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Evaluating the short-term trajectory of small-scale living shorelines within a socioecological context

Ella DiPetto

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Advisor: ***Dr. Eric L. Walters***

Living shorelines are seeing a surge along developed, privately owned properties. These shorelines differ markedly from those in less-developed regions, harboring lower biodiversity, increased habitat fragmentation, and altered hydrology. Additionally, the importance of individual resident values exacerbates these socioecological considerations. This ongoing study follows five living shorelines pre- and post-restoration to investigate the trajectory in protective service indicators over 2 years. Preliminary results reveal significant variation in short-term development of elevation, vegetation, and oyster recruitment. This study will improve our understanding of living shoreline effectiveness and provide guidance for practitioners and landowners in navigating the complexities of these unique shorelines.

Biography: Ella, also known by the unofficial title of "Marsh Mistress", is a 3rd year PhD candidate in Dr. Eric Walters' Avian Ecology Lab. When not knee-deep in research (and mud), she enjoys obsessively worrying about said research anyways. Her work explores social and ecological considerations of nature-based coastal protection along developed shorelines.

Fun fact: In her spare time, Ella organizes fiddler crab fashion shows across various coastal wetlands. They strut their stuff down the marsh showcasing the latest crustacean fads, while fellow crabs give them loud rounds of a-Claws.

Wetlands and protected areas in Hampton Roads

***Zlatka Rebolledo Sanchez*[1], *Swati Mishra*[2], *Rohit Chaudhary*[3], *Prashant Tomar*[3]**

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Advisor: ***Dr. Erik Yando***

Wetlands are among the most productive ecosystems on the Earth, providing numerous ecosystem services. Even so, they are among our most endangered ecosystems. This project is established to determine the coverage of wetlands in the surrounding area of Hampton Roads, Virginia. A geospatial data analysis was conducted using ArcGIS Pro and PowerBI to study conservation areas and wetlands. The primary protocols to develop this project are designed around available GIS data. The principal data layers used in the targeting models are – Wetlands, Conservation Lands, Priority Conservation Areas, and Boundaries of Hampton Roads. The project analyzes the protection of wetlands in Hampton Roads. This study will help to understand the dynamics in wetland ecosystems and may help establish key steps to achieve innovative management and conservation techniques for coastal ecosystems that are being impacted. The project was developed during the Hampton Roads Datathon 2022 and won third place in the competition. Our results show that less than 35% of the total area of wetlands in Hampton Roads are part of protected land, and only 6% of the total protected/managed area contains wetlands. When we take a closer look at each city, we find that Virginia Beach has the highest number of Protected Areas with Wetlands. In contrast, Norfolk, Portsmouth, Williamsburg, and New Kent have fewer Protected Areas with Wetlands. We recommend that areas that are highly threatened and have a high priority for conservation status need more attention, and an increase in protected lands and restoration efforts, especially in low-income areas. In conclusion, interdisciplinary teams and efforts must be made to manage and restore these vital ecosystems effectively. Policymakers, scientists, non-profits, and community members in each section must be involved to achieve the greatest conservation returns.

Biography: Biologist from Simón Bolívar University, Caracas, Venezuela. Member of the Coastal Plant and Ecotone Ecology Lab, studying marine and coastal ecosystems with a spatial ecology perspective. Virginia Sea Grant 2023–2025 Graduate Research Fellow. Rising TIDES Scholar of the Coastal and Estuarine Research Federation, and winner of the ODU SEES Mentoring Leader Award 2023.

Fun fact: Zlatka studied musical theater for 2 years.

Longleaf restoration strategies and their effects on avian and plant communities

Alex Wright

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Advisor: ***Dr. Eric L. Walters***

Longleaf pine ecosystems, once expansive across the southeastern United States, now face significant fragmentation and degradation, with only a fraction of their original extent remaining. Many land managers are faced with a dilemma: determining what method should be used to restore longleaf across its former range when the space is occupied by loblolly and slash pine plantations. Is it best to just start from scratch and clearcut the non-native pines, then plant longleaf seedlings? Or perhaps there is a way to convert the site to longleaf but preserve the integrity of the biological communities that use these managed forests. While working with Nokuse Plantation, the largest privately owned nature preserve in the Southeastern United States, I aim to answer how to restore longleaf pine forests that is most beneficial to their growth and survival, but also which strategies help maintain the diverse understory and avian communities that exist there.

Biography: Graduating from UNC Charlotte in 2022, Alex came to ODU to initially study how urbanization effected avian communities. Although she is still interested in the topic, she has shifted focus to restoration and conservation ecology, with special interest in longleaf pine forests.

Fun fact: Alex used to work as a veterinary assistant for 4 years.

Spatial and temporal genetic variation between two populations of Toothed Ponyfish (*Gazza minuta*) from the Philippines

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Advisor: ***Dr. Kent Carpenter***

Understanding how aquatic species adapt to anthropogenic influences has become increasingly important as the world's oceans see unprecedented changes. Areas of high species richness, such as the Philippines, are of particular interest. Since the late 19th century, the Philippines has undergone drastic changes brought on by wars, industrialization, and increasing populations (Nadeau, 2020). The USS Albatross conducted a fisheries survey of the Philippines from 1907 to 1910 and collected thousands of fishes from across the country which now reside at the Smithsonian Museum (Smith 1999). One such fish, *Gazza minuta*, is commonly found across much of the Indo-Pacific and is a food source for residents of the Philippines. Contemporary duplicates of collections from Jamilo Cove and Basud River provide the opportunity for temporal and spatial population genetics comparisons. The goal of this research is to compare the population genetics for G. minuta collected in Jamilo Cove in 1908 to a contemporary counterpart collected in 2018, and populations collected in Basud River in 1909 to a contemporary counterpart collected in 2019. A spatial comparison will then be made between the Albatross collections and between the contemporary collections. The results of this study will give valuable insight into the evolution and marine biodiversity of Philippines fishes. The USS Albatross specimens were initially fixed in ethanol-based solutions, which preserved the DNA integrity. However, the age of the specimens leads to natural degradation over time (Lindahl, 1993), and the high water content of ethanol can lead to a degradation of the DNA by hydrolysis (Overballe-Petersen et al., 2012). Due to these factors, we expect to see low quantities of viable DNA. The DNA sequencing method used for this research is restriction-site associated DNA sequencing or RADseq. RADseq is a sensitive method of DNA sequencing that clips restriction sites from a genome and sequences the DNA attached at both ends of the site to find single nucleotide polymorphisms or SNPs. The potential issues with DNA quality are not insurmountable, and the initial processing of *G. minuta* showed promising levels of quality DNA.

Biography: I am an avid scuba diver and love all things nature.

Fun fact: I have spent more than 2 and a half years at sea.

Evaluation of T cell development as a cause for Tc1 vaccine failure during chronic schistosomiasis

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Advisor: ***Dr. Lisa M. Shollenberger***

Schistosomiasis is a neglected tropical disease (NTD) caused by blood flukes of the genus *Schistosoma* with greater than 200 million people infected globally. Chronic infection with *S. mansoni* has been shown to cause host anti-inflammatory, Th2 immune biasing and immune suppression after the initial pro-inflammatory state during acute infection. This anti-inflammatory, immune-suppressed state is a poor environment in which to generate CD8+ T cell vaccine responses. Indeed, previous studies have shown that DNA vectors are unable to generate Tc1 vaccine responses in mice with chronic schistosomiasis when *Listeria*, a strong inducer of CD8+ immunity, can generate robust vaccine responses, begging the question: why the disparate response? Here, we plan to investigate T cell development during chronic schistosomiasis as a possible reason for the impaired CD8+ T cell responses seen after DNA vaccination. We hypothesize that chronic schistosome infection and/or vaccine vector modifies T cell development in the thymus. We will test this hypothesis through successful completion of our specific aims: (1) evaluate thymus size (weight and total T cell numbers) relative to infection status and vaccine vector, and (2) determine (by flow cytometry and RT-PCR) if ratios of the double negative (DN), double positive (DP), and single positive (SP) T cell compartments of the thymus are skewed based on infection status or vaccine vector. Results of this study will provide the next step in determining the mechanism of Tc1 vaccine failure during chronic schistosomiasis toward improved global vaccine efficacy.

Biography: Niaylah Means is a Master's student working towards a Master of Science in Biological Sciences with a Concentration in Microbiology and Immunology. Under the supervision of her mentor (PI), Dr. Lisa M. Shollenberger, she is committed to help raise awareness about neglected tropical diseases and studying vaccine delivery methods that could benefit immunocompromised individuals.

Fun fact: Niaylah loves to sing.

Examining 100 years of human impacts on the genetic diversity of the common pony fish, *Leiognathus equula*

John Schaefer

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Advisor: ***Dr. Kent Carpenter***

Severe human impacts have led to a decrease of biodiversity in the marine environment, but there is a knowledge gap of the impact at a genomic level. This project examines the changes of genetic diversity of the common pony fish, *Leiognathus equula*, over the last century. The species is found in the Philippines, which is the epicenter of marine biodiversity. Knowledge of genetic change in tropical ecosystems, such as the Philippines, is even less despite intense human impacts here. To make this comparison, the genetics of *L. equula* will be examined from collections made by the USS Albatross in the Philippines from 1907–1909 and from contemporary collections. A shotgun sequencing library pipeline is followed to sequence the DNA and examine the genetics. To measure the changes of genetic diversity, heterozygosity and allelic richness will be compared between the Albatross and contemporary samples. The result of this study attempts to confirm preliminary research which found support for a decrease in genetic diversity consistent with a reduction in population size. This study presents one of the first assessments of the effects of human impacts on coral reef species populations. Knowledge generated will provide an understanding of genome-level evolution of marine fishes. Findings will be valuable for resource management and contribute to local conservation efforts in the Philippines. This will support fisheries management and ensure food security through quantifying human impacts on fish populations utilized for food, for over 100 years.

Biography: John originally grew up in Woodbridge, Virginia before moving to Norfolk in 2020. After finishing his bachelor’s at ODU in biology with a concentration in marine biology in 2022, he became a master’s student there in 2023. His research interests are in marine conservation.

Fun fact: John has been playing soccer and following his favorite team, FC Bayern Munich, for most of his life.

Understanding tick-borne disease dynamics: insights from small mammal reservoirs in Richmond, Virginia

Nathaniel Ostrum

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Advisor: ***Dr. Wayne Hynes***

Tick-borne diseases pose a significant public health challenge as they continue to proliferate. The escalating prevalence of these diseases, characterized by symptoms ranging from skin rashes to flu-like symptoms, underscores the urgent need for research and intervention strategies. Historically concentrated in the northeastern United States regions, the incidence of Lyme disease has encroached into southern territories over the past two decades. Lyme disease is the most common tick-borne illness in North America which has been associated with the geographic expansion of the human-biting hard tick species, *Ixodes scapularis*. *Ixodes* spp. known to feed on a diverse array of mammalian hosts, interact with host species, influencing the dynamics of tick-borne pathogens. Recent studies have shed light on the pivotal role of small rodents as competent vectors for *Borrelia burgdorferi*, the bacterium responsible for Lyme disease in humans. Among small mammals, mouse species, chipmunks, squirrels, and shrews have been identified as reservoirs for tick-borne pathogens, with the white-footed mouse, *Peromyscus leucopus*, serving as the primary host of *B. burgdorferi*. Small mammal live trapping was conducted using CDC trapping protocols to understand the ecology of ticks and their hosts. Ear biopsies of small mammals' samples were obtained through trapping methodology undergo molecular analysis using quantitative polymerase chain reaction (qPCR) to assess the presence of *Borrelia burgdorferi* and *Rickettsia* spp. The project focuses on four different species – eastern meadow vole (*Microtus pennsylvanicus*), white-footed mouse (*Peromyscus leucopus*), hispid cotton rat (*Sigmodon hispidus*), and eastern chipmunk (*Tamias striatus*) – to add information to their role as potential reservoir hosts for tick-borne pathogens. This research aims to bridge existing knowledge gaps in the Richmond, Virginia region regarding the dynamics of tick-borne diseases. By continuing to uncover the relationship between small mammals and tick-borne pathogen transmission, this project provides additional evidence supporting the crucial role of small rodents in pathogen dynamics. Ultimately, a deeper understanding of tick-borne disease dynamics will inform the development of effective prevention and control measures, mitigating the impact of these diseases on human and animal health.

Biography: Nathaniel Ostrum is a biology master's student with a concentration in One Health. He has worked as an EMT for the past 4 years, likes to lift, and train martial arts. He would like to become a data analyst after graduation.

Fun fact: Nathaniel has three cats: Lennon, Hendrix, and Elliott.

Estrogen, progesterone, and hCG: gatekeepers or enablers? Hormonal impacts *on Listeria monocytogenes* trojan horse translocation across the placental barrier

Ayesha Atique

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Advisor: ***Dr. Rishi Drolia***

Listeria monocytogenes (Lm) is a deadly opportunistic food-borne pathogen that causes listeriosis with a 94% hospitalization rate of a ~30% case fatality rate. Lm breaches the protective placental barrier and harms the unborn fetus, which can potentially cause miscarriage or stillbirth. Pregnant women are 20 times more at risk of listeriosis as compared to other individuals, but the reason remains unclear. Previous work in our laboratory created a physiologically relevant placental barrier co-culture system. This model comprises the placental BeWo cells that occupy the apical side and the primary Human Placental Vascular Endothelial Cells (HPVEC) cells that occupy the basolateral side. Barrier integrity was validated using immunostaining of tight junctions (occludin and claudin-1) and a fluorescein isothiocyanate (FITC)-dextran permeability assay. Lm-infected human monocytic THP-1 cells (Trojan horses) were exposed to the co-culture model in a Transwell set-up for two hours. Upon exposure to the Lm-infected THP-1s, the placental model showed a five-fold increase in barrier permeability. Relative to uninfected or nonpathogenic L. innocua-infected THP-1 monocytes, a significant increase (~200%) in the translocation of Lm-infected THP-1s across the placental barrier was observed. Immunostaining of co-culture exposed to Lm-infected THP-1 monocytes revealed attachment of the monocytes to the barrier and severe disruption of occludin and claudin-1 tight junctions.Hormones are crucial in regulating placental structure and function, including permeability. Although the hormones influence placental permeability, how elevated hormones impact Lm infection is not yet understood. We hypothesize that key hormones in pregnancy (progesterone, estrogen, and Human Chorionic Gonadotropin (hCG)) impact the translocation of Lm-infected monocytes across the placental barrier. We will test this hypothesis using the co-culture model developed in our laboratory. Briefly, the model will be treated with physiologically relevant concentrations individually with progesterone, estrogen, and hCG and in combination and infected with Lm "Trojan horses." Treated samples will be analyzed for translocation of infected monocytes, placental-barrier permeability (FITC-dextran permeability and TEER), and tight junction architecture via immunofluorescence and confocal microscopy. The outcome of the proposed study will define the hormonal changes that impact susceptibility to Lm infection, providing the fundamental knowledge required to develop better preventive and therapeutic strategies.

Biography: Ayesha Atique is an international dentist currently in their third semester pursuing a master's degree at ODU. Ayesha's research delves into the intricate process of *Listeria monocytogenes* penetrating the placental barrier, with a specific focus on understanding hormonal influences. Upon completing their master's, Ayesha is contemplating a path toward dental school or pursuing a Ph.D.

Fun fact: Ayesha loves photography and makeup.

Breeder dispersal in the cooperative breeding Acorn Woodpeckers (*Melanerpes formicivorus*)

***Chi Wei*[1], *Eric L. Walters*[2]**

(*she/they*)

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Advisor: ***Dr. Eric L. Walters***

Cooperative behavior is widespread among animal taxa and forms a fundamental principle of animal sociality. Social groups, particularly those composed of kin, engage in cooperative activities, presumably to enhance fitness, either directly or indirectly. In the cooperative breeding of Acorn Woodpeckers (*Melanerpes formicivorus*), social groups consist of polygynandrous reproductive (breeders) and non-reproductive individuals (helpers). Helpers, often the offspring of breeders within the same social group, delay dispersal and aid their groups by defending territories, detecting predators, and feeding young in the nest to increase fitness benefits. The longevity of Acorn Woodpeckers (up to 19 years) makes them ideal organisms to investigate how social status and reproductive opportunities change over time. With a long-standing study population of Acorn Woodpeckers at the Hastings Natural History Reservation in central coastal California, this study aims to determine why breeders disperse. I hypothesized that both among-group and within-group relatedness will facilitate breeder dispersal, with females being more associated with among-group relatedness, and males being more related to within-group relatedness. Breeder dispersal, recorded as binary outcomes, occurred when a breeder dispersed to another group. Relatedness measures were calculated using the median of pairwise relatedness coefficients between the focal breeder and related adults in other groups or within its group, divided by the number of related individuals. A total of 178 breeder dispersal events from 1980 to 2022 were identified. Using generalized linear mixed models with individuals nested by coalition dispersal as the random effect, it was found that breeder dispersal exhibited a significantly positive relationship with within-group relatedness, suggesting a stronger drive of within-group competition. Moreover, the effect of within-group relatedness on breeder dispersal remained consistent in male breeders, whereas female breeders showed no significant relationships with relatedness measures. Since among-group relatedness showed no significant relationship with breeder dispersal, further examination of potential drivers such as reproductive success and food source availability may offer valuable insights.

Biography: Chi Wei is a second year PhD student from the Walters Avian Ecology Lab. Chi is interested in behavioral and community ecology. Her study focuses on the evolving dynamics of the cooperatively breeding Acorn Woodpeckers in central coastal California.

Fun fact: Chi has a larger head, so she used to believe as a child that a large shirt meant she could fit her head through it.

Distribution of *Hermundura americana* in the Chesapeake Bay

Maizer Sparkman

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Advisor: ***Dr. Daniel M. Dauer***

Understanding benthic estuarine ecosystems in the Chesapeake Bay is important for the overall health of the area. In 2009 a non-indigenous polychaete of the pilargid family named *Hermundura americana* migrated to the mesohaline areas of the Chesapeake Bay's tributaries and has greatly increased in population since, starting in the Southern Branch of the Elizabeth River, spreading to the James River shortly thereafter, and eventually spreading to the Rappahannock River. Salinity is believed to be a major barrier that influences the abundance per meter squared of *H. americana*, but this is an area for future studies. Studies underway include a stable isotopic analysis to determine the trophic niche of *H. americana*. Monitoring this species in the future will be important for mitigating any deleterious effects it may end up having on the Chesapeake Bay environment.

Biography: Maizer obtained Bachelor of Science majoring in biology with a marine emphasis with a minor in energy sciences from Western Washington University. Currently pursuing a master's in biology from ODU with a focus on benthic invertebrate ecology and taxonomy.

Fun fact: Maizer is a musician who can play the flute and bassoon.

Proposed investigation of cell fate redirection via 3D-bioprinted mammary organoid models

Annette Berkin

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Advisor: ***Dr. Wayne Hynes***

The cellular microenvironment found in the mammary gland has been shown in past studies to redirect cell fate, integrating stem cells of various lineages into functional mammary glands, and suppressing the formation of tumors. Meanwhile, three-dimensional (3D) bioprinting has emerged as a technique to create organoids from cultured cells, using a 3D printer to print cells and form tissue structures that are more biomimetic than two-dimensional cultures. Chimeric organoids, which have different cell types co-printed together, can serve as useful models to interrogate how different cell types may interact, and how stem cells may differentiate in accordance with their microenvironment of surrounding cell types. Bioprinted organoids can also be printed into various substrates, such as collagen or tissue-derived extracellular matrix, which are then part of the microenvironment in which the printed cells grow. The use of specific substrates allows an additional avenue for researchers to manipulate the microenvironment in which bioprinted organoids grow, and to observe the resultant effect upon cell fate. The research proposed here aims to use the 3D bioprinter to investigate whether bioprinted neural stem cells are redirected to assume a mammary cell fate when printed into organoid models of the mammary gland. Organoid creation techniques will include chimeric bioprinting to co-print neural stem cells with mammary epithelial cells, as well as the use of extracellular matrix derived from mammary tissue as a growth substrate for bioprinted cells. These two techniques will be used in conjunction, to see if the neural stem cells are redirected to a mammary cell fate by the combination of two factors, (A) neighboring cells of mammary epithelial origin, and (B) mammary-derived extracellular matrix, can redirect the neural stem cell fate. These two factors will also be investigated individually, to elucidate whether neighboring mammary cells may be sufficient to redirect the cell fate of neural stem cells in a collagen substrate, and whether mammary-derived extracellular matrix may be sufficient for cell fate redirection even in the absence of mammary epithelial cells.

Biography: Annette Berkin is a student pursuing a Master’s degree in Biology at Old Dominion University. After graduate school, she plans to work in the field of Science Communication.

Fun fact: Annette likes to do ballroom dance!

FilterABM: an agent-based model of trait-based environmental filtering

Oleksii Dubovyk

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Environmental filtering framework suggests that composition of ecological communities is a product of (1) dispersal abilities and stochastic processes allowing taxa to disperse into a local ecosystem, (2) suitability of the local abiotic and biotic factors, and (3) interspecific interactions with the taxa that already are present in the local community. To illustrate the concept, I developed an agent-based model that simulate such processes. First, a metacommunity is simulated wherein the distribution of trait within taxa follows a normal distribution and taxa abundance is mapped through a trait abundance distribution that is assumed to follow Cauchy distribution. Individuals disperse from metacommunity into local habitat that consists of a sequence of cells with different levels of an environmental factor and independent resource. Individuals are allowed to disperse into neighboring cells. Each individual consumes local resources to reproduce into two individuals and is eliminated when its age exceeds a set threshold. The amount of resource consumed depends on (1) amount of resource available, (2) difference between individual trait value and environmental factor, and (3) difference between individual trait value compared to other individuals within the cell. Simulations suggest that taxonomic and functional diversity in local communities are highly dependent on dispersal from the metacommunity and between cells, as well as spatial configuration of the environment.

Biography: Finished undergraduate degree at Ivan Franko National University of Lviv (Ukraine), where studied conservation value of urban parks and suburban forests for avian diversity. As a Fulbright scholar, joined the Walters Lab at ODU where conducted work on spatio-temporal patterns of functionally rare bird species across North America relative to level of urbanization. This led to a doctoral project tackling trait-based environmental filtering of avian communities relative to a gradient of urbanization.

Funny fact: Oleksii makes loud funny sounds when somebody tickles him, but highly discourages everybody to test it.

People's Choice Award

Please submit your favorite talk using the URL or the QR code below

https://forms.gle/12FgfcRUZmUYgyaAA

Acknowledgements

Organization Committee

Oleksii Dubovyk, President, Biology Graduate Student Organization
Chi Wei, Treasurer, Biology Graduate Student Organization
Zlatka Rebolledo Sanchez, Vice President, Biology Graduate Student Organization
Katelyn Overstreet, Wetland Officer, Biology Graduate Student Organization
MyKenna Zettle, Secretary, Biology Graduate Student Organization

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Dr. Isaura Simoes, Associate Professor, Department of Biological Sciences
Dr. Christina Steel, Senior Lecturer, Department of Biological Sciences
Dr. Eric L. Walters, Professor, Department of Biological Sciences
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