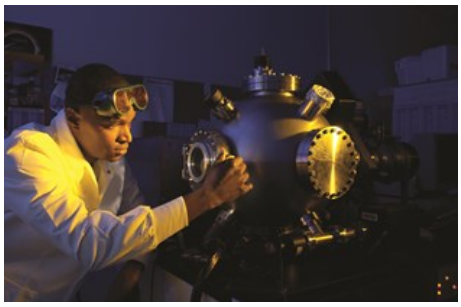
Life Sciences South Florida

2016 STEM Undergraduate Research Symposium

Saturday, April 2, 2016

8:45 a.m. - 3:00 p.m.

Broward College North Campus
1000 Coconut Creek Blvd
Omni Auditorium
Coconut Creek, FL



LifeSciences SOUTH FLORIDA
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BROWARD COLLEGE℠
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J. David Armstrong, Jr., President

Dear Friends,

It is my honor to welcome you to Broward College North Campus for the fifth annual Life Sciences South Florida (LSSF) Undergraduate Research Symposium.

Since its inception in 2010, LSSF has worked to stimulate economic growth in Science, Technology, Engineering and Math (STEM) industries through innovation, talent development and attracting businesses to South Florida. Through their efforts and collaboration with partner organizations, South Florida is one of the fastest growing regions for technological innovation.

The importance of STEM education is paramount to creating highly-skilled graduates who can meet the needs of this growing labor market. As educators, we must provide our students with opportunities for interaction, debate and dialogue with likeminded colleagues from other institutions so as to foster collaboration and creativity.

Eighty brilliant students have chosen to participate this year, making today the largest event in the Symposium's five-year history. The original scientific presentations they've submitted show the depth and breadth of knowledge South Florida students possess on various STEM fields. I invite you to walk through to view the outstanding poster entries, then hear from nineteen students as they demonstrate their proficiency before judges during the oral presentations.

Broward College is proud to collaborate with LSSF and other academic institutions to offer a challenging life sciences education experience. It is only through the exchange of ideas do we uncover breakthroughs that can impact the world.

We extend a sincere congratulations to students presenting today and we wish much success to all STEM students during their academic journey.

Sincerely,

J. David Armstrong, Jr.
President

Representative Kristin Jacobs

Kristin Jacobs is a member of the Florida House of Representatives. She was elected in November 2014 to represent Florida's 96th district.

Kristin currently sits on four committees in the House, Health Quality, Higher Education and Workforce, Local and Federal Affairs and Agriculture and Natural Resources Appropriations Subcommittee, where she was selected the Democratic Ranking Member. In her two sessions, Representative Jacobs has filed a bi-partisan bill to regulate the sale of kratom—"the new bath salts"—a dangerously addictive opioid substance that has recently been gaining popularity in Florida and is completely unregulated. She is also championing a bill to foster interagency collaboration in order to enhance State resilience and preparedness against natural hazards. Additionally, during the 2016 Legislative Session, Representative Jacobs was selected to serve as the Vice Chair of the Women's Legislative Caucus.

Prior to being elected to state office, she served as Broward County mayor.

Throughout her tenure, Broward County Mayor Kristin Jacobs championed issues to improve and protect Broward County's quality of life. As a neighborhood activist, she was elected to the County Commission in 1998 to represent the residents of District 2 where she served until November 2014.

She quickly earned the trust of her community by identifying problems and organizing divergent groups to work together to bring about real change. Her work has earned her recognition as an expert in sustainable growth, clean water and smart public transit. Recognizing that the welfare of a community is dependent on a healthy environment, Kristin began promoting green environmental practices upon taking office.

Over the years she created several task forces focused on sustainability, including the Climate Change Task Force, Water Advisory Board and the Coastal Ocean Task Force, Broward Leaders Water Academy, Broward Water Resources Task Force, many of which she was Chair. In 2008, Kristin created The Regional Climate Change Compact, a regional four county compact that addresses the future impact of climate change in Florida.

In 2011, Kristin was selected to serve as Chair of the White House National Ocean Council's Governance Coordinating Committee, which advises President Obama on local government perspectives on ocean policy. Kristin also is a member of SmartGrowth America's Local Leaders Council and an ICLEI Resilient Communities of America inaugural signatory.

As Mayor, her legislation included the Tri-County Compact, an agreement between Broward, Miami Dade, and Palm Beach Counties to work together as a region to accomplish mutual goals. She also celebrated the passage of Broward Complete Streets Program and the Broward County WAVE project, both of which support sustainable public transportation.

Kristin lives with her husband Stuart in Coconut Creek. She is the proud mother of three children and has three grandchildren.

Broward County Commissioner Chip LaMarca

Chip LaMarca is a lifelong resident of Broward County. He is married to his wife Eileen of twenty years and the couple lives in Lighthouse Point with their two rescue dogs.

Chip attended Broward College, Florida Atlantic University, and Boston University, before returning home to follow in his late father's footsteps by helping bring jobs to Broward through the construction industry. Chip started LaMarca Construction in 2006.

Chip was elected to the Lighthouse Point City Commission in 2005 and is proud to serve the people of District 4 as a Broward County Commissioner since 2010. Chip has worked hard to improve Broward's economy through job creation in his position on the Board of the Greater Fort Lauderdale Alliance.

Commissioner LaMarca is a dedicated member of the National Association of Counties where he serves as the Vice-Chair of Large Urban County Caucus and the Florida Association of Counties where he chairs the Finance & Tax Administration committee. He is most proud of his work with the Greater Fort Lauderdale Alliance and the Six Pillars project, where he serves as Co-Chair of the Steering Committee.

Life Science South Florida
STEM Research Symposium 2016
Program

8:40 a.m. Breakfast - Open during Registration

9:15 a.m. Opening Remarks.....Dr. Avis Proctor
President North Campus, Broward College

9:18 a.m. Welcome Address ..... Dr. Linda Howdyshell
Provost & Senior Vice President Broward College

9:20 a.m. Guest Speaker .....Honorable Chip LaMarca
Broward County Commissioner

9:40 a.m. Introduction of Keynote Speaker..... .Dr. Linda Howdyshell
Provost & Senior Vice President Broward College

9:45 a.m. Keynote Speaker ..... Honorable Kristin Jacobs
Florida State Representative District 96

10:30 a.m. – 12 p.m.
Oral Presentation I – Building 51 Room 101
Oral Presentation II – Building 51 Room 102
Oral Presentation III – Building 51 Room 103
Oral Presentation IV – Building 51 Room 104

10:30 a.m. – 11 p.m.
Poster Presentation Odd #'s 1-61 – Omni Auditorium
11:15 a.m. – 11:45p.m.
Poster Presentation Even #'s 2-60 – Omni Auditorium

12:15 p.m. Lunch – Omni Auditorium to 1:30 p.m.
Poster Exhibit Open Session – Omni Auditorium
College/University Programs – visit tables – Omni Auditorium
Visit Health Fair Building 62 Regional Library

1:45 p.m. Awards Presentation ..... Dr. Donald P. Astrab, Dean Broward College
Alexina Alonso, Coordinator, FIU Office of Engagement

Life Sciences South Florida STEM Undergraduate Research Symposium 2016

Oral Presentation #1

Increased Requirement for yKu Function in cdc13-1 Mutant *Saccharomyces cerevisiae*

Wesam Azaizeh, Lauren Sanchez, Sue-Ann Flores, Jovans Lorquet, Maxime Jean, Christoph Hengartner, Ph. D., and Leticia Vega, Ph.D.
Barry University, Miami, Fl.

Abstract

Telomeres are the physical ends of eukaryotic chromosomes that protect DNA ends from degradation and from end-to-end fusion. Telomeres consist of stretches of repeated C/G-rich DNA ending with 3' single stranded G-rich overhangs. The enzyme telomerase and accessory proteins such as Ku and Cdc13p maintain and facilitate telomere functions. In *S. cerevisiae*, cdc13-1 is a temperature sensitive allele of Cdc13p, an essential telosome protein that binds to single-stranded G-tails to prevent telomere degradation. The yKu heterodimer, composed of yKu70p and yKu80p, functions in DNA non-homologous end joining, recombination, and telomere end protection. Yeast cells lacking Cdc13p or the yKu complex have uncapped telomeres and long single-stranded G-tails. This study examines the effects of mutations in y*Ku80* on *cdc13-1* strains. We introduced a library of 125 mutant y*Ku80* alleles into the *cdc13-1* background by plasmid shuffle and determined the effects on viability and telomere end protection of the various *yKu80* mutant alleles. We found that 30 out of 125 *yKu80* alleles tested increased the temperature sensitive phenotype of cdc13-1 strains, suggesting a telomeric end protection role in the *yKu80* alleles. We are currently characterizing the telomere phenotypes of double mutant strains and analyzing DNA damage levels under the *cdc13-1* background. Initial characterization of *cdc13-1*, *yKu80* double mutant strains show that temperature sensitivity may be uncoupled from telomere shortening in these strains.

Oral Presentation #2

A population model of the Burmese Python in the Florida Everglades

Kelly Merrill, Wesam Azaizeh, Cassandra Denning, Kristina Pazienza, and Sanja Zivanovic Advisor, Ph.D.
Barry University, Miami Shores, FL

Abstract

The Burmese python is an invasive species in the Florida Everglades (FE). Invasive species do not only compete with endogenous species, prey on them, and pose a threat to biodiversity, but they can also cause harm to ecological resources. The FE is a home to a large variety of species, such as an array of mammals, reptiles, avians, and more. In the past years, the Burmese python population in the FE has been growing at an alarming rate, which in turn had a drastic effect on the population of avian and mammal species. This decrease has been even more dramatic in endangered and almost extinct species. Therefore, understanding and estimating the advancement of these non-native species is essential to FE native species and its ecosystems. We use a well-known Predator-Prey model to model population size of Burmese python in the FE. We use estimates of mortality rates, birth rates, and diet of both predator and prey in order to model the dynamics of Burmese python.

Oral Presentation #3

Lightning Initiation

Istvan Kereszy and Anthony De Lia, Ph.D.
Broward College, Coconut Creek, FL

Abstract

While there have been large efforts invested in the detection of lightning as well as the mitigation of its adverse impacts, the direct cause of lightning is not well understood (Gurevich and Zybin, 2005). The electric field necessary for conventional breakdown is approximately 2MV/m, while the field measured in thunderclouds is an order of magnitude less (i.e. below 200kV/m). This paradox has led to theoretical explanations that aim to reconcile electric fields that are too weak for breakdown, with the fact that we see lightning at such a high rate.
One of the prominent theories called runaway breakdown (RB) was proposed by Gurevich in 1990. Runaway breakdown arises from extensive atmospheric showers (EAS) initiated by energetic cosmic rays (above 10^16 eV), as fast electrons above the critical energy ionize neutral molecules, new free electrons are created, some of which have energies above the critical energy, thus these also ionize new molecules, and an avalanche of free electrons is created. The theory predicts that the charged particles along the axis of the EAS create the seed for the lightning discharge. To experimentally test the predictions of the theory, we have set up experiments in the State of Florida, over the land mass and 20 miles off shore, using cloud-to-ground and cloud-to-cloud lightning data from November 1, 2010 to October 31, 2015. Our study aims to find how the Heliospheric Magnetic Field (HMF) polarity and its reversal during Heliospheric Current Sheet (HCS) crossings might modulate the galactic cosmic ray flux, and in turn the frequency and magnitude of lightning over Florida.

Oral Presentation #4

A comparative survey of *Gopherus polyphemus* hemoparasites in four different South Florida habitats

Brian Cooney, Dana Elhassani, Evelyn Frazier PhD, Joseph Caruso PhD
Florida Atlantic University, Boca Raton, Florida, 33431

Abstract

The gopher tortoise (*Gopherus polyphemus*) is a keystone species, for its burrows house more than 300 species of animals. Habitat destruction and its consequent fragmentation have led to a decline in populations within southeastern ranges of the United States. Hemogregarines (Apicomplexa: Adeleiorina) are intracellular protozoan parasites that have previously been identified in the blood of gopher tortoises. High levels of blood parasitaemia have shown to be a potential indication of stress resulting from overcrowding. The goals of this study are: (1) to characterize hemoparasite species through the use of Polymerase Chain Reaction (PCR) from tortoise blood samples and the ticks attached to tortoises and (2) to determine if free ranging gopher tortoises that live in poorly maintained habitats exhibit higher prevalence and parasitaemia levels within their blood when compared to tortoises inhabiting better maintained

sites with prescribed fires. Research goals will be examined at four sites: Blazing Star Preserve (BSP), Pine Jog Preserve (PJP), Florida Atlantic University Preserve (FAUP), and Johnathan Dickinson State Park (JDSP), with each location differing in size and abundance of gopher tortoises. PJP and JDSP are sites currently practicing fire management and herbicides, whereas FAUP utilizes mechanical and chemical management while BSP is not managed. **We hypothesize that parasitaemia will be higher in poorly managed sites as a result of crowding, when compared to well managed sites.** This study will benefit current conservation and management practices for gopher tortoises in South Florida and help provide a baseline study for reptile hemoparasites.

Oral Presentation #5

Progress toward Synthesis of Glycopeptide Libraries based on MUC1 Protein

Eric Patino, Mohammed Al-huniti, and Mare Cudic Advisor, Ph.D.
Florida Atlantic University, Boca Raton, FL

Abstract

Although death rates for all cancers combined continued to decline in recent years, metastatic cancers remain a major public health problem, and new and efficient therapies are still needed. One of the novel therapeutic approaches involves targeting heavily glycosylated cell-surface mucin protein (MUC1), of which the expression and glycosylation patterns change with progression of cancer. These glycosylation changes from long to short-chained carbohydrates, also called tumor associated antigens (TACA), are usually associated with poor prognosis. Due to the random arrangement of TACAs on extracellular portions of aberrant MUC1, we hypothesize that replicating the variety of glycosylation patterns present on the surface of cancer cells will allow us to study the role of altered glycosylation of cancer cells in tumor progression and metastasis.

Our approach involves solid-state synthesis of the MUC1-derived glycopeptide library carrying TACAs at typical glycosylation sites at serine (Ser) or threonine (Thr) within the MUC1 20-mer repeat. A key component in the preparation of this library is the determination of isokinetic ratios of glycosylated to non-glycosylated amino acids necessary for equimolar coupling at each possible glycosylation site. We have established protocol for the simple mixture of two components and determined the isokinetic ratios for coupling to the neighboring amino acids and/or glycosylated amino acid.

Future studies will involve determination of isokinetic ratios for four component mixtures incorporating three TACAs and non-glycosylated amino acid. The proposed MUC1-derived glycopeptide library will be an invaluable tool for increasing our understanding of the role of MUC1 in cancer cell biology and immunology.

Oral Presentation #6

Nuclear Analysis of Invasive *Ctenosaurus similis* on Keewaydin Island as a Measure of Population Diversity

James Karl Till, Paul Faelnar, Phil Allman, and Jan B. DeJarnette
Florida Gulf Coast University, Fort Myers, FL

Abstract

In populations with low genetic diversity, inbreeding depression and subsequent crippling of the population's viability is expected to occur. However, the *Ctenosaurus similis* population on Keewaydin Island (KI), Florida has flourished despite founder effect. This is corroborated by the finding of one ND4 haplotype across all KI individuals sampled in a previous study (Nacarrato et al., 2015). This conservation demonstrates that all individuals are from a single matrilineage; however, it gives no intimation to the male progenitor(s)'s genetic contribution. Therefore, this project aims to investigate how an inbred population may be able to flourish by examining the degree of genetic diversity in nuclear genes. For this study, five sets of primers were used to amplify standard molecular measures of diversity: 18s rDNA, c-*mos*, and the second exon of the MHC class II DR beta gene – an exon with hypervariable regions amplified by three separate primers. Sequencing of cloned products, produced by primer pair MHCIIBF22 and MHCIIBR29, resulted in pertinent data for the MHC class II DR beta gene. Subsequent amplification, cloning, and sequencing of DNA from four additional lizards yielded a total of two alleles thus far, as demonstrated by ClustalW alignment and comparison to MHC-II sequences deposited in GenBank. These findings are indicative of an inbred population enduring limited contribution from both male and female ancestry.

Oral Presentation #7

Microfluidic Incubators for Picoliter-Scale Biochemical Assays

Karla A. Montejo, Wesley Q. Cochran, Alexander K. Price, Ph.D., and Brian M. Paegel Ph.D.
The Scripps Research Institute, Jupiter FL

Abstract

Drug discovery relies on costly and inaccessible robotic high-throughput screening technologies for parallel processing of 100,000 – 1,000,000 microplate-based assays. We are exploring miniaturization of these platforms in the form of microfluidic devices that continually generate and analyze millions of microscopic assay droplets at the picoliter scale. Because microfluidic reaction vessels are mobilized by oil flow, precise droplet incubation is only possible by addressing the dispersion that Poiseuille flow causes, and the accumulating back pressure. We explored geometry and placement of oil-skimming channels that discourage droplet intrusion into oil resevoirs and achieve uniform incubation. We also examined the placement of inductive chambers that regulate back pressure resulting from droplet packing. The dispersion ratio (R), a measure of droplet-to-droplet deviation in incubation time, provided a quantitative metric of device performance. Flowing 200 nL/ min oil/surfactant, and 200 nL/min aqueous generated 730 ± 20 pL droplets at 4.7 Hz. Packed droplets reached incubation times up to 3.2 minutes with an average dispersion ratio of 0.19 (n = 11). These findings show promise for precise on-chip incubation in cost-effective integrated circuits containing this component.

Oral Presentation #8

Modeling *Wolbachia* transmission in natural populations of *Anopheles* mosquitoes

Haroldo Rodriguez, Katherine Cartagenas, Austin Mishoe, Lauren Childs, Ph.D,
Robert Shaw, Ph.D., and Flaminia Catteruccia, Ph.D.
Florida International University, Miami, FL

Abstract

Wolbachia are intracellular bacterial symbionts that infect arthropods via maternal transmission and are known to affect the host's immune and reproductive systems. Prior research has shown that experimental *Wolbachia* infections in *Anopheles* can reduce *Plasmodium* load by inducing an immunological response. Recently, a new strain of *Wolbachia* was found in natural populations of the malaria vector *Anopheles gambiae*. Using mathematical modeling, the aims of this project were to: 1) understand the stable prevalence of *Wolbachia* in natural *Anopheles* mosquitoes, and 2) to predict what factors affect the prevalence of *Wolbachia* in the *Anopheles* host. A model of Wolbachia infection of Anopheles populations was developed to predict the number of adult progeny according to sex and *Wolbachia* infection status after many reproductive cycles. Baseline rates were obtained from a literature search and were used to run population dynamic simulations in MatLab. Parameters consistent with the levels of *Wolbachia* found in the natural populations were determined. A sensitivity analysis showed that the most significant alterations in population dynamics were caused by changes in the proportion of females in their reproductive stage that lay eggs depending on their *Wolbachia* infection status and the transmission rate in the progeny of infected females. Results from this model can be used to predict reproductive cycles in experiments carried in more controlled environments. Nevertheless, caution should be used when interpreting these results, since there could be other factors that were not taken into account that could be maintaining *Wolbachia* infection in *Anopheles* mosquitoes.

Oral Presentation #9

Automated N-Glycan Analysis in Pharmaceutical Manufacturing

Megan Geraghty[1], Joe Higdon[2]
[1]Indian River State College, Ft. Pierce, FL; [2]Frederick Manufacturing Center, Frederick, MD

Abstract

Analytical determination of protein glycosylation profiles has become a critical tool used in the development and production of biopharmaceuticals such as monoclonal antibodies (mAbs). Glycosylation is a post-translational modification that can affect a variety of biophysical attributes of the target protein. In the case of mAbs, glycosylation can impact the conformational stability, serum half-life, and binding affinity for the Fc gamma receptor. The glycosylation profile for a given therapeutic protein can be a primary determinant of the product's efficacy whereas changes to that profile may result in reduced efficacy or potential adverse impact to the patient. Due to the potential for negative immunogenic responses or other adverse patient impact as a result of glycosylation variability, regulatory agencies such as the FDA are expecting to see the inclusion of glycoanalysis for each product as part of the overall analytical characterization package.

This presentation covers experiments designed to evaluate the feasibility, accuracy, and repeatability of the N-glycan sample preparation using the automated workflow on the Agilent Bravo AssayMap and Prozyme GlykoPrep-plus reagents. Detection and analysis of N-glycan structures are facilitated through the use of Ultra High Performance Liquid Chromatography (UHPLC) and Hydrophilic Interaction Liquid Chromatography (HILIC) separation. Human IgG standards, Product A (mAb) and Product B (mAb) purified material were used to demonstrate the repeatable measures of the Bravo AssayMap platform.

Oral Presentation #10

Isolation, genome assembly, and characterization of a cluster A2 mycobateriophage

Chris Holland, H. Wiersma-Koch, T. D'Elia.
Indian River State College, Fort Pierce, FL

Abstract

As part of the HHMI-SEA PHAGES program, over 6800 mycobacteriophage have been isolated and 1,086 have been sequenced and classified into 26 clusters. Mycobacteriophage SnapTap was isolated through the enrichment of soil samples from St. Lucie County, Florida using the host *Mycobacterium smegmatis* mc^2155. Molecular characterization and electron microscopy indicate that SnapTap belongs to *Siphoviridae*, which have double stranded DNA genomes, long flexible tails and make up 90% of all mycobacteriophages. DNA from SnapTap was isolated and , and 334,421 reads were produced by genome sequencing. Sequencing reads were filtered based on Phred quality score and then a combination of *de novo* assembly and genome mapping to references were performed to generate the entire SnapTap genome consensus sequence. The 51,106 bp completed genome has a GC content of 63.5%, 98 total open reading frames, is 97.3% coding and has 10 bp 3' overhangs. BLASTn analysis places SnapTap within the A2 subcluster with closest matches to SweetiePie and Power, 99% sequence identity. This research expands the diversity among cluster A mycobacteriophages and provides an insight to the evolutionary characteristics of mycobacteriophages.

Oral Presentation #11

Properties of Photonic Band Gap Material at Microwave Frequencies: Application to Ultrarefraction

Emanuele Costantino, Soumia Souchak Ph.D.
Miami Dade College, Miami, FL

Abstract

The study concerns the properties of Photonic Band Gap Material (PBGM) in the microwave frequency range. The PBGM, which we studied was made of dielectric or metallic rods disposed in an isosceles right-angled triangle. First, the transmission diagram is calculated with a numerical code developed in the University of Glasgow [1], and then validated with the High Frequency Simulator Structure HFSS software

developed by Ansoft [2]. In the first allowed frequency band, the dielectric Photonic Band Gap Material with and without defects behaves like homogeneous medium. The metallic structure behaves like ultrarefractive medium. In the forbidden band frequencies, the surface defects create new electromagnetic modes in the dielectric and metallic photonic band gap material.

Oral Presentation #12

Towards Carbon-Based Nanotechnology: Electrostatic Shielding and Deshielding Effects on the ^{13}C NMR Spectrum of Buckminsterfullerene, C_{60}, within a Cyclic β-peptide Nanotube Host

Kassandra Fernández, Andrea Vásquez, Lissandra Maceda and Servando Muñoz
Miami Dade College, Miami, Florida

Abstract

Through cooperative intermolecular hydrogen bonding the nonapeptide monomer cyclo [(L-β-aminobutyric acid)$_9$] self-assembles into a peptide nanotube such that a net macromolecular dipole results that is directed away from the electron-deficient amino groups towards the electron-rich carbonyl groups on opposite termini. Quantum chemical analysis using hybrid Hartree-Fock Density Fuctional Theory self-consistent field calculations, at the EDF2 6-31G* level of theory, show that the ^{13}C NMR spectrum of Buckminsterfullerene depends on the nanotopography of the cyclic β-peptide host. When the C_{60} molecule is adsorbed near the electron-rich carbonyl torus it experiences an upfield chemical shift 138.3 ppm compared to that of the free guest at 144.4 ppm. Conversely, when C_{60} resides near the electron-deficient nitrogen torus on the opposite terminus, the guest experiences a downfield shift to 146.7 ppm. We attribute the upfield and downfield chemical shifts to electrostatic interactions between C_{60} and the β-peptide walls at the nanotube termini.

Oral Presentation #13

The Physiological and Behavioral Effects of Sleep deprivation: An Integrated Analysis

Christopher Sarmiento[1], Lauren Hill[2], Margaret Smith[2], Travis Craddock[2], Ana Fins[2], Jamie Tartar[2]
Miami Dade College, Miami, FL[1]; Nova Southeastern University, Davie, FL[2]

Abstract

Sleep deprivation (SD) impacts various aspects of health and behavior. Behaviorally, SD decreases cognitive performance and increases emotional instability. Physiologically, SD alters immune and endocrine processes. However, the findings on the physiological changes after SD are inconsistent. For example, some studies report decreases in immune functioning after SD while others do not. Through examining changes across behavior and physiology, we aimed to move beyond the typical single marker approach show the integrated effect of SD on humans. To that end, 23 participants (14 males) were tested during a baseline session and after 1 night of SD. In addition, typical sleep behavior of participants was assessed through 1w of actigraphy recordings.

During baseline and the SD day (0700-0830), participants were tested on a series of clinical health measures, a suite of cognitive tasks, measures of hunger and satiety (ghrelin and leptin), HPA axis functioning (cortisol), and inflammation (IL1-β, IL-6, CRP). Findings from this study showed system-wide changes. There was a significant decrease in cortisol with a related increase in inflammation markers IL-6 and CRP, but no change in leptin or ghrelin. There were also deficits in cognitive task performance after SD and increased mood disturbance. Changes to behavioral and physiological measures were analyzed independently and in combination. Combined, these findings advance the understanding of the deleterious effects of SD by demonstrating systems-wide changes in humans after SD. These findings are particularly relevant for understanding the potential health costs in careers that commonly involve SD (e.g. medical professionals and military personnel).

Oral Presentation #14

Circumvention of Learning Increase Intoxication Efficacy of Engineered Bacteria

Cyril Manchery, Olena Bracho, Evan C. Haskell, Ph.D., Christopher A Blanar, Ph.D.,and Robert P Smith, Ph.D.
Nova Southeastern University, Fort Lauderdale, FL

Abstract

Synthetic biology holds promise to engineer systems to treat infectious diseases. One critical facet of designing such systems is the interplay between the engineered system and the pathogen. Understanding this interplay may be critical to overcoming resistance against the system. Using the principles of synthetic biology, we engineer a strain of *Escherichia coli* to attract and kill the model nematode *Caenorhabditis elegans*. Our bacteria are engineered to expresses a nematicidal toxin and an AHL attractant. When independently expressed, our engineered bacteria successfully intoxicated and attracted the worms, respectively. However, in combination, the efficacy of our bacteria was reduced due to learning in *C. elegans*. To overcome this learned resistance, we dynamically regulate gene expression to increase intoxication by circumventing learning. Our results detail the creation of a novel nematicidal bacterium that may have application against nematodes and unravel unique constraints on circuit dynamics that are governed by *C. elegans* physiology.

Oral Presentation #15

Improved Retinal Blood Velocity and Vision in Retinitis Pigmentosa patients following Electro-stimulation

Jeslyn Vayalil; Mark Jaffe, DPM; Ava Bittner, OD, PhD
Nova Southeastern University; Ft. Lauderdale, FL

Abstract

The purpose of this research was to examine whether changes in retinal blood velocity (RBV) are helpful for understanding whether participants with retinitis pigmentosa (RP) in a randomized controlled trial developed improvements in vision after receiving Trans-corneal Electrical

Stimulation (TES). Four eyes of three TES subjects who developed significantly improved vision (i.e., >4 lines visual acuity or >100% log retinal area for visual fields) and six other eyes that received TES but did not have a significant vision change were compared to three control subjects' eyes that received placebo sham intervention (inactive laser acupuncture) and had no visual changes. RBV was measured at two baseline visits and post-intervention using an analysis system to track the non-uniform distribution of red blood cells within a macular capillary. Retinal arterial blood flow was significantly reduced at baseline among participants with greater loss of visual field area at time of study enrollment (p=0.03). The eyes with and without visual improvements had a significant 32% and 19% increase in RBV on average in the macular arteries, respectively, after two TES sessions when compared to control eyes (95% CI: 16-48%; p<0.001)(95% CI: 0.3-38%; p=0.047). The eyes with visual improvements had a significant 31% increase in RBV in macular veins after 2 TES sessions (95% CI: 4-59%; p=0.02), but those without visual changes post-TES had no significant RBV change in veins (p=0.70) compared to control eyes. RBV measurements are novel, reliable outcomes in support of a physiological basis for vision improvements in RP subjects who received TES.

Oral Presentation #16

Analysis of Limonene samples using FT-IR, VCD, and ROA/Raman Spectroscopy

Juanita Sanchez; Rina Dukor, Ph.D. Becky Mercer, Ph.D.
Palm Beach State College, Palm Beach, Fl.

Abstract

Homo-chirality is an important property in life chemistry and is always present in nature. Nineteen of the twenty common amino acids that form proteins are chiral, as are a host of other biologically important molecules related to the senses of smell and taste. Essential oils, as limonene, are organic compounds extracted from natural sources and used in a variety of commercial products. Traditionally essential oils have been extracted using steam distillation, carbon dioxide, and organic solvent extraction. In this experimental process we test different extraction, purification techniques, and concentration methods to study Limonene (1-methyl-4-prop-1-en-2-yl-cyclohexene) samples from orange and lemon peel to confirm its chiral structure.

The sample analysis of each enantiomer was obtained using different spectroscopic techniques including Fourier Transform-IR (FT-IR), Vibrational Circular Dichroism (VCD), and ROA/Raman spectroscopy available at BioTools.Inc. The spectroscopic tools used allow the analysis of the secondary structure of polypeptides and protein conformation in H-O base solutions. These studies help us confirm and visualize the identical secondary structure of Limonene (R-limonene and S-limonene), stereoisomer comparison for chiral molecules, and provide more information about the chemical properties of limonene currently used for research due to its anti-carcinogenic properties. This exemplifies the need for a reliable method of extraction of limonene and other natural oils from its natural source (citrus rinds), followed by a quantitative analysis of the extract for limonene content, and structural analysis of its chiral nature.

Oral Presentation #17

Differential gene expression in drought-tolerant and drought-susceptible Andean native potato varieties from Peru

Laynet Cornelio[1], Indira Perez[1], Carlos Vazquez[1], Diana Martinez[2], Olga Patricia Ponce[2], Emi Murata[2], Luz Noemi Zuniga[3], Dora Pilar Maul Ph.D.[1], and Carlos Merino Mendez[2].
[1]St. Thomas University, Miami Gardens, FL; [2]Universidad Peruana Cayetano Heredia, Unidad de Genomica, Lima, Peru; [3]Instituto Nacional de Innovacion Agraria, Estacion Experimental Santa Ana, El Tambo – Huancayo, Peru.

Abstract

Potato (*Solanum tuberosum*) is the world's most important non-grain food crop and is central to global food security. Commercial potato varieties are very sensitive to drought injury, which results in slow growth, small tuber formation and tuber deformation. Andean native potatoes are ideal candidates for gene expression studies associated with drought. Because of their high genetic diversity, they are well adapted to the harsh environmental conditions that prevail in the high Andes, including drought. The Universidad Peruana Cayetano Heredia (UPCH, Lima, Peru), in collaboration with the Instituto Nacional de Innovacion Agraria (INIA, Huancayo, Peru) and St. Thomas University (STU, Miami Gardens, FL), are in the process of studying changes in gene expression in native potatoes associated with early and late drought responses, as well as after recovery from drought conditions. Using RNA-seq analysis, the UPCH has identified a large number of candidate genes associated with drought. UPCH and STU students conducted a drought experiment with both tolerant and susceptible native potato species, using an aeroponics growth system at the INIA Experimental station in Huancayo. After selecting seven drought-associated candidate genes from the RNA-seq analysis, and designing primers for their amplification, quantitative RT-PCR (RT-qPCR) is being used to look for differentially expressed genes in the drought tolerant varieties.

Oral Presentation #18

Optimization of Solar Energy by Power Factor Correction

Javier Rojas and Alberto Varela, Ph.D
St. Thomas University, Miami Gardens, FL.

Abstract

The power factor of the water pumps from the Organic Research Garden and Chickee Hut, which are powered by the solar station, were measured, calculated, and corrected. By using a Fluke 43B Single Phase Power Quality Analyzer, the values of real and apparent power were obtained, and with these values, the reactive power and power factors were deduced. The computer software that was used to provide the numerical results was Excel and MatCad, which gathered these results from the manually implemented formulas. Based on these results, it was concluded that the water pump for the Organic Research Garden required the installation of a 177 µF capacitor in its circuit, whereas the water pump from the Chickee Hut required the installation of a 120 µF capacitor. The effect of adding the corresponding capacitors to each of respective water pumps' circuits resulted in a rise in power factor from 0.76 to 0.98 for the Organic Research Garden and 0.82 to 0.98 for

the Chickee Hut. Upon analyzing the amount of energy saved by this correction every year, total energy savings would be 163.80 kWh/year for the water pump from the Organic Research Garden and 6.09kWh/year for the Chickee Hut water pump.

Oral Presentation #19

Gold Nano-Particle (GNP) Colorimetric Quantification of Drug Concentrations to Determine Intervertebral Disc (IVD) Diffusion Coefficient

Stephanie Cheng, Lu Yu, and Na Li, Ph.D.
University of Miami, Coral Gables, FL

Abstract

Efficient quantification of drug diffusion through avascular tissues, such as intervertebral discs (IVDs), is vital to biomedical research seeking to optimize treatment efficacy. Prior investigations suggest that IVD diffusion coefficients vary with such factors as pressure, orientation, hydration, and electromagnetic charge of the drugs involved. Studies to obtain diffusion coefficient most commonly utilized dual-chamber diffusion cells, where solute concentrations are measured up- and/or down-stream of an IVD disc. In supplementing said research, the current investigation seeks to develop quick, facile, and affordable quantitative methods of determining antibiotic concentrations using colorimetric analysis of Gold Nano-Particles (GNPs).
For proof of concept, GNP colorimetric analyses (mainly wavelength absorbance ratio: A650nm/520nm) of Oxacillin solutions at varying concentrations were used to develop calibration curves by which solutions of unknown concentration could be quantified. Salt-titration (NaCl) methods were used to enhance colorimetric response to low Oxacillin concentrations, improving resolution in dilute ranges (0 – 100 mM). A dual-chamber diffusion cell was used with Polyacrylamide Gel Electrophoresis (PAGE) gel discs in place of IVD tissue samples. Oxacillin diffusion tests were run with 250mM upstream solution and DI water on the downstream. Testing of both chambers after varying diffusion periods was conducted using GNP solution (8nM, 15.6nm) and the Biotek Synergy 2 micro-plate reader in absorbance capacity. The A650/520 indicated reasonable correlation with Oxacillin concentrations in the 100-250mM range. Preliminary manual salt-titration trials demonstrate reasonable correlations but with low precision, therefore subsequent salt-titration trials using micro-plate reader are to be conducted.

Oral Presentation #20

Role of Carbonic Anhydrase in Tracheal Filling

Mark Keroles and James Baker, Ph.D.
University of Miami, Miami, FL

Abstract

The tracheal system of insects develops as a fluid filled epithelium. Fluid is replaced with a gas of unknown composition in a process known as tracheal filling. Tracheal filling often begins with bubbles forming in the central portion of the tubes, followed by expansion toward the ends that are open to the atmosphere. We sought to test if the enzyme carbonic anhydrase might function to generate said gas bubbles. A bioinformatics study of the gene family in *Drosophila* identified fourteen carbonic anhydrase genes. We elected to study two of these genes, Cah2 and CG6074.

Both genes are expressed in trachea with probable signal peptides; this suggests that they are secreted into the tracheal lumen. These two genes are also developmentally regulated, expressed more highly in the late embryo and early larval stages. We used CRISPR/Cas9 targeted mutagenesis to mutate both Cah2 and CG6074. Through this mutagenesis we recovered five independently derived phenotypic strains for each gene. These strains, supplemented by two publicly available lines containing transposon insertions in the Cah2 and CG6074 open reading frames, were used as stocks for further molecular and phenotypic analysis. All of these stocks show some larval lethality in the 1st to 2nd instar with defects in the air filling of their trachea, many instances of collapsed trachea and aberrant larval behavior.

Poster Session, Poster # 1

A proper probability distribution analysis of manipulated variables of nonlinear models

Wesam Azaizeh, Kamren Livingston,Daria Vasilyeva, Sanja Zivanovic, Ph. D., and Maurizio Giannotti, Ph.D.
Barry University, Miami, Fl.

Abstract

It is a common strategy when dealing with nonlinear data sets to manipulate the collected measurements in order to conform to the standard linear regression technique. A nonlinear transformation of the measurements is carried out to achieve a linear relationship between the new variables. The standard linear fit technique, however, strictly relies on the assumption of normally (Gaussian) distributed data but Gaussianity is generally lost when data is nonlinearly transformed. Consequently, the use of the linear fit equations may be unjustified. This leads to an incorrect calculation of a physical parameter. We analyze this problem starting from the probability distributions of the original and the transformed measurements and provide proper equations to use in the instances where the data is manipulated. Finally, we will discuss applications to some interesting cases.

Poster Session, Poster # 2

Efficiency of air conditioning at Barry University

Cassandra Denning, Wesam Azaizeh, Rainn Zabaleta, Vania Arboleda, Michael Wise, Maurizio Giannotti, And S. Zivanovic. Barry University, Miami Shores, FL

Abstract

After years of complaints from professors, staff, and students that certain rooms and/or buildings at Barry University are very cold, we decided to look into efficiency of air conditioning that is in use. There are several items that can be looked into when it comes to improving A/C efficiency such as temperature of the room, humidity, air quality, A/C unit itself, and level of CO2 in the room. For the purpose of this project we will focus on evaluating room temperature based on the outside climate conditions. In particular, we will collect temperature measurements of several classrooms. To do this, we use the Arduino platform to develop an economical temperature logger. Arduino is an open-source microcontroller unit that utilizes an 8-bit AVR chip and other hardware which allow it to be easily programmable and interfaceable. We interface an Arduino UNO R3 with a data logging shield for SD data storage and real time clock capabilities, and an HTU21D-F high precision temperature and humidity sensor. The Arduino is programmed to awaken from sleep at set intervals of time to write the sensor values to the SD card. Once data is collected, we will compare it with recommended room temperature, calculate possible energy savings, and essentially obtain cost savings.

Poster Session, Poster # 3

Tissue changes during wound healing in wild type *Danio rerio*

Gabriela Hernandez, Victoria Hoelscher, and Brenda Schoffstall
Barry University, Miami Shores, FL

Abstract

Danio rerio (zebrafish) have been shown to completely regenerate heart, fin, and tail tissues without loss of function or formation of permanent scars. We have recently established zebrafish as a model to study regeneration in skeletal muscle and surrounding tissues following deep tissue

burn puncture wounds. Preliminary data suggest that it takes approximately 30 days for zebrafish to recover from the wound; our current project focuses on attempts to characterize the changes in tissue over the healing time period, as evidenced by histological techniques. Tissue samples were cryopreserved on specific days post-wounding, cut using a cryostat, and stained with Hematoxylin and Eosin (H&E) and Trichrome stains. Samples were collected over a 42 day period. We were able to discern specific changes in cell types over the course of healing. At six days post-wounding, loose connective tissue formation was already clearly visible. By Day 12, fat cells were beginning to infiltrate the area of the wound, and by Day 16 were predominately visible. Muscle tissue appeared to be re-establishing within the wound site by Day 16, and by Day 18 appeared to be re-organizing in distinctive bundles. Others have demonstrated that in would healing processes, fat cells may de-differentiate and re-differentiate into specific other cell types like muscle. This project is ongoing; we will further explore the hypothesis that fat cell re-differentiate into muscle in zebrafish as they heal and fully regenerate working tissue damaged by the burn puncture wound.
NIH-NIGMS MBRS RISE: R25 GM059244-15.

Poster Session, Poster # 4

Using the Ant Colony Optimization Algorithm to Enhance Blood Vessels in Retinal Images

Luis Khawly, Julian Dasilva, and James Haralambides, Ph.D.
Barry University, Miami Shores, FL

Abstract

We present a probabilistic algorithm that enhances the blood vessels of retinal images to support medical diagnosis and clinical study. Extraction of blood vessel features is important for the diagnosis of diseases and the application of appropriate treatments. The algorithm is applied in two stages. During the first stage, pixel values of blood vessels are intensified through edge detection using Gaussian filters. During the second stage, enhanced images are explored to identify strong features such as the underlying graph structure of blood vessels using the ant colony optimization algorithm. Strong features allow for the detection of natural or abnormal medical conditions in the retina.

Feature augmentation is achieved with the use of two-dimensional Gaussian filters. During the execution of the ant colony optimization algorithm, pixels that correspond to blood vessels are visited by “ants” using a weighted cost function whose parameters include color intensity and frequency. Color intensity reflects the enhanced value produced by the first stage. Frequency is a dynamic parameter that favors blood vessel pixels visited by a larger number of ants. Probabilistic selection of ant routes that combine color intensity and frequency helps identify pixels that represent strong features of the underlying graph structure. Frequency values are filtered to allow for varying levels of detail. Experimentation is carried for a number of different configurations in which parameters such as the number of ants, the number of ant travel stages, and the number of frequency updates are fine-tuned to achieve results of better quality and shorter execution times.

Poster Session, Poster # 5

First description of the anatomy of the caudal spine mechanism of the blue tang, *Acanthurus coeruleus.*

Shaynell Monreal & Michael P Robinson
Barry University, Miami Shores, FL

Abstract

Surgeonfishes (Acanthuridae) all share a trait unique to this family, one to several sharp spines (also called scalpels) found on the caudal peduncle directly anterior to the caudal fin. The function of these spines is unknown although it is believed to be used during intraspecific aggression. These

spines differ among the acanthurids. In some genera the spine is fixed and in others it is mobile and retracts into a depression. To understand better the evolution of these spines, we examined the anatomy of the retractable spine in the blue tang, *Acanthurus coeruleus*. Via dissection, clearing and staining, and microscopical analyses, we identified a previously unknown ligament. This ligament originated far to the anterior, passed through much of the myotomal musculature and inserted on the base of the spine. This suggests that contraction of this ligament is most likely how the scalpel is extended. This ligament is probably critical to the flexible use of the spine based on different behavioral contexts.

Poster Session, Poster # 6

Comparative analysis of the colors of the caudal spines of surgeonfishes (Acanthuridae)

Eva Paulus & Michael P Robinson
Barry University, Miami Shores, FL

Abstract

All species of surgeonfish (Acanthuridae) have one to multiple spines on the base of their dorsal fin presumably used as weapons in intraspecific combat. These spines vary among species in their conspicuousness. In some species these spines are apparently advertised with colorful accents whereas in other species the spines almost appear absent because of masking colors. Surgeonfishes also have a diverse array of social systems, ranging from territorial individuals to schools of hundreds. We are attempting to determine the role of the spine and the social reasons some fish would advertise while other fish hide their spines. We conducted online surveys to assess how conspicuous the spines of the surgeonfishes are. Humans rated the conspicuousness of the caudal spines on a scale from 1 (least conspicuous) to ten (most). Fish ranged from 1 to 10 with an average value of 5.324±0.042. Using these data in combination with phylogenetic analyses, we determined that group-living species were more likely to have conspicuous spine coloration than solitary ones. This does not obviously support the idea that the coloration of these spines is to advertise them for intraspecific coloration.

Poster Session, Poster # 7

qPCR Microbial Array Screen for Identification of Bacteria in a Zebrafish Biofilm Model

Peter Rodriguez, Jessica Ricketts, and Brenda Schoffstall
Barry University, Miami Shores, FL

Abstract

Recent advances in microbiology focus on “biofilms” as a leading cause of persistent infection. Biofilms are an accumulation of a multicellular mass embedded in polysaccharide matrix with incredible adhesive abilities. Once initially formed, biofilm becomes quite complex, recruiting multiple species of microorganisms to become part of the multicellular mass. Due to its complexity, biofilm has a remarkable ability to impede normal host immune responses and medical intervention. Previous research has focused on in-vivo biofilm models using rodent, Drosophila, or rabbit models. Here, we establish *Danio rerio* (zebrafish) as an *in-vivo* biofilm model within which the formation, growth, and treatment of biofilms can be analyzed. We have previously established wounding methods to deliver a penetrating burn injury to zebrafish. We have utilized the Qiagen Microbial DNA qPCR Array for Sepsis to screen for microbes growing in penetrating burn wounds of zebrafish at 24 and 48 hours post-wounding, with no antibiotic treatment. We have identified some endogenous or environmental bacteria that might cause infections in these types of wounds. Our screen identified 2 different species of aquatic bacteria, 2 specific species of bacteria commonly associated with fish, and 1 species known to participate in human wound

infections. Interestingly, two species are known initial biofilm-formers. Our goal is induction of biofilm by inoculating wounds with known initial biofilm-formers, which may recruit other bacteria into the complex structure. Future studies will focus on novel methods to disrupt biofilm formation using our *in vivo* model, with potential to discover treatments for complex human biofilm infections.

Poster Session, Poster # 8

Investigation of a new hypoxia model to induce cardiomyocyte proliferation in zebrafish

Fabio Frech, Johan Sanchez, Kevin Williams, and Brenda Schoffstall
Barry University, Miami Shores, FL

Abstract

Although human cardiomyocytes are capable of some cell division, this response is neither sufficient to repair damaged cardiac tissue nor efficient to compensate for pathological stress. In response to forced swimming exercise to induce excessive cardiac overload stress, *Danio rerio* (zebrafish) hearts respond with high proliferative capability. Zebrafish cardiac stress models are used to identify molecules that could be targeted to initiate cardiomyocyte proliferation in humans. We are developing a new zebrafish cardiac stress model using extreme hypoxia exposure as the stress event. Other hypoxia models expose zebrafish to harsh chemicals to either reduce O_2 in water or to induce anemia in fish; we propose a chemical-free model, using an anaerobic chamber. We first determined the length of exposure time in an extremely low oxygen environment that is sufficient to induce excessive cardiac stress, but not death. Preliminary results indicate that dissolved oxygen (DO) levels in individual fish tanks within the hypoxia chamber can be reduced by an average of 84%, as compared to water exposed to air, after 2 hours. After 10 hours, effects of hypoxia are too severe, inducing a 50% death rate. We are currently collecting data at other time points to determine optimal exposure time required to induce a significant cardiac stress that would result in cardiomyocyte proliferation similar to that seen with excessive exercise stress. This hypoxia model can be used to study molecular mechanisms that may act as a "switch" to turn on proliferation in zebrafish cardiomyocytes. Support:NIH-NIGMS RISE Grant, R25GM059244-15, Barry University

Poster Session, Poster # 9

A Study of Crystal Movement in Solvents during the Recrystallization Process

Damoy Roberts, Russell Betts Ph.D., and David C. Perdian Ph.D.
Broward College, North Campus, Coconut Creek, FL

Abstract

Various organic crystals ranging in size from 1 mm to 1 cm exhibit spectacular movement while recrystallizing in solvents. Due to the size of the crystals this phenomenon is visible by the naked eye. The velocity of the crystals moving in the solution is as high as 5 cm/s. The effects of solvent, intermolecular forces, vapor pressure, surface tension, as well as thermodynamic properties of the solvent are studied to determine the root cause of the movement as well as the range in velocities. Current crystals being studied are naphthalene, benzyl, and an anhydride adduct. The solvents being studied include methanol, ethanol, acetone, and water. These systems represent good models for educational demonstrations and fundamental research into crystal formation.

Poster Session, Poster # 10

Determination of Sulfate concentration in Aqueous Solutions via Cu^{2+} absorption by UV-Vis Spectrophotometry

Thomas Kent and David C. Perdian Ph.D.
Broward College, North Campus, Coconut Creek, FL

Abstract

A new analytical method is described that is able to quantify the concentration of sulfate ion (SO_4^{2-}) in aqueous solution based on the ion's impact on the absorption of Cu^{2+} ion in the visible spectrum. Sulfate is a polyatomic ion present in all natural water sources. The presence of sulfate is the result of both natural and human sources. The Environmental Protection Agency suggests that the concentration of sulfate in drinking water should be less than 250 mg/L. Current methods to determine the concentration of sulfate in aqueous solutions utilize either gravimetric methods involving the precipitation of sulfate, chromatographic separations, or turbimetric methods. Each of these methods require numerous sample preparation steps and/or specialized equipment. Determination of sulfate ion concentration via copper absorption is a much simpler method that achieves a detection limit of less than 50 mg/L using only a standard UV/VIS spectrophotometer.

Poster Session, Poster # 11

Effects of Methionine Sulfoxide Reductase (Msr) on
Drosophila Melanogaster Larval Development using RNAi

Tevin Ali; David Binninger Ph.D
Department of Biological Sciences, Charles E. Schmidt College of Science, Florida Atlantic University, Boca Raton, FL

Abstract

Oxidative damage to macromolecules within cells plays a role in the aging process and age-associated neurodegenerative diseases such as Parkinson's disease and Alzheimer's disease. Methionine, a common amino acid in proteins, is readily oxidized to methionine sulfoxide, which often results in the loss of protein activity. Methionine Sulfoxide Reductases (Msr) are a family of enzymes that repair oxidized methionine and restore its biological function. Msr is also thought to play a role in regulation of some protein activities as well as function as an intracellular antioxidant. Previous studies in our lab found that the absence of any Msr activity leads to a slower rate of growth during the third larval instar of *Drosophila*. My experiments involve the use of tissue-specific RNA interference (RNAi) knockdown of Msr to help delineate which tissues require the Msr activity for normal larval development. Ultimately, the results of these experiments should lend insight into the underlying molecular mechanism. The results of proposed studies will contribute to a more detailed understanding of the roles of oxidative damage and Msr in contributing to aging and age-associated disorders, especially the neurodegenerative diseases.

Poster Session, Poster # 12

Identification of fauna associated with *Gopherus polyphemus* burrows
at the Florida Atlantic University Preserve

Laura De Souza, Jessica Huffman, Evelyn Frazier

Abstract

Gophers polyphemus is a burrowing chelonian species prevalent to the southeastern portion of the United States. This herbivorous reptile is considered a keystone species due to their extensive burrows which provide shelter for more than 350 commensal species. The gopher tortoise is classified as threatened due to diminishing populations mostly due to habitat destruction and fragmentation which

leave small isolated populations. Our preliminary work is focused within the Florida Atlantic University Preserve (FAUP), which is a 90 acre fragmented scrub habitat containing 80-100 tortoises. We are randomly setting up 10 cameras in the vegetation and 10 cameras in the grassland in order to identify fauna who come around and/or utilize the gopher tortoise burrows here at the FAUP. **We hypothesize that animal species will use gopher tortoise burrows differently based on vegetation cover.** This study will allow us to identify the species of animals associated with gopher tortoise burrows and unveil the types of interactions that exist between them. This information will add to the body of knowledge on the gopher tortoise and its importance in this ecosystem.

Poster Session, Poster # 13

Streamlining fractionation methods for high-throughput screening of marine invertebrates

Patricia Le, Joubin Jebelli, Walter Pierre, Paul Scesa, and Lyndon West, Ph.D.
Florida Atlantic University, Boca Raton, FL

Abstract

Marine invertebrates are a rich source of chemical diversity with great potential of application towards pharmaceutical and related therapeutic developments. This abundance of marine natural product facilitates the need of cost-effective as well as labor and time-efficient fractionation methods for future high-throughput screenings. Isolation of marine invertebrate extracts are performed by preparative high pressure liquid chromatography (HPLC) via HP20SS. Extractions are integrated with LC/MS fractionation protocols to create partially purified natural product libraries for ready high-throughput screenings and rapid drug discovery. Spectroscopic analysis done by 1D and 2D NMR spectroscopy. Project findings in process.

Poster Session, Poster # 14

Investigating Ground Penetrating Radar (GPR) Limitations and Potential for Detection of Gopher Tortoise Subsurface Nests within South Florida Soils

Sarah Mitchell[1], Jessica Huffman[2], Dr. Evelyn Frazier[2], Dr. Xavier Comas[1]
Department of Geosciences[1], Department of Biological Sciences[2]
Florida Atlantic University, Boca Raton, FL.

Abstract

Gopherus polyphemus is a burrowing species endemic to the southeastern portion of the U.S. This herbivorous reptile is a keystone species due to the extensive burrows it excavates that provide shelter for 350 various species. The gopher tortoise is threatened throughout its range due to diminishing populations caused by numerous factors. Population declines are creating a need to improve the ability to accurately locate their subsurface nests to assess egg-clutch survival and population viability. Current nest detection methods (wire-probing) are highly invasive and time consuming. Recent studies have suggested potentially non-invasive methods (GPR). Our preliminary work is focused within the FAU Preserve (FAUP), a 90 acre fragmented habitat containing 80-100 tortoises. Previous FAUP studies suggest disproportional age distributions (few juveniles and sub-adults) and inability to detect nests using wire-probing techniques. In 2014, a single egg was found, suggesting nesting potential; however, more efficient techniques are needed to fully characterize the FAUP. Utilizing GPR, we imaged a tortoise burrow to detect the presence of chicken eggs as a pseudo-nest. The eggs acted as point-reflectors in GPR profiles, allowing characterization of their extent and depth. This study aims to determine GPR's limitations for detecting subsurface nests, and determine whether GPR is a feasible alternative to wire-probing by comparing time consumption and accuracy. We hypothesize that GPR will be able to accurately characterize gopher tortoise nest profiles, allowing for efficient and reliable detection. This has

implications for understanding GPR's limitations, gopher tortoise conservation, and better understand gopher tortoise reproduction within fragmented populations.

Poster Session, Poster # 15

Methionine Sulfoxide Reductase Expression in Response to Anoxic Stress Conditions in *D. melanogaster*

Evgeniya Rakitina, and David Binninger, PhD
Florida Atlantic University, Boca raton, FL

Abstract

Anoxia is the condition of oxygen deficiency. Mammals poorly tolerate anoxic stress. In contrast, *D. melanogaster* endures hours of anoxia with no apparent problems. In response to anoxia, flies suppress overall energy levels and enter protective comma - spreading depression. Animals recover from comma after being returned to normal oxygen levels. Period following reintroduction of oxygen is characterized by abundance of Reactive Oxygen Species (ROS), which oxidize vital molecules in cells. Methionine is exceptionally susceptible to oxidation by ROS, but can be catalytically restored by enzyme Methionine Sulfoxide Reductase (Msr A/B). Currently, little is known about the relationship between Msr activity and recovery from anoxic stress in Drosophila. Expression of Msr genes in response to anoxia is the subject of this study. Methods used are anoxia chamber to induce protective comma in flies, followed by Drosophila Activity Monitor to record average recovery times. Western Blot analysis is used to visualize expression patterns of Msr genes before and after anoxic stress. Preliminary results show, that single mutant flies do not take significantly longer than wildtype flies to recover from spreading depression. Furthermore, survival of single mutant flies following anoxia is also comparable to wildtype. However, double mutants take significantly longer to recover from anoxia and a greater number of Msr-deficient flies die as a result of anoxia. Failure to recover from anoxia becomes more pronounced as the animals approach senescence. These studies have the potential of offering new insight into the role of oxidative damage during reperfusion period following cardiac stroke.

Poster Session, Poster # 16

Mechanisms of Neuronal Survival Under Conditions of Oxidative Stress

Howard M. Retz and Howard Prentice, Ph.D.
Florida Atlantic University, Boca Raton, FL

Abstract

Parkinson's disease is an irreversible and progressive brain disease that affects approximately 5,000,000 people worldwide. It has been shown that production of free radicals by excess glutamate leads to oxidative stress and plays an important role in the progression of the disease. Taurine is a known neuromodulator that can combat free radicals and reduce oxidative stress. **The objective of this study is to determine the value of Taurine in enhancing neuronal cell survival upon oxidative stress challenges.** The PC12 cell line, a rat model of neuronal cell function will be pre-treated with different concentrations of taurine followed by Glutamate administration to induce excitotoxicity and oxidative stress. The viability of the cells will be tested using the Adenosine Triphosphate (ATP) Cell Viability Assay (Promega). Preliminary results show that treatment with 10 mM Glutamate decreases PC12 viability by 46%. Upon pre-treatment of cells with 1 mM Taurine for an hour the decrease in viability was reduced to approximately 30% after Glutamate challenge. Upon pre-treatment with Taurine at 10 mM and 20 mM the cell viability was reduced to approximately 27% and 28% respectively. Values were obtained as averages of three independent experiments. We are now furthering this study by determining the protective effects of taurine in PC12 cells after Cobalt Chloride (chemical hypoxia) treatment.

Determining the efficacy of Taurine in preventing neuronal cell death induced by oxidative stress may increase our understanding for treatment of Parkinson's disease and other neurodegenerative diseases.

Poster Session, Poster # 17

Inhibition of Semaphorin7A Decreases Mammary Tumor Growth and Metastasis

Michael Simoes, Ramon Garcia-Areas, Nathalia Gazaniga, Vijaya Iragavarapu, Ph.D.
Florida Atlantic University, Boca Raton, FL

Abstract

Developing an understanding of the tumor microenvironment is critical for developing treatments for breast cancer patients. Poorly differentiated blood vessels can fashion an oxygen-deprived microenvironment that triggers the expression pro-tumorigenic proteins. We discovered that breast tumors express high levels of Semaphorin7A (SEMA7A). To study the role of SEMA7A we generated 4T1 and 4T07 murine mammary tumor cells that were either silenced for the SEMA7A or expressed a Renilla control vector. Using the SEMA7A-specific hairpin shRNA we achieved a greater than 10-fold knockdown in SEMA7A gene expression. Mice bearing 4T1 and 4T07 SEMA7A silenced tumor cells showed a decreased tumor growth rate, decreased metastasis, and increased survival. Primary tumors from mice bearing SEMA7A silenced tumors showed a decreased production of angiogenic molecules, less hypoxia-induced necrosis, and a large reduction in immune infiltrates. Our study shows that inhibition of tumor-derived SEMA7A can limit tumor-induced inflammation and improve prognosis.

Poster Session, Poster # 18

Characterizing extensive variation in spade-like structures of oak toads

Taylor Hancock and Phil Allman
Florida Gulf Coast University, Department of Biological Sciences, Ft. Myers, FL

Abstract

Many toad species have enlarged tubercles or spade-like projections on their hind limbs used for digging. The presence of this structure is well documented in spadefoot toads, but is not well described in other species. The purpose of this study is to characterize and fully describe variation of the spade-like structures found in the Oak Toad, *Anaxyrus quercicus*. We collected morphometric data on 23 toads captured on the campus of Florida Gulf Coast University (FGCU) and on 98 preserved toads at the Florida Museum of Natural History (FMNH) collected from throughout the Southeastern US. We characterized spade structure based on shape, length, and keratinization. For both samples, spade length increased with snout-vent length (FGCU: $p=0.00182$; FMNH: $p<0.001$) and snout-vent length differed among shape (FGCU: ANOVA, $F_{1, 17}=9.147$, $p=0.00765$; FMNH: ANOVA, $F_{1, 73}=5.245$, $p=0.0249$), keratinization was not explained by morphological features (FGCU: ANOVA, $F_{3, 17}=1.699$, $p=0.20509$; FMNH: ANOVA, $F_{2, 73}=1.767$,$p=0.1781$). Oak Toads displayed extensive variation in spade structure: one spade or two spades, simple tubercles to highly keratinized spades, and spade length 1.37% to 8.29% of hind-limb length. Since individual size does not fully explain the diversity of the spade-like structures, genetic variation and phenotypic plasticity may have an influence. Toads captured at FGCU were often found in sandy soils but some individuals were found within seasonally flooded habitats containing muddier substrates. This observed variation may influence digging performance and capabilities across microhabitats. Additional experiments are necessary to elucidate the genetic and environmental influences that likely impact the spade's structure.

Poster Session, Poster # 19

The impact of survey methods on sea turtle nesting behavior in Southwest Florida

Jaimie Kittle and Phil Allman
Florida Gulf Coast University, Department of Biological Sciences, Fort Myers, Florida

Abstract

Florida has one of the world's largest loggerhead turtle (*Caretta caretta*) nesting populations. It is also the third most populous state with over 19.9 million people, and many studies have analyzed the potential impacts humans have on sea turtle nesting behavior and success. Nesting surveys are one approach approved by the FWC and utilized for monitoring and protecting turtle populations, either by surveying at night or in the morning. Despite the surveys being a highly accepted conservation tool, the impacts such surveys have on nesting success have not yet been documented. To determine whether survey method influenced sea turtle nesting success, the false crawl, nest, and depredation numbers were collected from 13-16 beaches in the Southwest Florida area for 1-16 years, and data were compared based on whether the survey occurred during the night or in the morning. It was found that timing of survey did not have an impact on the nest to false crawl ratios of *C. caretta* in Southwest Florida, yet results for predation were determined inconclusive due to large amounts of variation. More information is needed to accurately assess the impacts of different survey methods on sea turtle nesting, and it is recommended that the central hub of detailed nesting data be made more complete and readily available to the public for the sake of research, education, and transparency.

Poster Session, Poster # 20

Kinetic and Mechanism Studies of U(VI) Bearing Groundwater Treated with Sodium Silicate at the Savannah River Site

Alejandro Hernandez (DOE Fellow), Vasileios Anagnostopoulos, Yelena Katsenovich
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Abstract

The Savannah River Site (SRS) was one of the most significant sites for the production of materials related to the U.S. nuclear program during the early 1950s to late 1980s. An estimated 3.4 billion gallons of hazardous waste solution was received in the F and H Areas. Constituents of concern associated with the F and H Area Hazardous Waste Management Facility (HWMF) groundwater plume include tritium, uranium-238, iodine-129, strontium-90, curium-244, americium-241, technetium-99, cadmium, aluminum, and mercury. The use of sodium silicate injections was explored as a cost-effective and environmentally benign technology to restore a neutral pH to the contaminated groundwater and immobilize the contaminants of concern. This research focuses on kinetic and mechanistic studies in order to elucidate the sorption properties of U(VI) for SRS soil at circumneutral conditions.

Poster Session, Poster # 21

Study of Synergetic Interactions between Uranium, Humic Acid, Silica Colloids and SRS Sediments at Variable pH

Alexis Smoot (DOE Fellow)
Dr. Ravi Gudavalli, Dr. Yelena Katsenovich (Mentors)
Applied Research Center, Florida International University
10555 W. Flagler St, EC 2100, Miami, FL 33174

Abstract

The Savanah River Site's (SRS) F/H Area Seepage Basins received approximately 1.8 billion gallons of acidic waste containing radionuclides and dissolved heavy metals. This led to the creation of a highly contaminated groundwater plume with uranium (VI) as a key contaminant of concern within the plume. Humic substances (HS) are major components of soil organic matter having the ability to influence migration behavior and fate of heavy metals and are being investigated for potential use in environmental remediation at SRS. HS are polyfunctional, organic macromolecules able to carry a large number of functional groups which is an important function in ion exchange and is a metal complexing ligand with a high complexation capacity. Humic acid (HA) represents the fraction of HS soluble at pH greater than 3.5. Silica, naturally found in soil, is the term applied to solid forms with the stoichiometric composition of SiO_2. The colloidal silica used in this work is amorphous and nonporous in suspension. This investigation studied the synergistic interactions between four key components: U(VI), humic acid (HA), colloidal silica and SRS sediment; the interactions were studied under varying pH conditions. Multi-component batch systems containing 30 ppm HA, 0.5 ppm uranium and 3.5 mM colloidal silica were constructed to effectively analyze the removal of U(VI). The expectation of this investigation is to observe a high percentage of uranium removal at the low pH range and a steady increase with an increase in pH.

Poster Session, Poster # 22

Migration and Distribution of Natural Organic Matter Injected into Subsurface Systems at F/H Area at Savannah River Site

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Abstract

The F-Area seepage basins at Savannah River Site (SRS) have received approximately 1.8 billion gallons of low-level waste solutions, containing nitric acid, radionuclides and dissolved metals due to plutonium separation operations. The waste solutions became a source of contamination for groundwater and soil at the site, with U(VI) and other radionuclides above their maximum contaminant levels (MCL). Use of humic acid (HA) as a remediation technology has shown to be a potential approach for controlling mobility of radionuclides. HA has strong sorption capacity and uranium develop a strong bond at slightly acidic pH, thus limiting the mobility of uranium with flushing of SRS groundwater. Column experiments were conducted using SRS soil from the F/H Area to examine the sorption and desorption properties of HA in SRS soil.

Poster Session, Poster # 23

Sab-mediated signaling sensitizes uterine cancer cells to chemotherapy.

Aymun J. Ahmed[1], Iru Paudel[1], Sean M. Hernandez[1], and Jeremy W. Chambers[1,2*]
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Abstract

Metastatic uterine cancer (UtC) has a 5-year survival less than 8%. This mortality is associated with treatment resistance in metastatic UtC cells. There is an urgent need to identify the mechanisms contributing to resistance in UtC patients with metastatic disease in order to improve the patient survival.Mitochondria control cell death responses, yet cancer cells can develop mechanisms to avoid apoptosis and evade therapeutic approaches. We propose communication between the cell and mitochondria becomes altered during metastasis, and metastatic UtC cells

have mitochondria that can no longer process cell death signals. To address if mitochondrial-cell communication was altered during metastasis, we compared a human cell line derived from a primary site tumor (SK-UT-1) and another isolated from a metastatic site (AN-3-Ca). Analysis of the signaling proteins on the surface of the mitochondria in these two cell lines revealed that a scaffold protein, Sab, was down regulated in metastatic AN-3-Ca cells compared to SK-UT-1. Our previous research demonstrated that elevated levels of Sab induced mitochondrial dysfunction and apoptosis, ultimately enhancing chemo-responsiveness in gynecological tumors. We examined the apoptotic potential of SK-UT-1 and AN-3-Ca cells by measuring the levels of pro-survival Bcl-2 proteins and pro-death BH-3 only proteins. Our results indicate that metastatic AN-3-Ca cells had considerably higher levels of Bcl-2 proteins, while SK-UT-1 cells had higher levels of BH-3 only proteins. We found that AN-3-Ca cells were more resistant to taxane and platinum treatment than SK-UT-1 cells. To determine if diminished Sab-mediated signaling played a role chemo-resistance, we ectopically expressed Sab in AN-3-Ca cells. Elevating Sab levels in AN-3-Ca cells rescued chemo-responsiveness by decreasing Bcl-2 protein levels and increasing BH-3 only protein concentrations. We surmise that Sab-mediated signaling plays a critical role in treatment responsiveness in UtC, and that inhibiting Sab expression is a critical event in metastasis and chemo-resistance

Poster Session, Poster # 24

Spatial Language Use of Middle Schoolers in Math Think-Alouds

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Abstract

Spatial language involves describing direction, shape, dimension, features, and quantity (e.g. *up, cube, three-dimensional*). Spatial language is one aspect of spatial reasoning, which is an important predictor of success in Science, Technology, Engineering, and Mathematics (STEM) fields (e.g. Shea, Lubinski & Benbow, 2001; Wai, Lubinksi & Benbow, 2009). The purpose of my summer project was to understand the role of spatial language in 6th graders' sketching and self-explanation of math problems. Sketching during problem solving potentially supports spatial thinking (Edens & Potter, 2008), and may improve understanding of abstract and spatial relationships (Jee et al. 2009). Self-explanation may support taking novel information and organizing it to fit prior beliefs (Lombrozo, 2006) and has shown benefits for 3rd-5th grade students solving arithmetic problems (Rittle-Johnson, 2006). Few studies have explored whether children who use both sketching and self-explanation see significant improvements in learning. I worked on data from an ongoing study in which sixth grade students from Philadelphia schools were randomly chosen for each of five conditions: (1) read-only, (2) self- explain only, (3) sketch only, (4) self-explain then sketch, and (5) sketch then self explain. To code of the spatial language, I adapted and expanded a spatial coding system used with younger children (Cannon, Levine, & Huttenlocher, 2007). Analyses are ongoing and will form the basis of my senior honors thesis. We expect more spatial language in the sketch and then self-explain condition, and hope to make recommendations for improvements in classroom practices.

Poster Session, Poster # 25

Humanized relaxin receptor mouse model for testing small molecule modulators.

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Abstract

Newly recognized functions of relaxin (RLN) include vasodilatory, angiogenic, and antifibrotic properties. Data from clinical trials of relaxin treatment in acute heart failure indicated a significant decrease in patient lethality. Short half-life *in vivo*, possible immune response, and high production costs complicate chronic use of RLN. We have identified small molecule agonists of human relaxin receptor, hRXFP1. Stability, comparable activity, and low toxicity make the agonist a promising pharmacologic agent. This agonist failed to activate rodent receptors due to divergence of the amino acid sequence in the allosteric binding site, hampering testing of RXFP1 agonists *in vivo*. To overcome this, we produced humanized RXFP1 mice. Using gene targeting of ES cells, we inserted human gene cDNA with the internal ribosomal entry site into one of the mouse RXFP1 (mRXFP1) introns. The resulting knock-in allele is driven by the endogenous promoter whereas the mouse gene is disrupted. Using quantitative RT-PCR we have shown a similar expression pattern of both alleles in different organs of hRXFP1/mRXFP1 animals. To generate a line homozygous for hRXFP1, we intercrossed mice with hRXFP1 and its deleted allele and to produce hRXFP1/hRXFP1 homozygotes. Both diheterozygous and homozygous females showed normal fertility. The pubic ligament of pregnant females was measured at day 18.5 of pregnancy and was fully dilated. Analysis of mammary nipple differentiation and reproductive tract suggested full complementation of the disrupted mouse gene by the homologue. Taken together, these data indicate that humanized mice express fully functional human relaxin receptor, allowing testing of small molecule agonists of RXFP1 *in vivo*.

Poster Session, Poster # 26

Role of aromatic amino acids in the structure and function of DREAM protein

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Abstract

Calcium binding to DREAM has been shown to regulate many intracellular processes, such as neuronal signaling and gene expression. In this study, site-directed and tryptophan fluorescence were used to investigate the role of aromatic amino acids in the structural and functional stability of DREAM protein. DREAM possesses a single tryptophan residue that is ideally located at core of its structure. Tryptophan fluorescence is a highly sensitive approach to monitor changes in the molecular environment surrounding this amino acid. Initially, guanidium hydrochloride (GuHCl) was used to unfold DREAM constructs in which F218, F219, F252, or Y174 were mutated to alanine, which allowed us to determine their folding state and stability. Plots of the tryptophan emission maxima, as a function of GuHCl, in all DREAM mutants was characterized by two notable transitions similar to the wild-type protein. Highlighting that the substitutions did not significantly affect the protein structure. All DREAM constructs showed an intermediate state at ~4 M GuHCl. In addition, the calcium binding affinity was measured using an NTA-EGTA buffer. Calcium binding provides insight into the functionality of the EF-hands in this protein and allow us to monitor the impact on activity of the mutations. Calcium binding reveals that the affinity of the mutants can be drastically affected by remodeling of the hydrophobic cores in the EF-hand. These findings suggest that mutations do not alter the structure of protein, but rather modify its activity.

Poster Session, Poster # 27

Study of kisspeptin receptor in behavioral and gonadal sex change in *Thalassoma bifasciatum*, bluehead wrasse

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[2]North Carolina State University, Raleigh, NC

Abstract

The objective of this project is to determine if kisspeptin receptor (kissr2) is directly involved in the behavioral and gonadal sex change of a coral reef fish, *Thalassoma bifasciatum*, the bluehead wrasse. Sex change in the bluehead wrasse can be induced by a change in social structure. The field experiment was conducted on various coral reefs off Key Largo, Florida. All of the bluehead wrasse on the experimental reefs were collected. The females were measured, tagged, and released back onto the test reefs. The males were relocated to a distant reef. Behavioral data were collected by observing focal female's behavior after the removal of the dominant males. Tagged females were then collected at different stages of sex change, and their brains and gonads were removed for lab experiments. In the lab, RNA isolation, cDNA synthesis, qPCR, nanodrop, and gel electrophoresis were conducted on all brain samples. The expression of kissr2 in whole brain samples was compared among all stages of the sex changing fish and non-sex-changing females (controls). Kissr2 had similar levels of gene expression in whole brain samples across all stages of sex change, including controls, with no statistical difference among groups. These results suggest that kissr2 does not play a role in sex change or that a subtle involvement of kissr2 is not detectable at this level. Future studies will focus on the preoptic lobe and may identify expression of kissr2, kiss2 and gnrh2 in specific neurons to determine the role of these genes in sex change.

Poster Session, Poster # 28

Fluorescent Selective Delta Opioid Receptor Peptides from Cyclic Library

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Abstract

A cyclic peptide library was built on mercaptomethylphenyl functionalized silica gel and modeled after a pentapeptide thioester scaffold. Position R1 always has glycine and R3 always has diaminopropionic acid. This library was tested on binding assays for the delta, kappa and mu opioid receptors. There was significant activity for mu and delta but not for kappa. Individual delta selective compounds were prepared and tested in assays for all three receptors. By screening the cyclic peptide library, the delta selective sequences are identified and the biologically active novel fluorescent peptides will be exhibited.

Poster Session, Poster # 29

Gene expression of brain aromatase during socially-induced sex change in a coral reef fish

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[2]Department of Biological Sciences, North Carolina State University, Raleigh NC

Abstract

Sex steroid hormones produced in the gonads are important in sexual differentiation, but less is known about the actions of sex steroids produced in the brain. Socially-induced sex change in fishes offers the opportunity to explore the roles of sex steroids in the brain on sex-specific behavior and differentiation. This project focused on expression of *cyp19a1b*, which encodes the brain form of aromatase in teleost fishes that synthesizes estradiol. Our model organism is the bluehead wrasse (*Thalassoma bifasciatum*), a species in which females and initial phase (IP) sneaker males can change to dominant terminal phase (TP) males when TP males are removed. This project assessed changes in *cyp19a1b* mRNA in the brain during socially-induced sex change. We tagged large females and induced sex change by removing TP males from the reefs. We measured expression of *cyp19a1b* mRNA in females, IP males, TP males, and sex changers. Our

results showed that females had greater expression of cyp19a1b mRNA than TP males, who had greater expression than IP males. Females and very early sex changers with functional ovaries had greater expression than sex changers whose ovaries were degenerating or had initiated testicular development. Importantly, since sex changers showed a change in behavior before *cyp19a1b* mRNA levels dropped, this may suggest that *cyp19a1b* may not be entirely responsible for behavioral changes and that expression is dependent on the gonads. Overall, a decrease in brain aromatase occurs with sex change in the bluehead wrasse and may facilitate sex change in teleost fishes more generally.

Poster Session, Poster # 30

Generation Time of *Candidatus* Liberibacter asiaticus using bacterial growth equations

Amelia Champion[1] and Mark Hilf[2]

[1] Indian River State College, Fort Pierce, Fl.

[2] United States Department of Agriculture, Fort Pierce, Fl.

Abstract

Candidatus Liberibacter asiaticus is responsible for causing the citrus greening disease in citrus varieties. Cultivation of the bacteria has been unsuccessful, leaving the majority of basic biological function unknown. In a plant with an established infection, the growth rate of bacteria in new flush has not been determined. The purpose of this research was to track the movement and colonization of *Ca.* L. asiaticus through new flush of *Citrus macrophylla* (Cmac) and *Citrus sinensis* (Ridge Pineapple) species. Using the averaged Ct values produced from real-time PCR assay, the population of each experimental group was determined. By applying bacterial growth equations to the data generated, the generation time of *Ca.* L. asiaticus in both species can be determined. Assuming binary fission as the mechanism of cell division for *Ca.* L. asiaticus the average population in Cmac and Ridge Pineapple samples increased over 30 and 60 days. By the 90 day sampling, *Ca.* L. asiaticus reached the stationary phase in each species. This research provides basic, necessary information about *Ca.* L. asiaticus that can be used in treatment of citrus greening.

Poster Session, Poster # 31

Mycobacteriophage in Southeast Florida: Genomic characterization of three new phage and comparative analysis of an expanding repository of isolates

Ivana Meservey, Santiago Hernandez, Brian Boring, Cayce Douthitt, Phaedra Geer, Kristin Lanzana, Megan Mcart, Morgan Miller, Jessica McMahon, Jessica Nelson, Esperanza Ortiz, Helen Wiersma-Koch, Tom D'Elia

Indian River State College, Ft. Pierce, FL

Abstract

During August of 2015, a total of eleven new mycobacteriophage capable of infecting *Mycobacterium smegmatis* mc^2155 were isolated and characterized from soil samples from southeast Florida. Additionally, the complete genome sequences have been generated, annotated and analyzed for three of these phage. Including previous phage isolates, there are now 22 total mycobacteriophage and six genome sequences collected from Indian River, Martin and St. Lucie counties in Florida. Comparative analysis of this repository has provided insight into phage genome evolution and diversity in subtropical ecosystems. Based on complete genome sequences available, the isolated phage belong to the A and L clusters within the mycobacteriophage classification system. When analyzing the phage diversity at the subcluster level, three A2, two A9 and one L3 phage have been identified based on whole genome sequence analysis. Further classifications based on restriction digestion and PCR analysis has predicted a more diverse phage population, with potential members of other subclusters. The sequenced A2 phage collected in this study were analyzed in comparison to the nationally collected A2 phage for genomic

signatures that could correlate to geographical location. Further phylogenetic analysis was performed to identify if a commonly used taxonomic gene (tapemeasure protein) could produce clades of related A2 phage based on geographical sources of collection. Understanding mycobacteriophage diversity and geographical distribution is important when designing new strategies to seek out novel phage. Insights gained from the unique mycobacteriophage will provide valuable insights of the molecular biology of the host/phage interactions and potentially lead to a richer understanding of *Mycobacterium tuberculosis.*

Poster Session, Poster # 32

Isolation and characterization of *Xanthomonas fragariae* bacteriophages

Morgan Miller[1], Helen Wiersma-Koch[1], Bill Turechek[2] and Tom D'Elia[1]

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[2] *United States Department of Agriculture, Ft. Pierce, FL*

Abstract

Bacterial angular leaf spot (ALS) is a potentially devastating disease of strawberries and is caused by the gram negative bacterium *Xanthamonas fragariae.* In order to evaluate potential control and prevention strategies, bacteriophages capable of infecting *X. fragariae* were isolated using enrichment methods. Leaves from 24 affected plants and 24 soil samples were collected from a strawberry crop which tested positive for ALS in Fort Pierce, Florida. Three isolates of *X. fragariae* collected from the same infected field were used to prepare enrichment cultures of the soil and leaves. A total of three individual plant and one soil samples tested positive for bacteriophages after spot testing the enrichment supernatant on lawns of host cells. Several unique phage from the separate samples were identified based on plaque morphology. Both the diameter and turbidity of the plaques varied for the isolated phage. Observations of the lytic phage recovered indicate variation in degrees of infectivity based on differential rates of clearing when grown on lawns of host cells. Enrichment strategies for isolating phage are not fully capable of representing the entire phage diversity present in a given environment. Therefore, the identification of distinct plaque morphologies indicates that the *X. fragariae* phage population may be diverse and warrants additional characterization. Further analysis of host range, thermal inactivation, UV sensitivity and genomic characterization will provide more insight to the potential use of these phage isolates in disease control for ALS.

Poster Session, Poster # 33

Taxonomic and functional analysis of a feather degrading microbial community using metagenomics

Karina Moesch, Sherry Bowen and Tom D'Elia

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Abstract

A disease known as pink feather syndrome has become an increasing concern over the last ten years. Feathers of swans that are affected by this illness become frail and lose their function in repelling water, ultimately leading to hypothermia and death of the swans. Previously, we utilized culture-dependent methods and screened bacterial isolates for keratinolytic activity. The results concluded that four isolates from the Firmicutes, Actinobacterium and Deinococcus-Thermus phyla likely provided the greatest contribution to the degradation of the feathers. This current study is the first report utilizing shotgun metagenomics DNA sequence analysis to analyze feather microbial communities and to screen for genes with functional capabilities related to protein degradation. Illumina DNA sequence data from two affected feathers was generated and analyzed by the metagenomics analysis server, MG-RAST. Taxonomic classifications and functional

annotations of the microbial community related to each feather were determined. At the phylum level, the two samples differed in the relative abundance of microorganisms significantly, and were primarily composed of Firmicutes (19.1%) or Deinococcus-Thermus (34.3%). These findings are consistent with the prevalence of these phyla detected with culture methods, and further support their association with microbial communities contributing to feather degradation. Functional annotation of metabolic genes compares between the sequence sets for protein metabolism (7-8% relative abundance), with 14-18% of the protein metabolism related specifically to protein degradation. These results provide a comprehensive analysis of relative abundance of key microorganisms related to feather degrading microbial communities, and potential metabolic pathways associated with this condition.

Poster Session, Poster # 34

On the occurrence of Leptogium species at North Miami

Boonrasee Akkarakij; M.; Ana Documet; Maylin Ginestra; Johana Gandur; Yohanna Mederos; and C. Fernandez

Abstract

Collemataceae ("jelly lichens") is a large family of fungi forming lichen symbiotic associations with cyanobacteria of the genus *Nostoc*. The main characteristic of these lichens is their gelatinous appearance when wet. Their epiphytic occurrence in shady humid forests is important because of their double function as a photosynthetic and a nitrogen-fixing symbiosis. The presence of a cortex is commonly used to separate the two common genera *Collema* and *Leptogium*. In the present work we describe the distribution of cortex-forming jelly lichens in twenty trees of a specific area at the North Campus of Miami Dade College.

Poster Session, Poster # 35

Phonoresponses of Syntomeida epilais (Lepidoptera, Noctuoidea) perched females to acoustic stimuli present in their environment

Alexandra Cano, Monica Navarro, and Frank Coro, Ph.D.
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Abstract

The study of the neural bases of behavior is an essential part of Neuroscience. A biological object with a complex behavior, such as courtship, and with a small number of neurons involved, would improve the success of such research. Syntomeida epilais is one of the few moth species that have two-celled ears and use acoustic communication during their courtship behavior. Other moth species with two-celled ears are known to acoustically interact with their predators, insectivorous bats. Our aim was to study the discriminating abilities of S. epilais perched females during their courtship time (3:00 – 6:30 AM) when stimulated with conspecific male and female emissions, as well as attack sequences from 3 insectivorous bat species. All the stimuli applied are within the same frequency range (between 15 and 55 kHz), which corresponds with the power spectra of the moth emissions. The acoustic stimuli applied and the phonoresponses from 23 females were digitized using a microphone sensitive in the ultrasonic range and further analyzed using BatSound software. The response variable measured was the number of modulation cycles (MC) emitted by the females when presented with the different acoustic stimuli. S. epilais females responded with more MC per second to their conspecific male signals than to the rest of the acoustic stimuli applied and also present in their environment. Considering the small amount of their auditory neurons, this moth species shows high discrimination abilities not previously described in other species with two-celled ears.

Poster Session, Poster # 36

Towards Carbon-Based Nanotechnology: Supramolecular Rectification via Electrostatic Doping of Metallic (9,0)-Zigzag Single-Walled Carbon Nanotubes.

Susana Cruz-Diaz, Michael Cartamil, Norton Nieves and Servando Muñoz.
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Abstract

Our research concerns molecular rectification in metallic single-walled carbon nanotubes via an electrostatic doping mechanism. Previous calculations showed that a guest (9,0) zigzag single-walled carbon nanotube becomes polarized within the cavity of a self-assembled cyclic β-peptide nanotube host made up of hydrogen-bonded cyclo-[(L)-(β)-aminobutyric acid]$_9$ monomers. Hartree-Fock 3-21G electrostatic potential maps showed that the polarization of the π-electrons on the carbon nanotube is antiparallel to the macromolecular dipole of the host. Hartree-Fock STO 3G calculations suggested that the frontier molecular orbitals of the guest are translocated to opposite termini under the host's electric field. We reasoned that the same effect should be observed if the multiatomic cyclic β-peptide nanotube were replaced by a dissociated KCl ion pair in which the corresponding cation and anion are permanently positioned on opposite tube termini separated by a distance equal to the length of the carbon cylinder. Hartree-Fock 6-31G* electrostatic potential maps and frontier molecular orbital calculations confirmed the presence of an electrostatic doping mechanism.

Poster Session, Poster # 37

Qualitative Metabolic Network Reconstruction of the Bacterium *Clostridium taeniosporum*

Salvador Rocha, Erick I.[1], Blinkova, A.[2], Hunicke-Smith, S.[2], Walker, J.R.[2], and Ginés-Candelaria, E.[1]1: Miami Dade College, Wolfson Campus, Department of Natural Sciences, Health & Wellness, Miami, FL2: Molecular Biosciences, College of Natural Sciences, University of Texas at Austin, Austin, TX

Abstract

Clostridium taeniosporum is a Gram-positive, nonpathogenic, and anaerobic bacterium that was isolated from Crimean silt. The organism is approximately 98% homologous in 16S rRNA gene to toxigenic *Clostridium botulinum* phylogenetic Group II strains. Using the software Pathway Tools it was possible to create an inferred metabolic cell-model for *Clostridium taeniosporum.* The metabolic reconstruction consisted of an automatic inference phase followed by a manual curation phase. The automatic phase was performed by the PathoLogic component of the Pathway Tools software, using the annotated genome of *C. taeniosporum*. We manually curated the inferred metabolic reconstruction by assigning reactions to ambiguous enzymes, creating complex proteins, inferring operons and creating new transporters. Our results predicted a total of 203 pathways along with 1231 enzymatic reactions catalyzed by 842 different enzymes and a total of 54 transporters involved in 77 transport reactions. The metabolic model for *C. taeniosporum* predicted chemical pathways that have been previously confirmed experimentally such as the production of both butyric and acetic acid. Our model also inferred metabolic pathways that have not been tested yet, such as resistance to triclosan and beta-lactam antibiotics. Using the metabolic reconstruction of *C. taeniosporum* it could be possible to construct a steady-state metabolic flux model. Such model can have diverse applications in metabolic engineering, phenotypic predictions, and studies of evolutionary processes. In addition, the metabolic reconstruction is the first major step in an effort to elucidate more complex metabolic mechanisms such as endospore formation, spore appendage generation and other relevant biochemical properties in *Clostridium taeniosporum.*

Poster Session, Poster # 38

Towards Carbon-Based Nanotechnology: Electrostatic Potential Maps, Molecular Nanotopography and Electrical Conductivity of Guest (9,0)-Zigzag Single-Walled Carbon Nanotubes Within Host Cyclic Peptide Nanotubes.

Liana Roque, Norton Nieves, and Servando Muñoz
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Abstract

Cyclic peptides made up of alternating (D)- and (L)-**α-aminoacids** are characterized by the parallel orientation of the C- and N-residues along their circumference. Self-assembly through intermolecular hydrogen bonding generates a nanotube with a net dipole of zero along the central axis. Cyclic peptides made up of **β-aminoacids** are characterized by an antiparallel orientation of the C- and N-residues along their circumference. Self-assembly through intermolecular hydrogen bonding generates a nanotube with a macromolecular dipole directed away from the electrophilic amino groups towards the electron-rich carbonyl groups along the cylinder's axis. Hartree-Fock 3-21G electrostatic potential maps show that a (9,0) zigzag single-walled carbon nanotube guest within a self-assembled α-peptide nanotube made up of cyclo [(D- Ala-L-Ala)$_6$] remains metallic as demonstrated by the extensive π-electron delocalization along the carbon cylinder's surface. Conversely, a (9,0) zigzag single-walled carbon nanotube guest within a self-assembled β-peptide nanotube made up of cyclo [(L-3-aminobutyric acid)$_9$] is polarized in a direction antiparallel to that of the host's macroscopic dipole.

Poster Session, Poster # 39

Towards Dioxygen Evolution from a Synthetic Spontaneously Self-Assembled Supramolecular Leaf: A Novel Mechanism for the Photooxidation of Water via the Keto-Enol Tautomerization of Chlorophyll a.

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Abstract

Dioxygen evolution from the photooxidation of water in green plant photosynthes is a fundamental event in energy transduction and storage. Absorption of four red photons causes two water molecules to be oxidized releasing dioxygen, four electrons, and four protons.To an organic chemist, the most intriguing structural property of chlorophyll a is the presence of a β-ketoester functional group in ring V. Thus the molecule can participate in keto-enol tautomerization. From a supramolecular perspective, the enolate form of chlorophyll a is amphiphilic and can spontaneously self-assemble in water: the macrocyclic ring is negatively charged and functions as a hydrophilic headgroup anchor while the long phytyl chain serves as the hydrophobic tail. We have used ab initio self-consistent field Hartree-Fock 3-21G and Density Functional Theory quantum chemical methods to study the interaction between water that is hydrogen bonded to the β-ketoester enolate. Spin density maps show that one-electron oxidation of the supramolecular assembly leads to hydrogen atom transfer from water to the macrocycle. Thus, intramolecular, single electron transfer "resets" chlorophyll while simultaneously generating a hydroxyl radical. Oxidation of two self-assembled cofacial porphyrin macrocycles within Van der Waals contact of each other produces a pair of OH radicals that recombine to generate a metastable hydrogen peroxide molecule, H_2O_2. Subsequent removal of two additional electrons releases molecular dioxygen, O_2, from the synthetic, spontaneously self-assembled, supramolecular leaf.

Poster Session, Poster # 40

Resonance as a Driver of Extinction in a Population of Engineered Bacteria.

Nina Argibay, Cortney Wilson and Robert P. Smith, Ph.D.
Nova Southeastern University, Fort Lauderdale, FL

Abstract

Bacterial communication plays critical roles in the regulation of gene expression, including genes involved in the organization and assembly of biofilm structures, and pathogenesis. Most often, communication between bacterial cells is mediated by a small diffusive molecule called an autoinducer. Here, each bacterium in the population secretes a given amount of autoinducer. Once the autoinducer reaches a critical concentration, it alters the gene expression. Previous studies have demonstrated that the spatial organization of bacteria cells is important in determining the critical concentration at which gene expression is altered. Despite this observation, it remains unclear as to how periodically reorganizing the spatial structure of a bacterial population can enhance, or disrupt, bacterial communication. In this study, we use a strain of engineered bacteria, which requires communication for survival, to investigate the effects of periodic spatial disruption to bacterial communication. Using a microfluidic flow chamber, we first quantified the effects that shaking a bacterial population had on their spatial distribution. Here, we observed a non-intuitive biphasic relationship between shaking time and average distance moved by the bacteria. Building on this, we next performed high-resolution microplate reader growth assays to determine the effect of this biphasic relationship has on survival of our engineered bacteria. Our results suggest that resonance between the bacterial population and the environment may alter the ability of bacteria to communicate successfully, which may have implications in the treatment of infectious diseases.

Poster Session, Poster # 41

Frozen Brain Atlas: Individualized Brain Mapping for Receptor Autoradiography Analysis

Samantha Bergoine, Natalie A. Builes, Dominick J. Casciato, John Reynolds, Benjamin Chilampath, Leena Couling, Robert C. Speth, Ph.D.
Nova Southeastern University Halmos College of Natural Sciences and Oceanography, Nova Southeastern University College of Pharmacy

Abstract

The Frozen Brain Atlas provides students, educators, and scientists with a tool to further explore the architecture of the brain. Current brain atlases enable users to navigate sectioned brain tissue using histological staining; however, they fail to capture naturally visible structures post sectioning. Through immediate post sectioning image collection, the natural contrast of the brain reveals unique structural details that are rarely seen by traditional staining procedures. By utilizing indexing and interactive labeling, the Nova Southeastern University Frozen Brain Atlas allows for the identification of brain regions when used as a correlative tool for modalities including receptor autoradiography, immunofluorescence, and other anatomical methods.

Poster Session, Poster # 42

Using Engineered Bacteria to Explore Biological Invasions

Josue Conde, Neil Thacker and Robert P Smith, Ph.D.
Nova Southeastern University, Fort Lauderdale, FL

Abstract

One critical ecological challenge is to circumvent invasion from non-indigenous organisms. Studying the factors that affect the ability of a non-indigenous species to colonize into a new territory is very challenging due to multiple confounding factors. Synthetic biology is often not

subject to these confounds, and thus we utilize it to explore factors that allow invasive species to successfully invade a new area. Specifically, we use engineered bacteria that are programmed to have an Allee effect, a fundamental growth dynamic that is observed in most invasive species. Using these bacteria, we take a two-pronged approach. First, we examine how the engineered bacteria spread in a continuously connected environment. Here, the bacteria were inoculated into a defined location of a microplate well and allowed to spread, the rate at which was controlled by the density of agar in nutrient medium. We used high resolution OD600 measurement to quantify growth at various area of the well. From this, we discovered unique growth patterns that may help to predict how fast an invasive species travels in a new environment. Second, we examined the effect of repeated introduction of the engineered bacteria into a novel environment. Here, we grew the bacteria in medium with different agar densities, which controlled their spread rate. At various intervals, we reintroduced a defined amount of bacteria and examined growth using colony forming units. Our results may indicate a unique principle that dictates survival and extinction for an invasive species with an Allee effect.

Poster Session, Poster # 43

Adenosine Deaminase SNP Associates with Evening Melatonin Levels and Self-Reported Sleep Measures

Franklin Hiffernan and Jaime L. Tartar, Ph.D.
Nova Southeastern University, Fort Lauderdale, FL

Abstract

Increased adenosine levels throughout the day promote sleepiness; this chemical is broken down by the enzyme adenosine deaminase (ADA). A single nucleotide polymorphism (SNP) in the ADA gene (rs73598374) has been shown to affect sleep regulation. This ADA SNP substitutes a G allele with an A allele, thus reducing ADA enzymatic activity and resulting in higher adenosine levels. Consistent with the idea that adenosine promotes sleepiness, carriers of the A allele show elevated sleep pressure and increased EEG measures of deep (delta) sleep. Aside from these findings, the extent to which lower ADA enzymatic activity is associated the homeostatic sleep factor, melatonin, is uncertain. This association is a distinct possibility, however, because adenosine has been shown to increase melatonin production in rat pineal glands. In order to test this possibility, we examined the extent to which the ADA polymorphism is associated with evening melatonin levels, along with several measures of self-reported sleep. Our findings support the idea that adenosine can enhance melatonin levels. Relative to the GG group, the AG group had significantly increased melatonin levels ($F(1,83) = 7.68$, $p < 0.01$). The GG group also had greater self-reported sleep difficulty ($F(1,83) = 5.45$, $p = 0.02$). There was not an effect of the ADA genotype on the a sleep quality global score; however, there was a significant effect of ADA genotype on the sleep duration PSQI component ($F(1,83) = 7.66$, $p < 0.01$). These results demonstrate newly discovered relationships between the ADA SNP, evening melatonin production, and sleep quality.

Poster Session, Poster # 44

Reactive oxygen species production during oxidative stress in lymphoblastoid cell lines in autistic children

Hannah Mathew, Jordan Spaw, Ana Castejon, Ph.D.
Nova Southeastern University, Davie, FL.

Abstract

Autism is a neurodevelopmental disorder that is characterized by deficits in social interaction, communication and repetitive behaviors. As the prevalence of the disorder increases, the need to understand the cause to account for its treatment increases. Besides the genetic factors that attribute to the cause, studies have examined other environmental factors that may lead to a diagnosis of

autism. Children with autism are thought to be more susceptible to oxidative stress, which may contribute to the pathological nature of the disorder. Studies have shown nearly 35% of autistic children have low glutathione levels. Glutathione is an antioxidant that the body creates to reduce oxidative stress; which could lead to oxidative damage to the brain and periphery. The purpose of this study will be to examine whether lymphoblastoid cells (LCLs) from autistic patients are more vulnerable to oxidative stress than cells of neurotypical controls. The study will investigate the effects of 2,3-dimethoxy-1,4-naphthoquinone(DMNQ), a mitochondrial oxidized stressor, on the LCLs. Very few studies have been conducted to understand how DMNQ induces cytotoxicity and its effects. Levels of intracellular reactive oxygen species (ROS) will be quantified via the use of dichlorofluorescein(DCF) assays in LCLs from both autistic and neurotypical children using a plate reader. We hypothesize that children with autism will have higher ROS levels at baseline and after treatment with the DMNQ. The findings of this study will advance our understanding of how LCLs from autistic patients respond to oxidative insult, which will contribute to future studies to reduce oxidative stress-induced cytotoxicity.

Poster Session, Poster # 45

Quick Contrast Sensitivity Function Testing in Adults without Ocular Disease and Patients with Retinitis Pigmentosa

Manonmani Murugappan; Jeslyn Vayalil; Mark Jaffe, DPM; Ava K. Bittner, OD, PhD
Nova Southeastern University; Ft. Lauderdale, FL

Abstract

The study objective was to determine the reliability and range of results for area under the log contrast sensitivity function (AULCSF) measures obtained with the quick contrast sensitivity function (qCSF) test in adults without eye disease and those with retinitis pigmentosa (RP). Nineteen RP patients and 63 adults with normal visual acuity (VA >20/25) and no ocular disease repeated qCSF testing at two sessions within ~1 week binocularly and monocularly, as well as with a 4% transmission filter simulating low illumination in a subgroup of normals and RP patients. Compared to younger subjects aged 20-49 years with mean AULCSF 1.73 and 1.44 for qCSF testing binocularly and monocularly, respectively, normal participants aged 50-69 had statistically significantly reduced AULCSF measures (mean 1.49 and 1.23; $p \leq 0.001$) and those over age 70 had significantly reduced AULCSF when compared to those aged 50-69 years (mean 1.19 and 0.99; $p \leq 0.01$). Normals aged 70-89 years had a significantly greater difference in monocular AULCSF with versus without the filter by 23% than normals aged 20-49 years (95% CI: 11-34%; $p<0.001$), likely mediated by natural rod sensitivity loss with aging. AULCSF results for some RP patients were significantly reduced relative to age-matched normals. Mean coefficients of variation for AULCSF were 2-9% and 7-12%, for normals and RP, respectively. We measured age-related declines in qCSF using this new, rapid test procedure that provides repeatable results across both younger and older adults with normal vision or RP, which may be used as a precise outcome measure during clinical trials.

Poster Session, Poster # 46

Urbanization Effects on Size and Fecundity of *Nephila clavipes*

Ashley Lonergan, Jake Ripp and Paul Arena, Ph.D.
Nova Southeastern University, Davie, Fl

Abstract

The Golden Orb Weaver, *Nephila clavipes*, is the largest non-tarantula spider species and commonly colonizes urban habitats. This species relies on trapping aerial prey in its large vertically oriented webs. Urban habitats tend to be warmer (due to the heat island effect), harbor an

abundance of light attracted prey species, and contain reduced densities of large native predators (bats and birds) when compared to natural areas. These attributes may provide *N. clavipes* with an optimal habitat which enhances their overall productivity. We examined the effects of increasing levels of urbanization and light intensity on body size and fecundity of *N. clavipes*. We hypothesized this species may be an urban exploiter and that individuals would be larger and more fecund in urban areas when compared to natural areas. Morphological and physical data were collected and lipid concentration was determined using a bioassay as a measurement of fecundity. Overall, urban spiders were significantly larger ($p<0.05$) than spiders in natural areas, supporting the notion that this species benefits from urban habitats. There was a weak correlation between spider size and distance to light source, as well as lumen exposure, indicating other factors may be contributing to the size differences noted in addition to light. Previous research has generally demonstrated negative effects of urbanization on local species, however, this study provides evidence suggesting that *N. clavipes* might benefit and exploit resources in this environment.

Poster Session, Poster # 47

Increased Proliferation of Human Neural Stem Cells Following Selective Agonism of Angiotensin II AT1 Receptor

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Nova Southeastern University Halmos College of Natural Sciences and Oceanography, Nova Southeastern University College of Pharmacy

Abstract

Angiotensin II is a potent hormone in the brain Renin-Angiotensin System. Altered levels of angiotensin II has been linked to synaptic dysfunction and neurodegenerative diseases. Recently, the angiotensin II receptor subtypes AT1 and AT2 were found to be expressed in neural stem cells. The purpose of this study is to enhance our understanding of how human neural stem cell (hNSC) proliferation and differentiation are affected by selective activation of the angiotensin II system through either the AT1 or AT2 receptor. We hypothesized that stimulating the AT1 receptor would induce proliferation and stimulating the AT2 receptor would induce differentiation upon addition of selective agonists. H-9-derived hNSCs were grown in cell culture medium supplemented with epidermal growth factor and basic fibroblast growth factor (proliferation medium) or without added growth factors (differentiation medium). The cells were treated with a nonselective agonist of Ang II receptors (Sar1, Ang II, 100 µM once daily) in the presence of the AT2 receptor blocker PD 123319 (10 µM once daily) to selectively stimulate AT1 receptors, CGP42112 a selective AT2 receptor agonist (100 µM once daily), PD123319 a selective AT2 receptor antagonist (10 µM, once daily), or saline for two weeks. Additional methods used included immunofluorescence, cell death assays, microscopy and N.I.H. ImageJ analysis. Statistical evaluation included ANOVA and post-hoc comparisons. Preliminary cell proliferation data demonstrate that AT1 receptor agonism significantly increased cell proliferation in differentiation growth condition but not proliferation growth conditions. These data suggest neurogenesis may be modified by the brain Renin-Angiotensin System.

Poster Session, Poster # 48

Effects of Editing Defective Alanyl-tRNA Synthetase on B-cell Lymphoma Development

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Palm Beach State College, Palm Beach Gardens, FL
The Scripps Research Institute, Jupiter, FL

Abstract

In 2015, the National Cancer Institute estimated 1,658,370 new cancer cases in the United States alone, 80,900 of which stemmed from lymphoma. Only 66.2% of all cancer cases survive 5 or more years after initial diagnosis. Such low survival rates have prompted a push for new therapeutic targets, including editing defective aminoacyl-tRNA synthetases (AARSs). It has recently been suggested that editing defective AARSs could be utilized to hinder cancer cell development. AARSs play an important role in protein translation by catalyzing the attachment of specific amino acids to their cognate transfer RNA molecule. Mutations in these enzymes can decrease protein translation fidelity through the mischarging of tRNA molecules, which ultimately lead to an intracellular accumulation of misfolded proteins followed my cell death. In this experiment, mutant mice with naturally occurring editing defective alanyl-tRNA synthetases (AlaRS) were crossed with an EμMyc B-cell lymphoma tumor model and followed for tumor development with a hypothesis that mice carrying at least a single AlaRS mutation would be saved from tumor development; however, findings revealed that crossing the AlaRS mutants with the EμMyc model appeared to enhance tumor development, suggesting that the mutation has no positive impact on the survival rates of the mice thus far. The transgenic animals will continue to be followed, with their tumors necropsied and scored by weight and size. In addition, the transgenic mice's survival rates will be compared to the survival rates of mice lacking the EμMyc oncogene to verify that death is the direct result of lymphoma.

Poster Session, Poster # 49

Utilizing Small Molecules to Inhibit Enzymatic Processing of Micro RNA

Anthony Vargas, Jessica Childs-Disney, Ph.D., Matthew D. Disney, Ph.D.
The Scripps Research Institute, Jupiter, FL

Abstract

The focus of this research is to identify and determine the potency of certain small molecules to bind to primary and precursor micro RNA in order to inhibit the function of the enzymes Dicer and Drosha. Initial compound efficacy was tested by measuring the displacement of the fluorescent indicator TO-PRO-1. After that we tested the compounds ability to block Drosha/Dicer binding by using fluorophore tagged DNA beacons that bonded to the RNA cleavage products of enzymatic processing. Of the initial 75 pentamidine and Hoechst-like compounds used in these assays only 4 showed potential competitive binding capabilities against Dicer and Drosha and of those only 2 showed specific affinity for the Drosha site. No Dicer site specific binders were identified in this protocol. Based on these results we will widen the search to include more compounds while continuing testing on the 4 successful compounds from this series of assays.

Poster Session, Poster # 50

Bacterial community patterns associated with different earthworm-based organic fertilizers.

Joana Almeida and Dora Pilar Maul Ph.D.
St. Thomas University, Miami Gardens, FL.

Abstract

While many bacterial species are commonly found in all types of soil, the bacterial community found in a particular type of soil depends on the structure of the soil, the vegetation, the nutrients and climate characteristics associated with it. Among the organic fertilizers, worm tea, made from earthworm castings is known to increase the bacterial population in the soil, thus providing the plants with more nutrients. Worm tea fertilizers are prepared with fresh castings brewed under oxygenated conditions with common sucrose and nitrogen additives. During the spring of 2015, an experiment conducted at the STU Organic Garden tested the effect of three different recipes for earthworm-based liquid fertilizers (worm teas) on the growth of arugula (*Eruca sativa*) plants. The

purpose of this study was to compare bacterial communities associated with soil fertilized with the different types of worm teas where the arugula plants grew. Using soil bacterial DNA isolation, primer design, polymerase chain reaction and agarose gel electrophoresis we were able to visualize to some extent the abundance and diversity of the bacterial community associated with soil fertilized with each type of worm tea. Bacterial universal primers revealed abundance of bacteria in all three worm tea-fertilized soil as well as in the control. Specific primers designed for a subset of bacterial species showed that bacterial community patterns differed among all three types of fertilized soils.

Poster Session, Poster # 51

In vitro citrus micropropagation as a potential system for the study of Huanglongbing disease (HLB)

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Abstract

Huanglongbing (HLB) also known as citrus greening is a bacterial disease caused by *Candidatus Liberibacter asiaticus (*CLas), a bacterium that lives only in citrus phloem. The Asian citrus psyllid (*Diaphorina citri*), is the vector responsible for spreading CLas from tree to tree. In addition to yellowing of leaves and shoots, HLB causes trees to produce hard and bitter fruit. Increasing yield losses every year in Florida are a big threat to the Citrus industry. Currently there is no effective treatment against HLB; once trees begin to exhibit symptoms they continue to decline. HLB is an especially challenging disease to research because it is caused by an insect-vectored, phloem-limited bacterial plant pathogen, and because research on citrus in general is difficult. We are interested in developing the simplest model system possible to study the effect of CLas infection on citrus. The objective of this project was to determine if the use of *in vitro* citrus plants can be used to study the effects of CLas infection on citrus. 26-month old *in vitro* Key lime plants were exposed to ACP known to be infected with CLas and then tested to determine if infection had occurred and if HLB symptoms subsequently developed. Twenty days following transfer to potting mix, DNA was extracted from tissue samples and assayed for CLas using quantitative PCR. We found that 20% of the plants exposed to the psyllids were successfully infected with CLas. Seedlings are being monitored to determine if symptoms of HLB become apparent.

Poster Session, Poster # 52

Antioxidant Performance of Popular Natural Extracts and Beverages

Luis E. Castellar, Christine Curiac, and Luis C. Fernandez-Torres Ph.D.
St. Thomas University, Miami Gardens, FL.

Abstract

A chemical clock or oscillating reaction is a complex mixture of reacting chemical compounds in which the concentration of one or more components exhibits periodic changes, or where sudden property changes occur after a predictable induction time. The aim of the present study is to evaluate the antioxidant presence in some popular beverages and supplements by using the Briggs-Rauscher reaction. When an antioxidant is present in any of the substances, the free radical production was staggered in the oscillating reaction. A free radical production is uncharged molecule (typically highly reactive and short-lived) having an unpaired valence electron. The various samples used, namely, pomegranate, açai, Vitamin water, and smoothies, showed the presence of antioxidants. Vitamin A was the antioxidant that showed no reduction in free radical production. We also did not observe UV degradation of the antioxidants, but exposure to open air did affect antioxidant performance.

Poster Session, Poster # 53

Is *in vivo* neuronal morphogenesis and wiring regulated by Hedgehog signaling?

Deliabell Hernandez, Leana Ramos, Normila Barthelemy, Milagros Mulero, Karla Rodriguez, Jossias Genao and Alexis Tapanes-Castillo Ph.D.
St. Thomas University, Miami Gardens, FL.

Abstract

Neurons exhibit complex and diverse morphologies. The shape of a neuron has important functional implications, as it determines what signals a neuron receives and how these signals are integrated into neuronal circuits. Work in *Drosophila melanogaster* has begun to identify mechanisms of neuronal morphogenesis and circuit formation that are evolutionarily conserved with vertebrates. Our study focuses on the Hedgehog signaling pathway. Previous data from cultured embryonic day 18 rat hippocampal neurons reveals that decreasing Hedgehog signaling activity reduces neurite length and branching (arborization), while increasing Hedgehog signaling activity increases neurite length and branching. Based on these results, we hypothesize the Hedgehog signaling pathway regulates neuronal morphogenesis *in vivo*. We predict that experimental manipulation of Hedgehog signaling proteins, using the GAL4/UAS system, will change dendrite arborization of class IV multidendritic larval body wall epidermal sensory neurons, as well as the circuit architecture of the nociceptive sensory nervous system. Using Sholl Analysis, we are comparing the dendritic arborization of wildtype control larvae, larvae expressing RNA interference (RNAi) constructs targeting *hedgehog* and *patched* mRNA, and larvae overexpressing *patched*.

Poster Session, Poster # 54

Coffee, Tea, or Chocolate?

Chelsea Trost, Kelnisha Lightbourne, Luis E. Castellar, Christine Curiac, Heather S. Hansen, and Luis C. Fernandez-Torres Ph.D.
St. Thomas University, Miami Gardens, FL.

Abstract

The effects of many antioxidants are presented by conducting a well-known oscillating reaction, known as the Briggs- Rauscher reaction. In this reaction there are methods that express the task of the antioxidants, in which they scavenge free radicals in the reaction and neutralize them. By observing the periods of time between each cycle of the Briggs-Rauscher reaction, it helps to see the effects of the antioxidants' presence. The reaction includes malonic acid, manganese (II) sulfate monohydrate, starch, potassium iodate, and sulfuric acid as the control reaction. The reaction published uses different amounts of each reaction at a bigger scale; when it is proportionally scaled smaller still behaves the same way for both. The period of oscillation usually is about 16 seconds. The oscillation period changes to an extended amount of time longer than the control time when the antioxidant is added to the reaction. The various samples used, such as caffeine (1%), coffee (1ppm), decaf (1ppm), black tea (1%), and dark chocolate (1%), show the presence of antioxidants. Finally, the effects of the antioxidants can be calculated by the Relative Antioxidant Performance (RAP), which measures the slope of the sample over the slope of the standard.

Poster Session, Poster # 55

Thin Layer Chromatography and Spectrophotometry: Chlorophyll Analysis in Okra (*Abelmoschus Esculentus*) and Everglades Tomato (*Solanum Pimpinellefium*) Plants Grown in Different Light Conditions

Anne Noel[1], Katerine Cortes[1], Ariana Ablan[1], Franklin Rodriguez[1], Jean Pierre Harland[2], Swan Pierre[2], Carlos Vazquez[1], Dora Pilar Maul Ph.D.[1], and Maria Pina Ph.D.[1]

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Abstract

Chlorophyll a is the principal pigment in higher plants. Chlorophyll b, carotenes and xanthophylls play a secondary role by transferring the energy they absorb to chlorophyll a for use in photosynthesis. Determining chlorophyll content in plants is one way of detecting nutritional deficiencies, and can be used to identify the right location in which to grow a particular species. The purpose of this study was to find an appropriate method to compare the chlorophyll content in okra (Abelmoschus Esculentus) and Everglades tomato (Solanum pimpinellifolium) leaves from plants grown in full sun versus those grown in the shade. This will create baseline information for future nutritional studies in this species in the STU organic garden. Pigments extracted from the leaves were separated by means of thin layer chromatography (TLC) using different solvent mixtures. Better separation of pigments was displayed for the dichloromethylene extracts in TLC using petroleum-ether, acetone, cyclohexane 5:3:3 as a mobile phase. Spectrophotometric analysis over a range of 370 to 700 nm at intervals of 15 nm was performed for both types of leaves. Total chlorophyll content was determined at 645 nm and 663 nm. Chlorophyll a and chlorophyll b content were determined using reported equations based on the absorbance of each type of chlorophyll. Preliminary results show similar chlorophyll a and b content for leaves of Everglades Tomato plants grown either under full sun or in the shade. Full shadow okra leaves displayed a slightly higher chlorophyll content than the full sun plants.

Poster Session, Poster # 56

Baseline Comparison of Home-Made Methanol-Ethanol Solutions for Mass Trapping of *Hypothenemus hampei* in Le Tortue, Haiti

Indira Perez[1], Laynet Cornelio[1], Tony St. Hubert[2], Emmanuel Buteau[1], Carlos Vazquez[1], Anthony P. Vinciguerra[1], and Dora Pilar Maul Ph.D.[1]

[1]St. Thomas University, Miami Gardens, FL; [2]Café Cocano, St. Louis du Nord, Haiti.

Abstract

World coffee production is currently been plagued by the coffee berry beetle (CBB), *Hypothenemus hampei* (Ferrari). Since most of the life cycle of the CBB takes place inside the coffee seed, it becomes very difficult to control it with chemical or biological approaches. Presently the main line of defense against CBB is to reduce the population by "mass-trapping". Researchers in various countries have tested traps with different ratios (depending on the area) of methanol: ethanol as a beetle attracting agent. This study aims to develop effective, home-made, affordable plastic traps for Haitian farmers by using recycled bottles, local beer and distilled liquor as substitutes for commercial methanol and ethanol attracting solution, and a home-made mix of soap and water was used as a killing agent. The experiment was conducted in Le Tortue, Haiti with the collaboration of Café Cocano, a coffee cooperative. Two types of trap designs CC and STU each with three ratios of beer to distilled liquor (3:1, 2:1, and 1:1), plus negative controls (0:0) were tested. Data was collected in the form of overall insects and CBB captured per trap every two weeks; each trap was also replenished with their respective attracting and killing solutions. Fractional distillation was utilized to determine the amount of methanol and ethanol per trap. This study found CC design traps more effective in trapping overall insects and CBB than the STU design. ANOVA analysis showed that traps with ratio 1:1 were more effective than the other traps in capturing CBB.

Poster Session, Poster # 57

Using gene silencing to study autism in cultured neurons derived from induced pluripotent adult human stem cells

Yoan Rodriguez[1], Rolain Pierre[1], Carlos Canales[1], Jossias Genao[1], Alexis Tapanes-Castillo Ph.D.[1], and Derek Dykxhoorn Ph.D.[2]

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Abstract

Autism spectrum disorder (ASD) is a neurological condition characterized by two core features: (1) impairments in social interaction and communication and (2) the presence of restricted interests and/or repetitive behaviors. ASD is associated with mutations in genes that affect the balance between neuronal excitation and inhibition. Excitatory neurotransmission in the human brain is primarily mediated by glutamate and a network of proteins at glutaminergic synapses, which are collectively referred to as the post synaptic density (PSD). Discs large homolog-associated protein 1 (DLGAP1), also known as GKAP, is a scaffolding protein, which interacts with post-synaptic density protein 95 (PSD-95). Recent work revealed that individuals with ASD exhibit differences in DLGAP1 gene expression levels compared to the general population. The goal of our project is to analyze the effect of manipulating DLGAP1 mRNA transcript levels in cultured human neurons, derived from adult induced pluripotent stem cells, which originate from the skin or blood. To accomplish this, we are genetically engineering several DNA constructs, which contain short hairpin RNAs (shRNAs) targeting DLGAP-1. We have also begun culturing neural progenitor cells from autistic and control patients.

Poster Session, Poster # 58

Withaferin A Promotes Neuroblastoma Cell Differentiation and Cell Death: Implications for Therapy

Amelia Bahamonde, Gregor A. Rodriguez, Anthony Sanchez, Claudia P. Zapata, Nico A. De Cordoba, Beatriz E. Hawkins, Sarah A. Samuels, Nadia Myrthil, Steven Vanni D.O., D.C., and Regina M. Graham PhD.*

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Abstract

Neuroblastoma (NB), the most common extra-cranial solid tumor in children, accounts for 15% of childhood cancer deaths. Despite an aggressive treatment regimen, the prognosis for high-risk NB remains poor. Differentiation of NB cells into mature cells represents a promising strategy for NB therapy. Currently, retinoids are used as differentiating agents; however, their use is limited due to intrinsic or acquired resistance as well as toxicity. We sought to evaluate the potential of the natural product withaferin A (WA), a steroidal lactone derived from the medicinal plant *Withania somnifera*, to induce NB cell differentiation. For differentiation studies, NB cell lines (NB1691, SK-N-BE2C, SH-SY5Y and the primary cell line SVBM15) were exposed to WA (100-500nM) for 7-10 days. Light microscopy revealed that WA promoted morphologic alterations (neurite outgrowth) similar to retinoid-treated cells. Fluorescent microscopy and western blot analysis indicated that WA increased expression of neuronal differentiation markers (neurofilament, vimentin, β-tubulin, MAP2) and decreased stem cell markers (BMi-1, musashi). The IC_{50} of NB stem cells was determined using MTS assay to be ~1M. Furthermore, WA significantly reduced the "stemness" of these cells even at sub-toxic concentrations (low as 50nM) as determined using sphere-forming assays. Lastly, effects of WA on NB cells was reversed with the anti-oxidant N-acetyl-cysteine, suggesting a mechanism of action whereby reactive oxygen species promote NB

cell death and differentiation. By targeting NB stem cells and promoting NB cell differentiation; WA represents a novel and potentially less toxic adjuvant therapy for the treatment of NB.

Poster Session, Poster # 59

Bsp1p, a Possible β-Adducin Homolog, Is Required for Vps13p-Dependent TGN Homotypic Fusion

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Department of Biological Chemistry[2], University of Michigan Medical School, Ann Arbor, MI

Abstract:

Yeast Vps13p is a cytosolic factor required for multiple vesicular transport/fusion events, including TGN-late endosome and late endosome-Golgi transport, TGN homotypic fusion and spore membrane maturation. Humans express four *VPS13* homologs (*VPS13A-D*) and loss of function mutations in these genes have been associated with distinct neurodegenerative or neurodevelopmental diseases. Chorea Acanthocytosis (ChAc) is an autosomal recessive Huntington's-like neurodegenerative disease caused by *VPS13A* null mutations. In addition to loss of striatal neurons, ChAc patients' exhibit aberrantly shaped red blood cells (RBCs), acanthocytes, suggesting defects in the actin cytoskeleton. Recent experiments showed that, in RBCs, human VPS13A is in a complex with ®-actin and ®-adducin, suggesting a role in actin organization. Bioinformatic analysis identified a possible ®-adducin homolog in yeast, Bsp1p, an actin-binding protein associated with cytokinesis. Here, we have found that extracts from *bsp1* mutant yeast cells are defective for *in vitro* TGN homotypic fusion. Bsp1p was purified from yeast as a soluble TAP-tagged protein. Purified Bsp1p restored TGN homotypic fusion activity to mutant extracts, suggesting that Bsp1p is directly required for this membrane fusion event. These results support the hypothesis that Bsp1p is a yeast homolog of ®-adducin and connect Vps13p function to the organellar actin cytoskeleton. Sequence alignments of fungal Bsp1p and metazoan ®-adducin homologs provide further support for this conclusion. Future studies will focus on how Bsp1p is recruited to membranes and whether Bsp1p and Vps13p function in complex with actin. Understanding the function of yeast Vps13p will further clarify the fundamental defects behind human *VPS13* diseases.

Poster Session, Poster # 60

Role of Perforin-2 at the Materno-Fetal Interface

Alyson Essex, Advisor Dr. Natasa Strbo. University of Miami

Abstract:

The gene encoding the 72kD Perforin-2 protein, the macrophage expressed gene-1 (MPEG-1), is expressed constitutively in macrophages, neutrophils and is induced by cytokines and/or infection in fibroblasts and endothelial cells (McCormick et al. 2013; Fields et al. 2013). In species with endometrial decidualization and hemochorial placentation (human and mice), leukocytes localize to early implant sites and contribute to decidual angiogenesis, spiral arterial remodeling and trophoblast invasion (Croy A., 2012). Our hypothesis is that decidual macrophages and granulocytes are equipped with Perforin-2 to withstand intracellular pathogen replication. The aim of our study was to analyze, by flow cytometry and immunohistochemistry, leukocytes present in the early and mid-pregnancy decidua and to determine the expression level of perforin-2 by qPCR and Western blotting. Pre-implantation uterus or timed gestational decidua were processed into single-cell suspension and stained with antibodies to delineate immune cell subsets. The day of vaginal plug detection was designated as gestational day (GD) 0.5. We found

that decidual macrophages (F4/80+CD11b+) and granulocytes (F4/80-Gr-1+), represent two major leukocyte population in mid-gestation pregnancy. Interestingly, macrophage frequency was significantly increased just before implantation of the blastocyst (GD 3.5) as well as perforin-2 expression. In Summary, we propose that Perforin-2 expressed by decidual macrophages represents a novel host-factor restricting pathogen colonization of the placenta. In initial studies we have established that Perforin-2 plays a central role in killing a number of intracellular bacterial pathogens and limiting acute disease in murine models of infection. We also found that Perforin-2 is abundantly expressed in placental tissue.

Poster Session, Poster # 61

Comparison of Beach Management Practices and Bacteria Levels at 316 Florida Beaches

Hannah Lockwood and Helena Solo-Gabriele, Ph.D.
University of Miami, Miami, FL

Abstract:

Through the Healthy Beaches Monitoring program, the Florida Department of Health has measured the quality of recreational beach water through measures of enterococci, a fecal indicator bacteria. When bacteria exceeds a specific threshold (104 colony forming units, CFU per 100 ml), the beaches are closed due to water contamination. One way to express the frequency of beach closures is to convert this data to percent exceedance. The causes of the exceedances are many times unknown. The objective of the study is to investigate connections between management practices and enterococci levels at the 316 monitored beaches in Florida. Beach management data was collected though a comprehensive survey completed by beach managers, which were compiled into a master excel spreadsheet and merged with the bacterial information. The merged data was analyzed statistically using t-tests. Questions chosen for preliminary testing of the collected data included whether the exceedances of enterococci differed between a) beaches that charge access fees versus those that do not, b) various seaweed density conditions, and c) the presence versus the absence of dogs. Results show that beaches requiring access fees had lower exceedances than those that did not ($p<0.02$). Beaches with reported "dense" seaweed conditions had higher exceedances than those with reported "medium," "sparse," and "zero" seaweed conditions ($p<0.03$). Beaches permitting dogs had higher exceedances than those that do not allow dogs ($p<0.02$). Overall results suggest that the cumulative effects of beach management practices can play a role in whether beaches comply with recreational water quality guidelines.

Poster Session, Poster # 62

Effects of Elevated Nutrient Levels and Thermal Stress on the Density of Algal Symbionts (*Symbiodinium* spp.) in Reef-Building Corals

Grace A. Snyder, Ana M. Palacio-Castro and Andrew C. Baker, Ph.D.
University of Miami, Rosenstiel School of Marine and Atmospheric Science, Miami, FL

Abstract

Coral reefs are highly biodiverse ecosystems threatened by changing environmental factors (such as warming temperatures, increasing ocean acidity and poor water quality) whose combined effects have led to reef degradation worldwide. Understanding how these factors affect coral physiology, both alone and in combination, is of great importance for conserving reefs over the coming century. Recent research has suggested that corals with higher relative abundance of algal symbionts (dinoflagellates in the genus *Symbiodinium*) may be more susceptible to coral "bleaching" (the stress-induced paling of corals due to expulsion of symbionts). Here we tested the hypothesis that decreases in water quality (nutrient

enrichment) increases the relative abundance of symbionts, thereby increasing their bleaching susceptibility. We exposed two species of Caribbean corals, *Montastraea cavernosa* and *Siderastrea siderea*, to elevated levels of nitrogen, nitrogen and phosphorus, or iron for a 200-day period, after which the corals were exposed to elevated temperatures (32-34°C) for three weeks. Subsets of corals were removed from the treatments before and after the thermal stress to determine the relative abundance of *Symbiodinium* (using microscopic counts of cells) and total lipid content. Chlorophyll fluorometry was also used to measure the photochemical efficiency of the symbionts. Initial observations suggest that overall pigmentation of corals did not change under nutrient enrichment compared to controls, however, total lipid concentrations and symbionts densities may have changed. During heat stress exposure, bleaching susceptibility was principally driven by the identity of thermotolerant *Symbiodinium*D1a, providing increased thermotolerance.

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Thank you to the institutions who tabled at the LSSF symposium. Providing resources and knowledge about next steps in academic careers to our undergraduate students is invaluable.

Barry University
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