

2022

NAMS Undergraduate Research Symposium



STOCKTON UNIVERSITY

School of Natural Sciences & Mathematics

Abstract #:1

Analysis and Comparison of Light Intensity Spectra Using Wavelet and Fourier Analysis

Buondonno, Gracie ; Ormond, KatieHaider, Amna; Weber, Courtney; Trout, Joseph ; Physics

This poster demonstrates our research on analyzing the light intensity spectra of stars with data provided by the Kepler Space Telescope. We analyzed the stellar light curves using Fourier Analysis and Wavelet Analysis. Continuous data of the light spectra intensities are used for the analysis of astronomical phenomena such as discovering the orbit of previously unseen planets. We are looking at various phenomena with stars and comparing the two techniques and seeing which one is more efficient and accurate. This poster presents the comparison of data collected and analyzed with Fourier Analysis and Wavelet analysis.

Faculty Mentor: Joseph Trout

Abstract #:2

Changes to the *Neurospora crassa* Metabolome as a Result of Defects in Arginine Catabolism

Urbanek, Alexandra; McCollum, Liam; Pollock, Elizabeth ; Biochemistry

Arginine is a secondary source of nitrogen in many plant and fungal species. Non-lethal mutations that impact arginine catabolism could cause secondary impacts on the metabolome as cells adjust to the lack of nitrogen availability via arginine. In this study, ¹H nuclear magnetic resonance spectroscopy (NMR) was used to compare the metabolomes of *Neurospora crassa* (*N. crassa*). A strain deficient in the arginase enzyme responsible for catalyzing the first step of arginine catabolism was metabolically distinct from wild type (WT) or urease knockout strains grown under the same conditions of Vogel's minimal medium (VM). Therefore, arginase knock-out strains (ArgKO) were supplemented with arginine, which exacerbated the differences in ArgKO strains. This exhibited changes in the composition of the amino acid pool, particularly alanine in comparison to WT grown in the VM. High-Pressure Liquid Chromatography (HPLC) is currently being used to help further identify metabolites due to spectral crowding in ¹H NMR.

Faculty Mentor: Elizabeth Pollock

Abstract #:3

Contemporary Presence of Humpback Whales (*Megaptera novaeangliae*) and the Menhaden Reduction Commercial Fishing Fleet off Cape May, New Jersey *Bariso, Heather & Laurino, Melissa ; NAMS*

North Atlantic Humpback Whales (*Megaptera novaeangliae*) utilize high latitude areas such as Cape May, New Jersey as integral feeding grounds during their extensive annual migration. In New Jersey, their main prey source is the Atlantic Menhaden (*Brevoortia tyrannus*), the most important fish of the sea. In addition to marine mammals, this keystone species is also an important food source for sea birds, predatory fish, and the primary target species for the Omega Protein Reduction Fishing Fleet. Reduction landings are responsible for the majority of menhaden take off New Jersey. Whale sightings data from the Atlantic Ocean in 2019-2020 was utilized from the Cape May Whale Watch and Research Center (CMWWR) database. This was combined with vessel Automatic Identification System (AIS) data from MarineCadastre.gov, a partnership between National Oceanic and Atmospheric Administration (NOAA) and the Bureau of Ocean Energy Management (BOEM). Data were manipulated and extracted using Python Pandas libraries and visualized using ArcGIS Pro. Vessel tracks in the Atlantic Ocean were represented using heat map density plots and overlaid with Humpback whale sightings. A total of 76% (n=93) of whale sightings intersected with locations where reduction vessels were occurring and 14% (n=13) of these sightings observed whales lunge feeding. Migrating Humpback whales are important to consider when establishing quotas and locations permitted for reduction harvests of one of their primary food sources.

Faculty Mentor: Melissa Laurino

Abstract #:4

Base-Free Transfer Hydrogenation Using a Novel Ruthenium-Based Catalyst *Citta, Richard; Kalman, Steven; Chan, Benny ; Chemistry*

While main group hydride salts have been traditionally used to reduce ketones and related functional groups, this method requires stoichiometric amounts of moisture-sensitive reagents. Metal-catalyzed hydrogenation with hydrogen gas is a viable alternative but requires high pressures and specialized equipment. Catalytic transfer hydrogenation can reduce pi bonds using easily-handled dihydrogen surrogates with good selectivity, thereby offering much value for

pharmaceutical and commercial uses. Many transfer hydrogen catalysts exist; however, only a select few can function in the absence of a base under aerobic conditions. Using an imidazole-2-carboxamide ligand, we have synthesized a novel ruthenium-based complex and characterized it using NMR spectroscopy, combustion analysis, and single-crystal X-ray diffraction. We find that this complex can catalyze the base-free hydrogenation of ketones and aldehydes under aerobic conditions using 2-propanol as both a hydrogen donor and solvent. A substrate scope study was performed to better characterize the complex's catalytic capabilities. Current work is being done to identify viable intermediates in-situ to better understand the catalytic mechanism.

Faculty Mentor: Steven Kahlman

Abstract #:5

Analysis of eDNA data for Characterizing the Finfish Population of a NJ Coastal Dredge Hole

Ozoria, Lizbeilyn; Harmer Luke, Tara ; BCMB

As part of a larger ecosystem characterization of finfish usage, this study uses environmental DNA (eDNA) data to help characterize the faunal community of Dredge Hole #90 in Atlantic County. Water samples containing eDNA were collected in the spring, summer, and autumn of 2020, filtered, and frozen for future analysis. Complete genomic DNA was extracted from these samples, further analyzed, a total of seven eDNA samples were sent out for Whole Genome Next Generation Sequencing. These files were analyzed separately and together using the web-based bioinformatics platform, Galaxy. Data reliability was assessed and adaptor sequences were removed for further analysis. Figures and basic data analytics were produced, collected, and analyzed. When analysis is complete, these data will be ground-truthed with results collected via traditional survey methods, and could potentially result in a less-invasive method for identifying faunal use of an ecosystem that is not dependent on invasive sampling techniques

Faculty Mentor: Tara Luke

Abstract #:6

Food Waste Recycling Bill A2371 Compliance Determination for the Sea Girt National Guard Training Center Dining Facility

Shank, Cassandra ; ENVL

Stockton University's Environmental Internship Program was tasked with developing and implementing a study to monitor food waste generation and management by the New Jersey Department of Military and Veterans Affairs Environmental Management Bureau in response to the Food Waste Recycling Bill (A2371). A2371 requires that all sites that generate more than 52 tons of waste annually and are within 25 road miles of an authorized food waste recycling facility must have their food waste sourced to those authorized facilities. To determine if the meal operations at Sea Girt National Guard Training Center were subject to A2371 food waste recycling requirements, we developed and implemented an experiment to quantify food waste generation for one day. Based on our data, we calculated that each diner generated about 0.0003 tons of food waste per day. Knowing that approximately 141,819 meals are served annually, we determined that the facility would generate approximately 12.68 tons of food waste annually. Based on these results, we determined that 539,137 meals would need to be served in one year to reach the 52-ton regulatory threshold. Additionally, we determined that there are currently no authorized food waste recycling facilities within 25 road miles of the site. Therefore, meal service operations at this facility are not currently subject to A2371 food waste recycling regulations. These results, as well as waste item observations and trends, waste minimization strategies, and various composting options, were included in a formal report, and provided to the facility superintendent for record.

Faculty Mentor: Dr. Tait Chirenje

Abstract #:7

Chemical Analysis of Newly Discovered Antibiotics from Soil Bacteria

Patel, Rani; Shah, Jairaj; York, Karen ; Biology

The increase in antibiotic-resistant bacterial infections is a growing health concern. To address this ongoing crisis, it is essential to discover new effective antibiotics. In this research project, we cultivated antibiotic-producing soil bacteria that inhibited the growth of known laboratory bacteria. We extracted chemical metabolites from these bacteria using ethyl acetate and confirmed antibiotic activity was present in the extract. We then used gas chromatography-mass spectrometry (GC-MS) to chemically characterize the metabolites by comparing fragmentation patterns to known compounds in the NIST library. The candidate compounds were assessed to determine if any were

previously identified as potential antibiotics. Two of the crude extract samples contained many interesting molecules not previously known to have antibiotic properties. In order to determine which of the metabolites had antimicrobial activity, we separated the metabolites using thin layer chromatography (TLC) and visualized the presence of bands using long and short UV light. The TLC separation can be optimized and then used to detect the biological activity of the bands. Then ultimately be used as a method to purify metabolites from a large-scale extract for further analysis.

Faculty Mentor: Karen York

Abstract #:8

Optimizing Bait and Trap Efficiency for Capturing Northern Red-bellied and Painted Turtles

; Holly, Donovan

Non-mammalian species have historically received less attention from conservation and research efforts. This has led to the continued decline of reptile populations that experience delayed management plans. The northern red-bellied cooter, *Pseudemys rubriventris*, is one such species. A subspecies of the red-bellied cooter from Massachusetts was listed as endangered in 1980, while leaving the species largely unprotected throughout most of its range. The USFWS currently has the Red-bellied Cooter under the National Listing Workplan to establish its endangered status. Basic ecological research is a precursor to developing plans that will rejuvenate vulnerable species. To contribute to ongoing and future ecological studies, we examined the efficacy of common turtle traps on catching red-bellied cooters and painted turtles, *Chrysemys picta*. Capture-mark-recapture studies have been one of the leading methods of establishing ecological trends for reptiles. Our capture-mark-recapture study was conducted at Stockton University's Lake Fred where a thriving population of red-bellied cooters exists. We sought to determine which bait types, temperature, and trap types would lead to the highest capture rates. Our bait types were sardines and strawberries, and trap types were hoop, caged hoop, and basking traps set on a daily basis during turtle active seasons. Due to the omnivorous diet of adult cooters, we hypothesized that the addition of plant material (strawberries) significantly increases the capture rates. Additionally, we expected that basking traps would work more

effectively in the spring when water temperatures are low, compared to late summer and fall when thermoregulatory opportunity is greater.

Faculty Mentor: Craig Lind

Abstract #:9

Lamprophyres: A unique volcanic rock type from Cortlandt and Beemerville Gulya, Matthew, Castle, Evans, Severs, Matthew ; Geology

The Cortlandt and Beemerville complexes and trend within Southeast NY to Northwest NJ are large igneous rock bodies that are thought to be related to one another. Within this trend are also dikes are primarily made of volcanic rocks called “lamprophyres” and are better characterized by an abundance of sodium, potassium, carbon dioxide and water along with lower silica content. The origin and association of these volcanic rocks is poorly understood and only those in the immediate vicinity of the Beemerville complex have been properly identified. A major goal of this project is to obtain a better understanding of these lamprophyres and their geochemical/mineralogical characteristics in order to understand their relationship to either/both the Beemerville or Cortlandt complexes and the source of these magmas. Field observations showed that the 29 sampled dikes show a great amount of diversity in their chemistry and mineral composition. The results of lab analyses show that these lamprophyres have a wide variety of crystal sizes and thus encompass a wide variety of different igneous rock names instead of all being lumped as “lamprophyres”. The geochemical analyses also suggest that the dikes show a variety of potential sources and that some show a relationship with the Beemerville, but others do not show a relationship with either Beemerville or the Cortlandt complexes.

Faculty Mentor: Matthew Severs

Abstract #:10

Scholarly Review of Literature: Which genetic components contribute to socialization?

Yasmin Mourad and Diane Imburgio, Ph.D. ; NAMS

Our study compiles a literature review that focuses on the emergence of common genetic themes associated with social behavior in animals including humans. Behavior in animals is a complex dynamic that is controlled by multiple factors including genetics. The availability of completed genome

sequences in many organisms has allowed for computer-based genome wide searches for common and variant genetic elements that correlate with both cooperative and aberrant behaviors. Identified candidate genes are then studied using more traditional genetic methods. Human syndromes such as autism spectrum disorders (ASDs) share the common feature of reduced language and communication (verbal and non-verbal) and may provide clues for genetic components that are essential in social interactions. In recent years, there has been identification of candidate genes found in ASD individuals indicating a genetic basis for the heterogenous disorder. Some genetic elements are found as increased or decreased copy number variants (CNVs). Single nucleotide polymorphisms (SNPs) are also identified in some genes. Our review presents data utilizing the social wasp, mouse, and human model organisms. We find that candidate genes that affect socialization encode for transcription factors that regulate the expression of other genes, signaling proteins that regulate embryonic development of the brain and proteins that affect the synthesis and release of neurotransmitters.

Faculty Mentor: Diane Imburgio

Abstract #:11

Impacts of offshore wind-farm processes (installation, maintenance, operation) on local pinniped populations: A review

Lauren Baier and Jacalyn Toth ; MARS

As the need for alternative energy sources increases, the construction and operation of offshore wind farms is becoming more frequent in the northeastern United States. Understanding how turbines impact surrounding ecosystems is essential for conscientious development of future wind energy systems. Various studies suggest that marine mammals are impacted at all stages of construction, maintenance, and operation, with noteworthy distinctions between pinnipeds and cetaceans. This review summarizes the methods, results, and significant conclusions of previous studies examining the effect of wind operations on local pinniped populations. Many of these studies originate in the North Sea, where most European Unions' offshore wind farms are located. Numerous behavioral studies suggest wind farm impacts on pinnipeds are primarily neutral and, in some cases, positive. Different stages of wind farm construction will be discussed - each of which may generate distinct behavioral reactions. For example, pinnipeds affected during wind farm

construction phases only may exhibit negative modified behavior during initial pile-driving operations. Pinniped auditory thresholds, along with frequencies related to wind farm construction and maintenance will be summarized. Suggested positive impacts will also be discussed, including the creation of artificial reef communities, increased prey biomass, and increased foraging opportunities. This review of pinniped populations co-occurring alongside varying stages of wind farm operations will increase awareness of potential impacts (positive, negative, neutral) to these important apex predators. As wind farm development becomes common in coastal environments, understanding outcomes from prior studies will help inform monitoring and impact assessments for future wind farm construction and operation.

Faculty Mentor: Jacalyn Toth

Abstract #:12

Phylogenetic Analysis of the Zona Pellucida Protein Complex and Zona Pellucida 3 (ZP3) in Vertebrates

Metzler, Matthew; Barbato, Guy F. ; BCMB and Biology

The zona pellucida (ZP) complex contains glycoproteins which are utilized in the formation of the “coat” surrounding oocytes. ZP glycoproteins have been shown to be involved in early fertilization events, as well as early embryologic development. The ZP3 gene codes for the predominant protein in the complex that surrounds the mammalian oocyte and plays a pivotal role in fertilization by mediating sperm binding in a species-specific manner, inducing the acrosome reaction, preventing polyspermy and protecting the embryo prior to implantation. Homology of the human ZP complex was examined and the evolutionary history of the ZP3 amongst vertebrates was investigated. ENSEMBL, MEGA-X, WebLogo, and UniProt aided in the visual representation of the homology and evolutionary history of the amino acid sequences within each vertebrates’ ZP3 alignment. High levels of evolutionary homology were seen amongst humans, other primates, and several classes of mammals. Radial phylogenetic trees were utilized to exhibit high conservation of ZP3 sequences amongst these groups as well as low conservativity amongst teleosts. The evolutionary conservation throughout vertebrates has reaffirmed the necessity and importance of the ZP3 in fertilization as the primary, although not exclusive, sperm receptor. As a key protein in reproduction, mutations in the gene may have distinct evolutionary disadvantages. Some vertebrates have

acquired due to mutation, specifically indels, in the gene causing poor oocyte fertilization, small progeny numbers, and longer gestation periods.

Faculty Mentor: Guy Barbato

Abstract #:13

Oyster recruitment and species richness and abundance on a living shoreline at Reeds Beach in Delaware Bay, New Jersey

Renna, Kylie ; MARS

Oysters are considered “ecosystem engineers,” filtering water and creating a stable habitat for many species of invertebrates as well as some vertebrates. They also create living shorelines, limiting the process of erosion, and protecting local communities. This study focuses on how artificial reefs can enhance biodiversity by providing habitat and the recruitment of oysters to Reeds Beach in Delaware Bay, NJ. In 2015, artificial reefs were made using bags packed with whelk shells. There were 15 inshore reefs and 8 offshore reefs, and each reef was monitored biweekly from August through October for mobile and encrusting species richness and abundance. Oyster size and density were monitored in October 2015 and April 2016 to assess recruitment and winter survival. The results of the study showed a significant difference in species richness with higher richness found on the offshore reef (mean: 10.4) compared to the inshore reef (mean: 8.7). When separating species abundances by taxonomic group, there was significantly higher density of bivalves on the inshore reef compared to the offshore reef. There was a significant difference in the size of oysters with respect to location and time with the offshore reef having larger oysters than the inshore reef, and April 2016 having larger oysters than October 2015. The conclusions show that the offshore reefs on Reeds Beach support a more diverse group of organisms and better oyster growth and survival. This proves that artificial reefs can create a suitable oyster reef habitat supporting a diverse assemblage of species in Delaware Bay.

Faculty Mentor: Christine Thompson

Abstract #:14

Optimization of CRISPR-Cas9 in the budding yeast *Saccharomyces cerevisiae*

Coulman, Jennifer; Maioriello, Johanna; Law, Michael ; Biology

CRISPR-Cas9 was discovered as a bacterial defense mechanism and is currently researched as a genome editing tool, enabling scientists to change an organism's DNA. Genome editing involves adding, removing, or altering DNA. This revolutionary approach is currently being investigated for gene therapy to treat diseases including sickle cell anemia and cancer. CRISPR-Cas9 can specifically target DNA sequences that will be cut by endonucleolytic cleavage. Once the DNA is cleaved, it needs to be repaired by the cell for continued cell divisions. Gene editing leverages endogenous DNA repair mechanisms and can be used to introduce any new DNA sequence of choice. In this project, we are implementing CRISPR-Cas9 for genome editing in the budding yeast *Saccharomyces cerevisiae*. Our goal is to optimize the CRISPR system in yeast so that we can apply it to biochemically dissect multiprotein enzymatic complexes and determine their roles in regulating cell divisions. The current investigation is aimed at disrupting the yeast gene ADE2 since inactivation of this gene results in a change in phenotype, turning the yeast red. Using bioinformatics, we have designed a targeting vector and repair template, which we have cloned for transformation into yeast. Yeast transformations will be performed on both diploid and haploid strains to determine the efficiency of generating homologous mutants. Future studies will include dissecting the complex of proteins associated with Set1 (COMPASS), which is a major focus in the Law laboratory.

Faculty Mentor: Michael Law

Abstract #:15

Petrogenesis of lamprophyre dikes in Great Falls Park, Virginia and Maryland *Caccamesi, Dylan D., Steup, Kadie J., and Severs, Matthew J. ; Geology*

Several igneous dikes were identified over 50 years ago that cut through the Potomac River along the border of Maryland and Virginia within Great Falls Park (George Washington Memorial Parkway and the Chesapeake and Ohio Canals National Historical Monuments). Originally identified as lamprophyre dikes, these differ from other mafic rocks (such as basalt or diabase) due to their high-alkali and volatile contents, which is reflected by an abundance of the minerals biotite and/or amphibole. Lamprophyre formation can occur in a variety of different tectonic settings such as subduction zones and continental rifts, and from melting a variety of source rocks such as an enriched mantle or metamorphosed lower continental crust rocks among others. This study aims

at identifying the specific type of lamprophyre present and understanding how it formed by examining the whole-rock geochemistry and the petrography of the dikes. Initial petrographic analysis of the Great Falls dikes shows enrichment in biotite, classifying these features as minette-type lamprophyres in conjunction with major element geochemistry to define the entire suite as basaltic trachy-andesites. Trace element geochemistry displays significant depletion in niobium and tantalum indicating an origin in a volcanic arc setting, likely placing this late during the Appalachian Orogeny. The long-term goal of this research is to utilize the petrology of the Great Falls lamprophyres in order to determine if there is a linkage between them and the local orogenic-type gold deposits found in the immediate area in Maryland, which will be completed over the upcoming summer.

Faculty Mentor: Matthew Severs

Abstract #:16

Diet of Pinnipeds in Great Bay, New Jersey

Talentino, Carla; Campbell, Jada; Jones, Symone; Alicea, Maya; Toth, Jacalyn; and Harmer Luke, Tara ; Biology, BCMB, MARS

The main goal of this project is to assess whether or not wind farm development has a negative effect on the fish and harbor seal population of Great Bay, NJ. As Great Bay is the largest haul-out site in the state, it is critical to identify the impact that building these structures may have on the seal population. We want to ensure that they are still able to use the land as a resting and thermoregulating site upon foraging at sea when structures foreign to them are present. We use environmental DNA (eDNA) analysis to determine the food habits of harbor seals that overwinter ahead of the construction of the Ocean Wind Project offshore of Atlantic City, NJ. A total of 10 Seal scat samples were collected per month from the Great Bay haul out site between November of 2021 through April of 2022 eDNA was extracted from these samples, amplified via the Polymerase Chain Reaction (PCR) using various primers that amplify regions of the mitochondrial genome of vertebrates. This allowed us to determine which primer sets were most effective for our purposes. Our next step is to prepare for Next-Generation Sequencing (NGS), which not only will determine the species of fish available during the winter and spring months, but also which types the seals ingest.

Faculty Mentor: Tara Luke

Abstract #:17

Structural and microscopic characterization of the Mount Powell Batholith, western Montana

Tapanes Steven, Kemble Richard, Reid Allison, Webber Jeffrey ; GEOL

Deeply eroded volcanic regions provide important locations to study the processes controlling the plumbing systems of volcanoes. Our study aims to understand the evolution of continental volcanic arcs during mountain building events in western Montana that experienced widespread volcanism during the construction of the North American Cordillera 70-30 Mya. We performed geologic mapping of the Mount Powell region at a scale of 1:10,000 to identify the locations of different rock types and collect samples for microscopic analysis and the characterization of crustal deformation. The field area displays different rock types including; granite, diorite, an altered diorite as well as sedimentary and metamorphic rock types. Cross-cutting relationships indicate that the granite intrudes the diorite and is later cut by younger mafic dikes. This suggests at least three distinct phases of volcanism since the Cretaceous. The granite exhibits a variety of textures including a unique exposure of orbicular granite composed of spherical orbicules (diameters 5cm-15cm) of plagioclase surrounding a core of granite. Microscopic analyses indicate a pervasive hydration of the granite that is not observed to the same extent in the diorite. This suggests a late-stage addition of hydrothermal fluids either during or post crystallization of the granite. Analysis of crystal orientations (n = 800) from a sample of quartzite host-rock indicates moderately high temperatures of crustal deformation that may have occurred during widespread extension in the Eocene. Ultimately, the Mount Powell batholith is a useful location for understanding the poly-phase magmatic and structural history of the North American Cordillera.

Faculty Mentor: Jeffrey Webber

Abstract #:18

Repression of Nutrient Foraging in Yeast

Parks, Alexandria; Campion, Katherine; Sirchio, Alexa; Ciccaglione Kerri; Law, Michael ; Biology and BCMB

Cells constantly survey their intracellular and extracellular environment to interpret signals that regulate life and death. When grown in nutrient-rich conditions, the budding yeast *Saccharomyces cerevisiae* will replicate via mitosis. However, in nutrient-poor conditions, yeast undergo nutrient foraging also known as filamentous growth. To achieve this switch from mitotic to filamentous growth, cells must alter their transcriptional program. Previous work conducted in the Law lab found that two transcriptional regulators, cyclin C and Jhd2, are required to inhibit filamentous growth when yeast are cultured in rich conditions. While this investigation was informative about the switch in cell division, it was performed using a non-canonical yeast strain, SK1, that has not been well-explored in filamentous growth. Intriguingly when the same mutations were made in the model filamentous strain, Σ 1278B (Σ), filamentous repression was maintained. This suggests that differences in the genetics of these two closely related strains are causing distinct environmental responses. Prior research performed in other labs found that carbon source is a key factor in the differing filamentous response mechanisms for SK1 and Σ . In this study, we explored the role of carbon source in filamentous growth repression for both SK1 and Σ yeast strain backgrounds. Using a combination of genetic and cell biology techniques, we found that carbon source is not as important for the filamentous response as inositol. Since inositol is synthesized from glucose, these results suggest that SK1 inositol catabolism is crippled in the filamentous mutants.

Faculty Mentor: Michael Law

Abstract #:19

The use of eDNA to Characterize Fish Populations in Marine Ecosystems

Aboagye, Marilyn; Bukhari, Nidaa; Patel, Janvi; Sylvestre, Keith; Norton, Emma; Stone, Jasmine; Harmer Luke, Tara ; Biology and BCMB

This project uses environmental DNA (eDNA) technology to identify various commercially and recreationally important fish populations from local marine and estuarine ecosystems. This technique results in significantly less disturbance to the aquatic environment when compared to traditional techniques like using nets and trawls to assess the population of fish inhabiting various ecosystems. Water samples were collected from several locations in and around the southern New Jersey coast, and whole genomic DNA was extracted from each sample. eDNA was PCR amplified using a variety of

primers that target regions of the mitochondrial DNA from animal samples, in order to evaluate the effectiveness of each primer set. This work provides a foundation for further analysis of these samples using Next Generation Sequencing techniques

Faculty Mentor: Tara Luke

Abstract #:20

Microbial Diversity of Sourdough

Ellis, Kaelie ; Biology and Sustainability

Sourdough is known for its diverse microbiome with yeast and various species of lactic acid bacteria. Even though wheat has been used for thousands of years to produce bread, the microbial diversity of sourdough bread starter remains not fully characterized. This research was conducted to identify whether there is a difference in microbial diversity based upon (1) location and (2) what variety of wheat is used. For our starter material, grains of Emmer wheat and Hard Red Winter Wheat were threshed and winnowed. The grains were then milled and sifted into flour. During a week long period, three samples of each species of wheat were distributed into campus woods, Stockton Sustainability Farm, and Lake Fred. Portions of the samples deployed outside were transferred sequentially into additional dough samples to provide microbes with additional nutrients. This transfer process occurred every week under sterile conditions. DNA isolation was performed and successfully completed for the six samples. DNA samples will be sent to a separate laboratory for 16S rRNA sequencing. These results will be discussed during the NAMS (School of Natural Sciences and Mathematics) Symposium. Once the data is analyzed in the future, this will result in a more detailed understanding of the microbial diversity of the samples.

Faculty Mentor: Ron Hutchison

Abstract #:21

As Simple as Possible, but no Simpler: Reduced Models of the Bromite-Iodide Clock Reaction

Citta, Richard; Olsen, Robert ; Chemistry

Clock reactions are kinetic phenomena characterized by the sudden appearance or disappearance of a substance after a well-defined period of time. In a large family of these reactions, clock behavior is visualized through an

intensely blue solution becoming abruptly colorless as iodine disappears. A detailed mechanistic understanding of clock reactions lagged their discovery by about a century. Today, we can apply modern techniques to further our understanding of their complex nature. We have reinvestigated a mechanism of the bromite-iodide reaction made up of 15 species and 22 reactions. The bromite-iodide reaction is a subsystem of the bromate-iodide reaction, a clock reaction whose rate law is determined in a Chemistry IV laboratory experiment. We take a computational approach to simplifying the mechanism while maintaining clock behavior over a range of conditions. We have developed several reduced models via sensitivity analysis by eliminating redundant species, finding that clock behavior can be maintained when BrO^- , IO^- , and HOIO are individually removed from the model. Clock behavior is sustained, albeit over a somewhat narrower range of conditions, when combinations of these species are removed. Notwithstanding this narrower range, we have several simplified mechanisms in hand and will proceed to identify the most important reactions through rate sensitivity analysis.

Faculty Mentor: Robert Olson

Abstract #:22

Garlic Tournament of Champions: Multi-Year Yield Analysis for Thirty-Nine Garlic (*Allium sativum*) Cultivars

Parks, Alexandria; Swenson, Jonathan; McBride, Sean ; Biology, Environmental Science, and Sustainability

Garlic (*Allium sativum*) is a common crop thought to have originated in Central Asia but has diverged into a highly variable crop worldwide. Garlic is historically grown in large-scale settings, but this study looks at its marketability in small-scale farming, as well as which cultivars are the most prosperous in the Eastern temperate climate of Southern New Jersey. We are presenting yield data for 39 varieties of garlic grown and analyzed over a three-year study period. The garlic was grown with 6-inch spacing on 30-inch beds on the Stockton University Sustainability farm. The garlic was grown according to standard procedures and was harvested when the bulbs approached marketable size, when the bottom third of the leaves died. This harvest date was generally between May 31st and the middle of July. Yield data was analyzed using RStudio with a Shapiro-Wilks, One-way ANOVA, and Tuckey's Test to compare between varieties; the large data set dictated the statistical methods applied. The cultivar type significantly

impacted the average yield weight. Our data can be used to inform growers in the Mid-Atlantic region of the optimal variety for their farming system. Specific relationships between varieties based on the yield data will be discussed further, in addition to the statistical processes applied. Future research will investigate the effects of planting dates on yield size and plant height.

Faculty Mentor: Ronald Hutchison and Matthew Olson

Abstract #:23

Harbor seal population dynamics within Great Bay (NJ): Preliminary findings on seal haul-out behavior and camera efficacy from a remote monitoring system

Zembricki, Emily; Toth, Jacalyn; Zimmermann, Elizabeth; Ambrose, David; and Evert, Steven ; MARS

As the need for renewable energy sources continues to grow, planned offshore wind-farm lease areas are widespread along the US east coast. Installation of a 1,100 MW wind farm off Atlantic City is underway (Orsted); this lease area is about 15-miles offshore of New Jersey's largest haul-out site for a population of over-wintering harbor seals (*Phoca vitulina*). To monitor population dynamics of these seals before, during, and after wind-farm installation, a TrueLook remote solar-powered camera system was installed on the adjacent Seven Islands (January 2022). The current study evaluates efficacy of the camera and haul-out patterns of harbor seals during the month of February relative to environmental factors. A full day of data (sunrise to sunset) was captured on 26 of 28 days, with seals present on 19 of these days. The highest number of seals hauled-out was 231 on February 3 (low tide, 0.01inch precipitation, barometric pressure 30.2Hg, wind 2.4mph), 252 on February 16 (high tide, zero precipitation, barometric pressure 30.6Hg, and wind 3.7mph), and 265 on February 22 (high tide, zero precipitation, barometric pressure 30.2Hg, wind speed of 4.9mph). Environmental averages on days when no seals were present did not vary from these three high-count days (n=7 days, 0.03inch precipitation, barometric pressure 30.3Hg, wind 7.7mph). The TrueLook remote camera was successful in capturing harbor seal haul-out behavior during the month of February and will help provide baseline information on these marine mammals in an important overwintering area as the neighboring wind farm becomes operational.

Faculty Mentor: Jacalyn Toth

Abstract #:24

Isofemale lines of *Drosophila melanogaster*: Phenotypic and genetic variation of natural populations in NJ

Walsh, Andrew; Williams, Dominique; Dougan, Colleen; Berardo, Caitlyn; Haralampoudis, Nicole ; Biology

Drosophila melanogaster, the common fruit fly, has been a staple of the scientific community for many decades. We have begun collecting wild *Drosophila* from a variety of geographic locations around New Jersey and have started to examine phenotypic variation among the lines using both morphometric and physiological measurements and experiments. A single female fly from each collection was allowed to lay eggs and produce progeny. Three females from the original vial were used to produce three replicate populations from each collection. The populations were then inbred using full-sib matings for ten generations prior to collecting phenotypic data, ensuring an inbreeding coefficient of 0.90. Currently, we have over 88 individual Isofemale lines derived from 35 collection sites. During routine reproduction of the lines, pupae are counted at 10d post-mating and adults are counted at 14d post-mating. Counts at 10d post-mating ranged from 0-190, with the mean being $74 \pm$. We have observed in the 14d post-mating adult counts ranging from 29 - 496, with a mean of 151 ± 85 . We also observed large differences in responses to cold temperature, dietary changes and other behaviors which will require quantification. Upon identifying phenotypic differences among the lines, we will make diallel crosses to estimate inheritance patterns and genetic variances.

Faculty Mentor: Guy Barbato

Abstract #:25

Environmental factors impacting settlement of Eastern Oyster (*Crassostrea virginica*) from 2014 to 2021 in the Mullica River

Leason, Matthew ; MARS

The Eastern oyster (*Crassostrea virginica*) is a critical species environmentally and economically in New Jersey as it supports the growth of habitat for many marine organisms as well as the continued growth of the shellfish industry. The species goes through a larval stage and a juvenile stage before reaching maturity. The juvenile or "spat" phase occurs as larvae from the water column settle onto a hard substrate and become fixed. The settlement of spat is affected by biotic and abiotic factors such as temperature and salinity. Spat

settlement and recruitment were calculated from biweekly spat bags (settlement) as well as seasonal bags (recruitment) from 10 sites within the Mullica River from 2014-2021. This data was collected each year from July to September and water quality data was obtained for May to September from the Chestnut Neck monitoring station within the Jacques Cousteau National Estuarine Research Reserve System (JCNERRS). We examined which monthly factors were most influential to yearly settlement and recruitment by creating multiple regression models. Spat settlement was high in 2016 and 2018-2020; it was low in 2014, 2015, and 2021. Recruitment was high from 2014-2016 and 2018-2020, while it was lower in 2017 and 2021. Settlement was negatively affected by May salinity, while positively affected by June through July salinity. Positive trends were also seen with May and July temperatures. Recruitment was found to have no statistical significance with any environmental parameter. This suggests that there may be more factors contributing to spatfall variability beyond water quality.

Faculty Mentor: Christine Thompson

Abstract #:26

Spermatogonial cells and Reproductive Success in *Drosophila melanogaster*
Dougan, Colleen; Walsh, Andrew; Berardo, Caitlin; Haralampoudis, Nicole ;
Biology

Fertility, per se, is a poor description of overall reproductive success. Having observed a range of progeny production among isofemale lines of *Drosophila melanogaster*, we selected 10 populations representing the range of reproductive outcomes. Beginning our investigation among males of the lines, we dissected testes under a dissecting scope and stained with DAPI. Germ cells are easily observed in the testicular tissue and were counted using ImageJ software. Germ cells were counted by three (3) independent students to minimize the observer effect. Correlation analysis between pupal and germ cell counts resulted in a negative correlation of -0.41. Our initial hypothesis was based on the assumption that a greater number of spermatogonia would result in larger numbers of spermatozoa – resulting in higher fertility. This was clearly not the case. Perhaps the males of the low producing lines were slower to mature than the others, or there were other systemic reasons for the inhibition of spermatogenesis.

Faculty Mentor: Guy Barbato

Abstract #:27

Characterization of *Vaccinium macrocarpon* Derived Peptides Associated With Inhibition of Bacterial Adhesion

(Harzold, Danielle), (Richards, Paige), (Rajput, Diviya), (Barbato, Guy) ; Biology

The purpose of this experiment was to analyze the size and charge of cranberry-derived peptides utilizing three different extraction methods. These peptides, found in *Vaccinium macrocarpon* (The American Cranberry) have been associated with antibacterial actions – based on their ability to inhibit adhesion of bacteria to eukaryotic cell membranes. The first protein pool, SAX RET A was retained on an anion exchange column (indicating that is positively charged), the SCX RET B pool was retained on the cation exchange column (indicating a positive charge), and SAX UN was unretained on either column (indicating a neutrally charged pool). SAX RET A, SCX RET B, and SAX UN were diluted 0.5x, 0.25x, and 0.125x and underwent polyacrylamide gel electrophoresis (10% PAGE). SAX RET A dilution 0.25x, SCX RET B (no dilution), and SCX UN dilution 0.5x exhibited the best visibility and were run on a separate gel alongside a protein ladder for comparison. SAX RET A was calculated to have a mass of 37.688 kDa, SCX RET B was calculated to have a mass of 37.386 kDa, and SCX UN was calculated to have a mass of 39.551 kDa. Each sample run on the resultant gel had only one band, indicating the presence of a large protein complex with multiple subunits. These data can be used for further research regarding the antibacterial agents in cranberries by separating the subunits by preparing the same samples with dithiothreitol to reduce the disulfide bonds.

Faculty Mentor: Guy Barbato

Abstract #:28

From book to bench: an introduction to polymer science in the undergraduate laboratory

Acharya, Hari, Cohn, Pamela, Rajaraman, Shanthi ; Chemistry

Polymers are at the foundation of many compelling discoveries in materials science. The characterization of polymers begins with determining molecular weight (MW) to understand the bulk properties of materials. The research seeks to introduce polymer chemistry and MW determination using end-group

analysis in undergraduate laboratories. The protocols include the synthesis of polystyrene at varying times and characterization using nuclear magnetic resonance (NMR) spectroscopy, with the goal of demonstrating how the polymerization mechanism influences the MW. When polymers proceed using chain-growth, there is a sharp increase in MW at shorter reaction times, followed by a plateau as time continues. The opposite occurs in step-growth, in which smaller MW forms at shorter reaction times and increases sharply with time. The breadth of MW is accounted for by the polydispersity index (PDI), a ratio of weight-average (M_w) to number-average (M_n) molecular weights. M_n is the ratio between the mass of a polymer and the number of repeating units, meanwhile, M_w is calculated based on the weight fraction of molecules to the MW of the polymer. For this study, polystyrene was synthesized under free-radical conditions for 15, 30, 45, and 60-minute reaction times. The resulting M_n value was determined using end-group analysis with 1H and ^{13}C NMR. A sharp increase in the M_n occurred at the 15- and 30-minute intervals, followed by a plateau at later reaction times. Findings are consistent with a chain-growth polymerization mechanism. Further analysis will focus on determining the PDI of the polymer using DOSY NMR spectroscopy.

Faculty Mentor: Pamela Cohn & Shanthi Rajaraman

Abstract #:29

Monitoring seagrass trends within Barnegat Bay

Dyson, Danielle ; MARS

In southern New Jersey, Barnegat Bay is an economically and ecologically important seagrass ecosystem comprised of two seagrass species: climax species *Zostera marina* and opportunistic species *Ruppia maritima*. Our objective was to: 1) identify overall trends in seagrass percent cover, and 2) determine the most appropriate sampling frequency to detect trends. Percent cover data were collected at ten sites biennially and at two sites annually from 2015 - 2021. As temperature can be an important determinant of seagrass health, water quality from NJ Buoys adjacent to field sites were assessed. Nonparametric tests with post-hoc were run to assess significant differences at each site across all biennial sampling years then again for yearly sentinel data. Additionally, a time series trend analysis was performed in Minitab for each species. Results indicate there has been an overall decline in percent cover of *Z. marina* and an increase in *R. maritima*. Time series analyses indicate biennial

sampling is sufficient to detect trends in climax species, such as *Z. marina*. However, this misses trends in *R. maritima*, the opportunistic species that has a more stochastic boom-bust population structure. Thus, yearly sampling should be conducted in order to fully understand all seagrass trends within Barnegat Bay.

Faculty Mentor: Elizabeth lacey

Abstract #:30

Characterization of Fertility-related yolk proteins in *Anas platyrhynchos domesticus*

Rajput, Divya & Richards, Paige; Dr. Barbato, Guy; ; Biology

Determining a method to detect high fertility in commercial avian species would be beneficial as it could improve environmental practices while meeting the industrial demands of the poultry industry. This study attempts to characterize fertility with respect to yolk protein composition, specifically vitellogenin (VTG) To investigate this topic, fertilized eggs from two family lines, S and J, were analyzed. Groups of high fertility and low fertility were determined from each line and a four pooled sample was used to determine if a varied fertility and/or varied extraction methods, either chloroform-methanol extraction or a triphasic ammonium sulfate extraction, impacts the breakdown of the VTG protein. An SDS PAGE was run on the samples and the banding patterns were analyzed using IMAGEJ software. The chloroform-methanol extraction led to reduced band visualization in the second averages (mid 2) of the high fertility groups in both families and in the second average of the low fertility group of family J. This separation technique also led to the increased band visualization in the first average (mid 1) of the high fertility group in family J. The triphasic ammonium sulfate extraction led to similar visualization of protein bands across averages, fertility groups and families. Having identified these differences the next step is to further investigate VTG presence to establish a correlation between fertility and protein expression, if present.

Faculty Mentor: Guy Barbato

Abstract #:31

High fat sex-diet interactions in *Drosophila melanogaster*

Luciano Rocco, Walsh Andrew, Barbato, G.F.; Biology

Recent reports in the *Drosophila* literature have suggested that the fly can be used as a model of diet induced obesity. In this study *Drosophila* were fed high fat diets from either coconut or olive oil. Olive oil is high in monounsaturated fat by 74%, while coconut oil is high in saturated fat by 65%. Each was added to the flies standard diet in portions of 20% by weight. The progeny of the exposed flies were mated in vials with normal (i.e., nonfat) media diet. *Drosophila* fed coconut oil died, however the flies fed olive oil survived. The progeny of the olive oil-fed parents had significantly heavier offspring than the controls. Showing a 25.96% difference, and an average increase of weight by 29.83% in the females. In males a 18.18% difference was observed, and an average increase of weight by 20%. Thus exhibiting significant sex-diet interactions. That is, females had a 69.62% greater increase in body weight than males (due to the high fat diet).

Faculty Mentor: G. F. Barbato

Abstract #:32

Snakes outperform turtles and a crocodylian on functional assays of innate immune performance

Tan, Xin Rou "Natalie" ; Biology

Disease is one of the primary threats to reptile populations, leaving them imperiled globally. However, modern immune research on these ectotherms has lagged behind endothermic birds and mammals. This imbalance leaves conservation biologists to act without a full understanding of reptile host-pathogen dynamics. Innate immunity involves cellular and acellular responses, including natural antibodies (NABs) and the serum complement cascade. The acellular innate immune system is responsible for eliciting a nonspecific, fast-acting response against microbial infections. The goal of this experiment was to examine interclade variation in acellular innate immune function amongst three major extant reptile clades. Specifically, we characterized innate immune performance in two Squamates (*Nerodia sipedon* and *Sistrurus miliarius*), two Testudines (*Chrysemys picta* and *Pseudemys rubriventris*), and a Crocodylian (*Alligator mississippiensis*). We hypothesized that immune performance would vary among groups and reflect phylogenetic relationships. We employed immune performance assays which challenged individuals' plasma against a gram-negative bacterium, *E. coli*, and mammalian erythrocytes in vitro. Bactericidal assays provide an assessment of complement mediated-lysis via

the classical and lectin-mediated pathways. Erythrocyte hemolysis assesses complement-mediated cell lysis via the classical and alternative assays, and erythrocyte agglutination reflects the activity of NAb. Complement performance of squamates was significantly better than turtles and crocodylians, which did not perform differently from each other. Our results support the hypothesis that the major reptile clades differ in complement performance and that differences may reflect broad phylogenetic relationships among clades, therefore, highlighting the need for further exploring of interclade variation in immune function among reptiles.

Faculty Mentor: Craig Lind

Abstract #:33

Behavioral Responses to Cold Exposure Among Isofemale Lines of *Drosophila melanogaster*

Berardo, Caitlin, Williams, Dominique, Recalde, Sara, Barbato, G.F. ; Biology

Environmental temperatures can affect an organism's adaptation across generations. *Drosophila melanogaster* is a common fruit fly used in scientific research. As an insect, *Drosophila* are poikilothermic. Lack of metabolic heat production causes the organism to enter a cold-induced coma at 0 degrees Celsius. The *Drosophila melanogaster* were taken from isofemale lines derived from different geographical locations across New Jersey. We measured the time of waking among both male and female flies exposed to 5 min of cold temperatures (in an ice bath). Wake times were recorded in order to compare populations' cold resistance. We recorded the time when the first fly awakened, and then the time at which all flies were awake and active. The time to first awakened fly exhibited significant line differences, whereas time to complete recovery exhibited both line ($P < .0001$) and sex ($P = 0.0056$) effects as indicated by ANOVA. The overall mean time of complete recovery was 216 +/- 4 sec and line by sex interactions were not significant. The quickest line to recover from the ice shock was the LES6 line ($s = 112$ sec, $P = 0.04$). The slowest to recover was the TLO3 line ($s = 272$ sec, $P = 0.004$). Male flies (mean = 227 sec) were slower to recover than females (mean = 205 sec).

Faculty Mentor: Guy Barbato

Abstract #:34

Detection of Decomposition Volatile Organic Compounds from Decaying Tissue

Lago, Jessica ; Biochemistry and Molecular Biology

Determination of a post-mortem interval (PMI), or time since death, is useful for forensic investigations as it develops a time frame for the occurrence of the crime. Current PMI determination methods are based on visual changes which separate corpses into immediate, early or the late post-mortem interval. Due to high variation caused by environmental factors, the estimation of PMI based on visual changes alone remains challenging. However, a novel approach is emerging which considers the release of volatile organic compounds (VOCs) at each stage of decomposition. In this study, a method for the sampling and analysis of the headspace gases above decaying tissue was developed for use in undergraduate research labs. Headspace samples were collected using a vacuum pump with a mass flow controller to measure flow through an in-line activated carbon Sep-pack cartridge (Waters corporation). Cartridges were extracted using methylene chloride, samples were filtered, and analyzed by gas chromatography-mass spectrometry (GC-MS). The tissue sample included a veal heart that consisted of cardiac muscle with congealed blood. Analysis of a sample collected after 8 days of decomposition showed polysulfide compounds including dimethyl trisulfide, dimethyl tetrasulfide and dimethyl pentasulfide. These results are consistent with VOC compounds detected in vertebrae decay studies found in the forensic literature. This methodology is now being used to test whether changes in type and amounts of VOCs are detectable at later points of decomposition.

Faculty Mentor: Dr. Kristen Hallock-Waters and Dr. Margaret Lewis

Abstract #:35

Effect of advanced glycation end products (AGE) on fetal mouse bone growth.

Havrylyuk, Valentina and Mili, Momota ; NAMS

Advanced glycation end products (AGEs) are molecules that are formed as a result of elevated levels of sugar in the bloodstream for long periods of time and have been found to have detrimental effects to health. High levels of AGEs are prevalent in individuals with Type I and Type II diabetes. AGEs are associated with several degenerative diseases, such as heart disease, kidney failure, and has been shown to negatively impact bone healing. In this study,

our aim was to observe a link between elevated AGE levels and the development of bone from cartilage templates in murine embryos. Fetal mice were obtained on day 14 of gestation and incubated with various doses of control and AGE proteins for 48 hours. The procedure required staining the cartilage of the embryos with Alcian blue stain and calcified bone with Alizarin red, and measuring the growth of bone in the forelimb skeleton with ImageJ, a software from NIH. Area of bone growth in the humerus, radius, and ulna was expressed as a percent of the total bone size. A comparison of treatment means (t-test) indicates that the lowest dose of AGE marginally reduced bone area in the humerus ($P < 0.2$), but this difference was not observed at the high dose. A high variability within treatment groups was observed and may be attributed to the small sample size currently available for this study. Increasing the N for each treatment group may reveal a link between AGEs and diminished bone growth in future studies.

Faculty Mentor: David Burleigh

Abstract #:36

Salt Marsh Sediment Accumulation Over a Small Spatial Area

Kelly, Sarah ; Geology

Salt marshes depend on sediment deposition and accumulation in order to survive through times of sea level increase. Sediment deposition in tidal salt marshes is well studied, but research typically focuses on larger areas, which could be less accurate for an entire marsh surface. The goal of this research was to determine the spatial variability of sediment deposition and accumulation in a New Jersey salt marsh over a very small area. Sediment traps were placed in the marsh at increments of 5 and 10 meters ranging over a 2800m² squared area. Traps were visited daily, weekly, and at the end of the month to collect sediment, which was then dried and weighed. Results will discuss the correlations of sediment deposition in relation to time, air pressure, water level, and weather. Discovering how the sediment accumulation varies in the small area is important as it allows us to assess the precision on previously published sediment accumulation data.

Faculty Mentor: Susanne Moskalski

Abstract #:37

Dissolved Inorganic Carbon in New Jersey Coastal Aquatic Ecosystems

Raptakis, Gavin ;Chemistry

This research is being conducted to understand inorganic carbon cycling in coastal NJ aquatic ecosystems. Measurements of high accuracy spectrophotometric pH, salinity, percent dissolved oxygen(%DO), and temperature were collected every thirty minutes during two to four week deployments at two locations on New Jersey's coast. Chestnut Neck and Beach Haven throughout spring and summer 2021 and spring 2022. These data were used to examine short-term and seasonal cycles in these parameters. Between deployments the instruments are cleaned, and the pH instrument is recalibrated. Historical lower accuracy pH data from January 2017 to January 2021, was used to supplement the high accuracy pH measurements. The historical data shows that the Chestnut Neck site regularly has a lower pH, %DO, and salinity than the other two sites. This site is further inland, and the samples are coming from the Mullica River, rather than closer to the ocean like the other two sites. The Beach Haven site has a higher level of salinity than Mantoloking, but the other variables are similar between these two sites. At all three sites, %DO has a large day-to-day variability in the summer, which tends to decrease in the winter. The short term variability in salinity and pH at Chestnut Neck is larger compared to Beach Haven and Mantoloking. All three sites have similar seasonal variability in temperature. These data will be used to evaluate what is driving the inorganic carbon cycle at these sites, and to predict future changes in the face of continued climate change.

Faculty Mentor: Dr. Sarah Gray

Abstract #:38

The synthesis and photophysics of 2,4-diaryl pyrroles as tetraarylazadipyrrin precursors

Furry, Matthew; Pemberton, Barry C.; Chemistry

The development and possible applications of near-infrared (NIR) emitting chromophores have garnered interest in the last decade, with a wide variety of applications from bioimaging to solar cells. Our goal is to expand the functionality of tetraarylazadipyrrins (a NIR emitting chromophore) and to understand the role large aromatic substituents play in the multi-emissive properties within these chromophores. We have synthesized 1,7-pyrene 3,5-

tolyl bis-azadipyrrin along with its pyrrole counterpart, 2-pyrene 4-tolyl pyrrole, and 2,4 di-tolyl pyrrole; the 1,7-pyrene 3,5-tolyl bis-azadipyrrin and 2-pyrene 4-tolyl pyrrole systems demonstrate solvent dependent multi-responsive emission properties accessed via selective excitation wavelengths. Herein this presentation we will discuss the synthesis of these molecules, which proceeds through well-established chemistry, including aldol condensations, Michael additions, and heterocyclic ring closures, along with the steady-state and time-resolved photophysical properties of some of these chromophores.

Faculty Mentor: Dr Barry Pemberton

Abstract #:39

Stock Origins, Micro-Habitat Preference, and Populational Health of *Morone saxatilis*

Handelman, Jared; Aguiar, Adam; Biology

Striped bass are the most sought-after inshore game fish on the east coast, generating tourism, business, and industry for New Jersey. However, there is ambiguity around the micro-habitat preference, migrational behavior, and stock origins of an important recreational, commercial, and ecological marine resource. Though the general migration patterns of spawning size striped bass are somewhat understood, there are nuances across fish size and age. The behavior of smaller bass is very different from the larger spawning size bass, and the former's behavior will vary across different areas. Striped bass have high fidelity to the spawning grounds in which they were hatched. The Jersey shore is not a major spawning ground, but rather a highway of mixed-migratory groups of stripers during spring and fall. The derived proportions from the major (and minor local) spawning grounds of this migratory stock are unclear. With the use of tagging instrumentation, catch logs, and scale and tissue sampling followed by DNA sequence comparisons, clarity maybe gained on 1) changes in migration and location preference and 2) the extent to which each spawning ground contributes to our local mixed-migratory stocks, and possibly illuminate differences between that of the fall and spring groups.

Faculty Mentor: Dr Adam Aguiar