-based biosensors and delivery systems that can be tuned for different biological uses.

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Novel Environmental Bacteriophages from the University of Rhode Island Demonstrate Antibacterial Activity Against Multidrug-Resistant *Staphylococcus aureus*

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Antibiotic-resistant *S. aureus* infections remain a significant clinical challenge, frequently limiting the effectiveness of conventional antimicrobial therapies. Bacteriophages are naturally occurring viruses that selectively infect and lyse bacteria and have emerged as promising alternatives or adjuncts to antibiotics for treating multidrug-resistant (MDR) infections. This study aimed to isolate and evaluate environmental anti-staphylococcal bacteriophages from various locations across the URI campus for their antibacterial activity against four genetically distinct MDR *S. aureus* strains. Samples were collected across four locations on the University of Rhode Island campus, with two ATCC phages used as comparators. (Phage 1) FIJI Fraternity House and Dorr Hall (Phage 2) Fascitelli Gym Pond (Phage 3) Meade Stadium (Phage 4) Library Pond (Phage 5) Intesti13 phage (control) (Phage 6) Sb-1 Phage (control). Environmental samples were then centrifuged at 4000 rpm for 40 minutes at 5°C and filtered twice through a 0.2µm filter to generate a working phage lysate stock. Phage lysate was propagated and evaluated against four genetically distinct Staphylococcus aureus biofilm-producing strains and one biofilm-negative strain. (1) B37 (*S. aureus* ATCC 19685), (2) B36 (*S. aureus* D712; USA100/ST5, DNS-VISA) (3) B23 (*S. aureus* ATCC 35984; strong biofilm producer), and (4) B19 (*S. aureus* M7; biofilm-negative strain). Phage titers were determined using a standard plaque assay. The starting bacterial inoculum was confirmed in duplicate (6.10 ± 0.19 $\log_{10}$ CFU/mL), and all experiments were performed at a target multiplicity of infection (MOI) of 1. Antibacterial activity was evaluated by monitoring bacterial growth kinetics at an optical density of 600 nm using a BioTek microplate reader over 24 hours following phage exposure, compared to growth control. Complete suppression of bacterial growth by 24h was observed against strain B37 with Phage 1 (Lagtime [600] 3:08:02; Max V [600] 0.390) and Phage 5 (Lagtime [600] 2:39:39; Max V [600] 0.260) indicating potent antibacterial activity throughout the assay. In contrast, phages 1-4 tested against B36, B19, and B23 primarily delayed bacterial growth kinetics and reduced maximal optical densities but did not achieve complete growth suppression by 24h. Lag times were prolonged by up to approximately 5h among susceptible isolates, demonstrating variable host-dependent antibacterial activity among environmental phage candidates. Four environmental phages were successfully isolated from URI, with phage 1 displaying potential therapeutic efficacy. Ongoing studies will focus on genomic characterization, host-range determination, and the evaluation of synergistic phage–antibiotic combinations to develop optimized phage cocktails.

This work was supported by RI-INBRE

Synthesis and Characterization of Aldehyde-Variant Salen/Salphen Ligands for G-Quadruplex-Targeting Metal Complexes with Potential Anticancer Applications

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G-quadruplexes (G4s) are secondary DNA structures which are formed by stacked planes of G-tetrads stabilized through Hoogsteen base pairing and coordination of monovalent metal ions. G4 binders, including small molecules and metal complexes, have shown promise for regulating telomerase activity and developing anticancer agents. This project investigates how variation in aldehyde structure, alongside a parallel study on diamine variation, affects the formation, structure, and properties of Schiff-base salen/salphen ligands, synthesized through condensation reactions between aldehydes and diamines. To date, this combined effort has produced a library of ten organic ligands. The aldehydes examined differ in aromatic ring size, electronic properties, and donor atom identity, factors expected to influence ligand stability and coordination behavior. Notably, varying the aldehyde identity produced ligands with distinct physical properties, including differences in color and in consistency, ranging from solids to oils, suggesting that aldehyde structure influences not only electronic and coordination behavior but also the physical characteristics of the resulting ligand. Synthesized ligands were isolated and characterized by NMR and IR spectroscopy. Metalation has so far been carried out with Ni(II), which favors a square-planar geometry well-suited for G4 binding. Crystallization of the resulting Ni(II) complexes has been set up to obtain structures by X-ray crystallography. Future work will extend metalation to Cu(II) and include binding assays to evaluate the interactions of these metal complexes with G4 DNA structures. Additional work will also explore ligands with more structurally complex components, expanding the range of aromatic systems and electronic properties investigated, and thus their impact on G4-binding potential. Together, these efforts will provide insight into ligand design principles and establish a foundation for the future development of G4-targeting metal complexes.

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Building the Foundation for Combinatorial Biosynthesis of Novel Catecholate Siderophores with Bioremediation Potential

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Siderophores are small iron chelating compounds that are produced by bacteria such as E. coli to scavenge Fe(III) from their environment, including from a host during infection. Beyond iron acquisition, siderophores are also known to acquire non-iron metals and modulate host functions. Combinatorial biosynthesis is the modification of natural biosynthetic pathways to expand the molecular toolbox of enzymes for the synthesis of unnatural natural products, and can be used to synthesize novel siderophores with unique properties. For example, novel siderophores with enhanced or altered metal-binding properties could aid bioremediation efforts, potentially helping sequester and remove toxic heavy metals from contaminated soils and wastewater.

As a new research lab at Providence College, we spent the summer establishing our lab space, protocols, and long-term research goals. As proof of concept for our biochemical workflow, we successfully carried out transformation, expression of His-tagged protein, Ni-NTA purification, and protein quantification via SDS-PAGE using known acyl carrier proteins (ACPs) as practice substrates. With this workflow validated, our key objective is to build a library of carrier proteins involved in siderophore production across various microorganisms, beginning with EntB, and to express and purify these proteins in E. coli. Sfp, a phosphopantetheinyl transferase from B. subtilis, will then be used to activate these carrier proteins in vitro, advancing our progress toward the combinatorial biosynthesis of novel catecholate siderophores with bioremediation potential.

This work was supported by Walsh Fellowship

Staining of *Clostridium novyi*-NonToxic Spores to Indicate Surface Composition and in Vivo Tracking Longevity

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Pancreatic cancer has a 12.5% five-year relative survival rate and is projected to become the second leading cause of cancer-related death within the next decade. One promising therapeutic strategy involves using engineered bacteria capable of selectively colonizing and lysing solid tumors. *Clostridium novyi*-NonToxic (NT), an attenuated, spore-forming anaerobe, is uniquely suited for this purpose because its spores germinate exclusively within the hypoxic core of solid tumors. However, despite its therapeutic potential, the longevity, behavior, and physiological transitions of *C. novyi*-NT spores in vivo remain poorly understood. To address this gap, reliable and reproducible fluorescent staining protocols are needed to visualize spores, characterize their surface chemistry, and track their fate in pre-clinical models.

This project evaluates several candidate stains with distinct mechanisms of interaction with the spore surface. CellBrite Fix membrane stains can penetrate and covalently bind the peptidoglycan layer, offering the possibility of long-term or permanent labeling suitable for in vivo tracking. Hoechst 34580 and propidium iodide (HO/PI) bind A/T-rich DNA regions and have demonstrated utility in both in vitro and in vivo systems, providing a potential route for identifying spores that have initiated germination. BODIPY-DPA is strongly considered due to its dual fluorescence-activation mechanisms: one triggered by phosphorylated proteins in the spore coat and another by oxidation via singlet oxygen, enabling sensitive detection of coat-associated biomolecules. HADA and FDL, fluorescent D-amino acid mimics, incorporate into newly synthesized peptidoglycan and therefore uniquely report on active growth, germination, and early vegetative transitions.

To establish a baseline protocol, carboxyfluorescein succinimidyl ester (CFSE) staining is used as the initial reference method. Building from this foundation, literature review and preliminary testing have identified several variables that must be optimized for *C. novyi*-NT spores, including dye concentration, incubation temperature, and the use of serum-based resuspension buffers to account for the impact of protein corona formation. Each stain will be systematically evaluated under modified conditions to determine its compatibility with anaerobic handling, spore integrity, and downstream imaging.
By comparing staining efficiency, stability, and biological relevance across multiple dyes, this work aims to develop a robust toolkit for visualizing *C. novyi*-NT spores. Establishing reliable staining methods will support future in vivo studies, improve mechanistic understanding of spore behavior, and ultimately contribute to the development of next-generation bacterial therapeutics for pancreatic cancer.

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Optimizing Calcium-Competency Conditions for Plasmid Uptake in *Clostridium novyi*-NT

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Pancreatic cancer has a 12.5% five-year relative survival rate and is projected to become the second leading cause of cancer-related death within the next decade. This severe clinical trajectory underscores the need for innovative therapeutic strategies that move beyond conventional chemotherapeutics. One emerging approach involves using engineered bacteria capable of selectively colonizing and destroying solid tumors. *Clostridium novyi*-NonToxic, an attenuated, obligate anaerobe, is uniquely suited for this purpose because its spores germinate exclusively within the hypoxic core of solid tumors, enabling intravenous delivery and highly selective localization. This tumor-specific niche provides a powerful opportunity to develop bacterial therapies that minimize off-target toxicity.

Despite its therapeutic promise, *C. novyi*-NT remains difficult to genetically manipulate. Its non-canonical sporulation biology, slow doubling time, and thick cell wall create barriers to plasmid delivery and stable genetic modification. As a result, fundamental tools required for engineering this organism (e.g., reliable competency protocols) are underdeveloped. This project aims to address that gap by adapting and optimizing a calcium competency protocol originally designed for *E. coli*, with the goal of enabling reproducible plasmid uptake in *C. novyi*-NT.

Because *C. novyi*-NT has a 24-hour doubling time (compared to ~20 minutes in *E. coli*), careful monitoring of optical density is essential to ensure cultures are harvested during true log phase growth. To achieve sufficient biomass, the initial culture volume is increased, which requires more frequent OD monitoring to avoid overshooting the growth window. Additional modifications include increasing calcium chloride concentration to 0.1 M- higher than the 0.06 M typically used for *E. coli* - to chemically weaken the cell wall and improve heat shock–mediated plasmid entry. Temperature, incubation time, and recovery conditions are systematically varied to identify species-specific parameters that maximize competency.

Two plasmids are used to evaluate uptake efficiency: pPUC19, a standard, commercially available control plasmid, and pNICKclos1.0, an erythromycin-resistant plasmid that serves as the backbone for our lab's CRISPR/Cas9n platform. By comparing transformation outcomes across conditions, this study seeks to establish a reproducible, optimized competency protocol tailored to *C. novyi*-NT.
Developing reliable genetic tools for *C. novyi*-NT is a critical step toward engineering next-generation bacterial therapeutics for pancreatic cancer. This work contributes foundational knowledge that will support future efforts in targeted genetic editing, virulence factor modulation, and therapeutic strain development.

This work was supported by RI-INBRE

Investigating the Effects of TDP-43 and SYNE1 Knockdown on Nuclear Homeostasis in ALS

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Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease characterized by the degeneration of motor neurons and the abnormal loss of nuclear TDP-43. TDP-43 pathology disrupts RNA metabolism and nuclear homeostasis, contributing to disease progression. The Linker of Nucleoskeleton and Cytoskeleton (LINC) complex, including the nuclear envelope protein SYNE1, plays a critical role in maintaining nuclear architecture by transmitting mechanical and structural signals between the cytoskeleton and nucleus. Disruption of the LINC complex may contribute to altered nuclear organization and TDP-43 localization during ALS.

To investigate this relationship, HEK293 cells were transfected with siRNA targeting TDP-43 and SYNE1, a major component of the LINC complex, and incubated for 48 and 72 hours. Immunofluorescence staining was performed using antibodies against TDP-43, with GFP serving as a marker of transfected cells. Cellular phenotypes were assessed by examining the localization and distribution of TDP-43. Quantitative image analysis was used to determine how disruption of the LINC complex influences TDP-43 localization following TDP-43 knockdown.

This work aims to determine whether depletion of TDP-43 and disruption of the LINC complex alter TDP-43 localization and nuclear organization. By quantifying changes in TDP-43 localization, this study seeks to provide insight into the contribution of LINC complex dysfunction to ALS-associated nuclear phenotypes and improve our understanding of the cellular mechanisms underlying disease pathogenesis.

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Quantum Mechanical Analysis of the Thermodynamic Stability of Secondary RNA Structure

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Bonding interactions and physical forces govern optimal folding and influence the ability to stabilize or destabilize bonds in secondary RNA (secRNA) structures, shaping the thermodynamic free-energy landscape in search of the lowest free-energy state to participate in biological processes and regulations. This study aims to understand the molecular interactions that stabilize secRNA structures via the application of quantum mechanical modeling of the physical forces that affect the thermodynamics. Of the 10 nucleotide dimers formed by combinations of adenine (A), cytosine (C), guanine (G), and uracil (U), Q-Chem software was used for the Canonical dimer formation of AU, CG, and non-canonical GU to apply the Density Functional Theory (DFT), which simplified the multi-electron body system into an electronic density where the Born–Oppenheimer approximation (BO approx.) allowed the nuclear motion to be separated from the electronic motion of the system. Q-Chem provided the data to calculate the enthalpy of binding (ΔH_B), the entropy of binding (ΔS_B), and the free energy of binding (ΔG_B). Results showed that the formation of AU, CG, and GU was all exothermic and stable, reaching order consistent with experimental data and literature based on $\Delta G_B < 0$ in a vacuum with a gas constant per temperature (RT = 0.592 kcal/mol). AU was found to be less stable (ΔG_B = −34.29 kcal/mol) than GU (ΔG_B = −34.78 kcal/mol). GC was found to be least stable (ΔG_B = −24.77 kcal/mol) in these conditions. Our preliminary results of gas-phase dimer formation showed a paradox in the stability trend due to the G monomer requiring a larger spatial range for the electronic orbitals, as the molecule contains a more polarizable conjugated purine ring due to the carbonyl oxygen functional group (C=O) participating in a third electrostatic interaction in comparison to A and U monomers having two. Biological conditions suggest that GC is expected to be more stable than GU/AU due to the aqueous solution producing an electric field that interacts with the field alongside the electrostatic force constructed by three hydrogen bonds. As the study proceeds, we seek to further characterize the stability that governs the other 7 dimer formations and determine if the stability is changed with the addition of a solvent that mimics a biological environment and increase the basis-set size that allows for greater spatial range for DFT on the energy landscape.

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Optimizing Fictive Locomotion Conditions for the Study of Locomotor Spinal Networks

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Locomotion is an essential motor activity generated by specialized networks of neurons in the spinal cord called Central Pattern Generators (CPGs), independently of higher brain centers. Although the cerebral cortex is responsible for voluntary movements and initiating and controlling locomotion, it is not required for the production of locomotion per se. In fact, locomotion can be produced in a decerebrate animal (in which the forebrain has been surgically removed), and in the absence of actual movements (using a neuromuscular blocking agent known as pancuronium, which prevents muscle contraction), in which case it is called fictive locomotion. The Manuel lab is studying the spinal neurons involved in producing this locomotor activity, but the preparation that is being currently used shows high variability between animals and often fails to exhibit signs of fictive locomotion at all. The goal of my research project was to standardize and optimize the decerebrate fictive locomotion mouse model by testing different surgical approaches for the decerebration and performing histological analyses of the brainstem post-decerebration. Decerebration was performed in adult mice following carotid artery ligation, tracheotomy, and craniotomy. Premammillary decerebration was achieved using a 20 or 45 degree angle guide to allow for reproducible transection rostral to the superior colliculi and and the mammillary bodies. Once the preparation was completed, locomotor activity was monitored during a 2-3 hour observation period. The brainstem was then dissected, post-fixed in paraformaldehyde, and cryoprotected in sucrose. Thereafter, the tissue was embedded in O.C.T and then sectioned into 30 µm tissue slices. The slices were stained with Nissl stain, and observed using an epifluorescence microscope to verify that significant brainstem regions such as the mesencephalic locomotor region (MLR), subthalamic locomotor region (SLR), medullary reticular formation (MRF), and pontomedullary locomotor region (PMLR) were not damaged by the decerebration procedure. Our results indicate that a 20 degree guide is preferred when performing premammillary decerebration because it provides a more controlled surgical approach with less bleeding. In contrast, a different 45 degree guide has shown to be associated with increased hemorrhage. When using the 45-degree angle guide, the cut was not rostral to the mammillary body. Overall, my project will contribute in establishing a robust model capable of fictive locomotion in order to study the spinal neurons that contribute to locomotion rhythm generation.

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Investigating Antibacterial Secondary Metabolites Produced by Streptomyces Strains Through OSMAC

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Streptomyces bacteria are the largest antibiotic-producing genus with them producing over half of the world's natural antibiotics. With the increasing prevalence of antibiotic-resistant bacteria, it is becoming ever more important to find new drugs able to combat this new threat. Recently, the One Strain Many Compounds (OSMAC) approach has emerged as a new strategy in discovering new metabolites produced by bacteria. The goal of this project was to maximize the production of antibiotic secondary metabolites created by three *Streptomyces* strains: *Streptomyces griseus*, *Streptomyces venezuelae*, and *Streptomyces avermitilis*. To do this, we created a custom liquid medium, named Super Streptomyces Soup (SSS), and grew the strains in this medium. To extract the created metabolites, we performed a solid-phase extraction using HP-20 resin. Analysis of compounds was done using HPLC-UV and disk diffusion. Compared to background HPLC readings, all three strains had distinct peaks. However, disk diffusion revealed no zone of inhibition. This leads us to conclude that while SSS did not allow *S. griseus*, *S. venezuelae*, or *S. avermitilis* to produce any antibiotic compounds, compounds were created in each of the strains. This suggests that a medium similar to SSS is unlikely to create antibiotic metabolites in these *Streptomyces* strains.

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HPLC Purification of Synthesized Peptides for Investigation of Quiescent Uropathogenic *E. coli*

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Of the 11 million urinary tract infections (UTIs) reported each year, twenty-seven percent of the patients that were already treated with antibiotics will experience a recurrence within twelve months. The leading cause of all initial and recurring UTIs is Uropathogenic *Escherichia coli* (UPEC), which has been found to enter a quiescent state within bladder epithelial cells that allows it to survive antibiotic treatment. Additionally, it is known that peptidoglycan stem tetra- and pentapeptides function as environmental cues that enable quiescent UPEC cells to regain antibiotic-sensitivity. This research will identify the peptide structures that best prevent uropathogenic bacteria from entering an antibiotic-tolerant, quiescent state, that may lead to a new treatment for recurrent UTI infections with multidrug-resistant strains. My role in this research project is to determine the best method to purify the newly synthesized peptidoglycan (PG) stem tetra- and pentapeptides using high performance liquid chromatography (HPLC) to contribute to future studies regarding the reversal of quiescent cells.

This work was supported by RI-INBRE

The Human Epidermal Melanocyte Non-Visual Opsin 5 (OPN5) Is Activated by Physiological Doses of Solar UVA and Leads to Ca^{2+}-mediated Increase in Melanin

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Melanocytes are neural-crest-derived cells located in the epidermis that produce and store the pigment melanin. Melanocytes respond to many external stimuli through activation of plasma membrane G-protein–coupled receptors (GPCRs), which trigger intracellular signaling cascades resulting in various cellular responses, including increases in intracellular Ca^{2+} and melanin synthesis. Because melanocytes reside in the epidermis, they are directly exposed to solar ultraviolet radiation (UVR), composed of ~95% UVA and ~5% UVB, a well-established human carcinogen. While the mechanisms by which UVB causes DNA damage and delayed pigmentation are well studied, far less is known about how physiological doses of UVA are detected and affect melanocytes. Our lab has shown that physiological doses of UVA activate a $G\alpha_{q/11}$-coupled signaling pathway, resulting in a transient change in cytosolic Ca^{2+} and a rapid increase in melanin synthesis. However, the GPCR used to detect and transduce the UVA signals remains unknown.

Our lab also showed that human skin melanocytes express light-activated GPCRs, including the non-visual opsin 3 (OPN3) and opsin 5 (OPN5), both predicted to signal though $G\alpha_{i/o}$ and modulate cAMP concentrations. Recent data suggested that OPN5 can couple to $G\alpha_{q/11}$ to transiently increase intracellular Ca^{2+} concentrations. This led us to investigate whether OPN5 in human epidermal melanocytes (HEMs) could function as the UVA receptor in melanocytes.

Here we show that melanocyte OPN5 is both necessary and sufficient to detect and mediate responses to physiological doses of UVA. We found that OPN5 is sufficient for UVA-induced Ca^{2+} responses: exogenously expressed OPN5 in cells that do not respond to UVA (HEK293T cells) renders the cells UVA-photopsensitive using a similar signaling pathway as in HEMs. To show that OPN5 is necessary for UVA responses, we used shRNA-mediated knockdown of endogenous OPN5 and found reduced UVA-induced Ca^{2+} and melanin responses compared to control shRNA.

Together, these findings identify OPN5 as a functional UVA receptor in human epidermal melanocytes and provide new insight into the molecular mechanisms underlying UVA phototransduction in skin. Our findings may reveal novel therapeutic targets for pigmentation disorders and melanoma while advancing our knowledge of melanocyte biology.

This work was supported by RI-INBRE

HPLC-Guided Isolation of a Natural Product from a Rhode Island Marine Shipworm

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The wood-boring marine bivalves known as shipworms are an underexplored biological resource for natural products chemistry. Shipworms rely on intracellular symbiotic bacteria (*Teredinibacter turnerae*) that live in their gills to provide enzymes for digesting cellulose and fixing nitrogen. To maintain a competitive advantage in their live environment, these symbionts synthesize complex secondary metabolites with potential antimicrobial properties.

This study aims to analyze the biosynthetic potential and metabolic production of a new *T. turnerae* strain. The strain, RIS004.S.0a.05, was isolated from the gill homogenate of a *Teredo navalis* shipworm specimen that was extracted from a piece of wood collected in Mt. Hope Bay. The pure strain was grown in liquid culture for genomic DNA and chemical extraction. The genome was analyzed using AntiSMASH v8.0.4 and revealed several interesting biosynthetic gene clusters (BGCs), including the tartrolon, turnerbactin, and several uncharacterized pathways. The chemical extracts were tested in a preliminary agar well diffusion assay and analyzed using HPLC-DAD. The HPLC showed a distinct peak with a UV-vis absorbance spectrum that is not found in closely related strains of *T. turnerae*, and was thus purified by semi-preparative HPLC. LC-MS analysis shows a $[M+H]^+$ ion at m/z =327.0350, with an isotopic distribution indicating the incorporation of a bromine, which does not match databases and is potentially a new compound. The compound is currently undergoing complete NMR characterization for structure elucidation. We are also continuing to pursue additional bioassays to determine the activity of this compound. This project shows that shipworms found here in Rhode Island contain endobacterial symbionts that possess the biological pathways needed for producing antibiotic compounds. These findings strengthen marine symbionts as promising resources in the discovery of new molecular families for drug discovery.

This work was supported by RI-INBRE

Nanostructured Bio- Barcode Immunosensor Based on Ferrocene and Copper Ions Polymer Bead Bioconjugate for Multiplex Electrochemical Detection of Cancer Biomarker Proteins

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Early detection of cancer through protein biomarkers offers a cost effective and rapid approach to disease monitoring, enabling timely diagnosis and improved patient care. Simultaneous electrochemical detection of the interleukin-6 (IL-6) and interleukin-22 (IL-22) in diluted calf serum would allow for a simple, rapid, low-cost method of quantifying these biomarkers in patient samples. Elevated concentrations of IL-6 and IL-22 are associated with cancers such as cutaneous T-cell lymphoma (CTCL). CTCL is a form of lymphoma that primarily affects the skin, producing symptoms including persistent scaling, tumors, severe itching, and skin lesions that resemble benign conditions such as eczema or psoriasis, making early and accurate diagnosis particularly challenging. The bio-barcode immunosensor strategy utilizes a sandwich assay built on Glutathione functionalized gold nanoparticles (AuNP-GSH) modified electrode coupled to electrochemical tag incorporated polymer beads (PB) as label. The electrochemical tag contained in the polymer beads, copper ion (Cu^{2+}) or ferrocene (Fc), could be effectively detected by square wave voltammetry (SWV) after dissolving the PB with organic solvent to release the electrochemical tags onto electrode surface. With the immobilization of two different antibodies onto the polymer beads surface, respectively, the position and intensity of the current peaks due to the two electrochemical tags could reflect the identity and level of the corresponding protein biomarkers. Preliminary SWV results showed that the copper (Cu^{2+}) and ferrocene (Fc) were successfully incorporated into the polymer beads. Cyclic voltammetry (CV) characterization in ferricyanide performed after each immunosensor fabrication step showed the peaks were decreasing, suggesting that the layers were successfully immobilized onto the electrode surface. Work is in progress to complete the calibration curve and assess the accuracy and precision of the multiplex immunosensor for both IL-6 and IL-22.

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Identification of Novel Microbial Factors That Regulate Vertebrate Metal Sensing

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Metals such as zinc, copper, manganese, and iron are essential trace elements that play critical roles in development, growth, and metabolism across all kingdoms of life. Disruptions in metal homeostasis, including both deficiency and toxicity, are linked to numerous metabolic and neurological disorders (Pajarillo et al., 2021), highlighting the importance of tightly regulated mechanisms that maintain metal balance at the cellular and organismal levels. In vertebrates, the intestine serves as the primary site of metal absorption and is densely populated by microorganisms collectively known as the gut microbiota. While the gut microbiota is a major regulator of host metabolism and nutrient absorption, including carbohydrates and fatty acids, its role in regulating host metal metabolism remains poorly understood. To address this gap in knowledge, we investigated whether commensal microbial factors influence vertebrate metal sensing using an engineered HEK-293 reporter cell line harboring a luciferase gene under the control of a metal response element (MRE) recognized by the vertebrate metalloregulator Metal Response Element-Binding Transcription Factor-1 (MTF-1). MTF-1 is a highly conserved intracellular metal sensor involved in cellular adaptation to stress conditions, primarily metal exposure but also hypoxia and oxidative stress. Upon activation, MTF-1 induces the expression of key metal homeostatic factors, including the metallothionein genes, which encode small, cysteine-rich proteins that scavenge toxic metals and free radicals (Günther et al., 2012). To identify specific bacterial species that promote MTF-1 activity, we performed luciferase assays with distinct zebrafish gut commensal bacterial strains, including *Aeromonas caviae*, *Aeromonas veronii*, *Vibrio cholerae*, *Enterobacter cloacae*, *Shewanella* sp., *Pseudomonas* sp., and *Acinetobacter calcoaceticus*. These responses were compared with activation induced by the trace metals zinc, copper, manganese, and iron. Notably, among the bacterial treatments, *Vibrio cholerae* culture supernatant and heat-killed *Enterobacter cloacae* elicited the strongest activation of MTF-1 signaling. Consistent with previous studies, zinc showed the strongest activation among the metals, closely followed by copper, whereas manganese and iron generated minimal activation. These results indicate that specific gut commensal bacteria activate host metal-sensing pathways and suggest that microbially derived factors can stimulate MTF-1 at levels comparable to zinc. Collectively, our findings reveal a potential mechanism through which the gut microbiota influences host trace metal homeostasis and establish a foundation for future studies investigating microbiome-mediated regulation of metal metabolism.

This work was supported by RI-INBRE

Making Mutants: CRISPR Knockouts to Test the Specificity of Temperature-Sensitive Pigmentation in Zebrafish

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Temperature-sensitive mutations have long been valuable tools for studying gene function, and pigmentation genes are especially useful for this because their phenotypes are easy to see. In the classic example of the Siamese cat, a missense mutation causes the tyrosinase enzyme to lose function at the higher temperature of the body but not at the cooler extremities (like the ears and tail). The zebrafish *oberon* mutant, isolated in a forward genetic screen for temperature-sensitive pigmentation alleles, was unexpectedly found to carry a premature stop codon in dystrobrevin binding protein 1a (*dtnbp1a*). Since nonsense mutations are expected to fully truncate the protein regardless of temperature, this raises the question of whether this temperature sensitivity is specific to *dtnbp1a*, the BLOC-1 complex in which *dtnbp1a* functions, or zebrafish pigmentation in general. To distinguish between these possibilities, we used CRISPR/Cas9 to induce nonsense mutations in three genes selected to test each level of this hierarchy. To ask whether temperature sensitivity extends to other BLOC-1 components, we targeted *bloc1s6*, and to test if it extends to pigmentation more broadly, independent of BLOC-1, we also targeted *pmela* and *slc24a5*. F0 bloc1s6 knockouts had a phenotype similar to, but more severe than, *oberon*'s, with lighter melanophores and abnormally dull iridophores. Embryos injected with gRNAs targeting *pmela* and *slc24a5* showed mosaic melanophore hypopigmentation but did not alter iridophore iridescence. To determine efficiency of CRISPR injections, genomic DNA was extracted from pools of injected embryos and uninjected siblings, amplified by PCR and sequenced. Analysis showed clear evidence of CRISPR-induced indels at the expected target site in each gene with a high efficiency of mutations in *bloc1s6* and *slc24a5*. Confirmed CRISPR-induced mutagenesis at the target site in each gene sets up raising stable lines and testing them across temperatures to address whether oberon's temperature-sensitivity is a quirk of this specific allele, a shared BLOC-1 feature, or a general property of pigment gene disruption.

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Detecting Early Larval Phenotypes of Temperature-Sensitive *oberon* Mutants

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Lysosome-related organelles (LROs) are specialized subcellular compartments that share some features with lysosomes. LRO function varies by cell type and includes roles in pigmentation, blood clotting, and the immune system. Mutations in the proteins responsible for LRO biosynthesis or transport cause human disorders such as Hermansky-Pudlak Syndrome or Chediak-Higashi Syndrome. In zebrafish (*Danio rerio*), the *oberon* mutant is caused by a nonsense mutation in dystrobrevin binding protein 1a (*dtnbp1a*) of the BLOC-1 complex. As BLOC-1 is required for melanosome formation, adult oberon mutants exhibit hypopigmentation. Interestingly, these mutants show a temperature-sensitive difference in the degree of hypopigmentation, an uncommon characteristic for nonsense mutations. Whether this temperature-sensitivity is also present in early larval stages remains unknown. To assess temperature-sensitive phenotypes at early larval stages, zebrafish embryos were reared 32℃ and 24℃ and imaged by brightfield microscopy at stages equivalent to 24 hours, 30 hours, and 5 days post-fertilization (5 dpf) at 28℃. RT-PCR was used to characterize dtnbp1a expression over the first five days of development. At the equivalent of 5dpf, *oberon* larvae raised at 24℃ had a larger average diameter of contracted pigment than those raised at 32℃, suggesting that increased pigmentation occurs at lower temperatures and that this temperature-sensitive phenotype is already present during early larval development. RT-PCR showed that dtnbp1a expression increased over the first three days of development, suggesting that this window is crucial in melanosome maturation. Together, these results support the presence of a temperature-sensitive, early larval phenotype in *oberon* mutants. Our findings fill a critical gap in our understanding of when this phenotype emerges, providing us with the ability to study this process at earlier, more tractable stages. Because BLOC-1 function is conserved across LRO-containing cell types, these findings may extend beyond melanophores to understanding how LRO biogenesis fails in disorders such as Hermansky-Pudlak Syndrome and Chediak-Higashi Syndrome.

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Comparing HA-3, HA-4, and HA-5 Cell Development During Inflammatory Challenge in *Ciona intestinalis*

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The innate immune system is crucial for protecting the body against infection, and its proper development is essential for health. Infection during embryonic development can disrupt normal innate immune system composition, causing lifelong adverse effects. Studying pathogen response in mammals and other vertebrates is challenging due to embryonic development not being easily accessible for experimentation and observation. It remains unclear whether infection alters immune cell fate decisions or activates cells that have already differentiated. *Ciona intestinalis* is an invertebrate chordate and the closest living relative to the vertebrates. *Ciona*'s rapid developmental time of ~3 days (fertilization to juvenile stage), full suite of molecular tools, single-cell RNA sequencing (scRNAseq) data of *Ciona* blood, and lack of a potentially-confounding adaptive immune system, make them an excellent model organism for studying immune system development. The overall goal of this research is to understand whether infection affects embryonic immune cell specification or if it alters differentiation of specified cell states. A better understanding of the mechanisms underlying infection during development could improve our knowledge of immune system dysregulation and how it plays a role in disease susceptibility. There are approximately 30 different cell types that constitute *Ciona* blood, but we were particularly intrigued by hyaline amoebocytes (HAs). This project focuses on three HA populations profiled in the recent *Ciona* blood scRNAseq study, HA-3, HA-4, and HA-5 cells. Unlike HA-3 and HA-4, HA-5 cells are thought to be vanadocytes, which uptake vanadium from the water, speculated to have an antimicrobial role. Since HA-5 cells are likely not rapid immune responders, we hypothesized that only HA-3 and HA-4 development will respond to a pathogenic agent. To test this hypothesis, we generated cell-specific reporter transgenes to label the three cell types. First, we investigated cell-specific gene expression databases, then PCR-amplified putative enhancer-promoter fragments from the highest expressed genes of each cell type. These fragments were then cloned into green fluorescent protein (GFP)-expressing vectors and inserted into fertilized *C. intestinalis* eggs via electroporation. After development into juveniles, specimens were examined under a fluorescent microscope to assess cell - state-specific GFP expression. Currently, we are using the lineage specific reporters and subjecting developing animals to inflammatory agents, such as LPS (bacterial) and zymosan (fungal), and quantifying abundance and temporal shifts in response of each cell type. This work is part of important first steps in understanding the molecular response to inflammation during development.

This work was supported by RI-INBRE

Investigating the Effects of Early Inflammatory Signals on Innate Immune Cell Lineage Specification in *Ciona intestinalis*

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Innate immunity is our first line of defense against pathogens and emerges before the adaptive immune system during development. Infection prior to innate immune system maturation can result in permanently dysregulated innate immunity later in life. However, we do not know how infection alters the development of the innate immune system. Understanding this problem is highly challenging in vertebrate models. To solve this problem, we aim to use the invertebrate model chordate, *Ciona intestinalis*. *Ciona*'s small size, genetic simplicity, and well-defined cell lineages allow us to see, visually and genetically, how inflammatory signals influence lineage specification and differentiation. Our overarching goal is to understand how early inflammatory inputs interface with developmental gene regulatory networks in shaping innate immune composition. The *Ciona* lifecycle begins by forming a simple tadpole-like free-swimming larva, but then metamorphoses into a sessile, filter-feeding adult, complete with heart, blood, and circulatory system. *Ciona intestinalis* has over thirty documented blood cell types. I chose to focus on three similar, but distinct cell types called unilocular refractile granulocytes: URG-1, URG-2 and URG-3. Many of the top expressed genes of URG-3 have known immune related functions (such as *TNFAIP6*, *HPGDS* and *ALDH1A2*), therefore I hypothesized that URG-3 cells are more likely to be influenced by immune challenges than URG-1 and URG-2 cells. To begin, I determined the top-expressed genes for each cell type. Then using PCR-amplified intergenic regions upstream of the top expressed genes, I cloned URG-specific enhancer/promoter regions into GFP reporter transgenes. These constructs were then electroporated into dechorionated *Ciona intestinalis* zygotes. We are currently in the process of observing expression patterns. Following this, we will test our hypothesis by exposing the developing embryos to fungal (zymosan) and bacterial (LPS) inflammatory agents, anticipating that one or both of the molecules will increase URG-3 quantity or onset of development. These experiments are beginning steps into understanding the phenotypic and transcriptomic changes brought about by infection during innate immune system development.

This work was supported by RI-INBRE

Exploring Hypothalamic Hunger Circuits Capable of Suppressing Competing Needs

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Survival depends on the brain's ability to evaluate and prioritize competing biological needs, such as hunger and fear. At any moment, an organism may have to decide between searching for food and staying safe from predators. The brain constantly weighs internal needs against what is happening in the environment, and understanding how the brain decides which needs take priority will help explain how behavior is flexibly shaped in dynamic environments. The hypothalamus senses the body's needs and drives behaviors essential for survival. Within the arcuate nucleus (ARC) of the hypothalamus, a specific subset of neurons known as Agouti-related peptide (AgRP) neurons act as the primary drivers of hunger-driven behavior. When AgRP neurons are activated using optogenetics, a technique in which blue light selectively stimulates genetically defined populations of neurons, mice immediately begin seeking and eating food. While this effect is well understood, it remains unclear how activity in these neurons affects behavior when hunger competes with other survival needs. We investigated whether this internal state is strong enough to overcome an immediate visual threat. A key downstream region where this integration between visual threats and hunger likely occurs is the periaqueductal gray (PAG). The PAG is critical for defensive behaviors like freezing or fleeing, and it is specifically responsible for reacting to visual threats. While we hypothesized that hunger-activated AgRP neurons might suppress activity in the PAG to prioritize hunger over responding to visual threat, we found that AgRP-PAG activation did not affect behavior on this assay. Future directions will explore how other AgRP projections might modulate food-directed behavior when hunger competes with other motivations.

This work was supported by RI-INBRE

Medial Prefrontal Cortical Ensemble Activation Alters Behavior in Presence of Competing Motivations

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Animals often encounter situations in which multiple needs compete for attention, requiring the brain to prioritize one behavior over another. Choosing whether to seek food or avoid danger, for example, is critical for survival, yet the neural mechanisms that guide these decisions remain poorly understood. Our previous work has shown that separate neural ensembles within the medial prefrontal cortex (mPFC) respond to hunger and predator threat, suggesting that these populations may help resolve motivational conflict by biasing behavior toward one competing need. In this study, we tested whether these ensembles are sufficient to influence behavior when hunger and threat are simultaneously present. Using TRAP2-Cre mice, we combined targeted recombinase in active populations (FosTRAP) with chemogenetic activation through designer receptors exclusively activated by designer drugs (DREADDS) to selectively label and reactivate mPFC neurons responsive to predator odor (trimethylthiazoline; TMT), food following food deprivation, or a neutral water control. After allowing three weeks for DREADD expression, mice received either clozapine-N-oxide (CNO) or vehicle before completing a series of behavioral assays. In a predator odor assay, food-deprived mice were presented with food placed next to TMT, creating a conflict between hunger and threat avoidance. Activation of TMT-responsive ensembles reduced food consumption, whereas activation of food-responsive ensembles increased food consumption and increased time spent in the odor zone. Neither manipulation affected food consumption when predator odor was absent, although activation of both ensembles did affect locomotion in an open field. Together, these findings demonstrate that distinct mPFC ensembles are sufficient to bias behavior only when competing motivations are present. These results support a role for the mPFC in integrating competing motivational information and selecting the behavioral response that is most adaptive for the current environment.

This work was supported by RI-INBRE

Comparative Analysis of Hyoid Depression Mechanics in High-Powered Suction, and Low- Powered Suction-Bite Feeding Sharks

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This study investigated how variation in the hyobranchial musculature contributes to feeding mechanics in two shark species with different feeding strategies: the high-powered suction-feeding *Chiloscyllium plagiosum* (white-spotted bamboo shark) and the low-powered suction - bite feeding *Squalus acanthias* (spiny dogfish). Although the coracohyoideus (CH) and coracoarcualis (CA), the primary muscles responsible for hyoid depression, are present in both species, differences in their geometry suggest distinct mechanical functions. In *C. plagiosum*, these muscles are positioned in a nearly straight line with the hyomandibular–ceratohyal joint at the onset of hyoid depression, creating a short in-lever that initially limits mechanical advantage. As the hyoid rotates ventrally, this alignment changes, increasing leverage and allowing greater power production during suction generation. In contrast, the generalist species exhibit a less specialized arrangement that likely favors versatility over maximal suction performance. The coracobranchialis (CB), although not always considered to be involved in depressing the hyoid, forms an important component of the hyobranchial complex. The CB inserts onto the hyoid skeleton and likely contributes to hyoid depression during feeding movements. Collectively, these findings suggest that modifications to the organization and mechanics of the hyobranchial complex, rather than major differences in muscle anatomy, underpin the enhanced suction-feeding capabilities of *C. plagiosum*, while enlarged divisions of the CB, that could be used to assist hyoid depression, in *S. acanthias* may have contributed to the increased versatility in feeding strategy.

This work was supported by RI-INBRE

Habitat-Associated Differences in Relative Neural Investment Between Two Coastal Shark Species: A Preliminary Comparative Neuroanatomical Study

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Brain evolution is thought to reflect the ecological and behavioral demands experienced by organisms through mosaic evolution, in which individual brain regions vary in relative size in response to differing sensory, motor, and cognitive requirements. Consequently, patterns of relative neural investment provide insight into how habitat and ecology influence nervous system evolution. The Atlantic Sharpnose Shark (*Rhizoprionodon terraenovae*) and Dusky Smooth-hound (*Mustelus canis*) occupy distinct coastal habitats and differ in aspects of their foraging ecology, making them an ideal system for examining whether ecological specialization is associated with differential investment among functional brain regions. We hypothesized that species occupying different ecological niches would exhibit differences in proportional investment in brain regions associated with sensory processing, motor coordination, and behavioral integration. Whole brains were dissected from three individuals of each species, and body mass, whole brain mass, cerebellar folding area, and the masses of the olfactory bulbs, cerebrum, cerebellum, optic lobes, and medulla oblongata were measured. Brain region masses were normalized to whole brain mass to quantify proportional neural investment independent of overall brain size, while cerebellar folding area was normalized to cerebellum mass. Independent-samples t-tests and Hedges' g effect sizes were used to compare normalized brain region measurements between species. Relative cerebrum size differed significantly between species ($p = 0.017$) and exhibited a very large effect size (Hedges' $g = 2.58$). Relative cerebellum and optic lobe sizes also demonstrated large effect sizes (Hedges' $g = 1.49$ and 1.32, respectively), although these comparisons did not reach statistical significance, likely reflecting the limited statistical power associated with the small sample size. Relative olfactory bulb size showed a moderate-to-large effect size (Hedges' $g = 0.92$), whereas differences in relative medulla size and normalized cerebellar folding were comparatively small. Although exploratory, these findings suggest that the two species differ in the proportional allocation of neural tissue among functionally distinct brain regions, indicating differences in relative neural investment rather than overall brain size. The observed pattern is consistent with ecological theory predicting that habitat use and sensory ecology influence investment in neural systems responsible for sensory processing, motor coordination, and behavioral integration. While additional sampling is needed to rigorously test these hypotheses, this pilot study provides a quantitative framework for investigating relationships among habitat, sensory ecology, and mosaic brain evolution in

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Retrograde Motor Neuron Labeling in the Rabbit Model of Cerebral Palsy

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Cerebral palsy (CP) is a movement disorder that affects around 1in 500 live births. A known risk factor for CP is hypoxia-ischemia (HI) injury around the time of birth. Motor deficits related to CP are typically the result of injury or damage to the developing central nervous system, but it is not clear why one muscle or group of muscles may be affected in one individual, while another individual with CP is affected in other muscles. This project specifically investigates motoneurons innervating affected muscle groups in CP, which remain poorly understood.

To study CP, we used an established rabbit model of CP based on prenatal HI that replicates key features of the human disorder. CP-like motor deficits are produced when fetal rabbits are exposed to HI at ~80% gestation. After birth, neonates are injected using a fluorescent dextran retrograde tracer at the wrist muscles (flexor carpi radialis and extensor carpi radialis) and lower hindlimb muscles (gastrocnemius, tibialis anterior) which are commonly affected in CP. Going forward, these will be performed specifically in the muscles that are determined to be hypertonic in HI rabbits and the corresponding muscles of uninjured rabbits. After injections, kits undergo a 5-10 day survival period to allow retrograde transport of dye to the neuronal somata that innervate these muscles. After the survival period, kits were euthanized followed by tissue harvest and processing either by fresh freezing, where the spinal cord is frozen in isopentane chilled by dry ice or by transcardial perfusion with 4% paraformaldehyde for tissue fixation. Transverse sections of the spinal cord were taken from segments of interest, C4-T1 and L4-S1. These segments are of interest because they are where we believe motoneurons innervating the injected muscles will be. Tissue was processed by indirect immunofluorescence with a primary antibody against choline acetyltransferase (ChAT), a marker of cholinergic neurons, as well as a fluorescent secondary antibody that is used to visualize our specific protein. We also used a fluorescent Nissl stain to serve as a base line of staining all neuronal pathways in our sample.

Co-labeling with dextran and ChAT will reveal specific populations of motoneurons innervating the muscles of interest we injected. This study will help us examine how developmental injuries impact the motoneurons and lead to CP. Mapping these neuronal populations will establish a foundation for future investigations into motoneuron organization, physiology, connectivity, transcriptomic properties, and pathological changes following HI injury.

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Targeting Acidic Environments with e-pHLIP

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The pH (Low) insertion peptide, pHLIP, has elevated the therapeutics industry through introducing specific and targeted cargo delivery of drugs. The most prominent characterisitic of pHLIP is that it targets the acidic extracellular enviornment of cells, specifically ones consistent in tumors. Due to the Warburg Effect, an excess of hydrogen atoms, lactate, and glucose molecules fabricte a low pH enviornment. When placed in such acidic enviornments, pHLIP goes through stages I,II, and III where ultimately, an alpha helix forms then inserting itself into cells' membranes. With pHLIP already in clinical trials, an attempt to now enhance pHLIP for a more efficient delivery of cargo has yielded enhanced pHLIP or e-pHLIP. This e-pHLIP technology is essentially 2 pHLIP peptides linked at the non-inserting ends. The larger peptide will be used for intracellular drug delivery aswell as delivering SIRNA. The idea behind e-pHLIP's composition suggests that the 2 pHLIP peptides will have faster and stronger cell membrane insertion rates and will be able to carry heavier, more polar cargo loads. Using cell culturing and tumor staining processes, the e-pHLIP-ICG compound shows significant binding compared to pHLIP through Invitrogen and Licore imaging. Furthermore, through in vitro imaging of mice treated with e-pHLIP-ICG, biodistribution of ICG fluorescence showed signal in tumors grown from in lab cells while other organs showed insignificant signal. Similarly, the Spectra Max IDS tests for fluorescence measurements and through HSA (Human Serum Albumin) binding experiments showed, that in spite of binding site competition, there is significant e-pHLIP binding to the albumin protein in blood plasma that allows e-pHLIP to be circulated throughought the body to ultimatley reach its target. Although we see that e-pHLIP is a strong enough peptide that can reach its intended target along with cargo, the true test lies in the insertion and exit rates of the cell membrane. The Biologic MOS 450 allows kinetics, circular dichroism, and pH dependance experiments to take place in which several trials reveal a graph that in each case pointed to quicker insertion rates, positive alpha helix formation necessary to insert in cell membrane, and finally the range of around pH 6.0 at which e-pHLIP inserts itself into the membrane. The possibilities associated with pHLIP were limited to the cargo and speed yet with e-pHLIP those very limitations have been breached to launch the therapeutics industry into more refined and efficient therapies.

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Occupational Participation After Brain Injury in Young Adults

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Importance: Traumatic Brain Injury (TBI) can result in persistent cognitive, physical, and psychological impairments that interfere with occupational participation. However, few studies have examined participation across multiple occupational domains among young adults.

Objective: To examine the association between a history of TBI with occupational participation limitations in young adults.

Design: Cross-sectional study

Setting: Community-based survey conducted electronically for young adults who reside in Rhode Island for at least a portion of the year.

Participants: A total of 1,008 young adults aged 18-25 who completed the 2024 Rhode Island Young Adults Survey.

Outcomes and Measures: TBI history was assessed using self-reported healthcare provider's diagnosis. Limitations in occupational participation were measured across nine occupational domains: body, daily activities, health management, education, labor, rest, play, leisure, and social participation. Separate multivariable logistic regression models estimated adjusted odds ratios (AORs) and 95% confidence intervals (CI's) controlling for confounders such as demographic factors (age, race/ethnicity, sex/gender), subjective social status, anxiety symptoms, depressive symptoms, and attention-deficit/ hyperactive disorder (ADHD).

Results: Among 1,008 participants, 138 (13.7%) reported a prior TBI diagnosis. After adjustment for demographic characteristics, subjective social status, depressive symptoms, anxiety symptoms, and ADHD, only limitations involving rest (AOR = 1.73, 95% CI = 1.14-2.61) and play (AOR = 1.69, 95% CI = 1.00-2.85) remained independently associated with TBI. Although unadjusted analyses demonstrated limitations across multiple occupational domains, these associations were attenuated after adjustment.

Conclusions and Relevance: Although young adults with TBI demonstrated limitations across multiple occupational domains in unadjusted analyses, only rest and play remained independently associated with TBI after adjustment. However, since the adjustment for demographic and mental health factors led to independent associations persisting only in rest and play, restorative and recreational occupations may represent uniquely vulnerable areas of occupational participation following TBI. These findings suggest that occupational therapy assessment following TBI should extend beyond traditional functional outcomes to include restorative and recreational occupations.

This work was supported by RI-INBRE

Barriers and Facilitators to Family-Centered Care Across Pediatric Feeding Disorder Practice Settings

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Family-centered care is considered best practice in pediatric feeding disorder (PFD) intervention because it promotes clinician-family collaboration, communication, and positive outcomes. However, speech-language pathologists (SLPs) may encounter implementation barriers that differ across practice settings. This study examined reported barriers and facilitators to family-centered care across PFD practice settings. A cross-sectional survey was completed by 97 SLPs serving children with PFD. Eligible participants were English-speaking SLPs practicing in the United States who held the ASHA Certificate of Clinical Competence and had at least one year of experience treating children with PFD. Most were experienced clinicians: 69.1% reported at least 10 years of practice within their discipline, and 60.8% reported at least 10 years working with feeding and swallowing disorders. Participants selected all applicable practice settings and identified perceived barriers and facilitators. Responses were summarized using counts and percentages. Barriers and facilitators varied across settings. Insurance policies were commonly reported barriers in non-hospital-affiliated outpatient clinics (50.0%) and private practice (59.5%). In contrast, 46.7% of early intervention providers and 57.1% of school-based clinicians reported no barriers. Individual interest was the most frequently reported facilitator, selected by 85 participants (87.6%). Other common facilitators included prioritization of family-centered care, selected by 72 participants (74.2%); adaptability to the practice setting, selected by 63 (64.9%); family engagement and patient interest, selected by 62 (63.9%); characteristics of the population served, selected by 57 (58.8%); and training and education, selected by 53 (54.6%). Findings indicate that clinicians' experiences implementing family-centered care differ across PFD practice settings. Addressing setting-specific barriers while strengthening existing facilitators may help clinicians and organizations identify where additional resources or support are needed. Insurance-related barriers may be particularly important to address in outpatient clinics and private practices.

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Development of Alginate Cryogels for Delivery of Immuno-Modulatory Proteins

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Hydrogel systems are widely utilized for delivery of immuno-modulatory proteins and have significant potential for regulating immune responses and improving therapeutic outcomes in many biomedical applications. However, conventional hydrogel crosslinking methods often can react with encapsulated proteins, potentially causing denaturation and loss of bioactivity. To address this limitation, injectable alginate cryogels were previously developed using bio-othogonal tetrazine-norbornene click chemistry, which enables rapid crosslinking without reacting with the protein payload. In addition, cryogelation occurs under frozen conditions, where ice crystals act as porogens and generate large, interconnected macroporous networks upon thawing. This unique architecture enhances mass transport, supports immune cell infiltration, and facilitates protein loading and release. In this project, we synthesized a series of alginate cryogels for delivery of immuno-modulatory proteins and characterized their morphological, mechanical and protein loading properties. Tetrazine- and norbornene-functionalized alginates (Alg-Tz and Alg-Nb, respectively) were synthesized and characterized by NMR, confirming successful functionalization with approximately 5% substitution for both groups. Cryogels were fabricated at 1-3% (w/v) polymer concentrations by mixing Alg-Nb and Alg-Tz at a 1:1 ratio in water using a luer lock syringe connector. Gels are cast into pre-chilled molds and crosslinked overnight at -20℃. Across all formulations, cryogels exhibited high interconnected porosity, favorable swelling behavior, and maintained structural integrity following compression and injection. Scanning electron microscopy and three-dimensional X-ray microscopy revealed large, interconnected macroporous networks characteristic of cryogel architectures. The cryogels encapsulated immuno-modulatory proteins CCL2, CCL5, and GM-CSF at nearly 100% loading efficiency as determined by ELISA. Protein release studies demonstrated sustained release of CCL2, CCL5, and GM-CSF over at least 7 days. These findings demonstrate that bio-orthogonally crosslinked alginate cryogels possess desirable structural, mechanical, and protein-loading properties for injectable biomaterial applications and support their continued evaluation as delivery vehicles for immuno-modulatory proteins.

This work was supported by RI-INBRE

Evaluation of PFAS Redistribution in Serum and Tissue Following Cholestyramine Intervention

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Per- and polyfluoroalkyl substances (PFAS) are synthetic environmental contaminants that are highly persistent and bioaccumulative in the environment and humans. PFAS exposure has been associated with adverse health effects, such as liver injury, dyslipidemia, immune dysfunction, and metabolic disease. Perfluorooctane sulfonate (PFOS) and perfluorooctanoic acid (PFOA) are among the most frequently detected PFAS and exhibit prolonged biological half-lives due to strong tissue binding and enterohepatic recirculation. Cholestyramine, an FDA-approved bile acid sequestrant, has been investigated as an off-label therapy to enhance PFAS elimination by interrupting enterohepatic recirculation and increasing fecal excretion. However, because PFAS accumulates in tissues, it remains unclear whether serum PFAS concentrations rebound after cholestyramine discontinuation. We hypothesize that PFAS stored in tissues, particularly the liver and kidneys, redistribute into the circulation following cholestyramine withdrawal, potentially masking reductions in total body burden

To investigate PFAS rebound following cholestyramine intervention, 40 adult male C57BL/6J mice, 8–10 weeks old, are undergoing a 5-day PFAS loading phase consisting of daily oral gavage administration of PFOS (5 mg/kg) and PFOA (5 mg/kg) for a total PFAS dose of 10 mg/kg/ for five consecutive days to induce tissue PFAS accumulation. 8 mice treated with vehicles ((0.5% Tween20 in PBS) will also serve as controls and undergo terminal necropsy following the loading phase to establish baseline hepatic endpoints. Following PFAS loading, a subset of PFAS-exposed mice will also undergo necropsy to evaluate serum and tissue PFAS accumulation prior to intervention. The remaining PFAS-loaded mice will be divided into 2 groups: 16 mice undergoing 1.5% (w/w) cholestyramine treatment and 8 mice receiving a control diet for 10 days. Following the intervention period, 8 of the cholestyramine-treated mice will undergo terminal necropsy while the other 8 mice go to a 7-day treatment withdrawal phase on a standard diet to evaluate PFAS redistribution after discontinuation of treatment. Serum samples collected at necropsy will be analyzed for PFOS and PFOA concentrations. Liver, brain and kidney tissues will also be collected for PFAS quantification, while liver weight and liver fat content will be evaluated. PFAS dosing solutions and laboratory materials were prepared using contamination-control procedures to minimize background PFAS contamination.

This study will determine whether dietary cholestyramine accelerates the elimination of accumulated PFOA and PFOS by lowering serum and tissue PFAS concentrations.

This work was supported by RI-INBRE

Investigation of Potential Detrimental Effects of Administration of Anti-Aβ Monoclonal Antibody in a Transgenic Rat Model of Cerebral Amyloid Angiopathy

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Cerebral amyloid angiopathy (CAA) is a neurovascular disease characterized by deposition of amyloid β (Aβ) along and inside cerebral blood vessels. Sporadic CAA is associated with Alzheimer's Disease (AD), while hereditary forms of CAA occur independently of AD and with an earlier age of onset. Dutch-type CAA (CAA-D) is a form of hereditary CAA resulting from a point mutation at codon 693 of Amyloid Beta Precursor Protein (APP), resulting in a glutamic acid to glutamine substitution at position 22 of the Aβ peptide (E22Q). Because the E22Q mutation neutralizes the negative charge at position 22, electrostatic interactions are disrupted, which accelerates fibrillogenesis and promotes deposition along cerebrovascular walls. The rTg-Dutch (rTg-D) rat model exhibits accumulation of both $A\beta_{40}$ and $A\beta_{42}$ isoforms in large arterioles, which is pathologically similar to the CAA-D phenotype in humans. Efficacy of anti-amyloid monoclonal antibody therapy in AD patients is controversial. AD patients with CAA treated with anti-amyloid antibodies have an increased risk for Amyloid Related Imaging Abnormalities Involving Microhemorrhages (ARIA-H), or edema (ARIA-E). It is theorized that ARIA-H could arise due to rapid disaggregation of cerebral vascular amyloid compromising vascular integrity and causing bleeds although the precise mechanisms remain unknown. Here we investigated the effects of anti-amyloid therapy in a rat model of CAA.

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