Life Sciences South Florida 2015 STEM Undergraduate Research Symposium

Saturday, April 4, 2015 9:00 a.m. - 3:00 p.m.

William and Helen Thomas STEM Center Indian River State College Pruitt Campus Port St. Lucie, Florida









April 4, 2015

Dear Friends:

It is my great privilege to welcome you to the STEM Center at Indian River State College – Pruitt Campus for the third annual Life Sciences South Florida STEM Undergraduate Research Symposium.

This event brings together some of the brightest undergraduate minds from across South Florida to facilitate a greater discourse in the areas of Science, Technology, Engineering and Math. The original scientific research presented today will contribute to the overall STEM knowledge commons, and I know it will help advance both life science academia and industry in the State of Florida.

We are quite fortunate to have two gentlemen with us this morning that have many accomplishments to that effect. Speaking with the symposium today are Dr. Richard Houghten, President and CEO of the Torrey Pines Institute for Molecular Studies, and the Honorable Ken Pruitt, St. Lucie County Property Appraiser and former President of the Florida Senate. Each of these individuals has been instrumental in not only growing the research footprint of this region, but enhancing research opportunities in Florida as a whole.

Life Sciences South Florida was established to help carry on this work, dedicating efforts to life science, biotechnology, and scientific research as a maturing industry in our state. Through research related, student engagement events such as this, we are meeting that commitment, building a pipeline of talented individuals ready to go from the classroom to the laboratory. This symposium is simply a springboard for many of you to outstanding careers in life science research.

Once again, many congratulations to all of the students who've chosen to participate here today. Please enjoy your time at Indian River State College and keep up the excellent work promoting STEM education in South Florida.

Sincerely,

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Edwin R. Massey, Ph.D. President

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Torrey Pines Institute for Molecular Studies

The Institute was founded in 1988, and began its operations in 1989 with eight employees. Now in its 22nd year, it has become internationally recognized for its scientific contributions in a wide range of fields, including chemistry, multiple sclerosis, diabetes, immunology, infectious disease, heart disease, cancer vaccines and pain management. The institute has grown to include over 150 scientists, technicians and administrative staff, all of whom work in an environment that emphasizes personal and professional growth by encouraging the development of independent research ideas as well as the development of collaborative efforts with scientists throughout the world.



Richard A. Houghten, Ph.D. Founder & President

Dr. Houghten received his doctorate in organic chemistry from the University of California, Berkeley, in 1975. Following positions at the University of California, San Francisco, and Mount Sinai School of Medicine, he joined The Scripps Research Institute in 1981. In addition to Torrey Pines Institute for Molecular Studies, he founded three commercial businesses, including one which became a publicly-traded biotechnology company.

His achievements have been recognized in the form of numerous honors and awards. Most recently, his contributions to the field of combinatorial chemistry and peptide science was acknowledged by the Bruce Merrifield Award in 2005. Just one year prior, he was awarded the 2004 Ralph F. Hirschmann Award in Peptide Chemistry by the American Chemical Society. Other honors received include the Vincent du Vigneaud Award for Excellence in Peptide Science (2000) and the UCSD Connect Athena Pinnacle Award for Empowering Women in the Workplace. His acceptance of the Athena Pinnacle Award in 1999 further distinguishes Dr. Houghten and his dedication to the mentoring and advancement of women scientists in the work place.

Dr. Houghten's scientific contributions include the "tea bag" approach, which was originally utilized to facilitate the synthesis of peptides in 1985. The tea bag method, in which solvent permeable packets are used during the synthesis process, has now resulted in not only the synthesis of millions of peptides, but also the synthesis of millions of low molecular weight compounds.

In collaboration with his long-time associates and colleagues at Torrey Pines Institute for Molecular Studies, he developed approaches in combinatorial chemistry which are invaluable for the rapid identification of individual compounds from millions to billions of others (positional scanning), the use of existing combinatorial libraries to generate entirely new diversities of compounds (libraries from libraries), the cross-referencing of library screening results with gene data bases in order to fine-tune the direction towards which further testing moves for a given disease target (biometrical analysis), and novel volatilizable solid supports. Many of these technologies have resulted in "leads", which are today undergoing further testing and analysis in pharmaceutical companies.

Guest Speaker

Ken Pruitt is a native Floridian and has called St. Lucie County home since 1977. Mr. Pruitt was elected Property Appraiser in 2010 and re-elected without opposition in May 2012.

Prior to his service as Property Appraiser, Mr. Pruitt served in the Florida Legislature from 1990-2009. His legislative tenure first began in the Florida House of Representatives from 1990-2000 and then the Florida Senate from 2000-2009. Ken Pruitt served as Appropriations Chair in both the House and the Senate and culminated his legislative service as President of the Florida Senate from 2006-2008.

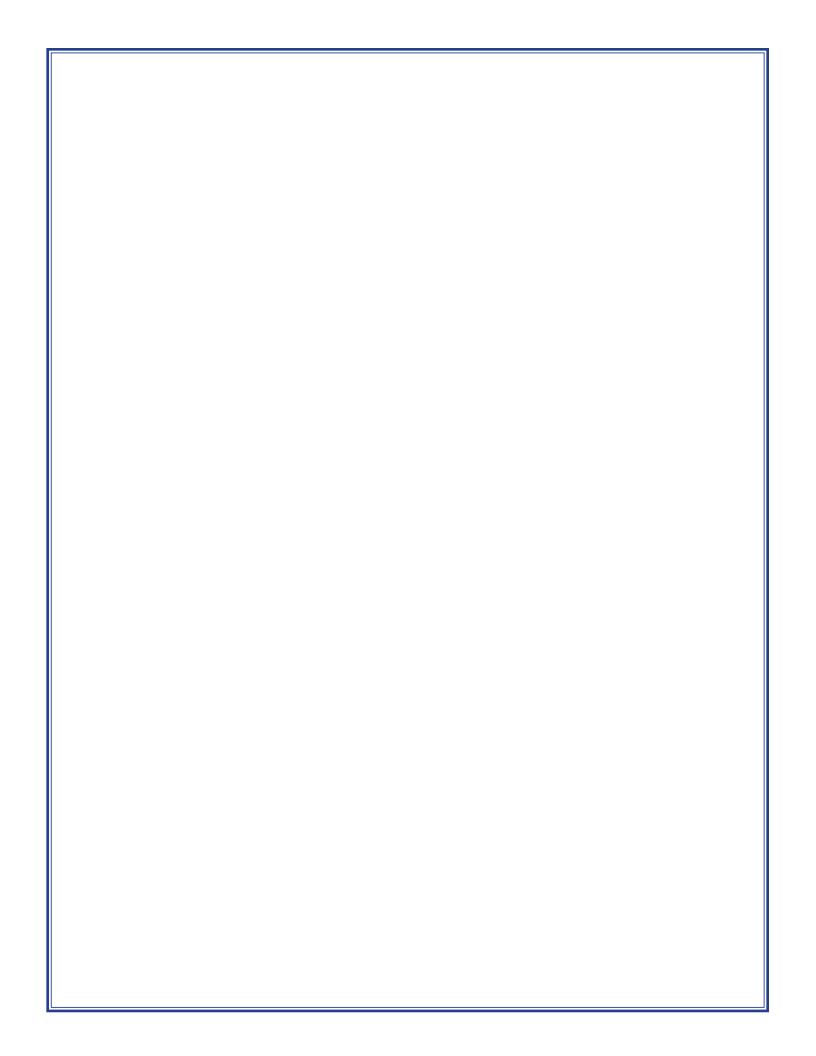


Ken Pruitt, Property Appraiser St. Lucie County

Mr. Pruitt's dedicated commitment to education during his tenure in the legislature was recognized with the naming of the Indian River State College in St. Lucie West as the Pruitt Campus.

Under Mr. Pruitt's leadership, the St. Lucie County Appraiser's Office was awarded the highly coveted 2014 International Association of Assessing Officers "Distinguished Assessment Jurisdiction Award," a recognition bestowed to only one office out of 7,000 in the world. Mr. Pruitt is also a recipient of the Paul Harris Fellow by Rotary International.

Ken Pruitt and his wife, Aileen, live in Fort Pierce and are proud parents of five children: Kenneth Jr. (deceased), Steven, Ashley, Michelle, Mark and granddaughter, Chloe. Ken and Aileen Pruitt are active in the community and are members of the St. Lucie County United Way Alexis de Tocqueville Society as well as the Martin Health System Foundation Barstow-Reed Society.



Life Science South Florida STEM Research Symposium 2015

Program

8:45 a.m.	Breakfast - open during Registration
9:15 a.m.	Opening Remarks Anthony J. Iacono, Ph.D. Vice President of Academic Affairs Indian River State College
9:18 a.m.	Welcome Address
9:25 a.m.	Guest Speaker
9:40 a.m.	Introduction of Keynote Speaker Charles R. Lunceford II Provost, Indian River County Indian River State College
9:45 a.m.	Keynote Speaker
10:30 a.m. to 12:30 p.m.	Oral Presentation I - Auditorium S108 Oral Presentation II - S204 Poster Presentation - S114 & S117
12:30 p.m. to 2:00 p.m.	Lunch - S108 & Cyber Cafe Poster Exhibit Open Session/Tour of Facilities
2:15 p.m.	Awards Presentation

RESEARCH PROJECT ABSTRACTS ORAL PRESENTATIONS

Designing drug-like compounds that target microRNAs

Tevin Ali^{1, 2}; Jessica Childs Disney, Ph.D.²; Matthew David Disney, Ph.D.² ¹Palm Beach State College, Palm Beach Gardens, Florida ²The Scripps Research Institute, Jupiter, Florida

Abstract

MicroRNAs (miRNAs) are a family of small non-coding RNAs that are 21-25 nucleotides long and regulate expression of at least 30% of all genes in a sequence-specific manner. Aberrant expression of miRNAs is associated with various human diseases such as Alzheimer's disease, Parkinson's disease, Muscular Dystrophy, and cancers among others. Thus, these small RNAs are interesting targets for therapeutic intervention. Unfortunately, RNA has been recalcitrant to drug discovery efforts. The Disney Lab, however, has successfully targeted RNAs that cause disease and inhibited their dysfunction in cellulo and in vivo by using non-traditional approaches developed in their laboratory. Unlike conventional methods that screen a validated RNA target for binding to a library set of compounds, they have developed a library-on-library screening approach to define the RNA secondary structural elements (motifs) to which a small molecule prefers to bind. The affinities of the small molecules for selected RNAs are then measured and the fitness of the RNA motif-small molecule interaction is calculated using a statistical approach. These motifs are then searched for in disease-associated RNAs and the corresponding small molecule is a lead compound. My role is to: (i) define RNA bulges that bind to small molecules; (ii) synthesize selected RNAs using Polymerase Chain Reaction (PCR) amplification and in vitro transcription using the T7 RNA Polymerase enzyme; (iii) measure the affinities of the RNA-small molecule interactions; and (iv) search for the selected bulges in disease-associated miRNAs.

Kappa-opioid receptor antagonist produces protective anxiolytic effect in stress prior to exercise

Ezana Assefa^{1,2}, Brendan Hare¹, Borivoj Golijanin¹, Jake Luceno¹, William A. Falls, Ph.D.¹ ¹University of Vermont, Burlington, Vermont ²Nova Southeastern University, Fort Lauderdale, Florida

Abstract

There are many beneficial qualities to exercise, including reducing anxiogenic and depressive symptoms caused by stress in humans and rodents. Studies show that stress prior to exercise interferes with the anxiolytic effect of exercise. Accumulating evidence indicates kappa-opioid receptors (KORs) and their endogenous opioid, dynorphin, modulate the stress response. NorBNI, a KOR antagonist, has anxiolytic and antidepressant qualities, suggesting it can be utilized to block the negative effects of stress to salvage the effects of exercise. The goal of this study is to assess whether norBNI administered prior to stress will prevent stress from interfering with the anxiolytic

effects of exercise. The acquisition of neither exercise nor the distance ran was affected by norBNI over a fourteen day period. Exercising groups showed blunted and reduced immobility times on days one and two of a test measuring depression while norBNI groups showed a reduction in a seven day protocol to measure anxiety. These findings propose norBNI does not interfere with the acquisition of exercise, the antidepressant effects of exercise and may have a short term or additive anxiolytic effect.

Neural stem cell proliferation, differentiation, and survival in response to AT1 and AT2 angiotensin II receptor-specific agonism

Brigitte Blanco*, Puja Patel*, Sujay Kamisetty*, James R. Munoz Ph.D., Robert C. Speth, Ph.D. Nova Southeastern University, Fort Lauderdale, Florida

Abstract

Major components of the brain Renin-Angiotensin System may provide modes of therapy for impaired neurons. Angiotensin II via its receptors, AT1 and AT2, induces proliferation and differentiation of rodent neural stem cells. This study was undertaken to determine if AT1 and AT2 receptor stimulation by Angiotensin II induces proliferation and differentiation of human neural stem cells (hNSC). This study will assess whether selective agonism of AT1 and AT2 receptors on hNSC could possibly induce proliferation and differentiation in damaged areas of the brain caused by stroke, traumatic brain injury, and several neurodegenerative diseases in a therapeutic manner. Using hNSC, this study aims to enhance our understanding of how neural differentiation and proliferation are affected by selective agonism of both the AT1 and AT2 receptor. It was hypothesized that stimulating the AT1 receptor would induce proliferation and stimulating the AT2 receptor would induce differentiation upon addition of selective agonists. Preliminary analyses of this ongoing research support the hypothesis, as there was a 78% increase in neuronal differentiation induced by AT2 agonism, and a 5% increase in proliferation with selective AT1 agonism. Further investigation of these preliminary results will determine if these trends are genuine and statistically significant.

*student researchers

Characterization of an HIV-1 capsid inhibitor

Angela Brady^{1,2}, Suzie Houssier, Ph.D.², Susana Valente, Ph.D.² ¹Palm Beach State College, Palm Beach Gardens, Florida ²The Scripps Research Institute, Jupiter, Florida

Abstract

Proper assembly of the viral capsid (CA) is essential to HIV maturation and infectivity, yet it is not the target of any current antiretroviral therapy. Preliminary work resulted in the development of a time-resolved fluorescence resonance energy transfer (TR-FRET) high-throughput screening assay, which was used to screen the 1280 molecules of the Library of Pharmacologically Active

Compounds (LOPAC) for drugs that inhibit HIV-1 capsid dimerization. Of the forty-two hits, twenty were screened in multiple-round infection assays, which identified Compound 1001 (C1001) as the most potent inhibitor of HIV-1 replication. Binding of C1001 to the CA C-terminal domain (CTD) was verified via Nuclear Magnetic Resonance Spectroscopy (NMR) using the isolated and purified CTD. The addition of C1001 to CTD protein resulted in NMR spectral changes consistent with tight binding. Confirmatory work is ongoing, using monomer- and dimer-only mutants of CTD along with compounds known not to bind CTD. To determine which step of the replication cycle is affected, HeLa cells were subjected to a single-round infection assay using a non-replicative virus, then challenged with various concentrations of C1001 as well as controls. Alu-PCR followed by qPCR allowed the quantification of integrated provirus. C1001 shows dose-dependent inhibitory effects in single-round infection, suggesting an inhibitory activity prior to integration, possibly interfering with the process of viral decapsidation and reverse transcription. Ongoing work will more precisely define the mechanism of action, by targeting the products of early post-entry and late-stage replication events.

Supramolecular metallofullerene atoms: hartree-fock 3-21G quantum chemical analysis of endohedral guest alkali and alkaline-earth metals within a buckyball host

Stephanie Cal, Heather Suchinsky, Servando Muñoz Miami Dade College, Miami, Florida

Abstract

The classical Bohr model of the hydrogen atom can be described in terms of a "planetary" electron orbiting a central positively charged nucleus. In our research we sought to find the supramolecular equivalent of the Bohr model of the atom. We placed a strongly reducing metal within C_{60} that would donate electrons to the carbon sphere. The resulting supramolecular superatom would be made up of a band of delocalized π -electrons on the fullerene surface and a positively charged metallic "nucleus" at the center. We used ab initio self-consistent field Hartree-Fock 3-21G quantum mechanical calculations to generate electrostatic potential maps, electron spin density maps, and frontier molecular orbitals to describe the process of intramolecular electron transfer from the endohedral metal atom to the electrophilic fullerene cage. Accordingly, lithium, sodium, and potassium metals irreversibly reduce C₆₀ such that the fullerene surface becomes negatively charged and the metal acquires a positive charge. The latter observation is consistent with the strongly reducing nature of group IA metals. Among group IIA metals, calcium readily transfers two electrons to the fullerene surface. The nanotopography of the highest occupied molecular orbital, HOMO, shows electrons from the donor metal become delocalized predominantly along the equator of the C₆₀ dianion sphere. By comparison, endohedral hydrogen which is a much weaker electron donor than the alkali and alkaline-earth metals does not transfer an electron to C₆₀ but remains in the neutral state.

Full Genome Determination and Characterization of Tobamoviruses

Kornelia Fillmer¹, Scott Adkins², Patchara Pongam¹, Tom D'Elia¹ ¹Indian River State College, Fort Pierce, Florida ²USDA Agricultural Research Service, Fort Pierce, Florida

Abstract

Viruses belonging to the genus *Tobamovirus* are responsible for reduced crop yield. Early and rapid detection of a specific virus is vital to prevent the spread of the virus and potential crop failure. Full genome sequences allow identification of multiple targets for detection and ultimately management. This study examined several procedures to streamline the process of developing full genome sequences of such viruses. From harvested leaves of underperforming plants showing typical mosaic symptoms, a procedure was developed and validated to determine full genome sequences of several representative emerging tobamoviruses in Florida by utilizing reverse transcription, polymerase chain reaction, capillary electrophoresis, and next generation sequencing. The first complete genome sequence of a Tomato mottle mosaic virus isolate recently reported from the United States was determined and comparative analysis showed it to be 99% identical to the sequence of the original virus isolate from Mexico. These new sequence data will be useful for the development of novel diagnostic methods and further studies of virus ecology and evolution, which will eventually yield improved management options.

Cloning and expression of a Bacteriocin gene from *Sinorhizobium meliloti* for killing plant pathogenic bacteria, *Liberibacter* species

Andrea J. Folds¹, Yong-Ping Duan, Ph.D.², Marco Pitino, Ph.D.² ¹Indian River State College, Fort Pierce, Florida ²USDA Agricultural Research Service, Fort Pierce, Florida

Abstract

Candidatus Liberibacter asiaticus, Ca. L. americanus, and Ca. L. africanus are three bacterial species responsible for citrus greening disease, also known as Huanglongbing (HLB). These uncultured *Liberibacter* species are devastating the citrus industry worldwide and scientists are desperate to find a method of eliminating these plant pathogens. Bacteriocins (microcins) are of interest as a potential control method of HLB. Bacteriocins are ribosomally synthesized proteins produced by various bacteria that exhibit antimicrobial and specific antagonistic activity against closely related species. Thus, it was imperative to utilize a phylogenetic evaluation in order to find a closely related species that produce a bacteriocin. It was established that *Sinorhizobium meliloti* 1021 does produce a microcin. As such, this study aimed to test the bactericidal activity of the microcin gene product from *S. meliloti* 1021. This gene was cloned into an expression vector and transformed into E. coli. The microcin protein was then isolated and purified to test against *Liberibacter crescens*, the only culturable *Liberibacter* species. It was found that the E. coli were storing the microcin protein into inclusion bodies, making extraction of functional microcin protein difficult. Therefore, an alternative method of expression was employed for protein production by using a tobacco plant as a heterologous host. The transient expression of the microcin gene product was achieved using

Agrobacterium plant transformation techniques. The protein product was then extracted and purified to test bactericidal activity against the *L. crescens* and the effects of the microcin protein will be discussed.

Increased CHI3L1 Levels due to Preexisting Pulmonary Inflammation Accelerates Breast Cancer Metastasis

Nathalia Gazaniga, Stephania Libreros, Ramon Garcia-Areas, Vijaya Iragavarapu Florida Atlantic University, Boca Raton, Florida

Abstract

Inflammation is known to play a significant role in cancer. Chitinase 3-like-1 protein (CHI3L1) is involved in pulmonary inflammation. We have shown that mice with preexisting pulmonary inflammation have accelerated metastasis and higher circulating levels of CHI3L1. Expression of CHI3L1 by myeloid derived cells has been shown to promote pro-tumorigenic effects. Thus, we **hypothesize that preexisting pulmonary inflammation leads to an increase in the production of CHI3L1 by myeloid derived cells resulting in accelerated breast cancer metastasis.** Flow cytometric analysis of wildtype mice with preexisting pulmonary inflammation showed a decrease in these subpopulations were further increased in these mice after tumor cell implantation. More importantly, CHI3L1 knockout mice induced with pulmonary inflammation showed a decrease in these cell subpopulations compared to wildtype mice and correlating with decreased metastasis. Targeting specific immune populations could lead to safer and more effective strategies against breast cancer.

Genetic regulation of the temperature-dependent egg-laying rate in C. elegans

Victoria Hoelscher^{1,2}, Kevin P. McPherson^{1,3}, Samuel Lasse¹, Erik Andersen⁴, Miriam B. Goodman¹ ¹Stanford University, Stanford, California • ²Barry University, Miami Shores, Florida ³Emory University, Atlanta, Georgia • ⁴Northwestern University, Evanston Illinois

Abstract

In humans, muscle function depends on temperature, but due to genetic complexity, it is difficult to identify genes responsible for this dependence. The genomes of humans and *Caenorhabditis elegans* contain many homologues, enabling *C. elegans* research to provide a blueprint for studying temperature-dependent muscle function in humans. Muscle function can be measured quantitatively in *C. elegans* by tracking egg-laying, since when an egg is laid, the vulval muscles of the worm must contract. These muscles function at different rates across a range of temperatures, meaning that the worms' muscles contract more often at certain optimum temperatures than at others. We have found that the egg-laying rates and optimum egg-laying temperatures also differ among strains of *C. elegans*, despite the presence of only minor genetic differences. By comparing the egg-laying rates and genomic sequences of two phenotypically divergent strains, N2 (Bristol) and CB4856

(Hawaii), we identified loci within chromosomes IV and X of the *C. elegans*' genome that may affect muscle function. After specific genes of interest are identified in *C. elegans*, homologous genes in humans can be studied for their roles in temperature dependence of muscle function.

CDC Bioreactor for cultivation of *Staphylococcus epidermidis* biofilm under flow conditions

Peter Rodriguez, Shashana Fiedler, Leticia Vega Barry University, Miami Shores, Florida

Abstract

Infectious disease resulting from bacterial invasion is a leading cause of death. Certain species of bacteria can form what is known as a "biofilm"- communities of bacteria embedded in a polysaccharide matrix. Accumulation of biomass from these bacteria have been shown to increase resistance to antimicrobial agents as compared to their planktonic forms. The first stage in biofilm formation begins with bacteria adhering to a surface, followed by the recruitment and accumulation of various numbers of different bacterial species. Staphylococcus epidermidis is a part of the normal skin flora of humans and has the ability to form robust biomasses once adhered to a biological surface or medical device. The purpose of this study was to compare biofilm formation of S. epidermidis under static conditions vs. flow conditions, which closely resembles an environmental niche. In addition, we troubleshot the setup of a CDC bioreactor in our lab to study growth under flow conditions. Biofilm formation was investigated for two wild type S. epidermidis strains, as well as mutant strains 1457 aap Δ , 1457 ica Δ , and 1457 aap Δ /ica Δ , which are deficient in biofilm formation. We found that the RP62A (WT) strain of S. epidermidis was able to form the most robust biofilm, compared to 1457(WT) and mutant strains of 1457. Our studies also confirmed that the *ica* and *aap* operons play important roles in the formation and accumulation of biofilms in S. epidermidis. These findings lay the groundwork for future studies of biofilm formation using the CDC bioreactor flow system.

Towards carbon based nanotechnology: construction of a supramolecular nanocable from a metallic guest (9,0)-zigzag single-walled carbon nanotube and a self-assembled cyclo-[(D-Ala-L-Ala)6] peptide nanotube host

Liana Roque, Servando Muñoz Miami Dade College, Miami, Florida

Abstract

(L)- α -Aminoacids are the basic building blocks of proteins. Depending on their secondary structure, proteins self-assemble into two distinct structural motifs: the α -helix and β -sheets. Our research is concerned with cyclic peptides made up of a sequence of alternating (D)- and (L)-aminoacids which spontaneously self-assemble into a cylindrical peptide nanotube through intermolecular hydrogen-bonding. Quantum chemical analysis demonstrates the ability of (D, L)-cyclic peptide

rings to undergo spontaneous supramolecular self-assembly into cylindrical nanotubes through non-covalent intermolecular hydrogen bonding. Accordingly, electrostatic potential maps show the complementarity between the electron deficient hydrogen atoms and the electron-rich oxygen atoms that make up the hydrogen bonded network stitching together the seamless peptide nanotube. We calculated electrostatic potential maps of (9,0)-Zigzag single-walled carbon nanotubes using ab initio self-consistent field quantum mechanical calculations at the Hartree-Fock 3-21G level of theory. Our goal was to assess whether a metallic (9,0)-Zigzag carbon nanotube guest placed within the insulating cavity of a peptide nanotube host can function as a nanocable. Electrostatic potential maps show that (9,0)-Zigzag carbon nanotubes are metallic, due to the continuous π -electron distribution along the cylinder's surface. Inclusion of the carbon nanotube within the peptide cavity does not significantly alter the extent of π -electron delocalization on the former. Consequently, the guest remains metallic and electrically-conducting. Under these conditions, the single-walled (9,0)-Zigzag nanotube behaves as a cylindrical carbon molecular wire surrounded by an electrically-insulating peptide matrix. Our calculations suggest that the resulting cooperative, supramolecular host-guest assembly can serve as a nanocable in microelectronics.

Single cell force spectroscopy to characterize the interaction between two *Plasmodium falciparum* domains and host immune cells

Shalondria Sears, Jordan Merritt, Andrew Oleinikov, Ewa P. Wojcikiewicz Florida Atlantic University, Boca Raton, Florida

Abstract

Plasmodium falciparum has the highest mortality of all malarial infections. Parasitic invasion of red blood cells (RBCs) is followed by *P. falciparum* Erythrocyte Membrane Protein 1 (*Pf*EMP1) clustering on the surfaces of infected RBCs (IRBCs). PfEMP1s mediate adhesion of IRBCs to monocytes. Parasite adhesion is limited by the ability of monocytes to recognize specific PfEMP1 domains presently expressed. During infection, monocyte phagocytosis of IRBCs is mediated by monocyte surface receptors, including scavenger receptor CD36 and Ig superfamily adhesion molecule, Intercellular Adhesion Molecule- 1 (ICAM-1). IRBC elimination elicits the over-activation of the immune response, perpetuating a cytokine storm, leading to excessive accumulation of monocytes at the site of infection. This hyperactivation may lead to tissue and organ failure. The objective of this study is to characterize the binding between monocytes and two prevalent domains within *Pf*EMP1s, using single cell force spectroscopy (SCFS). Preliminary results show that monocyte work of de-adhesion for the CIDR1_{PBF0010w} to CD36 was ~94% greater than control binding. Adhesion decreased by ~66% in the presence of soluble CD36, confirming CD36 binding specificity. Monocyte work of de-adhesion to DBL2C2_{PF11 0521} was ~98% higher than control. A ~95% drop in adhesion was observed in the presence of soluble ICAM-1, confirming binding specificity to ICAM-1. Together, our results have quantified adhesion between PfEMP1 domains and important monocyte receptors. Characterizing the interaction between PfEMP1s and monocytes is integral toward the development of tailored anti-adhesion therapies aimed at reducing the severity of the infection and malaria death.

POSTER PRESENTATIONS

1. The Effects of Ultra Marathon on Myocardial Hypertrophy

Naimah Alamin, Steven Hammer, Ph.D. Indian River State College, Fort. Pierce, Florida

Abstract

Ultra-marathon events are a growing trend in today's society. However, little is known regarding cardiovascular effects of extreme, prolonged exercise. The possible effects of chronic exercise may result in hypertrophy and or dilation. Increase in the size and thickness of all four cardiac chambers could be due to the volume and pressure load imposed by repeated bouts of exercise (Gerche et al. 2013). This study examined changes in chamber electrical activity due to ultra-marathon running that can be used to detect hypertrophy and/or dilation. The ECG criteria for diagnosing hypertrophy are very insensitive (sensitivity ~ 50 %), which means that participants with hypertrophy might not be detected by the ECG criteria. The results indicates that clinical hypertrophy examined in the pre-race and post-race values with the values of the pre and post exceeding the border line measurement in the determinant of clinical hypertrophy. ECG measurements indicating RAE showed above clinically normal value of 2.5 mm in leads II, III and avF, however no significant changes were noted over the distance measures. Examining p-wave duration in lead II for extended duration indicating LAE showed normal pre-race values with some of the 100 mile runners reaching the cutoff criteria of 0.12 sec by the end of the race. RVH was noted as border line normal pre-race with an increasing trend towards clinically significant RVH with many of the runners showing clinical criteria at 100 miles. These results show clinically significant changes in the heart of the Ultra Marathon runners, which tend to increase with increasing mileage run.

2. Insight into the calmodulin and DREAM protein complex interaction, mechanism and function

Walter G. Gonzalez, Andres S. Arango, Jaroslava Miksovska Florida International University, Miami, Florida

Abstract

DREAM (Downstream regulatory element antagonistic modulator) is a neuronal calcium sensor which has been shown to modulate gene expression as well as being involved in numerous neuronal processes. In this report, we show that association of calcium bound calmodulin (CaM) with DREAM is mediated by a short amphipathic amino acid sequence located between residues 29 and 44 on DREAM N-termini The association of CaM with a peptide analogous to DREAM(29-44) or to full length DREAM protein is calcium dependent with the dissociation constant of 136 nM and 3.4 μ M, respectively. Thermodynamic and kinetic studies show that the observed decrease in affinity for the native protein is due to electrostatic interaction between the basic N-terminus and an acidic surface on DREAM. These results are further supported by molecular dynamic simulations, circular dichroism and binding studies. Additionally, in fluorescence anisotropy decay measurements, a rotational correlation time of 10.8 ns for a complex of CaM with a DREAM(29-44)

peptide was observed, supporting a wraparound semi-spherical model with 1:1 stoichiometry. Furthermore, the interaction between a IEDANS labeled CaM construct with DREAM is best modeled as a heterotetramer. The CaM:DREAM heterotetramer adopts an elongated conformation with correlation time of 45 ns in the presence of Ca2+. We also demonstrate that association of CaM with DREAM eliminates the nonspecific interaction of DREAM with the DRE dsDNA sequence of human prodynorphin gene. The presented work provides an molecular insight into the CaM:DREAM complex and its potential role in modulation of gene expression.

3. Dynamic Regulation of Toxic Engineered Bacteria Prevents Learning in the Model Nematode *Caenorhabditis elegans*

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

Abstract

Infections due to parasitic nematodes result in nearly 125,000 deaths annually. Strikingly, this rate remains nearly unchanged in the past 50 years likely owing to the fact that treatment options are either inefficient or inaccessible. Prior to infecting humans, most parasitic nematodes begin as larvae where they feed nearly exclusively on bacteria. This unique property may offer an opportunity to develop new biological control agents with the use of synthetic biology. Recently, we have engineered a bacterium, consisting of an attraction module and toxin module that lures in and kills nematodes, respectively, using the principles of synthetic biology to act as biological control agent of the model nematode *Caenorhabditis elegans*. While independently characterizing of the two genetic modules governing the behavior of the engineered bacterium was successful, combining both modules in the same bacterial cell resulted in a reduction in attraction and killing efficacy. In this study we show that this reduction in efficacy is due to the ability of *C. elegans* to learn that our engineered bacterium is deadly. To circumvent learning, and thus increase efficacy, we dynamically regulate the modules of our engineered bacteria. We demonstrate that the order to activation of the modules is critical to successful attraction and killing of *C. elegans*. Our study paves the way for the engineering of autonomously regulated modules that may be optimized to be specific against diverse parasitic nematode species.

4. Targeting Abnormal Metabolism in Breast Adenocarcinoma Cell Lines to Induce an Immunogenic Phenotype

Rachel Berrie, Kevin Lang, James Hartmann, Ph.D. Florida Atlantic University, Boca Raton, Florida

Abstract

Most standard chemotherapies induce cell death by targeting DNA. Cancer phenotypes exhibiting the Warburg Effect primarily obtain ATP from glycolysis, producing a highly acidic tumor

environment. 3-BromoPyruvate (3BP) inhibits enzymes required for aerobic glycolysis, forcing oxidative phosphorylation, free radical production and death. Whether 3BP will induce an apoptotic-immunogenic cell death, maximizing uptake and presentation of dying breast cancer cells to the immune system is unknown. Mouse breast cancer cells exhibited 50% apoptosis at a concentration of 3BP 1000X lower than the therapeutic dose while doxorubicin required a dose equivalent to its therapeutic dose in order to achieve 50% apoptosis. Since 3BP does not cause severe immunosuppression seen with doxorubicin therapy, my results indicate it may be superior in inducing an apoptotic-immunogenic cell death. Discovering whether 3BP elicits markers of immunogenic death, such as HMGB-1, may further our understanding of cancer immunotherapy.

5. Chitinase-3-like-1 (CHI3L1) expressed during allergic pulmonary inflammation promotes metastasis of mammary tumor cells to the lung

Camilla Silva Castro, S. Libreros, R. Garcia-Areas, V. Iragavarapu-Charyulu Florida Atlantic University, Boca Raton, Florida

Abstract

Inflammation contributes to tumor initiation and metastasis. Our studies have shown that preexisting pulmonary inflammation accelerates primary tumor growth, increases metastasis, and shortens survival in mammary tumor bearing mice. We and others have reported that chitinase-3-like-1 protein (CHI3L1) is upregulated during allergic pulmonary inflammation and tumor progression. CHI3L1 expression is implicated in the regulation of tissue repair and immune response during inflammation. However, the role of CHI3L1 in establishing a pulmonary pre-metastatic niche is still unknown. We hypothesize that pre-existing pulmonary inflammation alters the lung parenchyma via upregulation of CHI3L1, and thus accelerates pulmonary metastasis. CHI3L1 KO allergic mice showed a decrease in mucous production, smooth muscle, and collagen deposition prior to tumor inoculation compared to WT. In addition, CHI3L1 KO mice showed a reduction in pulmonary inflammation and tumor burden. Delineating the contribution of pre-existing pulmonary inflammation in the progression of breast cancer could lead to targeted therapies.

6. Isolation of **11** mycobacteriophages from Florida ecosystems and genomic characterization of mycobacteriophages Lumos, Pioneer, and SnapTap

Nina Davis, Arthur Domingas, Nick Heuter, Chris Holland, J Houk, Laura Molina, Michael Sonntag, Connor Swinford, Olben Saintfleur, Krystal Villalobos-Ayala, Megan Carroll, Adrienne Cottrell-Yongye, Ph.D., Tom D'Elia, Ph.D. Indian River State College, Fort Pierce, Florida

Abstract

Mycobacteriophages capable of infecting *Mycobacterium smegmatis* mc² 155 were isolated through enrichment of soil samples collected in Indian River, St. Lucie and Martin Counties, Florida. This analysis represents the first look at the diversity of the mycobacteriophage population in these

areas. As part of the HHMI-SEA PHAGES program, over 5,800 mycobacteriophage have been isolated and 1233 have been classified into 23 clusters. Here we report the isolation of eleven phages representing two confirmed clusters. Electron microscopy and molecular characterization indicate that all isolates belong to *Siphoviridae*, which have double stranded DNA genomes, long flexible tails and make up 90% of all mycobacteriophage. The complete genome sequence was determined for phages Lumos, Pioneer and SnapTap. Comparative genomic analysis classified Lumos within subcluster L3, which has 2 other members. Lumos has a 75,586 bp genome with 59.3% GC content (*M. smegmatis* has 67.4% GC), and initial analysis has predicted 130 open reading frames (ORFs) and 10 tRNAs. Pioneer was identified as an A9 subcluster member, with a 53,219 bp genome and 62.6% GC content. Of the approximately 100 ORFs predicted in Pioneer, less than 20% were assigned function, which is representative of the diversity that exits in these phage genomes. Finally, SnapTap was identified as a cluster A2 phage, with high sequence identity to SweetiePie, an A2 phage with a genome of 53,184 bp. This study helps to expand the diversity of cluster L phages and provide a more thorough understanding of mycobacteriophage ecological and genomic diversity.

7. Tip60-mediated reduction of cancer cell proliferation requires its nuclear localization

Simon Davis ^{1,2} and Daniel S. Ginsburg ² ¹Palm Beach State College, Palm Beach Gardens, Florida ²Long Island University, Brookville, New York

Abstract

Tip60 is a lysine acetyltransferase that plays a vital role as a tumor suppressor in cancer. Tip60 interacts with various genes such as p53 in processes of DNA repair and apoptosis. Previously, we have shown that Tip60 decreases proliferation in some cancer lines; however, the mechanism by which this is achieved is not well understood. In this study, we attempt to investigate the mechanism by which Tip60 decreases proliferation in various cancer cell lines. This was done by transfecting lung, pancreatic and breast carcinoma cells with Tip60 followed by treatment with the chemotherapeutic drug paclitaxel. Once treated, the cells were observed at various time points over a total of 72 hours. We have also previously shown that nuclear localization of Tip60 and observing levels of nuclear localization. The effect of the NLS addition resulted in a dramatic increase in nuclear localization. In this investigation, we compared nuclear localization of Tip60 when a signal is added to the C-terminus of the protein as well as both the N-terminus and C-terminus.

8. Transgenerational Nutrient Effects in Aedes aegypti Infected with Dengue Virus

Bradley Eastmond¹, Kylie Zirbel², Barry Alto, PhD.² ¹Indian River State College, Fort Pierce, Florida ²University of Florida IFAS, Fort Pierce, Floirda

Abstract

Transgenerational effects arise when the environment experienced by parents influences offspring phenotypes. Since transgenerational effects influence offspring life histories and can lead to changes in host-pathogen interactions, studying these effects addresses an intellectual gap in our understanding of mosquito-borne diseases. Transmission requires virus infected blood ingested by the mosquito replicate in the midgut and disseminate through the body and into the salivary glands. Dissemination to the legs is an indicator that the virus has escaped the midgut, a prerequisite for transmission. In this study, Aedes aegypti was used as a model system to determine how the parental larval nutrient environment influences offspring susceptibility to dengue-1 virus (DENV-1) infection and dissemination. Parents and subsequent offspring were reared in either high or low nutrient conditions. To assess whether parental nutrition influenced offspring susceptibility to infection, female offspring were provided with a DENV-1 infected blood meal. Fed mosquitoes were held for 14 days and then dissected into three parts: abdomens, thoraces, and legs. Female offspring were assayed using quantitative RT-PCR for the presence of DENV-1 RNA in the abdomen. Legs of mosquitoes positive for DENV-1 were then tested to determine whether or not the virus was able to escape the midgut and disseminate to other tissues. Contingency table analysis was used to identify transgenerational effects. Findings suggest that nutrient mediated transgenerational effects occur in this system as related to infection with and dissemination of DENV-1. This research increases our understanding of factors influencing the mosquito immune system and interactions with arboviruses.

9. Enhancement of Gα expression with co-expression of Ric8 on a baculovirus genome.

KeiAuyndria Edwards¹, Jacob Mahoney², Roger Sunahara² ¹Barry University, Miami Shores, Florida ²University of Michigan, Ann Arbor, Michigan

Abstract

G protein-coupled receptors (GPCRs) are the largest family of cell-surface receptors in the human genome and play a role in regulating most physiological functions. GPCRs interact with intracellular proteins called G proteins to initiate signal cascades that modulate cellular processes. G proteins are heterotrimeric, containing α , β , and γ subunits. Structural and biochemical studies of receptor-G protein interactions have historically been hindered due to complications with purifying large quantities of protein. However, it was recently discovered that co-expressing G-proteins with chaperones enhances purification. The aim of this study was to enhance G α expression by combining G α with the Ric8 family of proteins on a baculovirus genome. Insertion of G α with the respective Ric8 into a pVL dual vector was attempted in order to generate a baculovirus that expresses both proteins. Through a series of validation steps, it was determined that Ric8 was not

successfully inserted. To address this, a new set of restriction enzymes will be tested. The ultimate goal is to examine gene expression of the recombinant virus in insect cells, thereby taking advantage of the ability of these cells to produce large quantities of eukaryotic proteins in a short amount of time. Protein expression will be examined after injecting the recombinant virus into insect cells. Future directions will include observing how receptors interact with different G-proteins to learn why receptors display selectivity for the G-proteins with which they interact.

10. Towards carbon based nanotechnology: construction of a supramolecular nanopeapod from a buckminsterfullerene guest and a self-assembled cyclic β-peptide nanotube host

Kassandra Fernández, Andrea Vásquez, Servando Muñoz Miami Dade College, Miami, Florida

Abstract

Nature uses α -amino acids as the basic building blocks of proteins. Depending on their secondary structure, proteins self-assemble into an alpha helix or beta sheet. Our research is concerned with the self-assembly of cyclic β -peptides into cylindrical nanotubes that can serve as molecular hosts for large organic molecules such as Buckminsterfullerene, C_{60} . Cyclic peptides made up of β -aminoacids are topographically planar such their side chains radiate outwardly while the carbonyl and amino residues point perpendicular to the plane of the ring. Consequently, cyclic β -peptides possess a net dipole directed towards the nucleophilic, C-residues and away from the electrophilic N-residues. Cyclic β-peptides interact with each other and spontaneously self-assemble into cylindrical nanotubes through non-covalent, intermolecular hydrogen bonding. In the resulting superstructure, the net dipole from each component peptide ring is magnified such that a net macromolecular dipole arises along the central axis of the cylinder. Space-filling molecular models show that nanotubes made up of cyclo-[(L-β aminobutyric acid)9] peptides possess an inner cavity about 10 angstroms in diameter that closely corresponds to the Van der Waals size of C₆₀. Thus, a supramolecular nanopeapod can be constructed by encapsulating Buckminsterfullerene molecules inside the nanotube. Quantum mechanical electrostatic potential maps calculated at the Hartree-Fock 3-21G level of theory demonstrate that the guest fullerene molecules in the supramolecular nanopeapod are polarized along the β -peptide nanotube's macromolecular dipole.

11. Why do Patients who are Going Blind Lose their Blue Color Vision First?

Mariana Ferraz, Mark Jaffe, D.P.M., Ava Bittner, Ph.D., O.D. Nova Southeastern University, Fort Lauderdale, Florida

Abstract

Retinitis pigmentosa (RP) is a slowly progressive, inherited retinal degeneration affecting roughly 1 in 4000 people, typically resulting in a loss of peripheral and night vision, with most legally blind by age 40^[1]. RP is characterized by the apoptosis of retinal rods and cones (photoreceptors). Cones are responsible for central and color vision, while rods provide peripheral and nighttime vision. Over 20 years ago, it was reported that some RP patients initially lose short wavelength cones (i.e., s-cones for

blue-violet colors; e.g., imagine a world in which shades of blue look grey), but no further research on this topic has been conducted. We explored factors that may predict which RP patients are susceptible to s-cone loss. Cone function was determined using the PC-based Innova Rabin Cone Contrast Test with 2 tests per session repeated at two visits. Of 18 RP patients tested, only three (17%) had normal s-cone sensitivity, while 14 out of 15 eyes (93%) in 10 patients with measurable s-cone loss had a greater reduction in sensitivity for the s-cones than longer wavelength cones for red and green colors. S-cone sensitivity loss was measurable in those with visual acuities between 20/25-20/50. Amount of peripheral visual field loss, ability to see stars as a child, and duration of night vision loss were not statistically significantly related to s-cone loss across subjects; however, the three participants with normal s-cone sensitivity were the only ones with rod-mediated night vision, indicating there may be a link between loss of rods and s-cones.

12. Temperature dependent variation in self-reported contagious yawning within a single season

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Abstract

Previous cross-cultural research on humans has shown that self-reported contagious yawning frequency varies between distinct seasons and climate conditions. However, it remains possible that differences in yawning across seasons may be a result of physiological circadian changes across the year. In attempt to address this question, here we discuss the results of a study investigating the variation in the frequency of self-reported contagious yawning within a single season in one geographic location. A total of 142 pedestrians were recruited outdoors during an 18-day period over the summer in an equatorial monsoon climate in southern Florida, USA. Consistent with the thermoregulatory theory of yawning, results showed that self-reported contagious yawning frequency varied only across temperature gradients. This was true after statistically controlling for variables relative humidity, time of day, time spent outside, testing day, age of participant and hours of sleep the night before. These findings provide further evidence suggesting a brain cooling function to yawning.

13. Synthesis of pentylcycloheptane

Amal Gayoushe, James Lopez, Evelyn Downs, Ilka Valverde, Elizabeth Smith, Danielle White, Erica Belkin, Emmanuel Escobar, Amber Gonzales, Daniel Hajek, Irene Ramirez, Frantzy Germain, James Ley, Ph.D. Miami Dade College, Homestead, Florida

Abstract

Naphthenes are a class of molecules made of carbon and hydrogen atoms that contain at least one ring of carbon atoms. Naphthenes are a significant component in petroleum products including

mineral oil, which is the single greatest contaminant in the human body. While naphthenes that contain six-carbon-atom rings have been well studied, those containing seven carbon atoms are less known. For example, pentylcycloheptane has not been previously reported in the literature. The purpose of this work was to prepare this novel molecule from commercially available starting materials. The synthesis was a 3-step procedure. First 1-pentylcycloheptanol was prepared by reacting pentylmagnesium bromide and cycloheptanone. Second, the alcohol was subjected to acid-catalyzed dehydration by phosphoric acid. This produced two alkene isomers, one with the carbon-carbon double bond inside the ring and the other isomer with the double bond outside the ring. The proportion of isomers was analyzed by gas chromatography and nuclear magnetic resonance spectroscopy (NMR). Third, the two isomers were hydrogenated with palladium on carbon to produce the target compound, pentylcycloheptane. All products were analyzed by infrared spectroscopy, ¹H-NMR, ¹³C-NMR, DEPT, COSY, and HETCOR NMR. The spectroscopic evidence was consistent with the structures proposed and showed that pentylcycloheptane had been prepared with no major impurities. The overall yield was 10% for this un-optimized first reaction beginning with 2 grams of cycloheptanone. For future work, this method will be modified using deuterium in the hydrogenation step to produce deuterated pentylcycloheptane. This would enable sample analysis for pentylcycloheptane by the isotope dilution technique.

14. Reassortment of Tomato spotted wilt virus, Groundnut ringspot virus, and Tomato chlorotic spot virus

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Abstract

Tospoviruses, including Tomato spotted wilt virus (TSWV), Groundnut ringspot virus (GRSV), and Tomato chlorotic spot virus (TCSV) are capable of infecting a wide variety of agricultural and ornamental crops. The ability of tospoviruses to reassort genome segments with each other may lead to the creation of new virus genotypes. This study focused on the frequency of reassortment between TSWV, GRSV, and TCSV, and whether or not the viruses compete for infection of the host. It was found that it was not terribly uncommon for inoculated plants to become infected with more than one virus at a time. In some cases of plants doubly infected with both GRSV and TCSV, GRSV seemed to outcompete TCSV, causing PCR results to show signs of infection of only a single virus. Extended incubation time and retesting revealed the presence of the second virus. Testing of local lesions induced by doubly infected plants showed the presence of only a single virus in 134 of 137 samples. Three samples showed evidence of the presence of two viruses providing indication of possible reassortment. Although infection of a single plant with two different tospoviruses was relatively common following experimental inoculation, reassortment of genome segments between two co-infecting tospoviruses appears to be a rarer event.

15. The over-expression of BDNF on adult neurogenesis and seizure vulnerability

Danick Joseph, Ceylan Isgor Florida Atlantic University, Boca Raton, Florida

Abstract

Epileptic seizures are characterized by the abnormal protrusion of cells into various brain structures such as the hippocampus. This region of the brain is one of the primary zones of adult neurogenesis, and it is characterized by concentrated amounts of brain-derived neurotrophic factor (BDNF). Other studies have shown how the exogenous infusion of BDNF affects neurogenesis; however, little is known in regards to how the endogenous over-expression of BDNF affects Adult neurogenesis and seizure vulnerability. We will use immunohistochemistry procedures combined with age-specific cell markers to compare the rate of adult neurogenesis (population size, maturation and survival of new-born cells) in our transgenic mouse model with those of the wild type (WT) controls. Understanding the mechanisms that contribute to the progression of seizures in this animal model will facilitate our ability to intervene and prevent this disorder.

16. Dioxygen activation by mononuclear non-heme iron oxygenases and the corresponding model complexes

Shanika L. Kingston¹, Laura Cunningham² and John P. Caradonna² ¹Barry University, Miami Shores, Florida, ²Boston University, Boston, Massachusett

Abstract

The activation of O^2 is a process that occurs naturally when enzymes containing iron centers, known as mononuclear non-heme iron enzymes, oxidize challenging substrates. The objective of this project is to develop synthetic model complexes that can mimic the reactivity properties of these mononuclear non-heme iron (MNO) enzymes. The use of iron in these catalytic systems is particularly attractive as this metal is earth-abundant and non-toxic and thus this effort opens new avenues in inexpensive and sustainable catalytic transformations. An N₂O₂ ligand set and its reaction with α -ketoglutarate to generate the Fe^{II}/ α -ketoglutarate complex was investigated as an MNO enzyme mimic. We have experimentally observed that the structurally characterized fac- $[Fe^{II}(N_{\alpha}O_{\alpha})(sol)_{\alpha}]$ + complex: (i) rapidly reacts with a variety of α -ketoacids to form 1:1 complexes, (ii) shows significantly enhanced oxygen sensitivity when coordinated by α -ketoacids, (iii) rapidly decomposes the α -ketoacid ligand to CO₂ and the corresponding carboxylate ligand, and (iv) generates an Fe-based reactive intermediate that is kinetically competent. A cyclic reaction was observed, where each mole of α -ketoglutarate added, gave rise to 1 mole of H₂O, formaldehyde, and succinic acid (completely coupled reaction). A Nash Assay was performed to determine the amount of formaldehyde within a sample. A Karl Fischer titration was used to determine the amount of water within a sample.

17. Synthesis of Fmoc-Hyp (O-beta-Gal)-OPF Building Block Residue for Incorporation into a Triple Helical Collagen-like Peptide Inhibitor

Brian Lenhart¹, Maceij Stawikowski² ¹Indian River State College, Fort Pierce, Florida ²Torrey Pines Institute of Molecular Studies

Abstract

Multiple Sclerosis (MS) is an autoimmune inflammatory disease in which the insulating sheaths of neural axons are slowly degraded, resulting in loss of communication between the central nervous system and body parts associated with the demyelination. MS is not considered a hereditary disease although numerous indicators from gene mapping experiments have found correlations between the genes of the affected and the expression of certain proteins. It is hypothesized that particular gelatinous matrix metalloproteinases (MMP) are associated with the degeneration of the nervous insulation. This research is targeted at synthesizing and incorporating specific building blocks of a triple helical peptide (THP) at key locations in order to help transport the allosteric MMP THP inhibitor across the highly specific blood-brain barrier (BBB). The synthesis and incorporation of the building block residue into the THP was successful, and we now turn our investigation towards in vivo testing to analyze the efficacy of this drug on crossing the BBB.

18. A novel approach to the synthesis of cannabinoids

James Lopez, Amal Gayoushe, Daniel Hajek, Evelyn Downs, Elizabeth Smith, Erica Belkin, Emmanuel Escobar, James Ley, Ph.D. Miami Dade College, Homestead, Florida

Abstract

Tetrahydrocannabinol (THC) is the principal psychoactive constituent of the cannabis plant. The human body contains CB1 and CB2 receptors that respond to THC. Some medical conditions may be treated or symptoms alleviated by the action of THC. Furthermore, it is possible to synthesize THC analogs, which have a similar molecular structure. These analogs can act selectively on CB2 receptors and avoid the psychotropic effects of THC. Therefore, the synthesis of cannabinoids that mimic THC are potentially very important. The research question is: can novel cannabinoids be synthesized from inexpensive starting materials. The Heck reaction was used to couple 1,3-iodobenzaldehyde with a commercially available natural product. This was followed by a Wittig reaction with n-butyltriphenylphosphonium bromide to yield a mixture of *cis*- and *trans*-alkenes. The double bond was reduced by hydrogenation with palladium on carbon. Reactions were monitored by thin layer chromatography. Products were purified by column chromatography with silica and then characterized by infrared spectroscopy, ¹H-NMR, ¹³C-NMR, DEPT, COSY and HETCOR nuclear magnetic resonance spectroscopy. The next step in this process will be an intramolecular Friedel-Crafts alkylation to form the middle ring of the phenanthrane nucleus. The long term goal will be to use this novel cannabinoid analog in biological research studies.

19. The role of Kisspeptin 2 in the social control of sex change in Bluehead wrasse *(Thalassoma bifasciatum)*

Alison Lukowsky, William A. Tyler, Ph.D. Indian River State College, Fort Pierce, Florida

Abstract

Kisspeptin 2 (KISS2) is a common gene expressed in neurons within the hypothalamus of the brain during sex hormone production. When active, KISS2 stimulates GnRH release which in turn, stimulates luteinizing hormone and follicle-stimulating hormone production allowing the gonads to produce estrogen. For this project, KISS2 mRNA was measured throughout the different phenotypes within the bluehead wrasse. This species is a protogynous hermaphrodite, and has the ability to change sex from female to male. Due to KISS2 playing a critical role during puberty and reproduction in vertebrates gives off the impression that this gene could have the potential to influence sex change, transforming a female with ovaries into a male with functioning testis. However, after performing qPCR it was discovered that there was not a significant change in KISS2 mRNA throughout the different phenotypes of the bluehead wrasse. These findings influence future studies of the gene using in *situ* hybridization, which could measure the quantity of neurons expressing KISS2 rather than measuring concentration at the whole brain level.

20. Properties of dielectric photonic band gap material at microwave frequencies Karen Manrique, J. Calavia, S. Souchak Miami Dade College, Miami, Florida

Abstract

The study concerns the properties of dielectric Photonic Band Gap Material (PBGM) in the microwave frequency range. The dielectric PBGM, which we studied made of dielectric rods disposed in an isosceles right-angled triangle. The transmission diagram is calculated with a numerical code developed in the University of Glasgow, and then validated with the High Frequency Simulator Structure HFSS software developed by Ansoft. In the first allowed frequency band, the dielectric crystals (PC) behaves like a homogeneous medium. In the forbidden band frequencies, the transmission decreases exponentially as the number of layers increase. The numerical results show that the dielectric photonic band gap prism behaves like homogenous and classical medium in its first authorized band frequency. In forbidden band frequencies the transmission decreases exponentially as the number of layers increases the transmission decreases exponentially as the number soft band frequencies and classical medium in its first authorized band frequency. In forbidden band frequencies the transmission decreases exponentially as the number of layers increases the transmission decreases exponentially as the number of layers increases the transmission decreases exponentially as the number of layers increases the transmission decreases exponentially as the number of layers increases the transmission decreases exponentially as the number of layers increases the transmission decreases exponentially as the number of layers increases.

21. Several Caribbean damselfish genera differ in UV-reflectance patterns

Kevin S. McCarty, Michael P. Robinson Barry University, Miami, Florida

Abstract

Ultraviolet (UV) radiation (200-400 nm) is located towards the short wavelength, high frequency end of the electromagnetic spectrum. Although ultraviolet radiation is not visible to the human eye, some animals, including many coral reef fishes, can perceive it. For example, two species of Pacific coral reef damselfishes (Pomacentridae) possess complex ultraviolet facial patterns that they can recognize and use for territorial aggression, identification, or other forms of communication. We used a UV-photography system to record the UV-reflectance of three species of Atlantic damselfishes: yellow tail (*Microspathadon chrysurus*), beaugregory (*Stegastes leucostictus*), and bicolor (*Stegastes partitus*). The fishes were placed into a small, single sided UV-transparent Lexan aquarium, which enabled us to photograph the fishes without harming them. The yellow tail and the beaugregory both had obvious ontogenetic changes and an overall decrease of the UVreflectance patches throughout their bodies. The yellow tail showed an overall UV-reflectance intensity around the occipital, suborbital, and preopercular regions, while both, the beaugregory and the bicolor showed similar UV-reflectance patterns along the anal fin during the juvenile stage. These complex patterns could likely be used for identification of individuals, mating selection, or aggressive territorial competition.

22. The inoculum effect offers an extended window for the evolution of antibiotic resistant bacteria.

Haley McKissack, Uzair Mohammed, Kyle Cahil, Steven Thomas, Louis Nemzer, Ph.D., Robert P. Smith, Ph.D. Nova Southeastern University, Fort Lauderdale, Florida

Abstract

Misuse of antibiotics, coupled with a lack of new antibiotics being discovered, has threatened our ability to treat bacterial infections. Confounding our ability to effectively combat antibiotic resistance is the myriad of ways in which bacteria can resist antibiotic treatment. One mechanism is the inoculum effect, a phenomenon in which the inhibitory concentration of an antibiotic increases with initial cell density. Previously acquired data has indicated a mutation exclusive mechanism by which resistance arises. However, it is currently unknown as to whether or not the generation of antibiotic resistant bacteria due to spontaneous mutation plays a role in the inoculum effect. The purpose of this study was to examine the role, if any, that spontaneous mutation plays in resistance due to the inoculum effect. To assess this, we grew *Escherichia coli* in the presence of increasing concentrations of the antibiotic resistant bacteria. Furthermore, by perturbing the cellular network responsible for the inoculum effect, we were able to alter the mutation frequency. To examine if spontaneous mutations could also arise in a dynamic setting, we built a microfluidic flow system that allowed antibiotics to be delivered at defined intervals to a population. We observed that under these dynamic conditions, spontaneous mutants could still arise but not completely account for the

total bacterial growth observed. Overall, our results indicate that the inoculum effect may provide an extended window in which antibiotic resistance due to genetic mutations can arise.

23. 5-HT1A Receptor Coupling Following Adolescent Drug Exposure

David Novo¹, Menglu Yuan², Frances Leslie, Ph.D. ² ¹Barry University, Miami Shores, Florida ²University of California, Irvine, California

Abstract

Adolescence is a critical developmental transition period in which the onset of psychiatric disorders and the initiation of smoking emerge. Eighty-eight percent of current adult smokers began during adolescence, and teen smokers are much more susceptible to develop psychiatric disorders and abuse other drugs. One of the key systems affected by exposure is the serotonin (5-HT) system, which is involved in regulating mood, anxiety, reward, and is believed to also play a role in addiction. Previous studies have shown that during adolescent drug exposure, 5-HT_{1A} receptors mediate the enhancement of cocaine self-administration. However, these effects are blocked by 5-HT_{1A}R antagonists. The enhancement of cocaine self-administration is due to increased 5-HT_{1A}R activity, however it is unclear what causes the increase in receptor activity although it is believed to be due to an increase in receptor coupling. To address this we perform GTP γ S audioradiography in rat brain sections. We quantify the audioradiography using MicroComputer Imaging Device (MCID), an image analysis program. Based on this data, we will be able to determine if increased receptor activity is due to an increase in receptor coupling or an increase in receptor sensitivity.

24. The effects of oxytocin and cortisol pre-and postpartum levels in mother–infant bonding

Jana Olivova and Nancy Jones Florida Atlantic University, Boca Raton, Florida

Abstract

Despite all the work on how oxytocin ("love" hormone) and cortisol ("stress" hormone) affect behavior, it is not well known how these hormones levels, *pre* and *post partum*, influence the mother-infant quality of bonding. Therefore, oxytocin and cortisol levels and mother-infant quality of bonding were studied to determine possible correlations. Hormones released were induced in mother-infant dyads by exposure to either a nurturing condition or to a stressful condition. Results have found no correlation between oxytocin and the nurturing condition, but positive correlations between oxytocin and the expressed feelings of mothers toward their infant, as well as a negative correlation between cortisol and less bonding feelings (afraid/resents infant). Understanding how mother-infant bonding develops into a lasting bond should be a valuable tool for pediatricians and psychologist in promoting behaviors that will benefit society at large.

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

Kiara Pazan, Yelena Katsenovich, Ravi Gudavalli Florida International University, Miami, Florida

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 from 1955 to 1988. 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 (MCLs). For remediation, humic acid (HA) technology has shown to be a potential approach for controlling mobility of radionuclides. Because sorbed HA and uranium develop a strong bond at slightly acidic pH, the mobility of the contaminant molecules should decrease with flushing of SRS groundwater. Column experiments are planned using SRS soil from the F/H Area to examine the sorption and desorption properties of HA in SRS soil. The data from these experiments will then be used to perform modeling of the migration and distribution of HA injected into the subsurface.

26. Characterization of ferret immunoglobulin-specific murine monoclonal antibodies

Thomas Penrose ^{1,2}, Greg A. Kirchenbaum ², Rayleigh Chan ², Ted M. Ross ² ¹Palm Beach State College, Palm Beach Gardens, Florida ²Vaccine and Gene Therapy Institute of Florida, Port St. Lucie, Florida

Abstract

The ferret is an ideal small animal model for influenza research because they are susceptible to infection with human isolates and exhibit similar symptomology including fever, lethargy and sneezing. Additionally, ferrets are capable of transmitting the virus through both nasal secretions and aerosol droplets. While the ferret is an extremely useful model for evaluating influenza pathogenesis and vaccine efficacy, there remains a severely limited set of reliable and well-characterized immunological tools available to the research community. In order to address this unmet need, we generated novel mouse anti-ferret immunoglobulin (Ig) specific monoclonal antibodies (mAb) using conventional hybridoma technology. These mAbs were initially characterized by enzyme linked immunosorbent assay (ELISA) and flow cytometry (FACS), and exhibit unique binding characteristics against purified ferret Ig and ferret peripheral blood mononuclear cells (PBMC). We further defined the specificities of these ferret Ig-specific reagents using multi-color FACS and fluorescently conjugated mAbs. Specifically, we were able to further categorize the ferret Igspecific mAbs based on their reactivity with defined populations of ferret PBMC, including B cells and monocytes. Based on these data, we generated multiple mAbs recognizing either the heavy chain (gamma) or light chain of ferret Ig. Collectively, these mAbs will aid in the study of humoral immunity in the ferret model, and have wider application beyond influenza research.

27. Use of XRF to Characterize Pre-Hanford Orchards in the 100-OL-1 Operable Unit

Christian Pino¹ (DOE Fellow), Amoret Bunn², Brad Fritz², Dominique Martinez³, Komal Rana⁴, and Leonel Lagos¹ ¹Florida International University Applied Research Center (DOE Fellow) ²Pacific Northwest National Laboratory • ³Austin College • ⁴California State University East Bay

Abstract

Prior to 1943, the Hanford Site included several small towns with approximately 8,000 acres of agricultural development. About 5,000 of those acres were used for orchards, with lead arsenate (PbHAsO) being the common pesticide for controlling coddling moths in fruit trees. Higher concentrations of lead and arsenic were recorded in the vicinity of the old orchards at the Hanford Site. In year 1980, U.S. Department of Energy's Richland Operating Office, Environmental Protection Agency, and Washington Department of Ecology investigated the lead arsenate residues under the Comprehensive Environmental Response, Compensation, and Liability Act (CERCLA) and designated the pre-Hanford orchards 100-OL-1 Operable Unit. Initial characterization activities included a pilot study to evaluate the use of a field portable x-ray fluorescence (XRF) analyzer and determine if the performance of the instrument provides results that meet quality assurance criteria for cleanup decisions. An optimization study was performed to evaluate the counting times and position of the XRF using soil collected from the orchards on the Hanford Site. The optimization study confirmed that the variability in the field was more significant than operator or instrument variability. The surface soil at four Decision Units (DU) OL-14, OL-32, OL-IU6-4 and OL-FR2-1 was evaluated with the XRF. Due to distinct past activities in each site, orchard activity may or may not have been present in every DU; however, all together they provide an adequate representation of the entire 100-OL-1 Operable Unit. Results indicated that there were areas in each DU with concentrations above the screening criteria for both lead (250 mg/kg) and arsenic (20 mg/kg).

28. Nutrient signaling is exaggerated in cells derived from patients with Huntington's Disease

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Abstract

Huntington's disease (HD) is characterized by the early loss of GABAergic medium spiny neurons in the striatum, which impairs motor and cognitive functions. Huntingtin (Htt) is a ubiquitously expressed protein whose polyglutamine (poly-Q) tract is expanded in HD; more than 36 glutamine repeats (36Q) in the N-terminal region results in production of a pathogenic mutant protein (mHtt).Previously we found that wild type Htt physiologically regulates the mTORC1 pathway, a major kinase induced by growth stimulants, amino acids (Pryor, 2014). mHtt further increases the mTORC1 pathway by amino acids. More importantly when mTORC1 is selectively induced in a HD mouse it leads to an exaggerated motor defects and premature demise of HD mice (Pryor, 2015). But whether mTORC1 pathway is altered in human HD patients is unknown. Now we have utilized fibroblast cells derived from human patients to confirm the mHtt-mTORC1 link. We cultured human fibroblast cells derived from healthy patients and HD patients containing either 69Qor 151Q. We starved the cells from amino acids and then re-stimulated with amino acids. Our results indicate that the activity of mTORC1 increases with increasing number of glutamine repeats in response to amino acid stimulation in these HD patient cells. This is significant, as high mTORC1 activity is observed not only in HD, but also in other neurodegenerative conditions. Therefore, interfering with the mTORC1pathway by controlling the patient's amino acid intake (diet) may have therapeutic potential for HD and presumably for other neurodegenerative diseases such as Parkinson's and Alzheimer's disease.

29. Enhancing Blood Vessels in Retinal Images using Gaussian Filters

Aarti Ragoonath, Lukas Bijaminas, and James Haralambides, Ph.D. Barry University, Miami Shores, Florida

Abstract

We present an algorithm that enhances the blood vessels of retinal images to support medical diagnosis and clinical study. Accurate imagery of blood vessel features such as diameter, curvature, and color is essential to the diagnosis of diseases and the application of appropriate treatments. The objectives of this work are in two main directions: a) locate, identify, and amplify blood vessel boundaries and structures, and b) exploit hardware parallelism to increase algorithmic efficiency. Delineation and augmentation of features is achieved with the use of Gaussian filters. A twodimensional Gaussian kernel function with non-uniform standard deviations for the x and y coordinates is used. The function is rotationally transformed twelve times in intervals of 15 degrees to achieve directional independence with respect to feature extraction. A 15x15 matrix holding filter values is applied to each image pixel in sliding window fashion. Normalization of computed values follows in order to parameterize feature intensity. Image filtering algorithms such as the algorithm presented here process large amounts of pixels in non-consecutive memory location and, therefore, suffer from memory read and write delays. We have designed a field-programmable architecture that takes advantage of the inherent concurrency of processes on hardware devices to minimize the effects of memory latency. This is achieved by prefetching and buffering memory words into smaller-size, independent block RAMs. Words stored in block RAMs can be accessed randomly at no additional overhead. Multiple pixels are processed at the same time for all rotational versions of the Gaussian filters reducing execution times substantially.

30. Females of *Syntomeida epilais* (Lepidoptera: Noctuoidea) phonorespond differentially to conspecific male and female acoustic emissions

Nicole Ramsay, Jessica Hernandez, Frank Coro, Ph.D. Miami Dade College, Miami, Florida

Abstract

Several species of noctuoid moths are known to interact acoustically with insectivorous bats by emitting acoustic signals when detecting bat calls. Some of these species also use acoustic emissions during their courtship behavior. In most cases studied, only males have emission organs. Syntomeida epilais is one of the few noctuoid species in which both genders emit acoustic signals, named modulation cycles (MC), during their courtship behavior. This species shows sexual dimorphism in some of the temporal variables of the MC, including repetition rate. Our aim was to study if virgin, perched females of S. epilais could discriminate between their male and female acoustic emissions presented at the same repetition rate. Ten S. epilais females were stimulated during their mating behavior hours (between 4:00 and 6:30 a.m.) with playback of male MC and female MC, as well as female MC converted into male MC, and male MC converted into female MC. Each of these 4 stimuli were applied in groups of 8 MC presented at the same repetition rate (between 8.3 and 20 MC/s, a range that includes the values of male and female emissions during courtship behavior). S. epilais females phonoresponded with more MC/s to the male MC series and to the female MC converted to male MC series than to the other 2 stimuli applied. We propose that these female moths, with two-celled ears, use the microtemporal structure of MCs presented repetitively as a cue for phonoresponding differentially to conspecific male and female acoustic emissions.

31. Evidence for ancient genetic structure between archaic hominins and modern humans

Brian Richardson, Robert K. Lowery, Ph.D. Indian River State College, Fort Pierce, Florida

Abstract

Conclusions have been made that low levels of Neanderthal (1-4%) and DenisovanDNA (6-8%) may have entered the gene pools of particular Modern Human populations. This supposition is founded upon D-statistic based comparisons of mutations and the sharing of haplotypes among these groups (Green et al., 2010; Reich et al, 2010). However, genetic structure analyses of human single nucleotide polymorphisms (SNPs) have suggested that common ancestry rather than admixture may explain the coincidence of stretches of DNA shared among these groups (Lowery et al, 2013). The latter study made this claim based on D-statistical results from of a very ancient set of human SNPs for which the derived state is found in both Neanderthals and Denisovans. The current study re-analyzed archaic-Modern hominin gene flow by using projected principal component analysis (PCA) of lineage-specific sets of alleles among the worldwide set of Modern Humans. PCA plots indicate a high retention of common ancestral DNA in populations previously said to have high Denisovan admixture (Green et al.2010), and thus said "admixture" may be explained by a retention of ancient alleles lost from other human population by genetic drift. Further, by using a

more recently developed structure analysis program with variant parameters and quality controls, (ADMIXTURE), even less support was found for inter-species gene flow than in the prior report of genetic structure relationships.

32. Wound healing and infection in adult Danio rerio wildtype zebrafish

Jessica Ricketts ¹, Victoria Hoelscher ¹, Precious de Verteuil ², Brenda Schoffstall¹ ¹Barry University, Miami, Florida ²University of Oregon, Eugene, Oregon

Abstract

Danio rerio (zebrafish) share many physiological and genetic characteristics with humans, making them an attractive model system for scientific research. Zebrafish have been shown to completely regenerate significant portions of heart, fin, and tail tissues without loss of function or formation of permanent scar tissue. However, the healing response following deep tissue burn puncture wounds has not yet been described for zebrafish. We have hypothesized that zebrafish should completely regenerate skeletal muscle and surrounding tissues in response to this type of injury-making them an interesting wound-healing model. Our initial investigations indicate that deep tissue burn puncture wounds of this type require approximately thirty days to heal, with minimal to no external scarring visible. We have also screened wounds for infection that occurs during the healing process, and have begun to identify the endogenous bacteria that cause these infections. Follow up studies include time point sampling for analysis of the wound healing process at tissue and molecular levels, as well as investigation of bacterial biofilm formation and specific identification of bacterial species causing infection during the healing process. Our preliminary results support the use of zebrafish as a model to investigate cellular and molecular regeneration and healing processes following deep tissue burn puncture wounds. Findings could translate into applications for treatment of burn puncture wounds to skeletal muscle in humans, such as those inflicted during military combat.

33. Evolutionary divergence of bacteriophages detected within the *Clostridium taeniosporum* genome

Erick Salvador Rocha¹, A. Gelman¹, D. Gelman¹, A. Tishena¹, S. Tobar-Potes¹, M. Moreno¹, K. Borrero¹, A. Blinkova², S. Barge², S. Hunicke-Smith², E. Satterwhite², H. Tucker², J.R. Walker², J.M. Cambridge², E. Ginés-Candelaria¹ ¹Miami Dade College, Miami, Florida ²University of Texas at Austin, Austin, Texas

Abstract

Clostridium taeniosporum is a Gram-positive, nonpathogenic, and anaerobic bacterium that was isolated from Crimean silt (Krasil'nikov, N. A. et al., 1968). The organism is approximately 98% homologous in rDNA to toxigenic *Clostridium botulinum* phylogenetic Group II strains. It is also unique in that it displays characteristic ribbon-like endospore appendages (Iyers, AV,

2008). *Clostridium taeniosporum*'s genome is approximately 3,264.846 Kbs in length. Upon further analysis of the *Clostridium taeniosporum* genome, various putative phages that integrated as a result of horizontal gene transfer were identified using the PHAge Search Tool, PHAST. To study the evolutionary divergence of phages detected within *Bacillus* and *Clostridum*, we identified and downloaded complete phage sequences from the NCBI's GenBank, representing those that infect these two indicated genera of Firmicutes. We then performed a MAFFT multi-wise nucleotide alignment (hosted under Geneious v.7.1.6), to construct a phylogenetic tree of *Bacillus* and *Clostridium* phage genome sequences both from NCBI and those identified as prophages within the *Clostridium taeniosporum* genome. Three putative prophages named Ct Prophage 1, Ct Prophage 2 and Ct Prophage 3, form clusters with other clostridial phages, which diverged from published *Bacillus* phage sequences in the NCBIS GenBank. Results seem to indicate that these sequences presumably diverged after integration into the *C. taeniosporum* genome. Studying the evolutionary divergence of phages detected within Firmicutes may possibly reveal common genome integration mechanisms, uncover close evolutionary relationships, and may provide further insights into the acquisition of cryptic virulence determinants within the group.

34. The potential for *igf2* and *yap1* genes as a proliferation switch in zebrafish cardiomyocytes

Johan Sanchez¹, Nicole H. Lopez², Brenda Schoffstall¹ ¹Barry University, Miami Shores, Florida ²Georgia Regents University, Augusta, Georgia

Abstract

Approximately 1 million people die annually from heart related disorders; the discovery of a "cardiomyocyte proliferation switch" may contribute to therapeutics that could solve this problem. Previous research has demonstrated that human cardiac cells are only able to proliferate until about 20 years of age, with the highest percentage of cell division between birth and the first year of life; the adult human heart has no ability to regenerate after myocardial infarction. Conversely, adult Danio rerio (zebrafish) hearts respond to excessive cardiac overload stress with cardiomegaly via cardiomyocyte proliferation. We have used a zebrafish model to identify specific gene pathways that may act as the switch that turns on efficient cardiomyocyte proliferation. Because of their involvement in cell division signaling, we have targeted *igf2* and *yap1* as proliferation switch candidates. Timed heart tissue samples were taken from zebrafish that were put through a rigorous exercise program for 4 weeks to promote cardiomyocyte proliferation. The *igf2* transcription levels appear to increase significantly during week 3 of the exercise trial, and decrease drastically during week 4, while *yap1* transcription levels appear to essentially be the same as controls during weeks 1-3 of the exercise trial, then decrease during week 4. Because phosphorylated Yap1 protein is inactive, our current and future studies focus on the hypothesis that dephosphorylation of Yap1 protein holds the key to its ability to act as a proliferation switch. Either igf2 or yap1 may prove to be the "therapeutic switch" that can turn on cardiomyocyte proliferation in human hearts.

35. New acidic terpenoids from Pseudopterogorgia acerosa

Paul D. Scesa, Lyndon M. West Florida Atlantic University, Boca Raton, Florida

Abstract

One new cembranoid and two new pseudopteranoids were found in the Gorgonian coral *Pseudopterogorgia acerosa* collected in the Bahamas. Isolation of these compounds was performed using a combination of column chromatography and preparative high pressure liquid chromatography. The structural elucidation was performed using extensive spectroscopic analysis, including mass spectrometry and 1D and 2D NMR spectroscopy. The structural elucidation of these compounds will be described.

36. Monitoring Mineralogical Changes Occurring in Sediments via the EARP Process

Aref Shehadeh (DOE Fellow), Dr. Yelena Katsenovich, Dr. Leonel Lagos Florida International University, Miami, Florida

Abstract

From 1955 to 1989, unlined basins at the Savannah River Site received approximately 1.8 billion gallons of acidic waste solutions, much of which seeped into the surrounding soil and groundwater. The mobilization of metals and radionuclides included soluble uranium (VI), which is now present in the F-Area sediments. In 2010, ARCADIS implemented in-situ injections of a carbohydrate substrate to establish anaerobic reactive zones for metal and radionuclide remediation via the Enhanced Anaerobic Reductive Precipitation (EARP) process at the SRS F-Area. The addition of a molasses substrate solution to groundwater in conjunction with the presence of anaerobic bacteria produces anaerobic conditions with redox values in the methanogenic or sulfate-reducing range conducive to the reductive precipitation of uranium. To determine the effectiveness of this process, a microcosm study was prepared with SRS sediments in a solution mixture augmented with molasses and sulfate. The sulfate reduction process can lead to an increased pH of the water, often to a near neutral condition. The study aims to determine whether forms of reduced iron such as siderite and pyrite would arise in the reducing zone and if any mineralogical changes can occur in the sediments during the re-oxidation period. These experiments can also explain the types of reactions that might occur in the anaerobic aquifer.

37. Effect of Sleep Restriction and Delay on Psychological Health and Biomarkers of Stress and Inflammation

Samuel V. Thomas, Ana I. Fins, Ph.D., Travis J.A. Craddock, Ph.D., Jaime Tartar, Ph.D. Nova Southeastern University, Fort Lauderdale, Florida

Abstract

Despite strong associations between sleep duration and health, there is no clear understanding of the mechanisms through which chronic sleep restriction (CSR) alters physiological processes that lead to poor health. In an effort to shed light on the complex sleep-immune-stress relationship we focused on biochemical and psychological factors that previous research suggests might be essential to uncovering the role of sleep in health. To that end, we analyzed the effect of selfreported volitional CSR and time of sleep on a series of sleep and psychological health measures as well as biomarkers of immune functioning/inflammation (IL-1β), stress (cortisol), and sleep regulation (melatonin) in young adult females. We found that across multiple measures, poor sleep was associated with decreased psychological health and a reduced perception of self-reported physical health. We found that self-reported volitional short sleep duration (i.e. CSR) is related to increased cortisol and increased inflammation as measured through IL-1 β levels. We separately looked at individuals who experienced CSR with and without a delayed sleep time and found that IL-1 β levels and cortisol levels were significantly elevated in both groups, relative to those who did not experience CSR or a late sleep time. Overall, our results show how an increase in a proinflammatory process and HPA axis activity relates to volitional CSR, with and without a delayed sleep time and how these mechanisms relate back to psychological and self-reported health.

38. The role of cdc2 in PMA-induced cell differentiation

Daria Vasilyeva, Pairat Dolinsky, Shashana Fielder, Alice Nakasone, Marithza Gaspard, Xiaotang Hu Barry University, Miami Shores, Florida

Abstract

The critical role of cdc2 (CDK1) in G2-M transition of the cell cycle control in mammalian cells has been well documented. However, whether this pluripotent CDK regulates cell differentiation is unclear. Thus, the effect of phorbol 12-myristate 13-acetate (PMA) on cell differentiation and the expression of cdc2 in a human myeloid leukemia cell line, TF-1a, were investigated. When TF-1a cells were treated with 10-5,10-6, and 10-7 PMA for 48 and 72 h, they showed marked macrophage-like changes, evidenced by significant decrease in nucleus/cytoplasm ratio and increase in the expression of IL-1 β . PMA treatment also caused time-dependent inhibition of cdc2 in both cytosol and nucleus of the cells, with maximal inhibition being observed by 48 and 72 hours, which paralleled with the cell differentiation course. In contrast, there was no significant cell differentiation and inhibition of cdc2 being observed in control human myeloid leukemia TF-1 and MV4-11 cells in response to PMA treatment. PMA treatment also rapidly induced phosphorylation of MAPK kinase (MEK and p44/42 MAPK), which persisted for 24 h, after which MEK and ERK return to base level, at which time the expression of cdc2 was still significantly downregulated, as compared with control cells treated with DMSO. Taken together, our data suggest that that inhibition of cdc2 is required for late differentiation of TF-1a cells in response to PMA stimulation. Whether activation of MAPK pathway inhibits expression of cdc2 is currently under investigation.

39. Towards carbon based nanotechnology: construction of an electrochemical, redox-switched (10,0)-zigzag single-walled carbon nanotube field effect transistor, FET

Daniel Villagomez, Servando Muñoz Miami Dade College, Miami, Florida

Abstract

The central processor unit, CPU, of modern computers is based on silicon transistors with a 22 nm architecture. Single-walled semiconductor carbon nanotubes can replace silicon transistors and increase the frequency of the processor because of their molecular size. In our research we use quantum chemical analysis to study electron transport through a semiconducting (10,0)-Zigzag single walled carbon nanotube, SWCNT, in the presence of an electrochemical gradient. We assembled a single-walled carbon nanotube field effect transistor, SWCNT-FET, using two capped, metallic (5,5)-Armchair carbon nanotubes that served as the source and the drain electrodes in contact with a semiconducting (10,0)-Zigzag nanotube. An electrochemical gradient was imposed across the semiconductor nanotube by placing sodium and fluorine atoms within the drain and the source electrodes, respectively. Quantum mechanical electrostatic potential maps calculated at the Hartree-Fock 3-21G level; of theory show that sodium becomes oxidized at the source and fluorine is synchronously reduced at the drain electrode. Thus, a single electron is transported across the nanotube "channel" over a distance of 32 angstroms. Our calculations suggest that redox-switched electrochemical field effect transistors made from (10,0)-zigzag carbon nanotubes may provide an alternative molecular technology to replace silicon-based semiconductors in microelectronics.

40. Relationship between diet quality and depressive symptoms in Blacks with and without Type 2 diabetes

Alejandra Vivas, Gustavo G. Zarini, Joel C. Exebio, Joan A. Vaccaro, Sahar Ajabshir, Fatma G. Huffman Florida International University, Miami, Florida

Abstract

The aim of this study was to investigate the relationship between diet quality and depressive symptoms in Blacks (Haitians- and African Americans) with and without type 2 diabetes. Recruitment of participants (n=507) for the study was conducted by community outreach in Broward and Miami-Dade counties, Florida. Beck Depression Inventory (BDI) was used to asses depressive symptoms, those who scored \geq 16 and or taking depression medication were classified as depressed. Willett's food frequency questionnaire was used to estimate the Healthy Eating Index 2005 scores (HEI-2005). Participants with a HEI score \leq 58 were classified as having a low diet quality and participants with a HEI score > 58 were classified as having a high diet quality. Independent t-test, chi square and logistic regression analysis were used to determine the association of these two variables. There was a higher percentage (50.9%) of subjects with depressive symptoms classified as having a low diet quality as compared to those with low depressive symptoms and a HEI-05 score \leq 58 (36.7%) (p=.007). Logistic regression analysis showed this relationship was significant for people without diabetes (p=.018). Participants with low diet quality were almost 2.5 times more likely to be classified as having depressive symptoms as compared to those with high diet quality after adjusting for age, gender, ethnicity and BMI (95% CI 1.16-5.22). A low diet quality was associated with depressive symptoms in Blacks without type 2 diabetes.

41. Development of enzymes for the production of fuel ethanol from pre-treated corn stover

Stacey Walter^{1,2} and Karen Hebbard² ¹Palm Beach State College, Palm Beach Gardens, Florida ²Dyadic International, Jupiter, Florida

Abstract

Corn stover contains high amounts of carbohydrates, which gives this material potential to become a low cost source for bioethanol production. The development of enzymes is essential for increasing efficiency and reducing the cost to produce ethanol for biofuel. Corn stover must be pre-treated prior to enzymatic hydrolysis due to potential bacterial growth, followed by dry weight determination. Saccharifications will be carried out using four of Dyadic International's enzymes. All samples undergo desalting prior to determining protein concentration. The amount of enzyme to be used is based on protein value deter-mined from BCA assay. 20 mg/g Total Solids enzyme concentration will be added to 10 grams (43.6 wet weight) corn stover. 500mM citrate buffer at pH 6.0 (with 0.02% sodium azide) will be added to reach a final weight of 100g. This saccharification is performed under conditions 50°C, in 250 ml Erlenmeyer flasks containing six 1/4" stainless steel balls shaken at 300rpm to mix. Hydrolyzing sugars will be determined by sugar analysis after 24, 48, and 72 hours incubation. HPLC will be used to analyze samples at flow rate .400 ml/min with 5mM sulfuric acid, 0-25 isocratic run for each sample. Concentrations of glucose, xylose, arabinose, and cellobiose will be determined using calibration standards of those sugars. Glucose concentration will be determined using YSI Biochemical Analyzer.

42. Sodium Silicate Treatment for Uranium (VI) Removal and pH Stabilization of the Groundwater Systems at the F/H Area of Savannah River Site

Christine M. Wipfli (DOE Fellow), Dr. Katsenovich, Dr. Anagnostopoulos Florida International University, Miami, Florida

Abstract

The Savanah River Site (SRS) was one of the most significant manufacturing facilities during the Cold War era for producing nuclear materials. At the end of the Cold War, the Site's mission changed to support the environmental restoration of the Site due to over six decades of research, development, and production of nuclear weapons. Currently SRS is a major hazardous waste management facility responsible for nuclear materials storage and remediation of contaminated soil and groundwater from radionuclides. This research focuses on two main objectives: to control the mobilization of the contaminants, specifically uranium (VI) located in groundwater plumes at the Sites' F/H Area Seepage Basin, where approximately 1.8 billion gallons of hazardous waste were deposited; secondly, to restore the pH of the treatment zone in an effort to create a stable environment suitable for biological life. This research specifically evaluates the potential use of sodium silicate which increases the pH of the treatment zone from an acidic state to an environment close to pH neutral, as well as achieves uranium precipitation from the aqueous phase, therefore immobilizing the contamination. Through a series of batch experiments, the optimum concentration of sodium silicate for the restoration of the pH was investigated.

LSSF STEM Research Symposium 2015 Judges

Judges play a vital role in the success of the LSSF Symposium and for that reason we express our sincere gratitude and thanks for their contributions.

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Life Sciences South Florida would like to extend their appreciation and thanks to the internal committee that served to create the symposium, define its characteristics and join our region's undergraduate student researchers together in a meaningful and highly productive manne.

Congratulations!

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