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CHARLES E. SCHMIDT COLLEGE OF SCIENCE

# SCIENCE FEST

**Fri., April 12, 2024**

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## Dr. Eric Shaw Excellence in Science Undergraduate Research Poster Abstract Book

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## Size and Sex Distribution of Blacktip Sharks in Southeast Florida

Savanna Arvin, Stephen Kajiura  
Department of Biological Sciences  
Florida Atlantic University, Boca Raton, FL

The Blacktip Shark (*Carcharhinus limbatus*) is a common species of large coastal shark found throughout the United States eastern seaboard from Florida to New York. This species has a well-established migratory pattern and overwinters in Southeast Florida from about January to March. During these months the sharks form large aggregations in the nearshore environment where they are targeted in a shore-based recreational fishery. Since 2014, researchers at Florida Atlantic University have undertaken targeted fishing for blacktips within 200m of the beach in Palm Beach County, Florida. Significantly greater fishing effort was expended during the winter months (January to March) when sharks are in greatest abundance, with only sporadic fishing at other times of the year. From these efforts, a total of 201 blacktip sharks were caught, of which 190 (94.5%) were male and 11 (5.5%) were female. Females ranged from 146 cm to 186 cm, with a mean of 167.6cm. Males ranged from 145 cm to 188 cm TL, with a mean of 171.0 cm. Clasper length and calcification indicated that all males caught were sexually mature. Sharks were captured from 26°24'09.6" latitude to 26°85'41.8" latitude with greater fishing effort north of the Palm Beach Inlet. These data help to inform us about the size and sex distribution of the blacktip shark aggregations at the southern terminus of their migration. It appears that the males migrate farther south and dominate the sex distribution with females remaining at higher latitudes and only rarely occurring in the large aggregations. This information is important for the recreational fishery that targets the aggregated sharks and may be selectively catching adult males. This may contribute to a healthy shark population which supports both a recreational and commercial fishery for this species.

## Analysis of Storm-Induced Subaerial Beach Morphology and Sedimentology after Two Consecutive Storms in Palm Beach County, Florida

Alondra Calderon, Leanne Hauptman, Tiffany Roberts Briggs  
Department of Geosciences  
Florida Atlantic University, Boca Raton, FL

Sandy beaches are among the most important coastal environments for supporting human population, providing habitat for various species, protecting coastal communities from storm impacts, reduction of coastal flooding, and economics. Beach erosion and accretion is a natural phenomenon, however, loss to the subaerial beach is becoming a widespread problem that has been affecting coastal communities due to factors of rising sea levels and frequency of major storms. The Atlantic basin is known for its active hurricane season and frequent or consecutive

storms can result in variable impacts to the subaerial beach. With the uncertainty in global climate, the frequency and intensity of storms could strengthen. Continued research is needed to understand the morphodynamics and sedimentological characteristics of sandy beach response after continuous storm impacts.

This study aimed to evaluate storm-induced subaerial sedimentology and morphology change after two consecutive storms during the 2022 hurricane season in Palm Beach County, Florida. Four sites were evaluated including three managed—beach and/or dune nourishment—beaches and one non-managed beach, which is being used as a control. Time-series beach profiles were collected using Real Time Kinematic Global Positioning System during pre-, post-, and recovery storm surveying events. Sediment samples were collected during each event at three cross-shore locations representing the back beach, mid beach, and mean high water line for each study site. Granulometric statistical analysis was completed using the moment method to establish the mean and standard deviation for the bulk sample. Using the Wentworth Scale, sediment was described qualitatively and quantitatively for each sample. Evaluation of beach response was completed for each study site after the impacts of two consecutive storms to compare varying responses in relation to morphology, sedimentology, and water levels. Results from this study have the potential to help future management efforts in understanding how sandy beaches respond to frequent storm impacts.

## **Reconstructing Environmental Change and Organic Matter Trends from a Boreal Peatland in Maine**

Kayla Connolly, Erik N. Johanson, Xavier Comas, Danielle Nering, Sabina Gyawali, Sanjeev Luintel, and Graham Morrison-Plumley  
Department of Geosciences  
Florida Atlantic University, Boca Raton, FL

This study presents the initial results of Loss on Ignition (LOI) analyses of a peat core collected in Summer 2023 from a boreal peat bog in Maine, USA. The recovered peat core is 7.5 meters in length and likely captures an environmental record of the entire Holocene following glacial retreat, but the core is currently undated. Our first step to reconstruct how climate and environmental conditions have changed at the study site was to reconstruct a high resolution (4 cm sample interval) record of Organic Matter (OM) and Inorganic Matter across depth. We expected high OM values across the record but decreases in the values likely represent drier climate periods. The project plans to continue with the addition of further environmental proxy analyses such as peat humification, charcoal and pollen analyses, magnetic susceptibility, and the development of an age-depth model to accurately date the timing of these changes. Connecting environmental proxy records to existing geophysical surveys of the study site can help identify how resilient the peatlands are to climate stress over time.

## Are Tomato Microbiomes Involved in the Resistance of Some Varieties to the Deadly Early Blight Disease?

Shan Damas, Michael Botey, Nwadiuto Esiobu

Department of Biological Sciences

FAU Microbiome Innovation Center

Florida Atlantic University, Boca Raton, FL

Tomatoes are vegetable fruits feasted on globally because they are delicious, rich in folate, vitamin C, and potassium which brightens the skin and supports robust immune response against inflammation. Its consumption and demand have increased and so has the pressure for improved average annual production rate. Unfortunately, tomatoes are very susceptible to many microbial blight diseases which threatens output from the USA, the third in total tomatoes harvested after China and India globally. *Alternaria sonali*, a fungus which has been devastating tomato crops in Florida is a major cause of early tomato blight disease. It is a disease that grows rapidly in many types of weather under the foliage of tomatoes and causes severe damage and harvest loss. Although resistant natural and hybrid varieties exist for this pathogen, there are other blights for which there are no other solutions than the spraying of dangerous pesticides and fungicides. Some farmers believe that completely removing the infected plant is a possible way to reduce the spread and all these, except careful rotations and agricultural practices have limited positive outcomes. The prospect of using well screened bio-control plant microbiomes is highly promising. But we do not know which organism(s) to use and their signaling requirements.

And although a lot is known about how plant immunity to disease works, there is little information on the mechanisms and role of microbes in plant response to infectious diseases. The role of human gut bacteria in determining the immune status of host was only recently discovered. So, as a critical first step, this study employed two varieties of tomatoes, one resistant to the early blight (Bush Grown Tomatoes - *Solanum centrale*), and another that is very susceptible (Everglades varieties - *Solanum pimpinellifolium*) to identify the contrasting and unique ribotypes (plant microbiomes) associated with healthy resistant tomatoes varieties. Also, we would cultivate the microbial compositions of the various niches in the tomatoes plant to isolate potential bio-control agents. The 16S rRNA sequence analysis will reveal microbial taxonomic profiles from which functional diversity and their potential role in conferring resistance to tomato plant during blight infections can be deduced. Our data will help create microbiome-based solutions to improve the resistance of Florida native tomatoes (Everglade).

# MUC-type O-glycosylation Affects Proteolytic Stability of APP Glycopeptides and the Binding Specificity to GalNAc-Specific Lectins

Gustavo Mundim<sup>1</sup>, Nancy Vela<sup>1</sup>, Ramya Ayyalasomayajula<sup>1</sup>, Ivet Boneva<sup>1</sup>, Dimitriy Minond<sup>2</sup>, Mare Cudic<sup>1</sup>

<sup>1</sup> Department of Chemistry and Biochemistry, Charles E. Schmidt College of Science, Florida Atlantic University, Boca Raton, FL, USA

<sup>2</sup> College of Pharmacy and Rumbaugh-Goodwin Institute for Cancer Research, Nova Southeastern University, Fort Lauderdale, FL, USA

Alzheimer's disease (AD) is one of the most common neurodegenerative disorders linked to aging. New evidence continues to emerge supporting the idea that deficiencies in amyloid- $\beta$  precursor protein (APP) trafficking and clearance of amyloid- $\beta$  (A $\beta$ ) peptides are the initiating events of AD pathogenic processes. Efforts to understand the role of proteolytic cleavage of the APP by  $\alpha$ -,  $\beta$ -, and  $\gamma$ -secretases into the toxic amyloidogenic pathway have sparked interest in the role of MUC-type O-glycosylation in the production and clearance of A $\beta$  peptides. Recently, we have provided important insight into glycosylation-driven changes in the intrinsic properties (secondary structure, secretase susceptibility, and kinetics of A $\beta$ <sub>40</sub> aggregation) of APP-derived glycopeptide models. Furthermore, we are interested in the potential role of glycosylation in neuroinflammation. The neuroinflammatory hypothesis provides a new and exciting lead in uncovering the underlying mechanisms of AD pathogenesis. A unique type of tyrosine O-glycosylation, found within short peptide fragments from the cerebrospinal fluid of AD patients, was shown to act as a ligand for the human macrophage galactose-type lectin hMGL, prompting interest in understanding the mechanism of this interaction. To gain a better insight into the role of glycosylation in the molecular mechanisms underlying AD, we synthesized APP glycopeptide models with a sequence that includes A $\beta$ -(1-9) at the C-terminal side, bearing the O-GalNAc moiety on Tyr681 and either IKTEEISEVKM or IKTEEISEVNL (NL=Swedish mutation) at the N-terminus to incorporate  $\beta$ - (BACE1) and  $\alpha$ -secretase (ADAM10) cleavage sites located near and within the A $\beta$ <sub>40</sub> domain, bearing the O-glycosylation site at Ser667 and/or at Thr663. Circular dichroism analysis was conducted in three relevant solvent systems to evaluate the peptide environment and O-glycosylation-induced conformational changes. Activity levels of  $\alpha$ - and  $\beta$ -secretase were measured using high-pressure liquid chromatography and characterized by mass spectroscopy. To determine the effect of different glycosylation sites on the binding affinity of GAlNAc-specific lectins to APP peptides, a preliminary enzyme-linked lectin assay screen against plant lectins VVA and SBA was conducted. Results show that the position and abundance of glycosylation sites play an important role in the conformation of the peptides, as well as their susceptibility to lectin binding and proteolytic cleavage.

## **Inlet-Adjacent Beach and Shoreline Variability at Decadal Scales**

Teagan Duenkel, Tiffany Roberts Briggs  
Department of Geosciences  
Florida Atlantic University, Boca Raton, FL

Healthy and thriving coastal ecosystems play a crucial role in shielding beachfront communities, bolstering local economies, and offering vital habitats for key species. However, the challenges of sea-level rise, expanding coastal development, and the increasing intensity of storms are accelerating coastal erosion. Addressing this challenge requires comprehensive and informed mitigation and management strategies. This study examines decadal-scale trends in morphology and shoreline variability at three inlet-adjacent beaches in Jupiter, Florida, spanning 30 years. Data was analyzed to determine volumetric and contour changes above the shoreline (0 m elevation) and across the entire profile. Notably, inlet contiguous beaches experienced the most significant morphological variations. Factors including storm events, nourishment practices, and sediment transport influenced these changes. Gaining insights into historical shoreline variability and patterns of erosion and accretion is crucial for adapting to coastal changes and formulating effective strategies for managing beach and inlet systems. The results underscore the effectiveness of this approach in uncovering long-term morphological trends and their driving forces, offering a foundation for future research to apply this methodology for more extensive spatio-temporal assessments of decadal beach patterns.

## **Unmanned Aircraft System Photogrammetry for Mapping Diverse Vegetation Species in an Inland Wetland**

Caiyun Zhang, Fiona Benzi, Abigail Eccles  
Department of Geosciences  
Florida Atlantic University, Boca Raton, FL

Inland wetlands play a vital role in maintaining ecological balance and providing essential ecosystem services. Accurate monitoring of wetland plant communities is crucial for effective management activities. This study explores the potential of contemporary Unmanned Aircraft System (UAS) photogrammetry techniques to assist with the delineation of wetland communities in central Florida. We acquired and generated fine-resolution optical UAS imagery products and then applied sophisticated artificial intelligence (AI) classification algorithms to map diverse wetland communities. This research leverages high-resolution UAS imagery to capture intricate details of inland wetland areas, facilitating the creation of precise photogrammetric products. Our findings demonstrate the efficacy of UAS-derived photogrammetric products in wetland mapping due to its centimeter-level imagery spatial resolution and complementary 3D elevation information. This study contributes to the growing

research hotspots using UAS as a tool for wetland monitoring, restoration, and management initiatives.

## **Soil Health Matters: How do Genetically Modified Glyphosate-Resistant Soybeans Affect Plant and Soil Microbiomes Over Time?**

Shania Henry, Nwaduito Esiobu

Florida Atlantic University, Boca Raton, FL

Genetically modified (GM) crops are a biotechnology phenomenon that is widely utilized in the agricultural industry. This farming technique has become increasingly popular over the years with farmers demonstrating a dependency on artificially manufactured plantations. More than 90% of the soybeans produced by U.S. legume companies are modified by genetic engineers (Maddell, 2019). This large percentage becomes worrisome when soil biodiversity comes into consideration. Most studies focus on the reliability of these crops including pest resistance and longer shelf life, with little to no regard for unveiling the potential dysbiotic effect that transgenic crops could have on the plant's microbial community. The concern then becomes the microbes' inability to flourish off the nutrients secreted from the plant. A change in plant genotype/genome could distort the plant's natural capability to support the microbes via root structure changes and altered foliar niche. More so, an alteration in the plant's genotype could lead to the accumulation of herbicides and agrochemicals which will directly affect endophytes, phyllospheric, and rhizospheric bacteria residency. And although these GMOs are engineered for beneficial agricultural traits in a changing climate; if the plant microbiome is adversely impacted, critical ecological activities - CO<sub>2</sub> sequestration, organic matter recycling, and biogeochemical cycling of gasses will be impaired over time.

This research will authenticate the genetically modified seeds and the organic equivalent by PCR. Both will be planted in replications in pot soils with various treatments. Endophytic, rhizospheric, and phyllosphere bacteria will be measured using 16S rRNA amplicon metagenomic sequencing at time zero, and one-month intervals for 4 months. Other measurements include plant biomass, pH balance, and soil parameters. We hypothesize that there will be a difference in the plant microbiome community structure of the genetically modified plant and the organic control. This study will attain a better understanding of the repercussions that transgenic plants could have on soil microbes.



## The Impact of Temporal Delay on Metacognitive Confidence in Memory Decisions

Isabella Klopukh, Kevin P. Darby  
Department of Psychology  
Florida Atlantic University, Boca Raton, FL

Metacognitive confidence judgments are frequently adopted as a measure of certainty in decision-making tasks, but the mechanisms that underly these judgments have been long debated. In this work, we investigate the effect of the timing of confidence judgments in memory decisions by querying confidence immediately after, with a 3-second delay, or in a separate phase within an associative recognition task. An additional control condition did not probe confidence judgments at all to investigate how metacognitive monitoring may influence the memory decision-making process itself. The results indicate changes in memory performance and response times in conditions where confidence judgments were made, as well as a stronger association between confidence and accuracy when confidence was probed following a 3-second delay. We discuss the theoretical and practical implications of these results regarding post-decision processing of metacognitive confidence and the bidirectional relationship between memory and metacognition.

## Developing Better Fluorescent Cholesterol Probes

Nicholas McInchak<sup>1</sup>, Dana Benavides<sup>1</sup>, and Maciej J. Stawikowski, Ph.D.<sup>1,2</sup>

<sup>1</sup> Department of Chemistry and Biochemistry, Charles E. Schmidt College of Science, Florida Atlantic University

<sup>2</sup> FAU Stiles-Nicholson Brain Institute, Florida Atlantic University, Jupiter, FL

Cholesterol is a vital component of eukaryotic membranes, playing key roles in membrane structure and various biological processes. A deeper understanding of its subcellular localization and trafficking mechanisms will lead to a better understanding of cholesterol-related diseases, along with potential treatments. Using fluorescent cholesterol analogs and live-cell imaging has proven to be a promising method to elucidate information about cholesterol's homeostasis, enzymology, subcellular localization, and transport. Our lab has developed a library of novel naphthalimide-based fluorescent cholesterol analogs utilizing molecular dynamics simulations to gauge how closely the analogs mimic cholesterol in model membranes. Previously, in our CND series, we developed fluorescent cholesterol probes with 1,8-naphthalimide fluorophore and amino acids as a linker connected to cholesterol via ester bond. Results from live-cell imaging, as well as studies in *C. elegans*, suggest that the ester linkage in the analogs could be subject to enzymatic hydrolysis. To address this hypothesis, several new CND analogs incorporating linkers with improved hydrolytic stability have been developed and characterized.

## Investigation of Melatonin's Role in *Nicotiana tabacum* Response to Environmental Stresses

Mia Michnik, Xing-Hai Zhang  
Department of Psychology  
Florida Atlantic University, Boca Raton, FL

Plant melatonin has been shown to play crucial functions stress responses and developmental processes. In this study, it was found that melatonin plays an important role in defense against environmental stressors in tobacco *Nicotiana tabacum*. Environmental stresses including radiation, sodium chloride and potassium chloride concentrations aggregated the CRISPR enabled melatonin-knockout plants as compared to the wild type control plants. Tobacco samples exposed to UV radiation exhibited visual signs of stunted growth and damage to plant tissue. We propose that due to the absence of melatonin biosynthesis, these knockout plants were unable to regulate the expression of various stress-response pathways. Lacking melatonin also leads to the impairment of photosynthetic process, such as biosynthesis of chlorophyll a/b. Under stress, these samples were subjected to manage stresses imposed upon them by spending more energy in either tissue generation or in root generation. The study provides insight into the role melatonin undertakes in alleviating damage caused by environmental stressors that plants face constantly during their life cycle of growth and development.

## A 1400-year Reconstruction of Fire History from a Landslide Formed Lake in Costa Rica

Danielle Nering<sup>1</sup>, Taber Friedel<sup>1</sup>, Erik N. Johanson<sup>1</sup>, Sally P. Horn<sup>2</sup>, and Mauricio Murillo Herrera<sup>3</sup>

<sup>1</sup> Florida Atlantic University, Department of Geosciences,

<sup>2</sup> University of Tennessee, Knoxville, Department of Geography and Sustainability

<sup>3</sup> University of Costa Rica, School of Anthropology

This study presents initial macroscopic charcoal trends from our study site, Laguna Arancibia, in Costa Rica. The sediment cores examined were recovered in 2019 from a small (1 ha), moderately deep (6.2 m) lake in the western portion of the Central Valley region. Laguna Arancibia, at 1250 meters elevation, is situated on the Pacific side of the Cordillera de Tilarán within the Puntarenas Province in an area prone to frequent landslide activity. The closed basin Laguna Arancibia occupies likely formed at ca. 1500 cal yr BP by a landslide or slump. Macroscopic charcoal deposited in lake sediments is a direct environmental proxy for fire activity within a watershed. Often influenced by major climate drivers or anthropogenic activity, fire events are frequent and variable even in the tropics. We analyzed macroscopic

charcoal to characterize the intensity and frequency of fire events over time. We counted macroscopic charcoal in two size ranges: 125 to 250  $\mu\text{m}$  and 250 to 500  $\mu\text{m}$ . Out of 162 sampled levels, 59 showed an absence of charcoal in either size range and 139 showed an absence of charcoal in the larger size fraction. The highest charcoal influx is found at a depth of 132.75 cm (ca. 520 cal yr BP). The initial results of this dataset are plotted by sampled depth and will later be compared to archaeological data, pollen and isotope analyses, and other additional datasets to reconstruct the environmental change occurring local to the region.

## Exploring Photodynamic Therapy-Induced Molecular Changes in Skin Tissue Using Raman Spectroscopy

Thi Nguyen, Andrew C. Terentis

Department of Chemistry and Biochemistry  
Florida Atlantic University, Boca Raton, FL

Cancer remains a significant global challenge, prompting ongoing efforts to improve treatment methods. Photodynamic therapy (PDT) has become a promising option in cancer research. PDT uses light-sensitive substances like porphyrins to target and eliminate cancer cells while protecting nearby healthy tissue. Porphyrins, known for their photosensitizing properties, generate reactive oxygen species upon light exposure, making them effective in PDT. However, optimizing PDT protocols to enhance treatment efficacy and minimize side effects remains challenging. This study aims to enhance cancer treatment precision via photodynamic therapy (PDT) by analyzing tissue changes with porphyrins and light using Raman spectroscopy while integrating machine learning for improved data analysis. Raman spectroscopy helps study polymeric membranes, revealing details about their structure and properties. Machine learning techniques, like principal component analysis (PCA), assist in analyzing complex data patterns. Here, we show that treating skin cancer specimens with porphyrin solutions and visible light induces distinct chemical patterns, as detected by Raman spectroscopy and analyzed through PCA, suggesting potential for enhanced cancer treatment precision. Our primary discovery reveals the molecular alterations in cancer tissues treated with porphyrins and light during PDT. Understanding how chemicals interact in PDT helps treat skin cancer better and sets the stage for creating treatments for different types of cancer. These discoveries hold significance as they help us develop better treatments, improve patient outcomes, and better understand cancer treatment methods.

## Treating and Researching Amyotrophic Lateral Sclerosis

Delilah Penate, Gary Perry  
Neuroscience and Behavior  
Florida Atlantic University, Boca Raton, FL

ALS is a motor neuron disease that results in the degeneration of the neurons that allow patients to move and that afflicts 31,000 people in the United States, majority of which are between 55 and 75 years old. Typically, within a few years someone diagnosed with ALS will die due to respiratory failure since they become paralyzed and lose the ability to breathe independently. Generally, most patients are going to have the sporadic type of ALS, but about 5-10% of patients will have a familial type of ALS. Gene mutations related to ALS often cause issues in proteins that are meant to process nucleic acids. Stem cells are used to both research ALS and to actually treat it, through the growth of motor neurons and astrocytes. Four genetic mutations - C9ORF72, SOD1, TARDBP, and FUS - contribute to the vast majority of familial cases of ALS, and some treatments exist to target these specifically. Notably, tofersen can be used for those with the SOD1 gene mutation. Other medications, like riluzole, edaravone, and a combination of sodium phenylbutyrate and taurursodiol.

## Next Generation Plant Booster: Proof of Concept via Expression of Green Fluorescent Proteins in Plant-Growth-Promoting Bacteria

Jon Declan Sullivan, Nwaduito Esiobu  
Florida Atlantic University, Boca Raton, FL

Traditional agricultural practice has relied on the use of antibiotics, pesticides and chemical fertilizers to combat issues such as stress, disease and nutrient deficiency. Genetically modified bacteria symbionts of plants represent a cost-effective and sustainable solution to issues like these. These organisms could act as micro-machines that could be easily engineered and customized to changing climatic conditions as well as tailored to specific plant needs.

The goal of this research is to examine the transformation efficiencies of bacteria already known to have beneficial impacts on plants, in expressing GFP (Green Fluorescent Protein) introduced via a monomeric plasmid and electroporation. Pseudomonas strains and Bacillus megaterium will be tested. If successful, this will serve as a proof of concept that PGPB (Plant Growth Promoting Bacteria) can be transformed with genes coding for hormones, nutrients and immune signals to aid their plant hosts more effectively in times of stress or nutrient deficiency. It is noteworthy that our engineered next-gen plant boosters will not be released into the environment. Specifically, bacteria native to the microbiomes of crops important to the economy and regional identity of South Florida, like citrus, will be targeted. The innovative delivery system is a subject of a different study.

The impact of this research could provide insight into developing alternative agricultural practices using indigenous bacteria to reduce operating costs and increase climate adaptation strategies and sustainability. On top of the agricultural and economic benefits the same practice could be expanded to conservation of endangered plant species by providing them with better mechanisms to deal with environmental stressors.

## **Interleukin-1 Type 1 Receptor (IL-1R<sub>1</sub>) is Implicated in Emergence and Severity of Progressive, Generalized tonic/clonic Epilepsy in a Transgenic Mouse Model**

Adrianna Tran, Tashi Dillon, Arthi Khan, Ceylan Isgor  
Florida Atlantic University, Boca Raton, FL

Post generalized electroencephalographic suppression (PGES) following the onset of a generalized tonic clonic seizure (GTCS) is suggested to be a biomarker for sudden unexpected death in epilepsy (SUDEP) risk. Interleukin-1 (IL-1) is an inflammatory cytokine with neuromodulatory properties in the CNS. The interleukin-1 receptor (IL-1R) elicits an inflammatory response that is exacerbated in epilepsy. There is strong evidence indicating that the release of inflammatory mediators produced by generalized tonic-clonic seizures influences the ontogeny of epileptogenesis. Preliminary experiments used a transgenic mouse model of adult-onset, progressive epilepsy with an overexpression of brain-derived neurotrophic factor (TgBDNF). During the progression of adult-onset epilepsy, the PGES duration prolongs, and cellular death is found in the nucleus pontis oralis, a brainstem arousal structure. We are investigating whether interfering with intracellular signaling cascades initiated by IL-1 binding to its type 1 receptor (IL-1R<sub>1</sub>) will alter the severity of the seizures in epileptic mice. TgBDNF mice are bred with IL-1R knockout (KO) strain to determine if the course or severity of epileptogenesis could change. Based on our current findings, the duration of PGES in TgBDNF/IL-1RKO mice does not increase as a function of successive GTCSs. This strongly suggests that IL-1R<sub>1</sub> signaling plays a role in the severity of successive seizures and can provide insight when elucidating the underlying mechanisms associated with death in adult-onset epilepsy.

## Conformational and Proteolytic Analysis of APP Model Glycopeptides

Maria Eduarda Vezzi<sup>1</sup>, Nancy Vela<sup>1</sup>, Ramya Ayyalasomayajula<sup>1</sup>, Ivet Boneva<sup>1</sup>, Dmitriy Minond<sup>2</sup>, Mare Cudic<sup>1</sup>

<sup>1</sup> Department of Chemistry and Biochemistry, Charles E. Schmidt College of Science, Florida Atlantic University, Boca Raton, FL, USA

<sup>2</sup> College of Pharmacy and Rumbaugh-Goodwin Institute for Cancer Research, Nova Southeastern University, Fort Lauderdale, FL, USA

The amyloid precursor protein (APP) is a type 1 transmembrane glycoprotein that undergoes proteolytic cleavage into a toxic amyloidogenic pathway via  $\beta$ -secretase, leading to the formation and consequent accumulation of  $\beta$ -amyloid (A $\beta$ ) peptides. Emerging evidence continues to support the idea that deficiencies in the processing and trafficking of these peptides are considered a possible initiating event of Alzheimer's Disease. Understanding the role of APP proteolytic cleavage by  $\alpha$ -,  $\beta$ -, and  $\gamma$ -secretases into the toxic amyloidogenic pathway has sparked interest in the function of MUC-type O-glycosylation in the production and clearance of A $\beta$  peptides. With this goal in mind, we have synthesized native and Swedish-mutated (Lys670Asn/Met671Leu) (glyco)peptides with O-GalNAc moiety on Thr663, Tyr681, or Ser667 to explore the role of glycosylation on conformation and secretase activity. The sequences incorporate the  $\beta$ -secretase (BACE-1) (M671~D672 or L671~D672) and  $\alpha$ -secretase (ADAM-10) (K687~L688) cleavage sites, located near and within the A $\beta$ <sub>40</sub> domain, respectively. CD analysis was conducted in four solvent systems to evaluate the peptide environment and O-glycosylation-induced conformational changes.

## Testing Song Preferences in Songbirds Using Operant Conditioning

Erika Wilczek, Jerry Gambrell, Rindy Anderson

Neuroscience and Behavior

Florida Atlantic University, Boca Raton, FL

Operant conditioning, a form of learning that uses rewards and punishments, is a successful method for testing the mating preferences of female songbirds because male song is inherently rewarding to females. This paradigm allows researchers to essentially "ask" female songbirds which qualities they find attractive in a male. Female songbirds determine a male's mating potential through his song qualities, making their preferences important information used during mate selection in songbirds. Previous operant conditioning research with songbirds required many wires to connect the operant perches and audio speakers to a single desktop computer. We built a new wireless prototype system that runs independently inside each sound isolation chamber. Each operant chamber contains two perches, and each plays a different song. Using this design, we can quantify hops on each perch to determine the

preferred song. My project aims to test the prototype setup's functionality and reliability, refine the setup, and complete a full-scale experiment testing the mating preferences for 10 female finches. Currently, I am testing the reliability of one chamber to ensure that the full system is operating with 100% accuracy. I am doing this by comparing data output from the operant system to video recordings of the female's behavior. Once the system is fully functional, I will test whether female finches prefer the songs of familiar males to unfamiliar males. I predict that the females will prefer the songs of familiar males because it is already known that female finches prefer males from their own population over distant populations, healthy males over unhealthy males, songs that were learned accurately over inaccurately, and the familiarity preference has already been shown in other songbird species. This project will add to the existing knowledge of what qualities females look for in males when choosing a mate by determining if the female finches prefer the songs of familiar males over the songs of males never encountered before, and how individual females vary in their preferences.