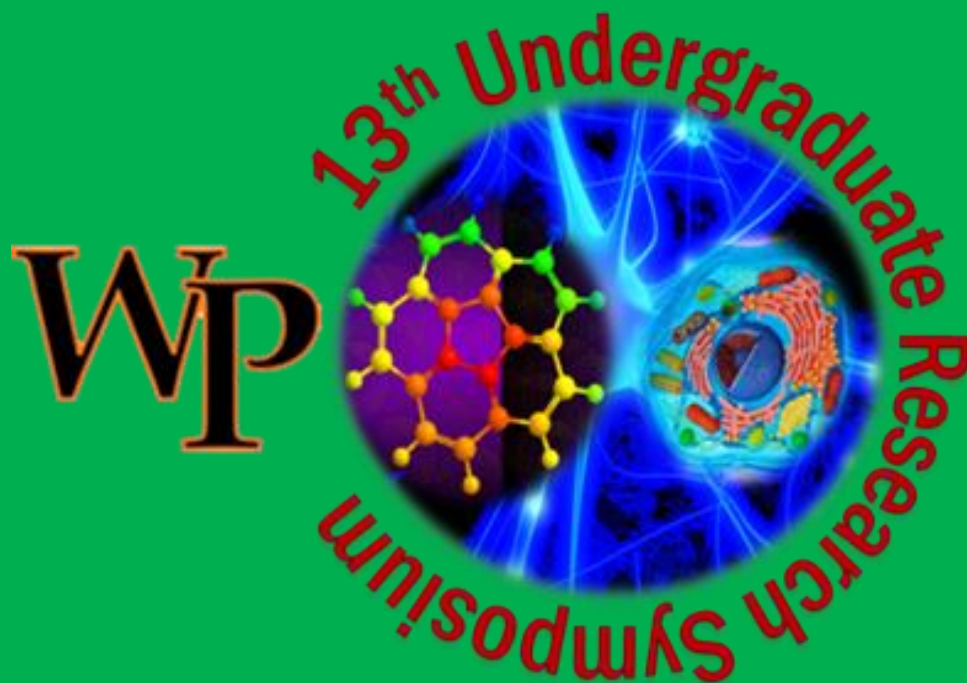


WILLIAM
PATERSON
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William Paterson University

Biological and Chemical Sciences

Program and Abstracts

Undergraduate Research Symposium

Saturday, April 6, 2019

300 Pompton Road, Wayne, NJ 07470

#WPSTEMRESEARCH

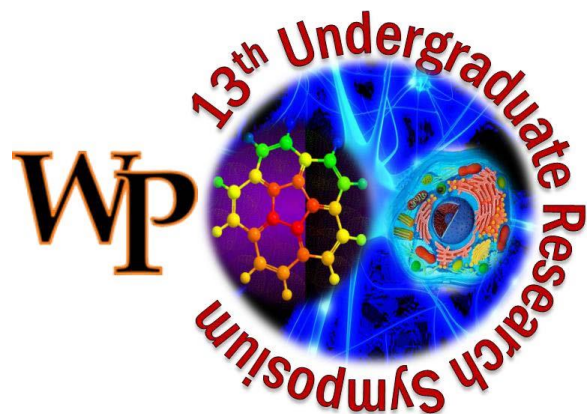
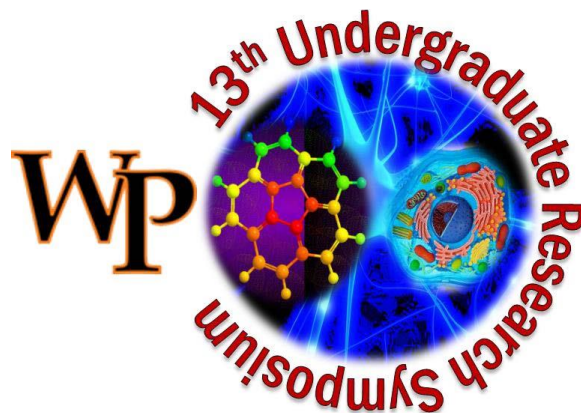


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“FEW WORDS FROM ORGANIZERS”



Few activities are as rewarding as research to the motivated students as well as faculty mentors. In addition to the acquisition of invaluable research skills, students learn how knowledge is created and experience the excitement of the “eureka moment”. To celebrate undergraduate achievements, a research symposium has been held since 2007 on the WPUNJ campus for students in biological, chemical and environmental sciences. This symposium provides an opportunity to the students to showcase their talents and share their research achievements with their peers from about thirty-four universities from the tristate area.

We would like to welcome all of you to an exciting 13th year of the Undergraduate Research Symposium at William Paterson University of New Jersey. This is an example of a budding community of undergraduate researchers. We want to thank all of the students from past and current who participated in the symposium and shared their research with us. We also want to thank all of the research mentors who have made it possible by investing their time, knowledge, resources and energy, so that the undergraduates gain their first hand research experiences.

We express our gratitude to all of our student volunteers who show great enthusiasm and worked very hard to make this symposium a success.

We are very much obliged to Dr. George Koob, Director, National Institute of Alcohol Abuse and Alcoholism, National Institute of Health, for

accepting our invitation as our keynote speaker and investing his valuable time to be with us.

This symposium could not have been successful without the moral support and continuous help from our Deans, Dr. Sharma and Dr. Fuller-Stanley, who worked very diligently with us so that everything is put together in a professional manner. Our special thanks are also due to Dr. Sandra DeYoung (Emeritus Dean/Interim Provost and Vice President of Academic Affairs), under whose direction and guidance this symposium was initiated.

We also want to thank Dr. David Slaymaker and Dr. Bhanu P. S. Chauhan, (Chairs of the Biology and Chemistry Departments) for their continued support. As well as the Office of Institutional Advancement and the Alumni Association for partly financing the event in various capacities.

Finally, yet importantly, we extend our gratitude to President Richard Helldobler for his leadership who continuously encouraged us and inspired us with his ideas to make this symposium a great success.

ORGANIZERS:

Dr. Jaishri Menon

Dr. Bhanu P.S. Chauhan

PLENARY ABSTRACT

“DRUG ADDICTION: THE GAIN IN THE BRAIN IS IN THE PAIN”

By

Dr. GEORGE KOOB

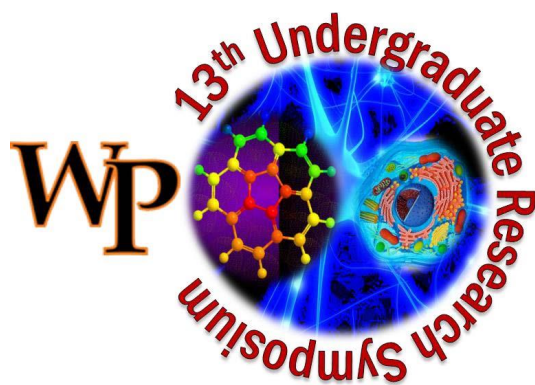


ABOUT DR. GEORGE KOOB

George F. Koob, is Director of the National Institute on Alcohol Abuse and Alcoholism (NIAAA) as of January 27, 2014. As NIAAA Director, Dr. Koob oversees a wide range of alcohol-related research, including genetics, neuroscience, epidemiology, prevention, and treatment.

As an authority on alcoholism, drug addiction and stress, he has contributed to our understanding of the neurocircuitry associated with the acute reinforcing effects of alcohol and drugs of abuse and the neuroadaptations of the reward and stress circuits associated with the transition to dependence. Dr. Koob has published over 700 peer reviewed papers and several books including the “Neurobiology of Addiction,” a comprehensive treatise on emerging research in the field, and a textbook for upper division undergraduates and graduate students called “Drugs, Addiction and the Brain.” He has mentored 11 Ph. D students and over 80 post-doctoral fellows.

He received his Ph.D. in Behavioral Physiology from Johns Hopkins University in 1972. He spent much of his early career at the Scripps Research Institute as the Director of the Alcohol Research Center, and as Professor and Chair of the Scripps’ Committee on the Neurobiology of Addictive Disorders. He has also served as a researcher in the Department of Neurophysiology at the Walter Reed Army Institute of Research and the Arthur Vining Davis Center for Behavioral Neurobiology at the Salk Institute for Biological Studies. Dr. Koob is the recipient of many honors, including membership in the National Academy of Medicine and award of the Legion of Honor (France).



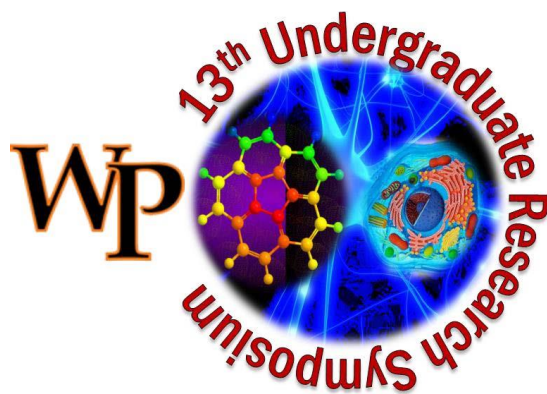
Symposium Organizing Committee

Organizers

Dz. Jaishri Menon
Dz. Bhanu P.S. Chauhan

Committee Members

Dz. Jean Fuller-Stanley
Dz. Michael Peek
Dz. Eileen Gardner
Dz. Jeung Woon Lee
Dz. Carey Waldburger
Dz. Pradeep Patnaik
Dz. Yalan Xing
Dz. Parminder Kaur
Dz. Jay Foley
Dz. Mihaela Jitianu
Dz. Emily Monzo
Dz. Mukesh Sahni
Ms. Kazyn Lapadusa



SCHEDULE OF EVENTS

7:30 am - 8:30 am	Registration, Breakfast & Poster Setup University Commons 171 A/B
8:30 am - 8:45 am	Welcome and Opening Remarks Provost Dr. Sandra DeYoung President Dr. Richard Helldobler Ballroom
9:00 am - 11:00 am	Poster Session A, Ballroom Cell & Molecular Biology: CMB 1 to CMB 8 Ecology & Environmental Science: EE 1 to EE 7 Microbiology: MB 1 to MB 6 Physiology & Toxicology: P & T 1 to P & T Nanochemistry: NC 1 to NC 7 Organic Chemistry: OC 1 to OC 8
11:15 am - 12:45 pm	LUNCH - Wayne Dining Hall
1:00 pm - 2:00 pm	PLENARY TALK - Ballroom Dr. George Koob Director, National Institute of Alcohol Abuse and Alcoholism, National Institute of Health
2:00 pm - 4:00 pm	Poster Session B, Ballroom Cell & Molecular Biology: CMB 9 to CMB 16 Behavior: B 1 to B 9 Ecology & Environmental Science: EE 8 to EE 14 Genomics & Bioinformatics: GB 1 to BG 5 Materials Chemistry: MC 1 to MC 8 Theoretical & Physical Chemistry: TPC 1 to TPC 9
4:15 pm - 4:30 pm	Refreshments, Coffee & Cake - Ballroom
4:30 pm - 5:00 pm	AWARDS CEREMONY - Ballroom

Poster Session A: Cell & Molecular Biology I

JUDGES: Dr. Pradeep Patnaik*
Dr. Cristina Cummings
Dr. Maria Shumskaya

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*Coordinator

Poster Session A: Ecology and Environmental Science I

JUDGES: Dr. Michael Peek
Dr. Ileana Soto
Dr. Edith Myers

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*Coordinator

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JUDGES: Dr. Emmanuel Onaivi*
Dr. Marjorie Squires

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JUDGES: Dr. Carey Waldburger*
 Dr. James Salierno
 Dr. Sara Reynolds

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*Coordinator

Poster Session A: Nanochemistry

JUDGES: Dr. Parminder Kaur*
 Dr. Demyan Prokopchuk
 Dr. Suresh Sahni
 Dr. Alfredo Castro

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*Coordinator

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JUDGES: Dr. Jonathan Foley*
Dr. Moni Chauhan
Dr. Frieder Jaekle

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Poster Session A: Behavior

JUDGES: Dr. Emily Monroe*
Dr. Marjorie Squires

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JUDGES: Dr. Joseph Spagna*
 Dr. David Slaymaker
 Dr. Marion McClary

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CHARACTERIZATION OF VANADIUM DERIVED INSULIN MIMETIC ON OSTEOBLASTOGENESIS AND CHONDROGENESIS DIFFERENTIATION

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Diabetes mellitus is a metabolic disorder in which the body's ability to produce/respond to the hormone insulin is impaired. Currently, this disorder affects ≈ 29.1 million people in the U.S. In addition, diabetes is considered a worldwide epidemic given its high socioeconomic impact on public health. Many complications are associated with diabetes, most notably increased fracture risk, impaired fracture healing, and adverse bone formation.

Diabetic bone healing animal models have demonstrated that treatment with insulin or insulin mimetic can improve bone healing. Vanadium compounds (VCs) are a type of insulin mimetic, which have been shown to improve bone healing through enhancement of endochondral ossification. Unfortunately, the mechanisms by which this occurs is unclear.

MC3T3 cells, a type of osteoblast cell line and ATDC5 cells, a type of chondrocyte cell line were used to analyze bone and cartilage formation. Osteoblasts and chondrocytes were treated with VCs, vanadyl acetate (VAC) and vanadium sulfoxide (VS04) at low (25 μ M), medium (50 μ M) and high (100 μ M) concentrations to determine if such treatments would enhance osteoblast and chondrocyte function. The cells were plated and treated with increasing concentrations of VAC and VS04 as well as appropriate controls.

The cells were collected post differentiation on days 1, 5, 7, 10, 14, 21, and/or 28. Cellular proliferation, calcium deposition, proteoglycan synthesis, collagen production, and cellular activity were measured utilizing various procedures.

In MC3t3 cells, the results demonstrated that low VC treatments positively affected cellular proliferation, calcium deposition, and proteoglycan synthesis. Higher concentrations of VCs either had little effect or inhibited these cellular functions. In both MC3t3 and ATDC5 cells, with low and medium VC treatment affected collagen levels while high VC treatment inhibited this process. In ATDC5 cells, VC treatment at all concentrations positively affected cellular proliferation, calcium deposition, and proteoglycan synthesis.

Insulin mimetics such as these VCs may be used in the future to treat diabetic patients with poorly healing fractures. Understanding the mode by which these compounds work to improve fracture healing will help provide better therapeutic approaches for those affected with skeletal complications.

IDENTIFICATION OF MULTI-DOMAIN PKS SEQUENCES IN A NON-TOXIC STRAIN OF *KARENIA BREVIS*

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Karenia brevis is a dinoflagellate that causes negative marine and human health impacts through its production of brevetoxins (PbTx), which are potent neurotoxins. Brevetoxins are produced by polyketide synthase (PKS) enzymes. PKSs require several catalytic domains, including the ketosynthase (KS), acyl transferase (AT), and acyl carrier protein (ACP) domains, which subsequently form multi-domain and multi-modular structured PKS enzymes. The objective of this study was to characterize newly identified multi-domain PKSs in a non-toxic (NT-

KB) strain of *K. brevis*. Using cDNA from a toxic strain (GB) known to have these multi-domain PKSs, PCR conditions such as annealing temperature and extension time were optimized. At a 67°C annealing temperature and 45 second extension, amplicons produced using NT-KB cDNA were consistent with both the amplicons from GB cDNA and the published sizes of the multi-domain PKSs for three of the contigs examined, 114143, 113789, and 134145. These results suggest the multi-domain PKSs are present in NT-KB, and future work will determine if there are any mutations in the NT-KB PKSs.

THE EFFECTS OF LEAD TREATMENT ON NERVE GROWTH FACTOR REGULATED DORSAL ROOT GANGLION DEVELOPMENT

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The effects of lead include memory loss, developmental delays, and at high enough concentrations, death. However, there is currently a lack of information surrounding the effects of lead in fetal neurodevelopment. Lead is a 2+ ion which easily mimics and takes the place of the 2+ ion calcium that is abundantly found in the human body. This can impact the function of calcium such as bone structure, cell signaling, and nerve function. The goal of this research was to study the effect that lead has on Dorsal Root Ganglions (DRGs). DRGs are clusters of nerves that develop into afferent neurons in the peripheral nervous system. These DRGs are found in the dorsal root of the spinal nerve in embryos. With only one tenth of the FDA approved safe level of lead, there has been a difference in cell proliferation, morphology of the DRG and axonal growth in response to nerve growth factor promoted process in cultures between experimental groups. Gene analysis is also currently being conducted using Reverse Transcription PCR and Quantitative PCR.

Three different cultures were tested; a negative control that consisted of harvested DRGs that were developed in culture media, a positive control that had DRGs, culture media, and NGF(200ng/ml), and an experimental group, which had DRGs grown in culture media with NGF, and a varying concentration of lead. The different concentrations of lead used in the experimental group was 0.1 uM/L, 0.3 uM/L, 0.5 uM/L, and 1 uM/L which showed the different responses nerve growth factor treated ganglion had to varying concentrations of lead. The results of this research showed that there are significant morphological differences between treated and untreated dorsal root ganglion. Observed morphological differences include ganglion shape, axonal growth, and the presence of cell death in lead treatment groups($p < 0.5$). Image J, Cellsens, and Zen have been used to image and analyze the ganglion over a 5 day period. Statistical analysis was conducted with T-tests and ANOVA. Support for this work was provided through the Dorothy Goodwin Scholarship to KV by The Woman's Advancement Initiative, advancing each woman's potential in the HCW tradition at the University of Hartford, and the Dean's research fund from the University of Hartford.

SYNTHESIS OF DAUMONE PRECURSOR AND ITS EFFECT ON AGING IN *SACCHAROMYCES CEREVISIAE*

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Nature has produced an abundant number of compounds that are seen to elicit medicinal properties. An example of this is the well-known natural product Spermidine, that was seen to extend lifespan by offering cardio protective

and neuroprotective effects in humans (Minois et al. 2014). Because of the medicinal importance of natural products, scientists in both fields of chemistry and biology are constantly investigating new natural products. One natural product currently under investigation is daumone. In the presence of poor environmental conditions (low nutrients and high population density) larval *Caenorhabditis elegans*, enter a resting state, that causes the arrest of larval development, termed the dauer stage (Golden et al., 1984). It was discovered that daumones, dauer pheromone ascarosides, secreted by larval *C.elegans* are responsible for inducing the dauer stage (Hollister et al., 2013). Since then, additional daumone compounds have been identified and synthesized; some having a more potent effect in inducing the dauer state compared to the first isolated daumone (Edison et al., 2009). However, the general biological properties of daumones, and their role in aging, are still under-characterized. The purpose of this research was to investigate and characterize the effects of a daumone precursor on cellular aging using *Saccharomyces cerevisiae* as a model. The daumone precursor was synthesized and the structure was confirmed and characterized by ¹H and ¹³C NMR. To test the effect of the daumone precursor on the chronological lifespan of *S. cerevisiae*, a colony forming unit and spotting test assay were conducted. Various concentrations (25 mM, 12.5 mM, 6.25 mM) of the daumone precursor suspended in DMSO were used for these biological assays. The data suggests that the daumone precursor provides a brief protective effect against DMSO's toxicity. This is supported by the yeast cells only being able to grow within the first fifteen minutes of exposure to the daumone precursor. Because the yeast cells were only viable within the fifteen minutes of exposure, we conducted a CFU assay using a more dilute dose (0.041 mM). The data indicates that the yeast cells exposed to the daumone precursor aged similarly to the untreated cells. Further testing will be conducted to lead to a more definite conclusion of the effects of the daumone precursor on *S.cerevisiae* lifespan. Future directions include the synthesis and biological characterization of another natural product under investigation is Actinopolymorphol B, isolated from *Actinopolymorpha ritulus*.

INVESTIGATING THE DEFENSIVE ROLE OF CYP72A ENZYMES USING *ARABIDOPSIS THALIANA* MUTANTS SUBJECTED TO COMBINED STRESSES

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Plants have evolved an arsenal of defenses to combat environmental stresses. Little is known about the mechanisms underlying metabolic changes for response to these stresses. Cytochrome P450 (CYP) enzymes are involved in primary metabolism and they also produce secondary metabolites that can help protect plants under different biotic and abiotic stresses. Environmental stresses such as heat and bacteria have damaging effects on plant yield, especially for crop plants. Therefore, studying the role of these enzymes using molecular and genetic techniques in a model plant, *Arabidopsis thaliana* will uncover how a combination of stresses affect plant metabolism through CYP mediated reactions. One CYP in Arabidopsis (CYP72A14) is induced by bacterial infection and its close relatives (A11/A13) are induced by abiotic stress. Therefore, we are testing the hypothesis that these enzymes are needed for combination stress responses.

Finding which multi-stress combination gives a robust phenotypic difference between normal plants and CRISPR mutant plants deficient in CYP72A genes can help unravel how stress metabolism functions in other plants as they are known to have orthologs of these CYP genes. If plants are missing gene products of defense genes, they will be more susceptible to stresses. We examined multiple CYP72A mutants under heat stress and *Pseudomonas syringae* infection. We see that bacterial growth is higher when multiple CYP72A enzymes are missing. This work contributes to a better understanding of plant chemical defenses. Further research can help us understand more about plant chemical diversity and potentially provide useful crop varieties of plants tolerant to certain environmental conditions.

NIEMANN-PICK TYPE C: DENSITY AND COLOCALIZATION OF DENDRITIC LYSOSOMES AND MITOCHONDRIA IN NPC1^{nmf164} MOUSE MODEL DURING POSTNATAL DEVELOPMENT

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Niemann-Pick Type C (NPC) is a lysosomal storage disease in which there is a dysfunction of lysosomes within the cells due to the deficiency of the NPC1 protein. Specifically, cerebellar Purkinje neurons (PN) are highly affected by the lack of the NPC1 protein, degenerating earlier and more severely than other neurons of the brain. Since the cerebellum is responsible for controlling motor movement, NPC patients and mouse models like the *Npc1^{nmf164}* mouse, exhibit ataxic behavior as a result of PN degradation. Despite this behavior being observed, it is not known how the lack of NPC1 affects the development of these neurons postnatally.

Previous experiments in our laboratory have shown that in *Npc1^{nmf164}* mice at post-weaning age (30 days) there is a significant decrease in mitochondria within the dendrites of the PN. The decrease in mitochondria could be attributed to either a decrease in biogenesis of mitochondria, or an increased degradation of mitochondria by lysosomes either through the mitophagy or autophagy pathways. Using confocal imaging and the three dimensional (3D) rendering software IMARIS, the density and colocalization between dendritic mitochondria (PDE⁺ immunostaining) and lysosomes (LAMP1⁺ immunostaining) was quantified within the dendrites of the PN immunostained with Calbindin at 15, 21 and 30 postnatal days. Using the IMARIS software it was possible to create 3D surfaces of the PN, along with the 3D spots tool that segregated the lysosomes and mitochondria to accurately measure the density and percentage of overlap between these two cellular structures. Our preliminary results showed that the densities of mitochondria and lysosomes were different through the examined postnatal ages between WT and *NPC1^{nmf164}* mice. An increased colocalization between mitochondria and lysosomes was found at 21 postnatal days when compared to the 14- and 30-days group, suggesting some form of mitochondrial turnover period before the post-weaning age.

GLUTAMATE RECEPTOR EXPRESSION IN MEMBRANE RAFT FRACTIONS FROM ADOLESCENT BRAIN: INFLUENCE OF ALCOHOL AND CAFFEINE

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Adolescence represents an important period of brain maturation and a time when many individuals have their first experiences with alcohol. Binge alcohol consumption is a serious concern that is amplified by co-use of alcohol and stimulants including caffeine. As a model for studying adolescent alcohol dependency, adolescent Long-Evans (LE) rats consume high levels of alcohol when presented in a liquid diet and develop a severe alcohol withdrawal syndrome, usually associated with a hyperglutamatergic state. In previous behavioral studies from our lab, liquid diets were exploited to model chronic alcohol-caffeine co-use (Pitchon et al., 2013; J. Caffeine Research 3:131-7). Administration of caffeine prior to and with alcohol resulted in decreased severity of alcohol withdrawal symptoms. If translatable to humans, caffeine may lessen the awareness of a growing dependence on alcohol by attenuating alcohol withdrawal symptoms.

The first goal of the present study was to determine whether lipid raft dynamics play a role in the cellular adaptations of adolescent brain membranes to chronic ethanol. Adolescent LE rats were fed an ethanol-containing liquid diet (3.5% w/v) or an isocaloric control formula for up to 3 weeks. Lipid raft fractions were isolated by

ultracentrifugation of detergent resistant membrane fragments from subcortical forebrain. Western blotting was used to analyze fractions for the raft marker flotilin, the endocytosis-associated protein caveolin, the scaffolding protein Homer, and the NMDA, mGluR1 and mGluR5 subtypes of glutamate receptor. Two fractions were found to contain flotilin with a relatively small percentage (<20%) of the marker found in the less buoyant raft (LBR) fraction. When the membranes were derived from ethanol-fed rats, there was a highly significant 2-fold increase of the raft marker flotillin in the LBR fraction. Raft fractions contained caveolin, Homer, and all 3 glutamate receptors (NMDA, mGluR1 and mGluR5). Thus, lipid raft dynamics characterized by increase in the LBR fraction may contribute to the hyperglutamatergic state of alcohol withdrawal as part of cellular adaptations to chronic alcohol consumption.

The second goal of the present study was to use our previous co-administration model to determine if lipid raft dynamics represent a site for interactions between caffeine and ethanol. Two additional treatment groups were developed: one receiving caffeine in the drinking water followed by caffeine in the isocaloric control diet, and the other receiving caffeine in the drinking water followed by caffeine in the ethanol-containing diet. The increase in the LBR fraction that was seen with ethanol-fed rats did not occur with the caffeine-ethanol co-administration group. Behaviorally, caffeine-ethanol co-administration groups showed significantly reduced alcohol withdrawal severity. The results suggest lipid raft dynamics may be associated with the ability of caffeine to antagonize some of the adaptive responses of the adolescent brain to chronic ethanol.

DETERMINING THE SIGNIFICANCE OF *CANDIDA AURIS* CLADE-SPECIFIC *ERG11* MUTATIONS ON AZOLE ANTIFUNGAL SUSCEPTIBILITIES

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Candida auris is an emerging fungal pathogen that has spread across the globe and caused hospital outbreaks. Currently, *C. auris* is divided into four major clades: South Asian, East Asian, South African, and South American. Strains of *C. auris* have been reported as non-susceptible to common antifungal agents, including azoles, emphasizing the importance of understanding resistance mechanisms in this yeast. Multiple mechanisms of azole resistance have been described in other *Candida* species, including mutations in the ergosterol synthesis pathway (primarily in the azole target *ERG11*). Due to limited genetic tools, we previously expressed *ERG11* alleles from various *C. auris* strains in *Saccharomyces cerevisiae* and measured azole susceptibilities through minimum inhibitory concentration (MIC) assays. Elevated azole MICs were detected in *S. cerevisiae* upon expression of *C. auris* *ERG11* alleles that encoded for Y132F or K143R amino acid substitutions identified in the South Asian and South American clades; however, expression of alleles encoding other clade-defined amino acid differences yielded susceptible MICs. For this project, we plan to determine how an amino acid substitution (F126L) widely identified in isolates from the South African clade affects azole MICs upon expression in *S. cerevisiae*. Thus far, we have obtained DNA from two isolates originating from South Africa, confirmed the Erg11 F126L amino acid substitution through PCR and sequence analysis, and taken steps toward the cloning process. Understanding which Erg11 amino acid substitutions lead to azole reduced susceptibility will help define molecular markers of *C. auris* azole resistance and allow for better treatment practices.

THE RELATIONSHIP OF VEGETATION STRUCTURE AND ANIMAL DIVERSITY IN NORTHERN NEW JERSEY

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The positive correlation between habitat structure and biodiversity has been well documented in the scientific literature. Biodiversity is essential for a natural habitat's ecological resilience as well as maintaining ecosystem services. Natural disturbances can benefit the heterogeneity of vegetation structure in a habitat; however, anthropogenic disturbances have been determined to have a homogenizing effect on vegetation structure. The goal of this research is to examine the relationship between vegetation structure and animal diversity in natural and disturbed areas in New Jersey. We will also determine the most critical habitat variables that correlate with diversity. A number of vegetation metrics will be quantified, i.e. canopy cover, average plant height, average plant density, depth of ground litter, and composition of the ground cover. Twelve sites have been identified for this study across 3 different habitat types: four forested sites (two along the Appalachian Trail in Vernon, New Jersey and two at Loantaka Brook Reservation in Morristown, NJ), four shrub sites (two at Ricky's Farm in Vernon, New Jersey, two along the Appalachian Trail), and four human impact sites (FDU Library Lawn, FDU Academic Lawn in Madison, adjacent to the FDU Student Center, and behind the FDU Student Center). Vegetation metrics and diversity data are gathered at a center point at each site and then along 25 meter transects North, South, East, and West of the center point. Diversity surveys last for a duration of 30 minutes. The survey consists of ground sweeps along the transects in each direction to compile mammal and avian richness and abundance data. Based on the Heterogeneity- Diversity theory, we hypothesize that greater canopy cover of the center point, taller plant heights, deeper litter depths, and a variation in vertical plant density will lead to overall increases in species richness and abundance. Mammalian richness and abundance was greatest at the forested sites. There were no significant differences in avian richness and abundance across the different habitat types surveyed. Canopy cover was positively correlated with both mammalian richness and abundance (strongest correlation of the vegetation metrics that were measured). Plant density was negatively correlated with mammalian richness, and litter depth was positively correlated with mammalian richness. None of the vegetation metrics were significantly correlated with avian richness and abundance. This study adds to the diverse array of research on Heterogeneity Diversity Theory. The results of this experiment may inform biodiversity management and indicate conservation priorities in local areas of New Jersey.

EXAMINATION OF A SUBURBAN LAKE FOR EFFECTS FROM NONPOINT SOURCE POLLUTION AND COPPER SULFATE TREATMENTS

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The natural process of eutrophication is accelerated by excess nutrients from nonpoint source pollutants, in which an inorganic compound, copper sulfate (CuSO_4), is used to conduct the reversal known as oligotrophication. Runoff in suburbanized areas combined with human practices such as, the spreading of fertilizers and pesticides that contain nitrogen or phosphorus, and application of rock salts composed of chloride, will promote damaging algal blooms. It is critical to determine the source of algal blooms as they can deplete dissolved oxygen in the water causing the aquatic ecosystem to suffer from non-point source pollutants. Packanack Lake in Wayne, New

Jersey was used to determine the influx of nutrients being deposited into the lake through eight surrounding drainways before and after a major rain storm. A secondary study was also conducted within the lake to determine the accumulation of copper from annual treatments of copper sulfate (CuSO₄).

Collected sediment and water samples from the targeted outfalls were used to analyze the different environmental variables and sources of water. Sediment samples from locations bordering the lake were tested for: pH, organic content, particle size and phosphorus. Water representatives from each selected outfall pipe, were tested for: pH, alkalinity, dissolved oxygen, turbidity, temperature, conductivity, phosphorus and certain anions. The secondary study tested for copper concentrations, pH, organic content within the sediment, alkalinity, and specific anions. Results from these field and lab methods of the sites showed neutral readings from sample day 1 (T1) to sample day 2 (T2) aside from Mountainside, Brookwood and Evergreen. Observations of algal blooms off the East shoreline of Packanack Lake, near Mountainside Drive, were made prior to the experiments. From T 1 to T2, evidence of inorganic phosphorus portrayed decreased concentrations in the water sample of Evergreen and increased elevations in the sediment sample of Mountainside. A nearby northern sample site of Mountainside called Brockwood, experienced a drop in sulfate and chloride anions after the rainfall. Furthermore, the geomorphology of Packanack Lake exhibits a cove in the region presumably confining anions and phosphorus as a result of the water moving from North to South towards the output in the South East corner. The phosphorus levels can be associated with swan droppings at Evergreen and the entrapped organic leaves in the particular area of interest at Mountainside. In summation, the water input poses no problem regarding infiltration and the subordinate study for the accumulation of copper within the sediment of the lake center sites presented no concern and concluded in minor concentrations of <2 ppb. Lack of circulation and the inflation of excess nutrients contributes to the eutrophication process.

INSECT BIODIVERSITY AT THE HIGH MOUNTAIN RESERVE IN SUMMER 2018

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With over a million species identified, and many still undiscovered, insects are a major portion of life on Earth, and are crucial in all land ecosystems. Insects are important because of their ecological role, and their influence on agriculture. They work to pollinate plants, disperse seeds, fertilize the soil, recycle nutrients back into the Earth, and much more. The purpose of this project is to identify and estimate the insect biodiversity at High Mountain Reservation in Wayne New Jersey. I captured insects throughout the Reserve with four different methods. I used aerial nets and sweep nets to sample the insect diversity of High Mountain Reserve, along with a beating sheet to trap insects that fall from trees and bushes. The beating sheet is placed under a tree branch while the branch is shook to capture and falling insects. It may also be placed inside a bush for the same result. The fourth capturing method was the kill jar, which is a glass jar about 1 pint in size. Underneath the sealed lid of the jar contained a paper towel damped with ethyl acetate. The purpose of the ethyl acetate is to essentially knock out and kill the specimen as quickly as possible because it is poison to insects. I then brought the specimens to lab for curation, including pinning, labeling and identification. I accumulated and identified 43 families of insects with 59 morpho-species categorized within seven orders. In total I was able to collect and identify 81 insects. With this collection data I was able to develop a species-area curve to estimate whether I had collected most of the species present, based on how many new findings I've collected during each sampling session. From my species accumulation curve I was able to determine that with my methods and timing I would only be able to find around 60-65 total families of insects in the Reserve. I also compared this year's insect data to similar data from last year to assess similarities and differences. This data can also be applied to future studies in determining how insect diversity changes as a result of climate change and other human impacts on the environment.

TRACING STORMS AND CLIMATE CHANGE THROUGH TREE-RING GROWTH PATTERNS ON COASTAL MARITIME FORESTS IN NY AND NJ

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This project focuses on coastal maritime forests located on Sandy Hook, NJ, Fire Island, NY, and Montauk NY, in an attempt to understand if major tropical cyclone activity is recorded in the tree-ring record and to determine how trees are responding to climate. Specifically, we aim to examine ring damage and/or growth releases in tree ring records as a result of severe storm events and/or saltwater inundation. Due to anthropogenic climate change creating more severe storms and rising sea levels, this study has become increasingly relevant and important in creating necessary foundational research on these unique forests. Cores were sampled from dominant tree species at the study sites. Following sample preparation, we measured tree-ring width and density using a high resolution scanner and CooRecorder, image analysis software. Using Coo-Recorder we will also evaluate Blue Intensity (BI), a relatively new image analysis derived methodology that analyzes the blue component of visible light reflected from scanned images of tree-ring cores. BI has been broadly interpreted as an indirect proxy measurement of wood density and can result in a stronger paleoclimate reconstructions. Once the RW and BI chronologies have been constructed using rigorous cross-dating techniques, we will use the site-specific meteorological data to determine the climate signal. We will also evaluate the oxygen isotopic composition of each ring in several of the older tree specimens to better understand the atmospheric dynamics, and potentially ‘fingerprint’ major storm events. Some of the trees sampled for this study date back to the early 1800s and will provide extended insights into forests response to climate change and storm frequency in this region.

DETERMINING METAL CONTAMINANTS IN TURTLE SCUTES THROUGH X-RAY FLUORESCENCE

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Environmental stressors on turtles that live near human development include heavy metal contamination. Such contamination in turtles is measured currently by ICP-OES methods, which can be prohibitively expensive if the equipment is not in-house, thus there is a need for a cheaper quantitative or semi-quantitative method for surveying multiple turtle samples. Scutes (shells) from a group of turtles found deceased in traps near JFK airport were used to see if a reliable quantitative or semi-quantitative method using TXRF and/or XRF could be developed to screen the turtles for heavy metal contamination. Turtle scutes are the outermost piece of keratin on a turtle’s shell and removing the scute is painless to the turtle as they are normally shed, so potentially this method could be applied to analysis of living turtles. Initially TXRF was used, as it is a more reliable method than XRF, to examine the turtle scutes. An analytical protocol was developed to prepare samples and the methods were calibrated to accurately quantify the present metals. The samples were also examined by using a portable XRF, which only measures elemental composition on the surface of the scute. Future steps will be to grind the samples into a powder, analyze the powder using the portable XRF, and compare the results to the TXRF and surface XRF spectra.

INITIAL EFFECTS OF ORGANIC AMENDMENTS ON EDAPHIC PROPERTIES AND BIOLOGICAL ACTIVITY

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The initial effects of biochar, composted chicken manure, and oyster shells to agricultural soil and its resultant effects on bean and eggplant monoculture and polyculture systems were analyzed. Three replicates of bean and eggplant monoculture and polyculture systems along with the amendments and control were planted for a total of 36 plots. Total seasonal crop yield along with soil carbon, enzymatic activity, nutrient availability, and pH were determined. Bean yield showed no differences among cultural method or amendment application, while eggplant yield was highest with compost application, though significantly lower in polyculture than in monoculture. Compost initially yielded a significantly different metabolic profile than the other amendments. No differences in available ammonium or nitrate were found among the treatments, though available phosphate was highest with compost. Oyster shell applications yielded highest soil pH. As organic amendments tend to have cumulative effects, future experiments should measure trends over multiple seasons. Within-season variance in yield and soil properties should also be analyzed. Bean density should be reduced in polyculture plots. Overall, amendments that stimulate high microbial activity should be combined with those that slow these effects to increase duration of biological activity, thereby sustaining its benefit throughout the season.

SOIL-BORNE FUNGI ASSOCIATED WITH SEEDS IN A FRAGMENTED LANDSCAPE

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Plants are subjected to a wide range of soil-borne pathogen pressures that affect plant growth, abundance, and diversity. Of particular interest are the interactions between pathogenic fungi and seeds, including the host range and pathogenicity of different fungal strains. As part of an ongoing project on landscape fragmentation and plant-pathogen interactions, our lab isolated fungi from approximately 2500 seeds. The goal of this study is to examine the ways plant diversity may be affected by pathogen pressure in fragmented landscapes through negative feedbacks. Landscape fragmentation is when larger pieces of land are broken into smaller patches, creating smaller isolated environments; smaller patches can differ drastically from larger patches due to higher exposure to the elements and lower plant richness and diversity. Through this study we will see if pathogen pressure is different in smaller patches versus larger patches. To test this, seeds were buried in an experimentally fragmented field site in Lawrence, Kansas in patches of different sizes. The seeds were then exhumed, surface sterilized, and plated on malt extract agar so the fungi that had penetrated the seeds could be grown and isolated. Over the past several months we have been subculturing these fungi and performing PCR to identify them using DNA barcoding. Over the course of this study we aim to use our genetic data along with Koch's Postulate tests to isolate and identify potentially pathogenic fungi. This data combined with our data on the patch they were buried will help to determine if there is a correlation between patch size and (1) fungal community composition and (2) pathogen pressure.

STRONG ANTIMICROBIAL ACTIVITY DISPLAYED BY NEWLY SYNTHESIZED HYDROXAMIC ACIDS AND THEIR DERIVATIVES

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Antibiotic resistant pathogenic bacteria are a growing worldwide health concern according to the Centers for Disease Control and Prevention. These bacteria are responsible for most infectious diseases and healthcare-associated infections in hospitals (HAIs). The need for new therapeutic approaches using novel antimicrobial compounds is becoming vital as the number of infections caused by antibiotic resistant strains of bacteria such as *Staphylococcus aureus* and *Staphylococcus epidermis* has drastically increased. The focus of our study is to test newly designed and synthesized therapeutic agents for antimicrobial properties. Several hydroxamic acids and their analogs were newly synthesized by the chemistry department and tested in our laboratory for antibacterial activity against five different ATCC strains of pathogenic bacteria. The antimicrobial activity of each compound was evaluated using the disk-diffusion assay and the liquid broth assay. All compounds displayed a various spectrum of antibacterial activity that will enable us to narrow down the potential active site or functional group in the molecules responsible for the activity. Future work will focus on designing and testing new derivatives with a broader spectrum of activity that will be further tested for cytotoxicity against plant and human cell lines.

RECOVERY OF DNA AND RNA FROM MICROORGANISMS IN WATER SAMPLES

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Natural water sources are essential for the growth and fitness of some of the most abundant microorganisms in the biosphere. These species are placed into three domains: Bacteria, Eukarya, and Archaea. This study focuses on the domain of Bacteria, whose many members can be broadly divided into two groups based on cell wall structure, Gram positive and Gram negative. Gram negative bacteria are then further classified as coliform (lactose-fermenting intestinal bacteria) or non-coliform. Because coliforms are commonly found in aquatic environments, and some are known to be pathogenic, this study aims to sample a local source of surface water fed by wastewater effluent and test for the presence of coliform populations. To do this, a technique needed to be developed to isolate DNA and RNA from microorganisms in those samples, and then use polymerase chain reactions (PCR) to amplify regions of the genetic material using species-specific primers. Preliminary research has found that adapting the commercial Qiagen AllPrep kit to incorporate PowerWater bead-beating technology should provide the greatest amount of quality DNA and RNA from water samples with consideration of both cost and ease of use. It was then necessary to test the DNeasy PowerWater Kit and the proposed adaption to the AllPrep DNA/RNA Kit using water spiked with *E. coli* to examine their extraction abilities. So far, DNA has been successfully isolated using the PowerWater Kit, as confirmed through gel electrophoresis. With the presence of DNA established, it then needs to be amplified through PCR, and the reaction products utilized to determine the identities of the organisms in the samples. Thus, the next task was to identify possible primers that would specifically amplify known DNA sequences to identify target species. As a BSL1 teaching facility, our laboratory does not have access to pathogenic species for PCR validation, thus we searched published literature for previously validated coliform-specific primers. We plan to use a systematically narrowing method of detection in which all coliforms will yield a PCR product targeted to the *lacZ* gene as our broadest detector of coliform bacteria. *LamB* presents a second gene present in three biologically important genera of coliforms: *Salmonella*,

Escherichia, and *Shigella*. There is only a single species of *Salmonella*, *Salmonella enterica*, of which some serogroups can cause typhoid fever. *S. enterica* can be detected by PCR using the gene *InvA*. Other research has also shown that *Escherichia* and *Shigella* are not different enough to reliably detect independently, thus both will yield a PCR product targeting the *Tuf* gene. The presence of wastewater effluent in our surface water suggested we could identify human pathogenic coliforms and so the genes *ConcaveA* and *SLT-I* have been selected to detect most pathogenic *E. coli* and the specific O157:H7 serogroup of *E. coli*, respectively. Moving forward, these genes will be PCR'd from both spiked and environmental water samples to ultimately confirm specificity, determine environmental microbial populations, and map out fluctuations in diversity due to factors including change in season and anthropogenic effects.

UNKNOWN BACTERIA FROM ECUADOR WITH STRONG ANTIBIOFILM ACTIVITY

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Bacteria can develop biofilms after attaching to surfaces. These biofilm forming cells generate an extracellular polymeric matrix. Once the biofilm has been established, it provides an environment for microorganisms to exchange genetic material between cells and to become resistant to our immune system and antibiotic treatment. Most infectious diseases in hospitals and device related infections, such as catheters are caused by biofilm forming pathogenic bacteria. The focus of our research is the identification and characterization of new anti-biofilm substances. Cell free extracts of unknown bacteria isolated from a volcanic spring from Banos, Ecuador, were tested against known pathogenic biofilm forming bacteria such as *Staphylococcus aureus*, *Staphylococcus epidermis*, *Escherichia coli*, and *Enterococcus faecalis*. Three out of several bacterial extracts that were tested showed strong antibiofilm properties against biofilm forming pathogenic bacteria including *Staphylococcus aureus* and *Staphylococcus epidermidis*. Further characterization will be conducted to identify the unknown bacteria as well as the active antibiofilm compound produced.

WHAT'S LURKING INSIDE A WASHING MACHINE?

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The organisms that persist inside of a washing machine is a subject of limited study, until now. The goal of this project was to determine the levels of bacteria/mold present in public washing machines, along with their identifications.

To perform this evaluation, sterilized generic cotton washcloths (washed and dried before sterilization) were washed at a variety of public laundromats, in multiple machines within each laundromat. The washcloths were then processed to extract the present microflora for quantification and for DNA extraction for external sequencing.

Results received to date show consistently high levels (over 5 logs) of bacteria and a microbiome unique to each laundromat.

The results received so far support the existence of persistent levels of microorganisms in washing machines at the different public laundromats examined. Initial identifications have reported organisms of potential public health significance.

DETECTING DIFFERENCES BETWEEN HONEY BEE GUT MICROBIOMES IN A QUICK, ECONOMICAL ASSAY

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The honeybee gut microbiome may provide a powerful tool for determining the health of bees and the effects stressors may have on those bees. The gut community of the adult honeybee is relatively simple, containing only nine bacterial species clusters. Previous studies have shown that the gut microbiome of honey bees has an affect on the host's health by means of nutrition, immune function and pathogen resistance. In addition, it has been shown that perturbation of the microbiome can affect the ability of the honey bee to maintain good health. Because of this, we are developing a simple and economical molecular method for microbiome analysis.

We characterized a subset of the taxonomic groups with a quantitative, nested-PCR approach. The relative abundance of the bacterial species was then used to detect for possible differences between-gut microbiomes between and within hives. The relative abundance of the bacterial taxon Bifidobacteria, showed more of the variation in Bee-gut microbiomes within a hive than did total bacteria. The variation in total bacteria and Bifidobacteria was greater within the spring-sampled hive than fall-sampled hives. The spring-sampled hive had lower total bacteria per bee. This proof-of-concept indicates we should be able to distinguish hives with a simple assay that could potentially characterize responses to stressors in longer-term investigations of bee colony health.

INVESTIGATION OF ANTIBIOTIC DOSAGE CONCENTRATIONS IN RELATION TO DEVELOPING AN AXENIC CULTURE OF *KARENIA BREVIS*

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The occurrence and intensity of red tides in the Gulf of Mexico have reached levels of environmental crisis. *Karenia brevis*, the cause of these red tides, is a dinoflagellate that produces neurotoxins called brevetoxins. *K. brevis* is studied in the laboratory under conditions that include the presence of bacterial species found in the marine niche where red tides occur, although very little research has been done on potential roles these bacterial community members may play in *K. brevis* growth and toxicity. In an attempt to create a bacteria-free (axenic) culture of *K. brevis* for comparison with bacteria-containing cultures, the Waldburger laboratory previously treated laboratory cultures with a variety of antibiotics. The results of that study revealed that some antibiotics permitted growth of *K. brevis* while others led to complete cell death of *K. brevis* cells in our laboratory cultures. The objective of this study was to determine the maximum allowable dose (MAD) at which those antibiotics that caused cell death could be used without killing *K. brevis*. In this study, we found that cultures that had been treated with antibiotics that were not lethal, *K. brevis* was now able to survive concentrations of antibiotics that had led to complete cell death previously. We propose that pre-treatment with permitted antibiotics may have led to survival in the presence of non-permitted antibiotics due to *K. brevis* or a critical bacterial species necessary for *K. brevis* growth acquiring broad-spectrum resistance. Alternatively, variation in the seawater properties or some other environmental factor may have influenced *K. brevis* sensitivity to specific antibiotics. Current studies include a continuation of our attempts to create an axenic culture of *K. brevis* by using the determined MAD for each antibiotic to treat cultures of *K. brevis* with multiple antibiotics in succession.

NEUROPROTECTIVE EFFECTS OF KCNQ POTASSIUM CHANNELS AFTER TRAUMATIC BRAIN INJURY WITH CHRONIC ALCOHOL USE

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Traumatic Brain Injury (TBI) affects millions of people each year. Characterization of TBI is defined as a direct injury to the brain followed by inflammation. Post-TBI recovery is often associated with negative changes in behavior as well as development of alcohol use. Studies have shown that alcohol slows down and impedes brain injury recovery. While acute alcohol usage has been suggested to have a neuroprotective effect, chronic usage is thought to have the opposite effect on brain tissue and behavior. While alcohol and brain injury have been studied previously, changes in brain morphology and behavior have not been well characterized with chronic use during the initial recovery period. This study used mice given a TBI and chronic administration of alcohol for a period of 21 days post-TBI. The goal of this experiment was to examine whether chronic administration of alcohol had a neurodegenerative effect on brain recovery identified through histological brain slices and multi-modal behavioral models. Additionally, we used a KCNQ channel opener as a therapeutic target since it underlies cell excitability.

DEVELOPMENTAL NEUROGENESIS AND HYPOTHALAMIC PEPTIDE LEVELS ARE ABNORMAL IN BRAINS OF EMBRYONIC AUTISTIC *BTBR* MICE: A PROTEIN AND HISTOLOGICAL STUDY

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Autism spectrum disorder (ASD) is a developmental disorder affecting almost 1 in 40 children in New Jersey, according to the latest CDC statistics. In this study, we used an animal model for ASD, the BTBR mice, to examine their neural development during the embryonic stage. In experiment 1, we harvested the embryonic brains of BTBR mice at embryonic ages (E12, E16, E18) and postnatal ages (P5 and P11). C57/BL6 were used as reference. These brains were homogenized using protein inhibitor and processed for the Western blot for detection of TH and endorphin. In experiment 2, we administered cellular developmental marker into the dams to label the rate of new neural birth in the brains of embryos at E14, E16 and E18. Animals were sacrificed 3 days later, brains of embryos were removed and post-fixed for histological examination. Results showed that NPY was present in the brains of both strains as early as E12 and rose postnatally before maximizing at adulthood. Our data also showed that TH was also present in both strains as early as E12 but remained constant throughout the rest of the mice's development. There was dramatic difference in brain development in BTBR compared to C57. The subcortical regions in BTBR had significantly larger number of newly born neurons vs. control. Moreover, the area of the subcortical region were significantly larger in BTBR mice at all embryonic developmental ages. This study showed that the BTBRs have significantly higher level of hypothalamic hormones as well increased developmental rate of neurons in the subcortical regions. This study showed that the developmental difference on ASD begins at much earlier age than predicted, and these changes involve both the neural and hormonal abnormalities.

THE ROLE OF CANNABINOID 2 RECEPTOR IN MODULATING MICROGLIA ACTIVATION AFTER A TRAUMATIC BRAIN INJURY IN FEMALES

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Traumatic brain injury (TBI) occurs when a sudden trauma is applied to the head and causes damage to the brain. TBI can result from a multitude of events including most commonly from sports injuries, vehicle collisions, violence, falls, and war. Injury can result in permanent disabilities and in severe cases it can be fatal. Symptoms after a TBI can be mild, moderate and severe depending on the extent of brain damage as well as location. Long-term behavioral effects can be characterized including depression, anti-social behavior, and fear/anxiety. Additionally, TBI injuries have shown symptoms that are closely related to Parkinson's and Alzheimer's like-symptoms. Currently, there are no specific treatments for a TBI injury. TBI occurs in two phases, the primary injury (physical aspect of the injury) and the secondary injury which consists of cellular process activated hours, days, and months after the initial injury. Neuroinflammation arising during the secondary injury can lead to neuronal death and involves the activation of microglia. The Endocannabinoid system (ECS) consist of two major receptors CB1 and CB2, including the endocannabinoids that activate these receptors and the enzymes involved in their synthesis and degradation. Previously published *in vitro* data indicates that activation of CB2 receptors in microglia decreased the production of pro-inflammatory factors; thus expression of CB2 receptor in microglia may play a role in the modulation of the immune response. This research evaluated the role of microglia activation after TBI by using female CB2 receptor knockout mice (Cx3-Cnr2) which would not express the characteristic neuroprotective effects on local neural circuits.

ADAPTIVE PLASTICITY TO PLASMA EXPOSURE: FASTER REGENERATION VERSUS DELAYED METAMORPHOSIS IN TADPOLES, *X. laevis*

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Adaptive plasticity is essential for many species to cope with changes in environment. Many amphibian species have exploited this trait by accelerating metamorphic development when threatened by desiccation in their aquatic habitat (Gomes-Mestre et al., 2013). The most important environmental variable for tadpoles is swimming in water for their survival (Denver, 1997). Our earlier studies have shown that tail regeneration is faster in plasma exposed tadpoles compared to control due to oxidative stress (Rivie et al., 2016). The current study was focused on the a) effect of plasma exposure on tail regeneration with its simultaneous effect on metamorphosis of tadpoles *Xenopus laevis* and b) immunohistochemistry and gene expression of antioxidant enzymes, superoxide dismutase (SOD) and catalase in regenerating blastema.

Tadpole tail was amputated at stage 57 according to Nieukoop and Faber, (1967). Following amputation, these tadpoles were exposed to plasma; and progression of each metamorphic stage was observed. Data for gene expression were obtained through qPCR of RNA isolated from plasma-exposed and non-exposed tail blastema.

Our results show that there is delay in metamorphic events unlike tail regeneration, which was faster (Rivie et al., 2017). This can be explained by the fact that tadpole tail was amputated at stage 57 (when hind limbs had not yet fully developed and forelimbs had not erupted) and exposed to plasma. These organisms were subjected to two kinds of stress: a) removal of the tail impeding movement in water and b) stress of plasma exposure. Restriction of swimming activity in absence of fully developed limbs, contributes to faster rate of tail regeneration for their survival, but at the expense of metamorphosis. Our immunohistochemistry results have shown that there is an increase in activity of both the antioxidant enzymes, SOD and catalase following plasma exposure and changes in gene expression of both these enzymes. These larval tadpoles have evolved sophisticated reactive oxygen species signalling pathways along with antioxidant defences to coordinate the subtleties of wound healing and regeneration along with the ongoing metamorphic process.

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VARIATION IN REPRODUCTIVE TRAITS AMONG MICE ADAPTED TO DIFFERENT REGIONS OF THE AMERICAS

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Although house mice, *Mus musculus domesticus*, are not native to the Americas, they have quickly adapted to a wide range of climates. For example, body size and nesting behavior are two traits linked to fitness that vary among populations from different latitudes, and those differences have been shown to have a genetic basis. Reproductive traits have a direct impact on fitness and life history theory predicts that both body size and climatic seasonality have the potential to affect reproductive investment. Here, we investigate whether litter size and pup weight vary among mice from different climates using new wild-derived mouse strains originating from New York, Brazil, Arizona, Florida, and Canada. We find significant differences in litter size among laboratory bred mice from these populations, both in early and middle late generations of inbreeding. Preliminary data also suggest differences in pup size. Overall, mice from higher-latitude locations tend to have larger litters and larger pups. These findings suggest that reproductive parameters may be either directly or indirectly selected on as populations of house mice adapt to more seasonal, temperate climates.

THE ROLE OF POTASSIUM CHANNEL (KCNQ CHANNEL) AFTER BRAIN INJURY

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Traumatic brain injury is a common type of brain injury that involves a cascade of cellular processes. These processes include, but are not excluded to hyperexcitability, excitotoxicity, and neuroinflammation, which ultimately leads to cellular death. There are currently no therapeutic treatments for TBI, only preventative measures. Neurons have M-channels which functions to control neuronal excitability. Retigabine, which is an anticonvulsant, has been shown to open M-channels, reducing cell excitability. This study investigates the neuroprotective effect of retigabine during various cellular processes of TBI in order to identify therapeutic treatments. The effects of retigabine on brain injury was observed by histologic assays 1h, 4h, 8h, 24h, 7d and 21d post injury.

C. ELEGANS ALTERED ODORANT RESPONSE AFTER TRICLOSAN EXPOSURE

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Triclosan (TCS) is an antimicrobial which is present in toothpastes and certain face cleansers, but has been banned by the FDA from most antiseptic washes. TCS induces oxidative stress in the nematode *C. elegans*. Oxidative stress is a disturbance in the balance of reactive oxidative stress species (ROS) production and the organism's ability to counteract that with antioxidant defenses. Oxidative stress can decrease longevity and reproduction. Paraquat, another chemical that induces oxidative stress, increases *C. elegans* sensitivity to octanol, a volatile repellent. We wanted to determine whether TCS elicited similar effects on odorant sensitivity. This is interesting because it suggests environmental toxin may sensitize nervous systems to other environmental stimuli. *C. elegans* were cultivated on agar plates with or without triclosan at concentrations of 0 ug/ml, 1.0 ug/ml, 2.5 ug/ml, 5.0 ug/ml or 10 ug/ml for 24 hours. After triclosan exposure, an octanol avoidance assay was performed on individual worms. The strength of avoidance was measured as the amount of time it took individual worms to move backwards, away from the octanol. We predicted that if triclosan had similar effects as paraquat, the time it takes a worm to avoid octanol should decrease. Unexpectedly, our data suggest that there is decreased sensitivity to octanol with triclosan exposure. A population assay was conducted as well where groups of worms were exposed to either 0 ug/ml or 5.0 ug/ml TCS concentration and avoidance of the population was measured after 30 minutes. A similar decrease in sensitivity was observed.

INVESTIGATING THE BEHAVIOURAL AND SYNAPTIC EFFECTS OF NITRIC OXIDE

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School of Natural Sciences

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Ethanol (Et-OH) effects inducible nitric oxide synthase (iNOS) activity by inhibiting the production of iNOS in cells. Acute doses increase the production of nitric oxide (NO) and endothelial NOS (eNOS). At higher dosages, ethanol impairs endothelial functions. NO has been found to suppress the feeding response in pond snails,

Lymnaea stagnalis, induce synaptic depression in crayfish, and inhibit the swimming rhythm of *Xenopus laevis* tadpoles (Aonuma, et al. 2000). This *in vivo* study has been performed in order to determine if synaptic depression is caused by NO, and if overall movements are decreased in *Procambarus forma fallax virginalis* (*P.f.f virginalis*) and *Procambarus blandingii*, in the presence of NO. Movement was assessed in a labeled gridded tanks of water, denatured ethanol (EtOH, 3 ppm), L-arginine (L-arg, Reagent grade, 1ppb) and chlorhexidine (CHX, 99.95%, 1ppb). There was an evident trend over a time interval of $6 \leq t \leq 8$ minutes, where the control, ethanol and chlorhexidine all had a stark drop off in activity, whilst L-arginine had a stark increase. It is hypothesized that this could be due to a metabolic pathway of L-arginine is converted through nitric oxide synthase (NOS) to L-citrulline (Racke, et al. 2010); whereas ethanol has proven to inhibit iNOS, and due to the cytostatic characteristics of chlorhexidine, it can be assumed that the correlation of chlorhexidine to ethanol lies in this pathway as well. Synaptic depression is shown where L-arginine is present, over a time interval of $0 \text{ ms} \leq t \leq 10 \text{ ms}$ (Aonuma et al. 2010); as found in the study, there is a correlation between L-arginine and chlorhexidine pre-wash, and it is hypothesized that this is from the terminal guanlyl group.

EFFECTS OF *Npc1*^{nmf164} MUTATION ON THE POSTNATAL DEVELOPMENT OF CEREBELLAR BLOOD VESSELS

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Npc1^{nmf164} is a mouse model of the autosomal recessive lysosomal storage disease Niemann Pick type-C (NPC). NPC features a mutation of the NPC1 transport protein which renders the protein dysfunctional in transporting cholesterol out of lysosomes, creating neurotoxic lysosomal cholesterol accumulation. NPC is additionally characterized by rapid neurodegeneration of Purkinje neurons (PN) within the cerebellum, inducing dramatic cognitive and motor decline leading up to childhood fatality. PNs, glial cells, and blood vessels (BV) develop postnatally in the cerebellum and due to metabolic dependencies, PN dendritic growth is coupled with cerebellar BV development. Despite being a fatal childhood disease, not much literature is available pertaining to the effect of NPC1 deficiency on postnatal development. Hence, we are conducting a blind study comparing 15, 21, and 30 day old *Npc1*^{nmf164} and wild type (WT) mice by quantifying cerebellar BV length, density, diameter, and branching to determine if there is a significant difference in cerebellar BV development linked with the *Npc1* mutation. Sample images are taken of the molecular layer (where PN cell bodies, dendrites, and synaptic connections reside) of mice cerebella stained with tomato lectin allowing BV visualization and imaging using fluorescent microscopy. BV lengths within sample images are quantified using the NeuronJ plugin available in the ImageJ program, allowing us to calculate the average BV density and length within the sample cerebella. Additionally, 3D images of BVs were produced using confocal microscopy of floating section cerebella in order to quantify BV diameter and branching. These images are analyzed using the filament tool available within the Imaris 3D imaging program. Our preliminary data shows that capillary complexity in the molecular layer increases with age during postnatal development. Differences in capillary patterns between the *Npc1*^{nmf164} and WT mice were also observed, suggesting that NPC1 deficiency affects the development of cerebellar BVs.

PHASE TRANSFER OF AQUEOUS GOLD NANOPARTICLES TO ORGANIC SOLVENTS

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and Dr. Bhanu P. S. Chauhan

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Gold nanoparticles have been commonly produced in aqueous solution, as the synthesis involves a simple pathway. Generally, they are transferred to organic media for more practical use. The direct production of gold nanoparticles in organic solvents is a more complex synthesis. Due to the variety of applications that require gold nanoparticles in organic solution, new routes to produce stable gold organic sols can be very useful and important. Polymers, as well as many biological macromolecules with strong coordinating ligands can be good stabilizing agents for nanoparticles.(10-13)

Recent research has shown that poly(hydro)siloxanes can provide a good balance between stability and reactivity for the nanoparticles.(14) Since hydrosiloxanes can reduce metal complexes to produce nanoparticles, additional reducing agents may not be needed. The unique activity of polysiloxanes has inspired the investigation of using monomeric hydrosilanes in order to transfer gold nanoparticles from aqueous to organic solution. This research presents a new approach to the dispersion and stabilization of gold nanoparticles from aqueous to organic solution through the use of alkylsilanes.

RHEOLOGY OF VARIOUS MATERIALS – CHARACTERIZATION AND CORRELATIONS

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Analytical rheology is the subject of determining the microstructure of a material from measurements of its viscoelastic response. In other words, it is an extension of analytical chemistry in much the same sense as other analytic methods predict on flow properties. Analytical rheology can be applied to any material system where the rheological response depends strongly on the microstructure. Layered double hydroxides (LDH) are clays of colloidal dimensions and present intractable rheological challenges that may be attributed mainly to their anisotropic physical and crystallo-chemical properties. Primary LDH particles usually exhibit plate-like morphology defined by edge and basal faces. Correlation of the rheological behavior of clays with interfacial chemistry and microstructure was used to probe the origin and nature of particle interaction forces.

Rheology, very sensitive to particle interactions, is characterized in terms of the apparent viscosity, shear yield stresses, critical shear stresses and elastic (G') and viscous (G'') moduli. The links between rheology, microstructure (buildup or breakdown) and interfacial chemistries as a function of applied stress or shear rate and time were established, while assessing the forces between particle aggregates at different stages of decomposition. Why rheology? There are two main reasons for using rheology: 1. It is a very sensitive method that detects very accurately the slightest change in particle arrangement and their structure and 2. The LDHs layered structure and plate-like particles meet the requirements for monitoring the smallest changes in particle array and/or constitution. Experimental methods of determining the linear viscoelastic LDHs functions are highly evolved such that accurate and reliable measurements can be made in a routine highly automated manner. Analytical rheology exploits this experimental capability and develops advanced methods of interpreting and utilizing standard rheological measurements.

CATALYTIC ACTIVITY OF A NEW GENERATION OF PLATINUM NANOPARTICLES

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Generation of hybrid polymers are an interesting field of study in that they can interact with both organic and inorganic functional groups. Our lab used a hybrid nano-material containing platinum nanoparticles and polymethylhydrosiloxane (PMHS), as a catalyst. The catalyst was made utilizing a general procedure that first used 0.1 mmol of potassium hexachloroplatinate and 6 molecular equivalents of PMHS, as a reducing and stabilizing agent. The reaction fostered a black gel. The same reaction was performed using cis-diamminedichloroplatinum, once again fostering a black gel. These catalysts were then used in the polymerization reaction of n-butylsilane.

Synthesis of the catalyst were observed using UV-vis which displayed a flat, featureless spectra. The catalyst was characterized using FT-IR revealing a disappearance of functional groups, previously present in the platinum precursor, and presence peaks associated with PMHS. Afterwards catalytic activity of the product was tested, 10 mg of catalysts was added to 0.1 mmol of n-butylsilane in organic solvent at room temperature for 24 hours. The resulting solution was a viscous liquid that was characterized using H-NMR and revealed the presence of n-butylsilane polymer.

ANTIBACTERIAL AND ANTIOXIDANT AGENTS DELIVERED IN NANOSIZED MATRICES

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Nisin is a suitable food preservative, used in more than fifty countries, because it is non-toxic, safe (food-grade), quickly digested, and it does not give cross-resistance in bacteria (which may lead to antibiotic resistance in subjects being treated for infections). Nisin is also considered a natural food preservative since it is not the result of any man-conducted chemical synthesis. The principal drawbacks of this agent are its lack of inhibitory activity against Gram negative bacteria, yeasts, and molds, its fast release in lipophilic environments, and its low stability. In the food industry, nisin is useful in controlling spoilage due to lactic acid bacteria in alcoholic beverages (wines, beers), salad dressings, bakery products, meats, fish, and cheeses. Nisin may be used as preservative in formulations for the skin. For all these applications the drawback is the fact that nisin leaks out fast when fats are present.

Tannins and tannic acid (a hydrolysable gallotannin) are strong antioxidants which make complexes with proteins. The wine industry uses them for wine clarification.

This study proposes encapsulation of nisin in chitosan nanoparticles. This approach targets a double benefit. The presence of the hydrophilic glucosamine units is expected to prevent fast leakage of nisin from the particles into fatty environments while the activity of nisin against Gram-positive bacteria will be complemented by chitosan, an agent active against both Gram-positive/Gram-negative and fungi.

A parallel set of nanomatrices will be prepared containing, besides chitosan and nisin, different amounts of tannic acid. Its influence is expected to be two-fold: antioxidant effect (enhancing chitosan, an antioxidant) and complexation of nisin having as result longer residence of nisin in the particles.

The comparative study will use the following characteristics of the particles: encapsulation efficiency, loading capacity, ratio of residual amino groups (important for antimicrobial activity), antioxidant activity, and kinetics of release from the particles.

DEVELOPING INVERSE OPAL TRANSITION-METAL DICHALCOGENIDE SEMICONDUCTOR FILMS FOR USE IN WATER SPLITTING APPLICATIONS

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There is an increasing demand for harvesting renewable and sustainable energy sources due to increasing global energy consumption. Hydrogen is an ideal renewable energy source that can be stored, is transportable, and can be converted to electricity using fuel cells as a clean energy source without producing CO₂. A key challenge, however, is to produce cost-effective and environmentally friendly renewable hydrogen on a large scale. Transition metal dichalcogenides, such as tungsten sulfide (WS₂) and molybdenum sulfide (MoS₂), have shown great promise because they are relatively abundant (much cheaper than platinum) and are active catalysts for the electrochemical generation of hydrogen from water. In here, we present our recent efforts of first attempt to develop inverse opal macroporous MoS₂ and WS₂ semiconductor thin films to enhance their catalytic activity using molecular precursors and polystyrene microsphere (500nm) as a template. We successfully developed self-assembled close-packed polystyrene microspheres and demonstrated the molecular precursor route is effective, high throughput method to form uniform semiconductor thin films. The structural, electrochemical, and optical properties of the MoS₂ and WS₂ thin films were characterized by Powder x-ray diffraction, cyclic voltammetry (CV), UV-Vis spectroscopy for water splitting applications. Surface morphologies of the films were obtained by Atomic Force Microscopy.

SYNTHESIS OF MAGNETIC SEMICONDUCTING IRON NANOPARTICLES GELS OF *n*-(2-AMINOETHYL)-3-AMINOSILANETRIOL

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The iron nanoparticles have very potent magnetic semiconducting and catalytic properties, therefore, have found applications from medical imaging to the development of specific treatments for different diseases, such as breast and brain cancer.¹ One of the problems often encountered in terms of storage of iron nanoparticles is that due to their strong reactivity with oxygen in air and water, their oxidation and demagnetization takes place. In this study, a facile three-step reaction for the production of magnetic iron nanoparticles is disclosed. The goal of our study is to stabilize iron nanoparticles with functional polymerizable silicon agents to create magnetic semiconductor gels, where the magnetic particles are protected from oxidation and are stable and active, by employing the silane, *n*-(2-aminoethyl)-3-aminosilanetriol², as stabilizing agents, iron nanoparticles were created which were stable and possess improved resistance to moisture and oxidation, while maintaining the nanoparticle magnetization.

Various analytical tools were used to conduct a thorough analysis of the resulting magnetic particles. Morphological analysis was carried out using transmission electron microscopy (TEM) and scanning electron microscope (SEM). Spectral characterization was carried out using Fourier Transform Magnetic Resonance spectroscopy (FT-IR) and UV-vis spectrometry (UV-vis) technologies. The TEM imaging analysis demonstrated that the magnetic semiconducting iron particles are uniformly coated with 2-AST, and the presence of 2-AST was also confirmed by FT-IR. We will also disclose possible use of such nanoparticles for the development of new technological equipment and drug development.

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² Chauhan, B. P. S.; Matam, S.; Johnson, Q. R.; Patel, A.; Moran, K.; Onyechi, B. Generation of Zerovalent Metal Core Nanoparticles Using N-(2-Aminoethyl)-3-Aminosilanetriol. *JoVE J. Vis. Exp.* 2016, No. 108, e53507. <https://doi.org/10.3791/53507>.

ADSORPTION OF Cr(VI) ON CASHEW NUT SHELL-BASED ACTIVATED CARBONS: THE EFFECT OF POLYETHYLENEIMINE IMPREGNATION

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Activated carbons were prepared from cashew nut shells by activation with phosphoric acid and heat treatment at 400°C. The prepared carbons were tested for the removal of aqueous Cr(VI), which is a human carcinogen. The adsorption capacity of carbons for Cr(VI), tested in the concentration range of 100 – 200 ppm, was found to be pH dependent. Carbons had higher capacities at lower pH, with a maximum capacity at pH ~ 2. It was also found that the washing time of carbons, after the heat treatment step, affected their adsorption capacities. The longer washing times resulted in higher capacities, which could be related to the changes in surface chemistry of carbons and the nature of surface functional groups. These groups were analyzed by FT-IR, where carboxyl, carbonyl, and phenol functional groups were detected on the carbon surface. Furthermore, carbons were impregnated with polyethyleneimine (PEI), to introduce nitrogen-containing functionalities to the surface, and tested for removal of Cr(VI). The results showed that the removal efficiencies of carbons with lower initial capacities were improved to a higher extent upon PEI grafting than those for carbons with higher initial capacities. The amount of PEI on the surface did not affect the removal of Cr(VI) to any significant degree. The results of this study demonstrate an effective way to utilize agricultural waste, in particular cashew nut shells, to produce activated carbon adsorbents for removal of water pollutants, and thus providing a solution for agricultural waste management and environmental remediation.

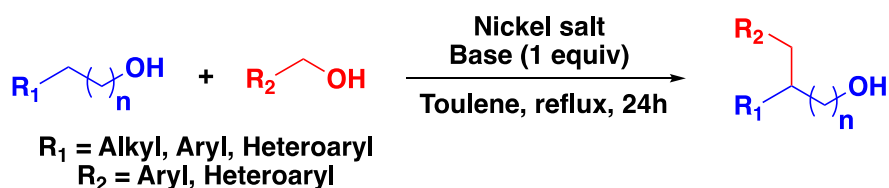
NON-PRECIOUS METAL CATALYZED DIRECT SYNTHESIS OF GUERBET ALCOHOL

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In the past decades, the development of transition metal catalyzed C-H functionalization boosted the scope of C-C and C-X (X = C, O, N, P, S) bond formation reactions. This methodology has had a great impact on the areas of synthetic chemistry, medicinal chemistry and material sciences. These reactions require the *in-situ* activation of the C-H bonds that results in a oxidative/dehydrogenative coupling leading to the formation of the desired product. Various transition-metal complexes especially palladium, platinum and ruthenium have gained tremendous success in carrying out various C-H activation reactions. These metals have broad synthetic scope and the possibility to control the selectivity of the transformations, which is an attractive feature in catalysis. Moreover, these metal complexes are stable, highly selective, have high turnover numbers and low catalyst loadings. However, these precious metals, although carry out rapid, time-effective and selective reactions, are expensive, more toxic, limited in supply and hard to remove from the reaction product. Hence non-precious metals (first row transition metals) have gained much popularity over these rare metals in recent years due to their low toxicity, and unique reactions mechanism.

In our current project, we are exploring the effect of non-precious nickel metal catalysts for the synthesis of Guerbet Alcohols, the reaction that involves the conversion of primary alcohols into the corresponding β -alkylated dimeric alcohol with the loss of water. The simple, inexpensive and readily available substrates make this an important and atom efficient reaction. Recently recyclable impregnated iridium oxide on magnetite as a heterogeneous catalyst was used for the synthesis of Gurebet alcohols.

Ruthenium catalysts was also used recently for the synthesis of α,β -unsaturated aldehydes. A wide substrate scope of the reaction was demonstrated to prepare a wide variety of Guerbet alcohol derivatives.^{24f} However, the methods reported till date only used the precious metals for the synthesis of Guerbet alcohols. In this project, we are exploring the use of nickel and nickel-complexes for the cross-coupling reaction of primary alcohols for the direct synthesis of Guerbet Alcohols. (Scheme 1).



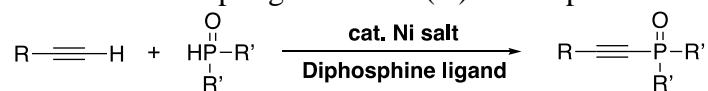
Scheme 1. Ni-catalyzed synthesis of Guerbet Alcohols

NICKEL-CATALYZED SYNTHESIS OF ALKYNYLPHOSPHONATES

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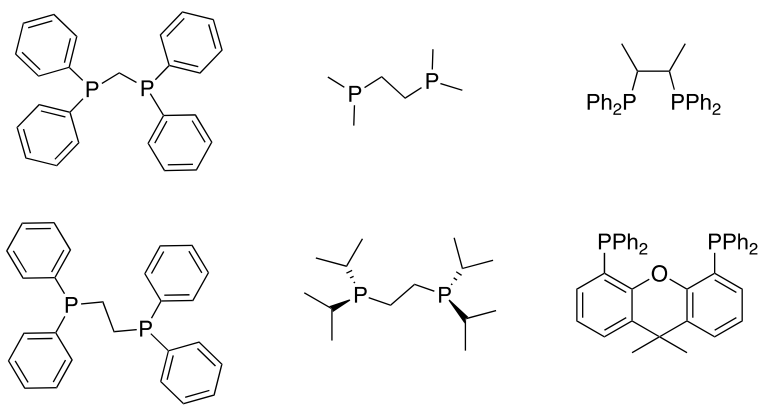
Alkynylphosphonates are an important class of organic compounds. They are excellent precursor for important transformations such as conjugate addition, cycloaddition, metellacycle, and hydration. Some of the alkynylphosphates containing molecules are also found to be bioactive and hence medicinally important.

The conventional procedure for the synthesis of alkynylphosphonates includes the use of nucleophilic substitution reactions involving toxic and moisture sensitive P(O)X compounds with metal acetylides under harsh conditions. But these procedures suffer from low functional group tolerance and use of hazardous conditions. Other methods for the synthesis of alkynylphosphonates involves the use of functionalized alkenes such as 1,1-dibromoalkenes, alkynyl sulfones, copper acetylides, and propiolic acids. In the last decade, the use of atom-efficient methods has been the area of great interest and one of the straightforward atom efficient methods for the synthesis of alkynylphosphonates is the direct cross coupling between P(O)-H compounds and terminal alkynes.



R' = Me, Et, *i*-Pr, Ph, Bn, CH_x

Diphosphine ligands:



Scheme 2 Ni-catalyzed synthesis of alkynylphosphonates

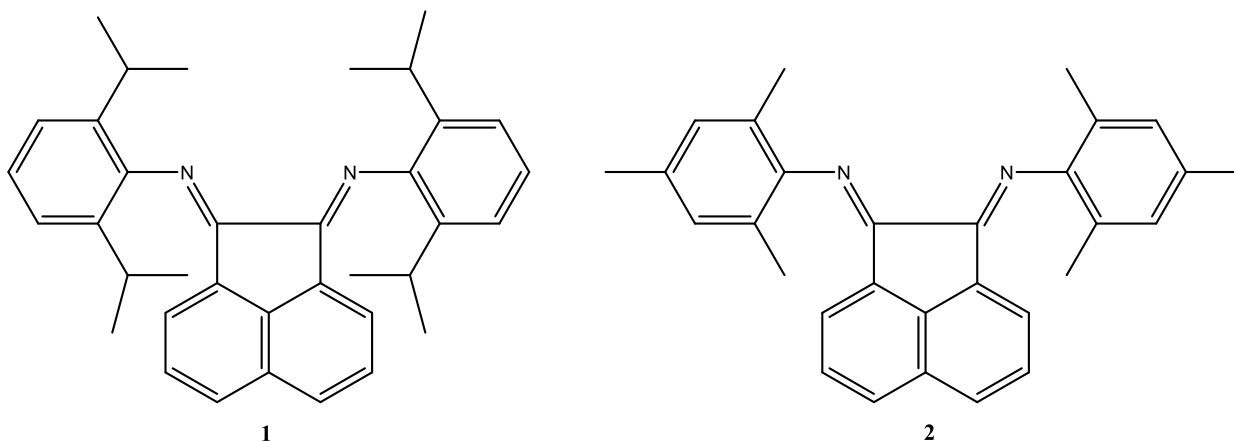
Last year, Han group reported the Ag free palladium-catalyzed dehydrogenative phosphorylation of terminal alkynes with hydrogen phosphine oxides. A good tolerance of functional group on alkynes was also reported.

Although elegant protocols have been reported in the last few years for the synthesis of alkynylphosphonates, but the use of non-precious metals such as nickel has never been used for the synthesis. In the current project, we are exploring the use of nickel salts and nickel complexes in presence of various phosphorus ligands for the synthesis of alkynyl phosphonates (**Scheme 2**).

A 60 MHZ NMR STUDY OF BIS(AMINO)ACENAPHTHENE MOLECULES

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and Dr. Colin Abernethy¹

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Bis(amino)acenaphthene (R-BIAN) molecules with sterically demanding substituents have been widely used as ligands in both transition metal and main group chemistry. The most commonly used compounds of this type are 1,2-bis[(2,6-diisopropylphenyl)imino]acenaphthene (dpp-BIAN, **1**) and 1,2-bis[(2,4,6-trimethylphenyl)imino]acenaphthene (mes-BIAN, **2**).

The Chemistry Department at Sarah Lawrence College recently acquired a new 60 MHz benchtop NMR spectrometer, and we wished to employ this instrument in our research projects involving the synthesis of new R-BIAN complexes of vanadium and other transition metal elements. However, the low field strength of benchtop NMR spectrometers can make interpreting the spectra large molecules such as R-BIANs extremely challenging. In order to assess the utility of our benchtop NMR spectrometer for our research, we first collected ¹H and ¹³C NMR spectra of R-BIAN compounds using this instrument. We then compared our spectra with the published data, which was collected on high-magnetic-field-strength instruments.

In our poster we will present our spectra and discuss the utility of low-magnetic-field NMR spectrometers for the characterization of complexes containing large ligands such as R-BIAN.

CARBOCATION CATALYZED IMINE FUNCTIONALIZATION'S: HYDRIDE TRANSFERS AND [3+2]-ALLYLSILANE ANNULATIONS

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Seton Hall University, South Orange, NJ

Chirality and enantiospecificity play an important role in the treatment of diseases by producing a desired effect when targeting an intended biological target. However, if the wrong region of the receptor is stimulated then it can cause a cascade of various side reactions producing effects. One case of a drug producing debilitating side effects was seen in thalidomide. The (*R*)-enantiomer of thalidomide cured nausea, while the (*S*)-enantiomer prevented the development of major blood vessels during pregnancy that lead to multiple physical and mental complications of newborn infants.

The purpose of this research project is to functionalize imines using Lewis acid carbocation-catalysis in order to produce chiral amines. Two methods were investigated; the asymmetric transfer hydrogenation of imines and [3+2]-allylsilane annulations. We first began by examining transfer hydrogenation of aryl ketone derived imines using Hantzsch ester as the hydride source. The reaction was found to be temperature dependent and the highest yield for amine formation (76%) was obtained at 80°C in DCE. Additionally, reaction efficiency also correlates to catalyst acidity, theoretically increases in acidity lead to increased efficiency. A proton sponge was used in order to show the reaction is Lewis acid catalyzed and not catalyzed by adventitious acid produced under the reaction conditions. Next, we studied the [3+2]-annulation method using allyl triisopropylsilane (TIPS) and aldehyde derived imines. The TIPS possess a silicon atom, silicon is electropositive and pushes electron density away from the central atom making the double bond of the alkene a good nucleophile. Upon imine activation by the carbocation catalyst the double bond attacks forming a new carbon-carbon bond. The lone pair of electrons attack the carbon containing the silane group causing a 1,2-silyl migration with concomitant cyclization to form the corresponding pyrrolidine products. The catalyst then reenters the catalytic cycle leaving the desired amine product. The best conditions are produced using trityl pentachlorostannate as the catalyst in dichloromethane at room temperature; the yield is 35% with a 67:33 mixture of diastereomers. Future plans include the development of more Lewis acidic carbocation catalysts and the use of chiral counterions to induce asymmetric transformations.

GREEN CHEMISTRY: BENZYLIC FUNCTIONALIZATION VIA VISIBLE-LIGHT INDUCED PHOTO REDOX CATALYSIS

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Visible-light photo-redox catalysis offers a promising synthetic technology which replaces traditional methods due to its mildness and high compatibility with functional groups. Visible light is considered as clean energy because of its high abundance, greenness, benign environmental impact, and sustainability. We developed a visible-light induced photo-redox catalysis for the efficient functionalization of benzylic/allylic C-H bonds with peroxides. This research was primarily conducted to functionalize various substrates at the benzylic position by the addition of a peroxide group. An organic dye, Eosin Y, is used as a non-expensive photocatalyst and the blue LED light was employed as the light visible light source. Various benzylic peroxides were synthesized under our optimal conditions in good to excellent yields. This reaction takes advantage of a Hydrogen Atom Transfer mechanism and features mild conditions, high functional group compatibility, and broad substrate scopes.

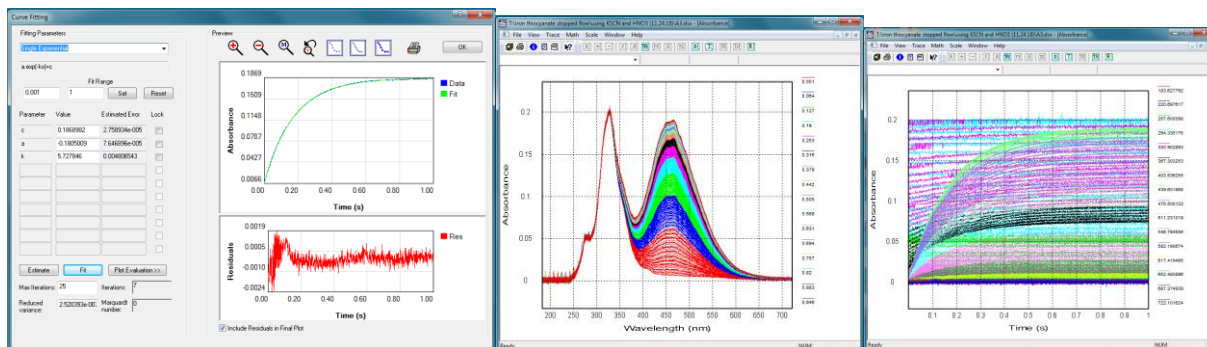
REVISITING THE SUBSTITUTION KINETICS OF THE FORMATION OF IRON (III) THIOCYANATE $[\text{Fe}(\text{SCN})]^{2+}$ COMPLEX^{1,2} USING APPLIED PHOTOPHYSICS STOPPED-FLOW SPECTROMETER KOMAL MIR(MCC)* Φ

Komal Mir and Dr. Phalguni Ghosh

Middlesex Community College, Edison, NJ

A Stopped-flow Spectrometer serves as a source for monitoring reactions that occur in timeframes as fast as milliseconds. The instrument rapidly mixes the reactants and examines the reaction's kinetics using a suitable spectroscopic probe. This paper explores the stopped-flow kinetics of the Formation of Iron (III) Thiocyanate.

The formation of Iron (III) Thiocyanate is a four-step reversible system, governed by various rate and acid dissociation constants¹. The experiment was carried out under Pseudo-first Order conditions. Since the dark red Iron (III) thiocyanate complex absorbed readily at wavelengths ranging from 440 nm to 460 nm, the rate constant values for the overall reaction collected by the spectrometer at 440 nm, 450 nm, and 460 nm for different Fe^{3+} concentrations and pH values were used to find the rate constants incorporated into the integrated rate equation and the results were compared with the reported values.



Currently, we are focusing on learning the enzyme kinetics and protein-ligand binding interactions using Stopped-flow and fluorimeter instruments. Specifically, we are studying Neutral Red (Ligand) interaction to Riboflavin-binding protein using UV-Vis and fluorescence quenching techniques³.

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THE EFFECT OF CD44 ON REDD1 IN BREAST CANCER

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Breast cancer is the most common type of cancer in the United States. In 2016, breast cancer made up 14.6%, or 246,660 of all new cancer cases, and resulted in around 40,450 deaths. A key contributor to cancer progression is the control of cellular metabolism. mTOR (mammalian target of Rapamycin) signaling is a known and well studied, dysregulated pathway in diseases. This pathway is known to regulate cell growth, apoptosis, cell survival, protein synthesis, cell proliferation, transcription, and translation. mTOR signaling is inhibited by REDD1, a gene that is response to hypoxia and stress. Our research has shown that over expression of CD44 in breast cancer cells results in a down regulation of REDD1 expression and REDD1 protein level in a hypoxia-induced dependent fashion. This regulation may result in altered mTOR signaling resulting increased cancer cells metabolism.

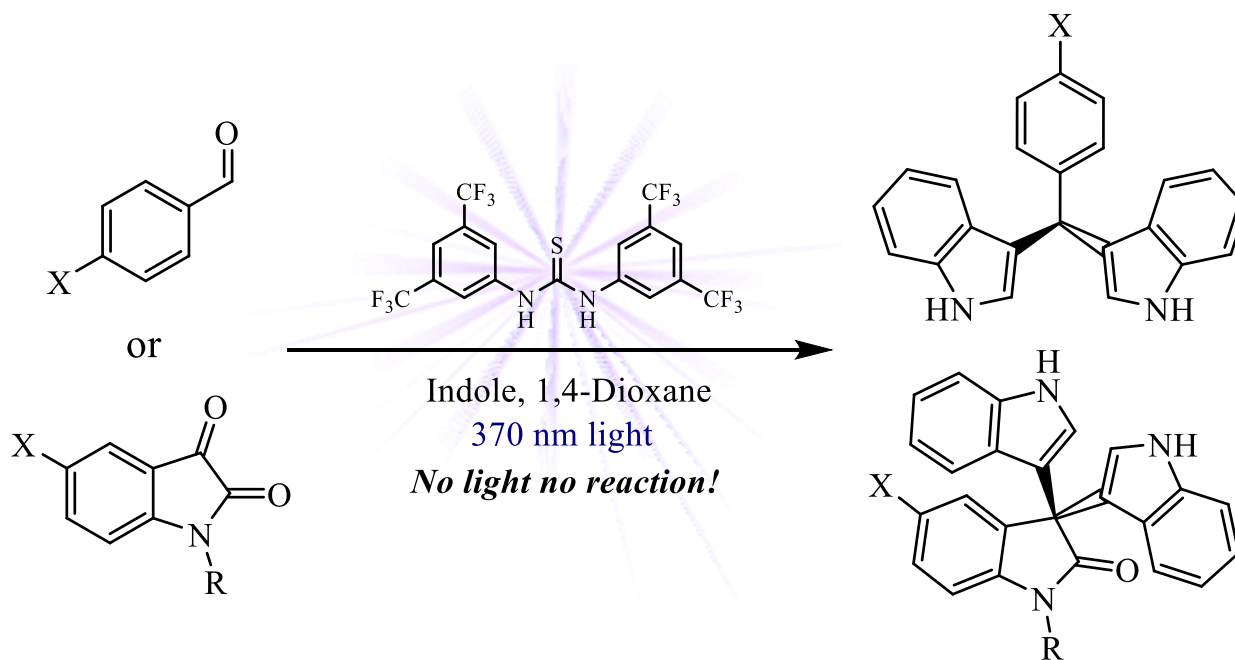
PHOTOACID CATALYZED FRIEDEL-CRAFTS ALKYLATION OF CARBONYLS

Zena Salem, Jason Saway, Samantha Chalet, and Dr. Joseph Badillo

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Photoacids are molecules that become orders of magnitude more acidic upon the absorption of light. Here we show that a simple organophotoacid, such as Schreiner's thiourea, is capable of being engaged in hydrogen bonding catalysis through visible light excitation to enable the synthesis of numerous bis(indolyl)phenylmethanes. Bis(indolyl)phenylmethanes are interesting therapeutics for drug discovery due to their ability to interact with various ligand binding domains within cancer cells to either induce cellular apoptosis or inhibit cellular growth. Initial studies for the addition of π -nucleophiles to carbonyl compounds show that in the absence of light, the thiourea-catalyzed reaction is completely shut down. Specifically, we have demonstrated that excited state N,N'-bis[3,5-bis(trifluoromethyl)phenyl]-thiourea facilitates the double addition of indole to aldehydes and isatins to form the corresponding 1,1-bis(3'-indolyl)-1-phenylmethanes and 3,3'-bisindolyl oxindoles. Reaction conditions including solvents, light sources, photoacids, catalyst loading, and a range of electrophilic carbonyls and nucleophilic aromatics have been investigated.



OXIDATIVE CYCLIZATION OF 3-INDOLE-ETHANOLS VIA LEWIS ACID CATALYZED ELECTROCHEMISTRY

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Electrochemistry has made major and recent contributions to organic synthesis through its “green” methodology, higher atom economy, and minimal waste. Organic electrosynthesis utilizes electrical current to drive the activation of organic molecules via the removal or addition of electrons in a reaction. As a result of its selective redox of organic molecules, organic electrosynthesis can perform reaction transformations that have not been generated traditionally through chemical reagents used in the past. Electrochemistry is a beneficial asset for chemists providing clean transformations, mild reaction conditions, simple scalability, high functional group tolerance, low energy consumption, and a step away from the use of toxic redox reagents. We have developed a Lewis Acid catalyzed oxidative cyclization of 3-indole-ethanols using electrochemistry. Csp²-H bond was activated and a new C-O bond to afford the furo[2,3-*b*]-indole structural motif formed under mild electrochemical conditions. This electrochemical transformation utilizes undivided cell and graphite electrodes as both cathode and anode. Currently, studies on screening different Lewis acid catalysts to identify the optimal conditions are undergoing in our laboratory.

BEHAVIORAL OUTCOMES OF CO-USE OF ALCOHOL AND AMPHETAMINE IN A RAT MODEL FOR ADHD

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Non-medical use of amphetamine and other stimulants prescribed for treatment of attention deficit hyperactivity disorder (ADHD) peaks in adolescence and is of growing concern when combined with binge consumption of alcohol. Previous studies in our lab modeled chronic ethanol-amphetamine co-use in adolescent Long-Evans rats and provided evidence that amphetamine attenuates alcohol withdrawal symptoms in a manner that may lessen an individual’s awareness of impending alcohol dependence (Popkin et al., 2018; Behavioural Pharmacology 29:547-550).

The current project was designed as a pilot study to test repeated ethanol-amphetamine co-use in adolescent Spontaneously Hypertensive Rats (SHR), an experimental model for study of ADHD. How will a brain, for which amphetamine is potentially therapeutic, respond to co-administration of ethanol and amphetamine?

SHR adolescents were randomly assigned at P33 to one of four treatment groups: control (no drug), ethanol (3.5%, w/v), amphetamine (20-40mg/L), or ethanol combined with amphetamine. Each group was administered the treatment as part of a liquid diet over the course of 19 days. Rats were withdrawn from treatment groups at three different time points: 5 days, 12 days, and 19 days and tested for alcohol withdrawal symptoms after 6-8 hours. Computer controlled activity chambers equipped with a dark box insert were used to assess general locomotor activity and anxiety-like behavior. Overall alcohol withdrawal severity was also evaluated.

After 5 days consuming alcohol, SHR adolescents showed marked hypo-activity typical of alcohol withdrawal. However, hypo-activity declined with additional periods of ethanol administration and there was surprisingly low overall withdrawal severity after 19 days. The SHR adolescents appeared resistant to progressive signs of alcohol

withdrawal used to gauge alcohol dependency in rodents. Moreover, amphetamine co-administration had no effect on withdrawal hypo-activity or overall withdrawal severity, but increased anxiety-like behavior at the 5-day time point. Thus, amphetamine did not attenuate the one observed symptom of alcohol withdrawal and exacerbated anxiety-like behavior not seen with ethanol alone. Amphetamine also had an anorexic effect not seen in control rats. Thus, as a model for ADHD, adolescent SHR showed altered responses to alcohol, to amphetamine, and to the combined administration of both drugs. The results speak to the importance of better understanding alcohol-stimulant interactions in an ADHD population in developing educational and preventive strategies.

ACUTE ALCOHOL USE AFTER TRAUMATIC BRAIN INJURY

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Between 30-50% of traumatic brain injury patients are found with a BAC 0.08 (the legal limit in the United States) at the time of the injury. It has been suggested by several studies that alcohol use at the time of TBI has an initial neuroprotective effect. However, what is not currently known is whether this neuroprotective effect is truly neuroprotective at the neuronal level when examining cell morphology in the initial phase of recovery. This study examined mice administered alcohol once before TBI and observed for the effects on behavior and cell morphology through histology. Additionally, this study focused on M-Type Potassium channels as a mechanism to evaluate neurodegeneration. The M-type channel opener is understood to decrease secondary effects of injury and enhance the neuroprotective effect of alcohol. Thus, this study examined whether a single dose of alcohol pre- and post-TBI can elicit changes in both cell morphology and behavior.

COMPARISON OF INDIVIDUAL BEHAVIORS BETWEEN BEAR SPECIES IN ZOOLOGICAL PARKS

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Zoological parks provide a source of public education on wildlife and conservation. However, these parks may not be ideal for certain species of animals. Bears in particular tend to display abnormal behavior in captivity, such as pacing and looping (moving in a repeated programmatic manner). The main goal of this study is to compare captive bear behavior in zoological parks to natural bear behavior as documented in the scientific literature. In addition, this research aims to analyze variations of behavior across different species of bears based on their morphology, biogeography and evolutionary history. The focal species for this study are the Polar Bear (*Ursus marinus*), the Brown Bear/ Grizzly Bear (*Ursus actors*), the American Black Bear (*Ursus americanus*), the Sun Bear (*Ursus malayanus*), the Sloth Bear (*Ursus ursinus*) and the Asian Black Bear (*Ursus thibetanus*). This study will examine these species across eight different zoological parks. Subjects were sampled utilizing the focal observation rule, recording instantaneous behavior every 10 seconds for a total of 30 minutes. Each individual bear in the study was examined between 1 to 3 times. I hypothesize that species that are more closely related will demonstrate similar behavioral patterns. In addition, I hypothesize that bears living in similar habitats with similar morphological features will display overlapping behavioral patterns. It was found that walking, pacing, swimming, and climbing behaviors significantly differed in frequency across the species under study. Polar bears

paced at the highest frequency, indicating possible increased stress in this species under captive conditions. Captive bears slept less under crowded visitor conditions. Pacing frequency decreased as temperature increased, and climbing behavior increased as temperature increased. The results of this study increase our knowledge of captive bear behavior. Polar bears, especially, seem to struggle under captive conditions highlighted by our research and supported by additional studies. Zoological and conservation managers are encouraged to address behavioral issues in captive bears, such as poor rate of conception, high infant mortality rates and poor captive adult survivorship rates.

EFFECT OF HOST SWITCH ON SEXUAL SELECTION OF AN HERBIVORE

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Female mate choice, is considered an important component in maximizing female fitness (i.e. her offspring numbers). To test this whether females with mate choice have indeed higher offspring numbers bean beetles are being used for my research at Fairleigh Dickinson University in Dr. Harald Parzer's lab. However, surprisingly few empirical studies support this notion. Interestingly, preliminary data collected in the course *Sophomore Research*, as well as other non-published data by my collaborator Dr. Deanne Soper (University of Dallas), showed that females which are paired with several males (sexual selection treatment) have in fact *lower fitness* than females which are paired with one randomly selected male (non-sexual selection treatment). Previous studies on this species indicate that male bean beetles are injuring females during insemination, presumably to increase their own fitness (at the cost of the female). Thus, “antagonistic sexual selection” might explain such intriguing pattern. Here, Dr. Parzer and I are predicting that while females might not benefit from sexual selection under “ideal conditions”, they might benefit from mate choice when exposed to stressful conditions due to increased genetic variability of their offspring. To test this, beetles are stored in containers with either mung beans, or adzuki beans. Data will be collected from how many eggs were laid by females when allowed to mate for a week with males in the same beans they were stored in at a 1:1; Male: Female ratio. The same will be done but with a 3:1; Male: Female ratio to determine if this will result in antagonist sexual selection. Then, beetles that were stored in mung beans will then be stressed by allowing them to mate for a week in adzuki beans, and vice versa. These treatments will be carried out in the 1:1; Male: Female ratio and in the 3:1; Male: Female ratio. So far, data collected has revealed that there females are laying fewer eggs when placed in a stressful environment when allowed to mate in the 1:1; Male:Female ratio.

AIRBORNE TRANSMISSION OF THE HONEYBEE WAGGLE-DANCE PHEROMONE

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Foraging honeybees pollinate the majority of crops around the globe. The waggle-dance pheromone is a mixture of four hydrocarbons emitted by waggle-dancing foragers to promote foraging behavior. The traits of known chemical communication in honeybees led me to hypothesize that direct contact is not necessary for the waggle-dance pheromone to produce a behavioral response. To test our hypothesis, foragers were observed during trials where they could not physically touch the pheromone. The initial number of waggle-runs was compared to the number of waggle-runs after the pheromone was introduced. The observed increase in waggle-runs, primarily

from nectar foragers, after the introduction of the pheromone supports the hypothesis that contact is not necessary for a behavioral response and suggests that nectar foragers respond more strongly to the pheromone than pollen foragers. These results provide important context to further study how foragers detect the pheromone and to use the pheromone to promote agricultural efforts.

COMPENSATION FOR LEG-LOSS IN ROTATING PREY-STRIKES OF “FLATTIE” SPIDERS (ARANEAE: SELENOPIDAE)

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Spiders in the family Selenopidae, commonly called “flatties,”- have been characterized as having the fastest rotational prey strikes of any animal. While previous work developed a model of rotational striking based on intact, eight-legged spiders, here this model was used as a basis to analyze the strikes of flatties missing one or two legs. Flatties (*Karaops* sp.) were collected in Australia and filmed using high-speed digital video cameras attacking fruit fly prey. Using rotational speed as a measure of performance, we found that spiders missing one leg were only marginally slower (13% reduction in speed, $p = .054$) than intact individuals (2.13 ± 0.38 deg/ms for seven legs, vs $2.48 \pm .61$ for intact spiders). By contrast, those missing two legs were much slower (54% reduction, $p < 0.001$, mean speed 1.15 ± 0.50 deg/ms), though all could successfully grab prey. The leg use of autotomized spiders was also compared to the model developed for close relatives in the genus *Selenops* by Zeng and Crews (2001). Analysis of changes in leg use by seven-legged spiders in rotational attacks showed that those that had lost a single rear leg would compensate by changing the roles of the back two legs, usually shifting the role of the inner flexion leg (IFL) to the next closest leg to the prey. This maintained the three different leg roles in 100% of attacks. This not only supports the proposed “spare leg” hypothesis proposed by Brueseke and colleagues in 2001, but provides evidence supporting optimality for the maintenance of the three leg roles and their typical pattern, though the effects of gait changes on prey capture and overall fitness remain unknown.

DOPAMINE INHIBITION AND EXITATION OF MOVEMENT IN THE CHERRY SHRIMP (*NEOCAIDINIA DAVIDI*)

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Desire in organisms correlates to seeking behavior or mediated movement toward a target. *Neocaridina davidi*, show food seeking movement mediated by the presence of stimulatory or inhibitory molecules. Glutamate and glucose act as stimulatory molecules, while dopamine acts as an inhibitor of glutamate stimulated movement, and insulin act as an inhibitor of glucose stimulated movement. Unexpectedly, dopamine can serve as either a stimulant or inhibitor depending on the context. Glucose and glutamate were used as stimulatory substances signaling the availability of food. Dopamine was inhibitory when combined with glutamate. Haloperidol blocked the effects of dopamine and partially restored movement. Shrimp showed increased movement when treated with glucose, and activity increased further in combination with dopamine. Insulin did not show a statistical difference from endogenous insulin in the presence of glucose. Dopamine inhibition of insulin is suspected as the mechanism producing a stimulatory interaction between dopamine and insulin.

STIMULATING DESIRE AND REWARD IN CHERRY SHRIMP (NEOCAIDINIA DAVIDI)

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Neocaridina davidi, (cherry shrimp), were used as the model organisms, due to their relatively simple neurobiology. Shrimp were placed in tanks in groups of ten, treated with stimulants or inhibitors, and their movements were recorded for twenty minutes. Experiments were conducted with dopamine, haloperidol, glutamate, and glucose, and behavioral responses were quantified by observing movement after treatment. The addition of glutamate (MSG) to shrimp tank water showed significantly increased movement over controls. Dopamine, despite being associated with stimulants, showed decreased movement in treated shrimp. This was true of dopamine on its own, or when paired with glutamate. Treatment with the dopamine inhibitor, haloperidol, resulted in restored movement. Glucose stimulated movement, but dopamine combined with glucose acted as a stimulant rather than an inhibitor, as was seen when dopamine was combined with glutamate.

THE ACTIVITY OF HERMIT CRABS DEPENDS ON THE CONSTANT CONDITION

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The hermit crab, *Coenobita clypeatus*, is a semi-terrestrial and tree-climbing hermit crab that is nocturnal. To determine if its nocturnal activities are endogenous and self-sustaining or exogenous and not self-sustaining, 7 crabs were placed in constant light conditions with food and water while another 7 were placed in constant dark conditions with food and water before observing both for activity at random times for a few weeks. The activity of hermit crabs in constant light conditions ranged from 17% to 20% during the evening but was 100% inactive during the day. The activity of hermit crabs in constant dark conditions was 43% during evening but ranged from 29% to 100% active during the day. These results suggest that although hermit crabs in constant darkness were more active than crabs in constant light conditions, they were active at times not expected for nocturnal animals and had activities that were exogenous and not self-sustaining. Hermit crabs in constant light conditions, although not as active as those in constant dark conditions, were active at times expected for nocturnal animals and had activities that were endogenous and self-sustaining. Based on these findings future studies on nocturnal hermit crabs should test them in both constant light and constant dark conditions.

ANALYSIS OF THE Mps1-PP1 INTERACTION IN VIVO

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Meiosis and mitosis, essential to the survival of all organisms, rely on the formation of a bipolar spindle to segregate chromosomes and complete cell division successfully. Many of the spindle assembly mutants are lethal, requiring the use of transgenic constructs (both wild type and mutant) to compensate for the lethality and study the protein. *monopolar spindle-1 (mps-1)* is a spindle checkpoint gene responsible for monitoring kinetochore attachment to the microtubules and ensuring that the spindle is properly built before giving the cell permission to enter anaphase and progress through the cell cycle (InteractiveFly: Genebrief alterreddisjunction 2018). Since *mps-*

1 null alleles are usually embryonic lethal, transgenic flies carrying a mutant (or wild-type) construct must be generated allowing for analysis in an *mps-1* null background, with the embryonic lethality bypassed. Here we present the results of attempting to generate 4 different *mps1* transgenic lines. Only the GFP-tagged construct with the native promoter and gene were viable and produced normal spindles; the GAL4 driven promoters and/or mutant *mps1* lines were sterile or inviable, demonstrating a dominant negative effect of mutant and/or over-expressed *mps1*.

USING HEK CELLS AS A MODEL SYSTEM TO STUDY AUTOPHAGY AND IT'S REGULATIONS

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The body has multiple mechanisms to detoxify and regulate itself to maintain homeostasis. Autophagy functions as a self-recycling mechanism involving protein degradation in autophagosomes. Autophagy is particularly important in neuronal function, and its disruption has been linked to diseases like Parkinson's and Alzheimer's. This study investigates using HEK (human embryonic kidney) cells as a model system to study autophagy and its regulation. LC3 labeling was used as a marker to show the formation of autophagosomes. Serum starvation of HEK cells induced autophagosome formation as shown by a 35% increase in LC3 cluster labeling. Wortmannin, a PI3 kinase inhibitor, inhibited starvation-induced autophagy by 31% when added to the starvation media. Chloroquine treatment induced increased expression of LC3 levels consistent with its blocking lysosome function. Initial investigations have examined the role of autophagy in regulating expression of neurotransmitter receptor GABA β_2 along with GABA RAP, following transfection into HEK cells.

SECONDARY STRUCTURE ANALYSIS BY SHAPE-MAP OF THE EGFR AND VEGFR2 PRE-MRNA TRANSCRIPTS: UNCOVERING NOVEL REGIONS FOR RNA ANTI-SENSE TARGETED THERAPY

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Splicing is the process where pre-mRNA is transformed into mRNA by removing introns and joining exons together. The pattern of which introns are removed, and which exons are joined together effects the characteristic of the protein. We have developed a gene therapy vector that delivers antisense RNA to block critical splicing elements of pre-mRNA transcripts. This can induce alternative splicing and reduce or alter the expression of oncogenic proteins. We are using this strategy to alter the expression of epidermal growth factor receptor which is overexpressed in 60% of Glioblastoma tumors. We sought to improve our current model, which is designed to have an antisense RNA molecule complementary to canonical and cryptic splicing motifs. Our therapy can be improved by determining novel targets which are not bound by protein or involved in RNA secondary, tertiary, or quaternary structure.

The secondary, tertiary and quaternary structure of the pre-mRNA transcript determines the splicing pattern. In order to therapeutically modify the pre-mRNA transcript, we are using tools to uncover the RNA structure of oncogenic transcripts., we have begun experiments to analyze the EGFR pre-mRNA structure using selective 2' hydroxyl acylation and primer extension followed by mutational profiling (SHAPE-MaP). The SHAPE reagent (1M7) reacts with the 2' hydroxyl of RNA molecules when the RNA molecule is in a conformationally flexible position creating a 2' O-adduct. The modified RNA is reverse transcribed, incorporating mismatches at the acylated positions; a comparison of unmodified to modified

RNA will allow us to determine RNA nucleotides that are involved in secondary structure, part of RNA-binding-protein complexes, or single stranded. Single stranded RNAs and RNAs with minimal structure are a preferential target of our therapy. We hypothesize that the secondary structure of the RNA of exon15-intron-15-exon16 will determine the most effective way to approach synthetically altering the splicing of the EGFR pre-mRNA. Also, the secondary structure of the pre-mRNA will give further insight into understanding the mechanism of alternative transcripts induced by nature.

SKMG-3 cells were grown in DMEM with 10% FBS. Cells were subjected to 1M7, 5-NIA or DMSO (control) in cellular and cell-free conditions. RNA was isolated using Trizol and phenol:chloroform:isoamyl alcohol respectively. The RNA was subjected to DNA degradation followed by reverse transcribed with Superscript IV under SHAPE conditions using a gene specific cocktail primer. Reverse transcription under SHAPE conditions includes the use of manganese chloride as the divalent ion for the RNA-dependent DNA polymerase subunit and is significantly less effective. It was determined that the most effective way to isolate pre-mRNA was to reverse transcribe with a gene specific cocktail primer mix. Primers were designed to target the EGFR transcript ranging from intron 15 to the 3' UTR. The cocktail consisted of 10 primers at 2 pmol/primer. RNA was converted to double stranded DNA and prepared for Oxford Nanopore sequencing. Nanopore sequencing will be performed at Monmouth University; the data will be analyzed by MaP technology to deduce the pre-mRNA secondary structure.

PATTERNS OF MITOCHONDRIAL INHERITANCE IN SEPTIN MUTANTS IN SACCHAROMYCES CEREVISIAE

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Saccharomyces cerevisiae (commonly known as budding yeast) is a single-celled eukaryote that is frequently used as a model organism in scientific research. The purpose of this research was to study mitochondrial inheritance in septin mutants *cdc11* and *cdc12*. Septins are GTP-binding proteins seen in eukaryotic cells to control the end of cell division. Septins normally assemble early in the cell cycle as a patch, forming an hourglass shaped collar. Septins located at the bud neck serve as a structural scaffold, which helped recruit different components that are involved in processes at certain stages during of a cell's cycle There are seven septin genes found in budding yeast including *cdc3*, *cdc10*, *cdc11* and *cdc12*. These four septin genes are identified to have defects in cytokinesis through temperature-sensitive mutants. Septin mutants may grow abnormally and produce elongated buds at higher temperatures. In addition, cytokinesis may not be able to be completed, and budding chains may grow too large. However, in our research we focused on the temperature-sensitive mutants, *cdc11* and *cdc12*. Septins normally assemble early in the cell cycle as a patch, forming an hourglass shaped collar.

To test if septins influence mitochondrial inheritance between the mother and daughter cells, wild type, *cdc11* and *cdc12* yeast were compared. In addition, we conducted mitochondrial and ER co-localization via fluorescence microscopy. The objective was to determine if the mitochondria and ER are located in the same cellular region, or if they are just in close proximity. MitoTracker Red CMXRos was utilized for staining the mitochondria samples. Mitochondrial localization patterns were studied throughout the cell cycle, including G1, S, G2, and M. In the *cdc12* mutant cells, at room temperature, a majority of the S-phase cells had a colocalization retention zone of mitochondria and ER located in the mother cell and the bud neck, while the majority of G2/M-phase cells exhibited no colocalization at all. When exposed to the elevated temperature, most of the S-phase and G2/M- phase *cdc12* cells exhibited colocalization solely at the bud neck. The results also indicated that the septin mutants had an overall change in mitochondrial localization at 37°C. For example, at room temperature, *cdc11* mutants had mitochondria that either appeared as dots or were circular shaped on the edges of the yeast bud in both the mother and the daughter cell. The septin mutant had a distorted spoon shape at 37°C, in contrast to the

round shape at room temperature. The mitochondria observed in the *cdc11* septin mutant appeared to have more spots at 37°C than room temperature. It was concluded that that the brighter spots could serve as possible fragments of mitochondria.

Serial dilutions on plates were also performed, using the *mgm1* mitochondria mutant as a control, which tested the growth of the septin mutant on different carbon sources. In future testing, we hope to compare our frogging experiment with the *mgm1* mutant as a control to a different mitochondria mutant, *mdm1*, as a control on the same carbon sources.

EVALUATING THE PHENOTYPIC EFFECTS OF PREVENTING AURORA KINASE BINDING TO INCENP

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Infertility affects 6% of couples worldwide. Although there are many pathologies that can cause infertility, the primary cause of miscarriage is aneuploidy that originated in eggs. The Aurora protein kinase (AURK) family has three members that regulate chromosome segregation during cell division. AURKA and AURKB are expressed in mitotic and meiotic cells, but AURKC expression is specific to meiotic germ cells. Distinguishing the roles of these isoforms is important to understanding the etiology of aneuploidy. During meiosis, AURKA and AURKC localize to the spindle poles and are important for establishing spindle bipolarity. AURKC also localizes on chromosomes, where it replaces AURKB as the primary Aurora kinase in the chromosomal passenger complex via binding INCENP, and prevents AURKA chromosome localization in mouse oocytes. However, the antagonism between AURKA and AURKC at the poles in meiotic cells is not understood. To explore this antagonism, we used an Aurora kinase inhibitor, ZINC08918027 (Zn), that prevents the interaction between AURKB and INCENP in mitotic cells. Our hypothesis was that Zn will inhibit the AURKC::INCENP interaction in mouse oocytes. If AURKC cannot bind INCENP, we expect it will shift its localization from chromosomes and concentrate at the poles. This shift will cause AURKC to antagonize AURKA, negatively affecting oocyte meiotic maturation. Our results from a western blot showed that the levels of AURK activity were altered in oocytes treated with Zn. Activated AURKA and AURKC levels in Zn-treated oocytes decreased compared to controls, but were not completely absent at high concentrations of Zn. Surprisingly, the activated AURKB level increased at higher doses. Based on these results, we suspect that there is a sub-population of INCENP-bound AURKA. We also suspect that there is a sub-population of AURKC that can be activated independently of INCENP. Furthermore, we observed a reduction in spindle length and increased incidence of spindle monopolarity or multipolarity as the concentration of Zn increased. These data together suggest that a strict balance of AURKA and AURKC activities is needed to secure spindle bipolarity and meiotic progression.

DELETION OF CUL3 IN THE MOUSE MAMMARY GLAND AND THE EFFECTS IT HAS ON TUMORIGENICITY

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Precise control of mitotic factors is crucial for the proper regulation of cell division. A major means of regulating proteins, including those involved in cell division, is by ubiquitin-mediated protein degradation, where a specific protein is targeted for destruction. The small molecule, ubiquitin, is attached to a protein, marking it for destruction by the proteasome. In the process of ubiquitination, an E3 ligase is used to determine which substrate

protein will be targeted. Cul3 is an E3 ligase which has been shown to target many different substrates for ubiquitination, by pairing up with different substrate adaptor proteins. One major substrate of Cul3 is cyclin E, which regulates the G₁/S transition of the cell cycle. Previous studies indicate that when there is decreased Cul3 activity, large amounts of cyclin E protein accumulate. When cyclin E is overexpressed, cells remain in S-phase for prolonged periods and are unable to proceed through mitosis normally. Some breast cancers and cell lines derived from breast cancers are shown to have overexpressed cyclin E, which results in a worse prognosis. We hypothesize this may be due to reduced Cul3 activity.

Therefore, we created a conditional knock-out of Cul3 in the mouse mammary gland to assess the effects of reduced Cul3 expression. Immunohistochemistry of Cul3-deficient tissue was utilized to evaluate effects of Cul3 loss on other cell cycle regulators, including p27 and p53. Additionally, we will investigate breast tumor cell lines to determine Cul3 and cyclin E levels. With this information, the levels of Cul3 will be silenced in different cell lines and the effects on tumorigenicity will be assessed for each cell line.

CHARACTERIZING THE ROLE OF CYP72A ENZYMES IN *ARABIDOPSIS THALIANA* UNDER COLD AND BACTERIAL STRESS

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As stationary organisms, plants have evolved a complex molecular system responsible for coordinating their metabolic activities. Environmental stressors, however, can affect the metabolic activities by causing gene up-regulation in a pathway that results in physiological and chemical alterations. Cytochrome P450s (CYPs) are a group of enzymes important in secondary metabolism that are known to aid plants by stimulating chemical pathways for defense metabolites. CYP72A is a subfamily found in flowering plants that appears to be important for defensive metabolism and removal of dangerous toxins. Gene expression data suggests that CYP72A enzymes are induced by abiotic and biotic stresses. To better understand the biochemical responses of plants, molecular biology and genetics techniques are used in *Arabidopsis thaliana* under combination of stresses. CYP72A15 is induced by bacterial and cold stress, while CYP72A11 and CYP72A13 that are close relatives are induced by abiotic stresses. Therefore, it is hypothesized that CYP72A enzymes are essential in defending the plants under a combination of stresses.

Plants with missing genes should be more susceptible to the combination of stresses since they cannot turn on the genes to protect themselves from the stressors. In order to determine the phenotypic differences between the wild-type plants and CRISPR mutants, cold stress was combined with *Pseudomonas syringae* infection. Individual gene mutations showed no differences, while multi-mutants showed differences in bacterial growth compared to that of the wild-type plants. While this work contributes to broaden our understanding of biochemical responses in plants, future research can help with understanding plant chemical diversity and help scientists better understand crop plant stress responses.

CLONING CelB2 ENDOGLUCANASE GENE INTO pET28a VECTOR FOR EXPRESSION IN *E.coli*

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Streptomyces lividans endoglucanase CelB2 is investigated as cellulose degrading enzyme for alternative fuel production. In this project, CelB2 gene was cloned into pET28a expression vector for expression in *E.coli*. pET vector-based expression system facilitates recombinant protein purification using metal affinity chromatography.

CelB2 gene was cloned out from pMAL vector that is currently used in the lab. Using pMal expression vector CelB2 is expressed as a fusion construct with maltose binding protein. Purification of this fusion construct requires protease digest and ion exchange chromatography in addition to affinity chromatography. These multiple purification steps result in low protein yield. CelB2 expression in pET vector-based system was tested. Purification of N-terminal His₆-tagged CelB2 was performed by Ni-NTA affinity chromatography. The results of purification were examined by SDS-PAGE and activity assay.

INORGANIC ARSENIC IN RICE-BASED PRODUCTS

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Rice and rice-based products are widely used by consumers worldwide. In 2012, the Consumer Products Safety Commission (CPSC) issued a report warning about the effects of high levels of inorganic arsenic in rice and rice products on human health. Rice plants are particularly good at absorbing arsenic from the soil because they grow in a lot of water. Inorganic arsenic is a common ingredient in pesticides and other products used in farming and can linger in the soil for a long time after it is used. It can be poisonous in high doses, but even small amounts can damage the brain, nerves, blood vessels, or skin and increase the risk of birth defects and cancer (McCarthy, 2016). According to a study published in January 2016, there were no regulations applicable to the concentration of arsenic in infant based rice products (Pastor, Antonio J. Signes., 2016). In 2017, the Federal and Drug Administration (FDA) set the level of inorganic arsenic in infant rice products in the United States to a maximum of 10 ppb (parts per billion). The FDA found that most infant rice cereal in the U.S. meets or is close to meeting this new limit. Out of 76 samples from retail stores in the U.S. in 2014, 47% met the standard, and 78% were at or below 10 ppb (Erickson, 2016). Clearly, there is an urgent need for compliance with regulatory limits for arsenic levels in rice-based products given its adverse effects on human health.

The quantitative determination of the levels of inorganic arsenic in rice-based products was carried out using an inexpensive, commercially available, and easy to use arsenic test kit. Different sample products (rice) were analyzed. The results were compared to the FDA standards in order to determine if inorganic arsenic contamination is in fact prominent in rice-based products. All samples measured well below the limit value of 10 ppb. White rice contained the highest amount of arsenic.

EFFECTS OF GARLIC MUSTARD (*ALLIARIA PETIOLATA*) ALLELOPATHY ON GERMINATION, GROWTH, AND MYCORRHIZATION IN WHEAT (*TRITICUM AESTIVUM*)

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Invasive plants species can cause significant financial damage to U.S. agricultural products annually and gain competitive advantage over native species through various mechanisms. Garlic mustard (*Alliaria petiolata*) is a non-native European biennial herb that was introduced by European settlers who valued its culinary and medicinal properties. It has proliferated in forest understories due to a number of adaptive traits, including allelopathy; the ability to produce and release chemicals that can directly or indirectly harm the fitness of other plants. The goal of this study was to assess how *A. petiolata* allelopathy may affect the fitness of wheat (*Triticum aestivum*). We hypothesized that *T. aestivum*, when grown in soils previously inhabited by *A. petiolata*, will have lower seed

germination rates lower root and shoot biomass, lower mycorrhization rates, and higher root:shoot ratio when inoculated with the mycorrhizae *Rhizophagus irregularis*. In the fall of 2019, surface soil samples were collected from a plot with abundant growth of first-year *A. petiolata* and from an adjacent plot without *A. petiolata* growth (control); these soil samples were used as a substrate to germinate *T. aestivum* and measure germination rates after 14 days. In a separate greenhouse experiment, commercial potting soil was grown with 0 (control), 1, or 3 *A. petiolata* seedlings (after cold-stratification) for 2 months, after which the plants were removed and the soil used to grow germinated wheat seedlings. After 1 month of wheat growth, the plants were harvested for measurements of biomass and root percent colonization by the mycorrhizal inoculant, *R. irregularis*. In the germination experiment, soils extracted from the *A. petiolata* field plot yielded a 4.4% decrease in total (after 14 days) germination and a 61.5% decrease in initial (after 1 day) germination for *T. aestivum* when compared to the control plot. In the greenhouse experiment, root:shoot ratio was 32% higher in the control/non-mycorrhizal treatment compared to control/mycorrhizal, 1-seedling/non-mycorrhizal, and 3-seedlings/non-mycorrhizal treatments. Percent root colonized by mycorrhizae was 65% higher in the control/mycorrhizal treatment compared to the 1-seedling/mycorrhizal treatment. Other metrics (root and shoot mass, total biomass, and root length) did not show any differences. The effects observed may be due to the interactions of *R. irregularis* with the allelochemicals produced by *A. petiolata*; *R. irregularis* colonization of *T. aestivum* roots appeared to be inhibited in some of the allelopathy treatments. Further research into the mechanisms of interaction and their significance in the field can be useful for determining best practices for the eradication of *A. petiolata* from its introduced ranges.

CHONDRICHTHYANS FROM THE LOWER CLAYTON LIMESTONE UNIT OF THE MIDWAY GROUP (PALEOCENE) NEAR MALVERN, ARKANSAS, USA WITH COMMENTS ON THE K/Pg BOUNDARY

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The Lower Clayton Limestone Unit (LCLU) of the Midway Group (Paleocene) near Malvern, Arkansas, contains an assemblage of chondrichthyans recently exposed by excavation for highway stabilization. Chondrichthyan teeth in this assemblage belong to at least 12 species including: *Ginglymostoma subafricanum*, *Carcharias* cf. *C. whitei*, *Carcharias* sp., *Odontaspis winkleri*, *Palaeohypotodus rutori*, *Palaeogaleus vincenti*, *Dasyastis* cf. *D. hexagonalis*, *Dasyastis* sp., *Hypolophites* sp., *Myliobatis* sp., *Rhinoptera* sp., and an indeterminate chimaerid. Locally, these chondrichthyans occur within a stratigraphic section directly above the Cretaceous-Paleogene (K/Pg) boundary that also contains chondrichthyans. This occurrence is uncommon in the global fossil record and provides an opportunity to: 1) assess chondrichthyan diversity across the K/Pg boundary in the Malvern region and Gulf Coastal Plain of southwestern Arkansas; and, 2) evaluate the timing of marginal to shallow marine chondrichthyan faunal turnover and extinction at a proximal location ≈ 1500 km from the Chicxulub, Mexico, K/Pg impact site. Observed patterns within this K/Pg stratigraphic section indicate that changes in chondrichthyan assemblages are primarily the result of sea level cyclicity and habitat losses that occurred across several million years.

SPIDER BIODIVERSITY IN THE HIGH MOUNTAIN RESERVE

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The goal of this research is to quantify the biodiversity of High Mountain Reserve focusing on the arachnids, particularly the spiders. Specific questions that were asked included: how many different types of spiders are there, and what types of methods are most useful for capturing them? In June and July, I hiked to High Mountain Reserve in Wayne, New Jersey every Wednesday to collect arachnids that were present. The collected specimen of that day was then identified and curated by storing them in alcohol in labeled vials. I found two different orders of arachnids- Araneae, or spiders and Opiliones, commonly called harvestmen or daddy-longlegs. The four families of spiders identified were Thomisidae (Crab spiders), with three species, Araneidae (Orb-weavers), with seven species, Salticidae (Jumping spiders), with three species and one Atypidae (Purse spider). Among the Opiliones, there were fifteen individuals. The collection of spiders were most commonly found near the trees, specifically on the trunk and the crevices of the branches. Majority of the spiders were captured roaming, but only a few were on their webs or in the process of building one. Opiliones, on the other hand, do not have silk glands thus they cannot build webs. This is the first year of a multi-year arthropod survey. This sample was limited by time, and could be improved by collected in late summer or fall when more spiders are mature and easier to identify. We will be collecting more data that will aid in the tracking of the spider diversity over time to see if there are changes in biodiversity and improve our understanding of how to best sample spiders in the habitats around William Paterson University.

A STUDY OF SYNTHETIC MELANIN AND ALOE VERA'S UV-ABSORPTION AND EFFICIENCY AS A POTENTIAL SUN PROTECTANT IN SKINCARE

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Recent media sources have reported that the currently marketed sunscreens are responsible for killing coral reefs due to their artificial composition which beg the question whether there may be a better alternative to protect human beings from the harmful ultraviolet rays of the sun. The purpose of this experiment was to create a more natural alternative for sun protection by way of aloe vera gel and artificial melanin, which is naturally produced in the human epidermis. The ultraviolet absorption levels of nine commercially available sunscreens were tested through UV-Visible light spectroscopy. The sunscreens were diluted in ethanol with a 0.25:100 ratio, respectively. The artificial melanin was dissolved in dimethyl sulfoxide (DMSO) and tested through UV-Vis spectroscopy. Aloe vera gel was extracted from an aloe plant and tested both with and without ethanol dilution. The melanin-DMSO solution and the aloe vera-ethanol solution were combined together through alternation of heat and centrifuging.

The results of the commercially available sunscreens showed that the sun protection factors (SPF) claimed on the sunscreen bottles do not follow a particular pattern. For some brands as larger factors should imply more ultraviolet absorption yet this was not always observed. The aloe vera gel proved to have UV absorption comparable with sunscreen with sun protection factor claims of thirty to fifty SPF. The aloe vera and artificial melanin proved to be very incompatible for use in combination, but a reading of the two combined in spite of limit of the very insoluble melanin gave a slightly better absorption than most of the sunscreens tested. The results of this experiment proved aloe vera to be a possible safer alternative for the currently marketed sunscreens, but artificial melanin being restricted by its very limited solubility would be an impractical alternative.

THE EXTINCTION OF THE MEGATOOCHED SHARK *OTODUS MEGALODON*: EVIDENCE FROM CLUMPED ISOTOPE THERMOMETRY

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The largest and most iconic fossil shark to have ever lived is *Otodus megalodon*. Fossil teeth and vertebra indicate this highly successful apex predator achieved lengths up to 20 meters, weights exceeding 20,000 kg, and global distribution throughout the Miocene and Pliocene (23-2.5 MYA). A general consensus indicates that the ability to thermoregulate in *O. megalodon* acted as a key driver for the evolution of gigantism that impacted its ecological role and success in surviving environmental changes. However, little agreement exists as to the primary cause for the disappearance of *O. megalodon* where models suggest predator-prey dynamics or environmental change resulted in extinction.

To address these alternative extinction hypotheses, ‘clumped’ isotope thermometry (CIT) was tested on modern shark teeth, with known thermoregulatory physiologies, to validate a previously reported calibration equation. Application of this calibration equation to fossils from *O. megalodon* reveal a high body temperature (~38-40°C), similar to cetaceans, which are known to thermoregulate. We hypothesize that, given *O. megalodon* was an apex predator, it would had to have consumed large quantities of prey in order to maintain such a high metabolic rate. Indeed, very high $d^{13}C$ values of the same *megalodon* teeth indicate that it was likely feeding at a very high trophic level. The high body temperature of *megalodon* favors the hypothesis that it had the thermoregulatory ability to withstand cooler waters during the Pliocene. Therefore, our preliminary results suggest that the extinction of *megalodon* was probably not driven by global cooling, but rather factors related to habitat loss produced by sea-level fluctuations and/or biotic changes such as prey availability and/or competition.

AGROCLIMATIC EFFECTS ON JASMONATE-MEDIATED DEFENSE IN MAIZE (*ZEA MAYS*)

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When attacked by pathogens or insect herbivores, plant reconfigure their metabolism to produce defense secondary metabolites. In maize, herbivore-induced biosynthesis of jasmonic acid (JA) and jasmonoyl-l-isoleucine (JA-Ile) trigger a cascade of transcriptomic and metabolomic responses targeted against the attackers. The level and pattern of accumulation of JA or JA-Ile affect the extent and duration of defense responses. Hence, studying variability in the jasmonate accumulation in natural populations provides the opportunity to understand plant defense responses at population level. The maize Nested Association Mapping (NAM) population is an excellent genetic resource that encompass huge genetic variability that is utilized to map the genetic mechanism behind phenotypic variability. Using this resource, it is possible to identify loci and/or gene(s) that affect quantitative traits. In the current study, we studied five selected members of the NAM populations that are adapted to grow in different agro-climatic regions (Texas, TX303; Wisconsin, W22; Ohio, OH43; North Carolina, NC350 and Missouri, MO17) to understand variability in jasmonate-mediated defense responses against larvae of *Spodoptera exigua* and *Spodoptera frugiperda*.

The five NAM lines collected from geographically diverse states in the US are used to test the hypothesis that the herbivore-induced accumulation of JA and secondary metabolites, and hence defense responses, are dependent on the geographic history of each maize line. To test variability in defense against insect herbivores, neonates (5d) of *S. exigua* were allowed to freely feed for five days on four-week old maize NAM plants and the masses of the caterpillars were determined. Overall, the data indicated variability in the caterpillar performance among the NAM lines; particularly, the caterpillars feeding on the TX303 lines gained significantly less ($p < 0.01$) mass. We measured the herbivore-induced JA and metabolite accumulation among the NAM lines to test whether the observed variability in caterpillar performance is correlated with defense traits. To simulate herbivory and induce the JA production, the third fully-expanded leaves of three week old maize plants were artificially wounded and treated with the oral secretions of *S. exigua* and *S. frugiperda*. The leaves were collected in liquid nitrogen to measure the levels of JA and secondary metabolites. Pending data analysis of phytohormone and secondary metabolite analysis, the data supports the hypothesis that plant defense against insect herbivory in NAM lines of *Z. mays* depends on their geographic range.

CHARACTERIZATION OF NEW CRYPTOCHROMES IN THE DINOFLAGELLATE *KARENIA BREVIS*

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Karenia brevis is a photosynthetic dinoflagellate responsible for the annual red tides in the Gulf of Mexico causing extensive marine life mortalities and human illnesses. Rhythmic cellular processes in *K. brevis* such as photosynthesis, carbon fixation, vertical migration, and phased cell division suggest a strong response to light. Cryptochrome DASH (KB CRY DASH) is the only known photoreceptor found in *Karenia brevis* to date. However, with *K. brevis*' newly expanded EST library we identified additional cryptochrome candidates. Using *K. brevis*' CRY DASH amino acid sequence as a query, 54 protein sequences were identified with E-values less than 1.0×10^{-5} that are homologous to other CRY DASH sequences, cryptochromes 1 and 2 (CRY 1 & 2), photolyases and other hypothetical proteins. Candidates were analyzed for the presence of conserved residues and narrowed down to eleven CRY DASH and seven CRY 1 & 2 candidates. Phylogenetic analyses provided additional evidence for having a distinct CRY 1 & 2 group from the CRY DASH candidates. This data provides evidence for the presence of new cryptochromes in *K. brevis* which will be further investigated. Characterizing new photoreceptor proteins will help in understanding *K. brevis*' cell cycle and possible control mechanisms of bloom proliferation.

TRPV1 AND THE HUNT FOR THE CB3 RECEPTOR

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Since the discovery of tetrahydrocannabinol (THC) in 1964, the world has experienced a new era of science and research surrounding *Cannabis* ^[1]. The plant contains a system that naturally produces molecules labeled as cannabinoids, terpenes, and flavonoids which has ushered in a new era of medicine. These molecules produced by cannabis plant have the potential to treat numerous diseases previously deemed "untreatable" by modern techniques. This was followed by the discovery of the human body's own natural cannabis-like system called the endocannabinoid system ^[2]. Originally, scientists believed that there was only one cannabinoid receptor (CB1R) localized throughout the body. In 1992 the cannabinoid 2 (CB2R) receptor was discovered in immune tissues and

throughout the peripheral system ^[3]. It turned out that CB2Rs are also localized in neurons and glia cells in the brain ^[9]. Now, thirty years later, there is a general consensus that there are other putative candidates, and a third cannabinoid receptor is being labeled as CB3 receptor (CB3R). The evidence points to the transient receptor potential cation channel subfamily V member 1 (TRPV1R) or commonly known as the capsaicin receptor. This is because there is a cross-talk between the endocannabinoid system and the TRPV1R ^[4].

Using a series of bioinformatics protocols, our researchers began to investigate this hypothesis to unravel the supporting evidence. This was done by obtaining the recent crystal structures of both the CB1, CB2 and TRPV1 receptors and replicating the docking, and analyzing the protein pocket to see any similarities between them ^{[5][6][7][8]}. These tools include UCSF Chimera, SwissDock, Swiss Target Prediction, Chem 3D Draw, and the RCSB Protein Data Bank. This also includes analysis of protein-ligand complexes, Gibbs free energy values from binding, and comparing them to known IC50 values. The new information obtained will help support evidence that TRPV1R may indeed be the CB3R, and that it may be reclassified and examined further for a deeper understanding of the endocannabinoid system in health and disease.

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NEXT GENERATION SEQUENCING ANALYSIS OF DEAD WOOD AS A METHOD TO STUDY DIVERSITY OF SAPROXYLIC FUNGI FOR BIODIVERSITY ASSESSMENT

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Dead wood is an important component to the conservation of biodiversity in forests. When left to decompose on the forest floor, it protects soil from erosion, promotes nutrient cycling, and provides a unique ecological niche for decomposers such as fungi. The species richness of dead-wood inhabiting fungi can therefore serve as an indicator of the overall health of the forest. Most species of dead-wood inhabiting fungi are cryptic and do not always produce visible fruiting bodies for study. The goal of this project to evaluate new techniques that can be used to quickly assess the diversity of undetectable species present in decomposing wood. Samples of tissue from trees in varying stages of decay were collected near Elizabeth river, NJ and mixed, then DNA was extracted, PCR of ITS gene marker performed and sent for Next Generation Sequencing (NGS). Resulting DNA sequences were

analyzed using SCATA pipeline and fungal species or OTU identified based on NCBI database. The results are to demonstrate how many dead wood trunks would require NGS assessment in order to collect information on dead wood fungi representative for the whole location.

EVALUATION OF NEXT GENERATION SEQUENCING TECHNIQUE AS A METHOD TO ASSESS SAPROXYLIC FUNGAL COMMUNITY COMPOSITION

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The focus of our research is to evaluate the potential of Next Generation Sequencing (NGS) method in identification of dead wood fungal species from a specific location, such as an urban park. In North America the research on biodiversity of dead wood fungi is still developing and there is no complete database so far. For our project, 37 fruiting bodies of various dead wood fungi were collected from Ocean County Park during October 2017. The species were identified morphologically where possible, with the conformation by DNA-barcoding. For the barcoding, DNA was isolated from each individual fungal body using DNeasy PowerSoil kit, then amplified by PCR using ITS specific primers to obtain a fragment of ITS gene, which serves as a barcode in fungal identification. This fragment was sequenced, the resulting sequence was compared to the database of fungal ITS sequences in NCBI portal using BLAST and species identified. As a result, a local database of the species found in Ocean County Park was created. NGS sequencing was used as a method allowing metabarcoding of a mixed DNA sample. This method allows to identify species all at once, without individual sequencing. The efficiency and reliability of this method in comparison to the individual species identification is discussed.

THIRD GENERATION SEQUENCING OF EGFR MRNA

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Glioblastoma multiforme (GBM) is the most common malignant primary brain tumor in adults with a mean survival of 14-15 months. 60% of GBM tumors are characterized by the dysregulation, upregulation or constitutive activation of epidermal growth factor receptor (EGFR), leading to tumor cell proliferation. With the advances in nanopore sequencing technology, we have developed a strategy to evaluate alternative splicing and polyadenylation patterns in the EGFR transcript. Our goal is to isolate alternatively spliced and polyadenylated lower abundant EGFR transcripts to characterize the expression of this oncogene. GBM cell lines, SKMG-3, U87MG, U118, and A172, were cultured in multi-layer flasks with total cell confluency of 87,500,000. RNA was isolated using the TRIzol™ Reagent RNA extraction protocol. Biotinylated DNA probes, 90 nucleotides in length, targeting EGFR mRNA exon junctions were used to capture the mRNA transcript. Captured transcripts were pulled down with streptavidin dynabeads, washed and purified. Generation of cDNA by reverse transcription with poly-dT versus EGFR specific primers were compared. PCR analysis demonstrated that biotinylated DNA probing of the EGFR mRNA transcript is a reliable method to retrieve gene specific mRNA. Repeated biotinylated DNA extraction experiments established an optimal molar ratio of 1:10:100 for our target mRNA: to DNA probe: to Dynabeads. EGFR mRNA was captured at a desired concentration of 66.7 ng/μL, polyadenylated using E. Coli Poly(A) Polymerase, purified with Agencourt magnetic beads and stored at -20°C for sequencing.

Our goal is to sequence EGFR transcripts without bias associated with reverse transcription and PCR. The Oxford Nanopore Technology MinION sequencer and accompanying cDNA-PCR sequencing kit provides VN primers

that encode transcript switching oligo (TSO) sequences to the 5' end and 3' end of each polyadenylated molecule during reverse transcription. EGFR mRNA samples are barcoded by cell type using the PCR Barcoding Kit (Oxford Nanopore Technology). The cDNA product is amplified with strand-switching oligo primers complementary to the TSO sequence. This technique generates complete second strand synthesis of the original cDNA strand. We expect full-length cDNA reads with higher yields than traditional cDNA-synthesis. To study different EGFR mRNA isoforms resulting from alternative splicing we will use the FLAIR (Full-Length Alternative Isoform analysis of RNA) bioinformatic pipeline for the correction, isoform definition, and alternative splicing analysis of our nanopore cDNA sequencing reads. By identifying lower abundant, less common variants of EGFR transcripts and alternative isoforms of EGFR, we expect to identify candidates for induction through antisense therapeutics to activate alternative splice sites through recruitment of splicing activators or inhibit critical splicing elements through the recruitment of splicing inhibitors.

DEVELOPMENT OF BSL1 ORGANISM REFERENCE TABLE VIA KIRBY-BAUER TESTING ON MUELLER-HINTON II AGAR

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In the development of BSL2 organism references already available for Kirby-Bauer tests, susceptibility and resistivity of many pathogenic organisms towards varying antibiotics are known already. This process can help in diagnosing what prescription to provide for a sick patient. However, the ability to do this same aspect in non-pathogenic organisms, BSL1, has not been developed yet. The ideology behind not having a reference in Kirby-Bauer testing for these organisms is that they follow the same patterns of their pathogenic relatives. However, with our research we expect find that this fact is not true in comparison to drug susceptibility versus resistivity of BSL1 and BSL2 relative organisms. With these findings, further referencing for BSL1 organisms can be developed in helping provide further understanding of non-pathogenic organisms in the college setting, where these are the focal organisms.

PATHOGENIC BACTERIA ON THE RISE IN HUDSON RARITAN ESTUARY

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Excess wastewater after rainfall leads to combined sewer overflows (CSOs) that contain untreated or partially treated waste with high toxicity and increased pathogenic bacterial concentration. CSOs have a high impact on water quality leading to compromised drinking water supplies and endangered human health. Our project focuses on studying the concentrations of pathogenic bacteria at selected Hudson Raritan Estuary (HRE) sites in correlation with nearby CSOs and rainfall events. Weekly testing and monitoring of water were conducted in designated sites for a period of 15 weeks. Modern bacterial identification techniques were used in the laboratory to determine the concentration of fecal coliform bacteria and Enterococcus bacteria. High concentrations were recorded at designated sites and days, showing poor water quality and the presence of potential pathogenic bacteria. The results of this study will not only inform management practices but will also become an important resource for decision-makers to advance environmental protection.

STUDY OF THE ANTIBACTERIAL ACTIVITY OF BLACK CUMIN SEEDS USING MULTIPLE EXTRACTION METHODS

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Black cumin (*Nigella sativa*), a widely used spice in the South-Asian and Middle Eastern cuisine, is a popular traditional medicine in those regions to treat a plethora of illnesses. The purpose of this study was to investigate if this “miracle herb” possesses any antibacterial properties, and to find the best method of extraction to maximize those properties. Seven different extraction processes were used to separate the bioactive compounds of black cumin, including oil, water, alcohol and acid-digestion extractions. Both whole and crushed seeds were extracted, and the organic as well as the aqueous layers of the extracts were separately tested. Various concentrations of the extracts were tested on *E. coli* colonies using the Kirby-Bauer disc diffusion method to measure the susceptibility of this bacteria to these extracts. Vancomycin was used as a positive control, and an empty disc as the negative control. For all the sample of the extracts, the inhibition zones were insignificant or zero, which indicates that the extracts did not prevent *E. coli* growth. Hence, this study concludes that black cumin extracts made using the above mentioned methods do not display any antibacterial properties against the bacteria tested. The observed medicinal effects of this herb is therefore not caused by its direct elimination of bacteria from the body, but possibly for its antioxidant, anti-inflammatory and immunity-boosting properties.

KILLING POTENTIAL OF PORPHYRINS ON MICROBES

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Porphyrins are light reactive chemical compounds that when exposed to light produce a reactive oxygen species with the potential to inhibit the bacterial growth of both gram positive and gram negative bacteria. Porphyrins are made up of heterocyclic macrocycle organic compounds, composed of modified pyrrole units. Synthesized porphyrin used in this experiment, synthesized by the Elshaer lab, to inhibit the growth in a gram negative bacteria like *Escherichia coli* and gram positive bacteria like *Staphylococcus epidermidis*. Gram positive bacteria have a single plasma membrane, while gram negative bacteria have a second plasma membrane. Porphyrins are able to disrupt the cell membrane of gram positive bacteria, but tend to have difficulty affecting gram negative bacteria because the oxygen reactions have issues reaching it. In order to determine porphyrin bactericidal activity other labs have utilized day old bacteria stored at 4°C (Carvalho, CMB., et al. Functional Cation Nanomagnet - porphyrin Hybrids for the photoinactivation of Microorganisms. *ACS Nano*. 2010;4(12):7133-7140) (Merchat, M., et al. Meso-substituted cationic porphyrins as efficient photosensitizers of gram-positive and gram negative bacteria. *J of photochemistry and photobiology B: biology*. 1996;23:153-157). In this study we utilized optical density during early logarithmic growth to determine forming unit# per ml (CFU/ml) of actively growing bacteria used to determine porphyrin bactericidal activity. The results of these experiments show that porphyrins at a concentration of 5mM show complete killing of both gram positive and gram negative bacteria. At a concentration of 0.5mM porphyrin continues to show killing potential of gram positive samples but gram negative bacteria show higher survivability. At concentrations of 0.05mM both gram negative and gram positive bacteria show survivability. Future tests are planned to use different synthesized forms of porphyrin, experiment on different gram negative and positive species, as well as examine killing potential and growth conditions like more warm environments.

CHARACTERIZATION OF A NEURO-IMMUNE-MICROBIOME ENDOCANNABINOID AXIS

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The endocannabinoid system (ECS) and its related bioactive compounds have been known to participate in numerous physiological processes that include immune and metabolic regulatory functions contributing to the maintenance of an organism's homeostasis. It is also known that the gut microbiota plays a critical role in immune system function. Considering the accumulating evidence of an interaction between the immune system, the gut microbiota, and the ECS, we hypothesized that a mouse neuro-immune-microbiome endocannabinoid axis provides anti-inflammatory benefits. We generated *Cnr2*-floxed mice to produce DAT-*Cnr2* and Cx3cr1-*Cnr2* conditional knockout (cKO) mice with deletion of CB2 cannabinoid receptors from dopamine neurons and microglia respectively. The cKO mice were used alongside a C57BL/6J control group for these experiments.

Experimental groups of mice were peripherally injected twice, 6 hours apart, with sub-acute doses of lipopolysaccharide (LPS) from *Salmonella* to cause a systemic inflammatory response. Behavioral data was collected using the elevated null maze and the locomotor activity monitor tests. We report that after the LPS treatment, locomotor activity of the animals was reduced with C57BL/6J < Cx3cr1-*Cnr2* < DAT-*Cnr2*. A similar pattern was observed in the test of anxiety. After 15 hours, all mice were euthanized by cervical dislocation, and forebrains were quickly extracted and preserved at -80°C. An antibody array targeting 23 neuroinflammatory cytokines was then performed on the brain homogenates and analyzed using a chemiluminescent western blot.

At the time of behavioral testing, fecal pellets were collected for microbiological testing and analysis of *Akkermansia muciniphila*, a potential indicator species for an anti-inflammatory mouse-gut microbiome. The dry weight and moisture content showed treatment and mouse-strain differences, indicating a differential gut-function response. A nested PCR protocol was used to improve sensitivity and specificity, and bias was limited by using a Real-Time PCR analysis of the first round to ensure that the amplification did not leave the exponential phase. We quantified *A. muciniphila*-specific 16S sequences in a nested SYBR Green qPCR protocol, with *A. muciniphila* DNA for concentration standards. Analysis of total bacterial content of the feces and the relative abundance of *A. muciniphila* supported the gut-function observations.

AMINE FUNCTIONALIZED SILOXY GELS FOR CATALYSIS

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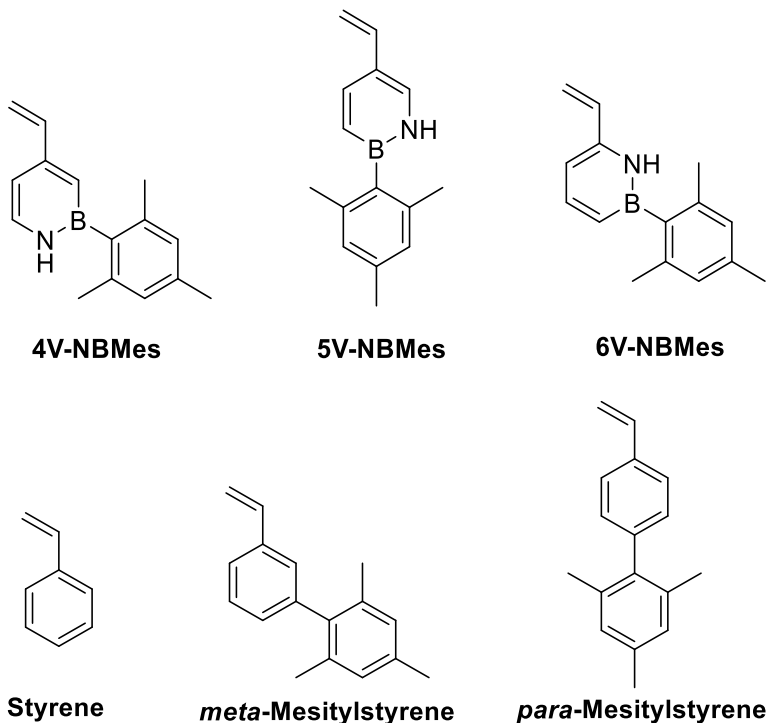
Preparation of new material can be approached by Sol-gel process. The essential aim for this research was to prepare a new material using compounds containing silicon. The purpose was to understand the chemistry involved during the preparation of the solid products by Sol-gel process. . In this presentation, a synthetic process in which amine functionalized siloxy gels are synthesized in a one step process will be described. The preparation of the silanes is done through the reaction with a silane, and halosuccinimide (NXS) forming a porous gel. The first step which was done was to learn how to make gel using different compounds. Sol-gel process is a chemical solution process used to make ceramic and glass materials in form of powders or fibers. When the solvent from the sol begins to evaporate the ions left begins to join to form a gel. This hydrolytic polycondensation reaction of

a Si-OR bond is a nucleophilic substitution of oxygen or the Si-OH bond on the metallic center of another molecule which leads to the formation of the Si-O-Si bonds. The condensation between the silane groups and ethoxy groups creates siloxane bridges (Si-O-Si) that form entire silica structure. We will present our detailed characterization studies. The final product properties are also investigated to develop a good understanding of gelation phenomenon. The silica gel synthesized was added to the p-tert-butylcalix[4]arene to act as a catalyst. Structural and spectroscopic analysis of these samples was carried out by NMR, TEM, SEM, FT-IR techniques.

AZABORININE POLYMERS AS B-N ANALOGS OF POLYSTYRENES

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Polystyrene and its derivatives are very significant in the polymer industry. There is a high demand for the development of analogs of styrene that are polymerizable and exhibit new functional properties. Selective replacement of carbon-carbon for the polar, isosteric, and isoelectronic boron-nitrogen bond has the potential to expand the reactivities and physical properties of polystyrene materials. Advances in the synthesis of 1,2-azaborines provide special opportunities towards their application in biomedical research, material science, nanotechnology, synthetic chemistry, and transition metal-based catalysis. In this project, we examined the polymerization and polymer physical properties of B-mesityl-4-vinyl-1,2-dihydro-1,2-azaborinine (4V-NBMes), B-mesityl-5-vinyl-1,2-dihydro-1,2-azaborinine (5V-NBMes), and B-mesityl-6-vinyl-1,2-dihydro-1,2-azaborinine (6V-NBMes)—each with the BN moiety in a different position relative to the polymer backbone. In addition, we prepared the respective all-carbon polystyrene counterparts and compared their properties to those of the B-N polymers.



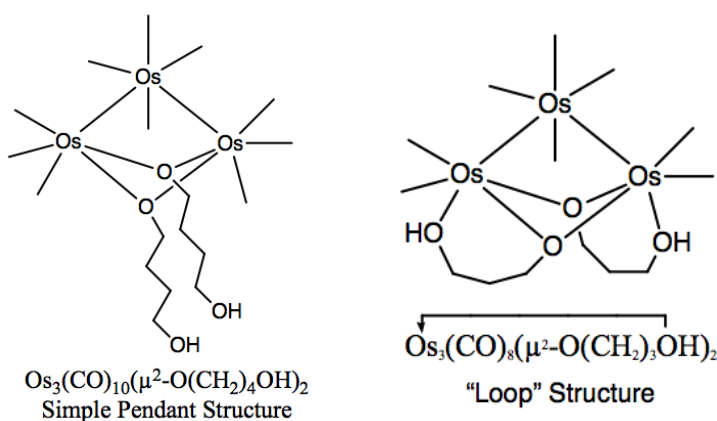
REACTIONS OF Os₃(CO)₁₀(OEt)₂ WITH DIFFERENT DIOLS

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Our investigations of the alkoxide substitution reactions Os₃(CO)₁₀(OEt)₂ with 1,3 propanediol and 1,4 butanediol we have found that 1,4 butanediol reacts to form Os₃(CO)₁₀(μ²-O(CH₂)₄OH)₂, a simple pendant structure in which one of the alcohols of the diol replaces the ethoxide seen in the figure below. In contrast, 1,3 propanediol reacts to form a compound believed to be which one end of the diol forms an alkoxide bridge and the other alcohol coordinates to one osmium to form a ring, or “loop” structure seen in the figure below.

Immediately after the formation, the pendant product can be generated by bubbling carbon monoxide into the solution.

Characterization of products is based IR to identify the carbonyl pattern of (CO)₁₀ versus (CO)₈ and H¹-NMR



HIGHLY EFFICIENT, RARE-EARTH-FREE SN(IV) COMPLEXES FOR POTENTIAL ORGANIC LIGHT EMITTING DEVICES

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Rare earth metal organic complexes have been widely developed for efficient organic light emitting diodes (OLEDs) because of their tunable optical and electrical properties. However, rare earth element-based phosphors are expensive and in limited supply. For this reason, efficient rare earth free metal complexes have brought much attention, including group IV and V. Tin (Sn) coordinated compounds have shown promising phosphorescent phosphor materials because of their versatile coordination and geometry. Herein we develop new efficient Sn (IV) complexes with 8-hydroxyquinoline derivative ligands, namely SnL₂X₂ (L=8-hydroxyquinoline and 5,7-dimethyl-8-quinolinol; X= Cl or F), which exhibit green emission applicable in the fabrication of organic light emitting device. To our knowledge, we first modified the molecular structure of Sn complexes via halide exchange reaction by utilizing ammonium hexafluorophosphate (NH₄PF₆) as a fluorine source to incorporate fluorine in Sn

complexes. Furthermore, the fluorinated Sn complexes enhance emission properties. The structural, optical, thermal, and electrochemical properties of Sn complexes were characterized by Single crystal x-ray diffraction, UV-Vis spectroscopy, fluorescence, thermal gravimetric analysis, and cyclic voltammetry (CV). We also fabricated solution processed Sn metal complex thin films for potential OLED application, which could lead to low cost, highly efficient light-emitting phosphors.

THE EFFECT OF VARYING CONCENTRATIONS OF COAGULATION AGENT IN RELATION TO LEAD ION REMOVAL USING BIOMATERIALS

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Lead compounds can be found in everyday products one uses such as paints, batteries, and gasoline. While the lead levels of these products are particularly low, lead can become a devastating problem when found in high levels. Even low exposure to lead can lead to kidney problems, intellectual disabilities, and cardiovascular complications. It is safe to say that lead exposure can be dangerous at any level. One factor that contributes to a high concentration of lead is the corrosion of lead pipes which allows lead to leech into drinking water. Biomaterials have been explored as a way to adsorb lead from aqueous solutions for they possess promising qualities such as biocompatibility, abundance, low cost, and a favorable chemical composition. Previous results show that there is a positive correlation between the percent cellulose in a biofilm and the percent lead removal, as well as there being a morphological effect related to the removal of lead ions in water. The purpose of this study is to determine how the morphology and chemical composition of regenerated cellulose and *Bombyx Mori Silk* biofilms will affect lead ion adsorption capabilities in relation to changes in the concentration of coagulation agent. These efforts will be measured using fourier-transform infrared spectroscopy, electrochemical analyzer, and X-ray scattering.

METHOD DEVELOPMENT FOR MEASURING THE CRITICAL MICELLE CONCENTRATION OF AEROSOL-OT IN A TWO-SOLVENT SYSTEM USING FLUORESCENCE SPECTROSCOPY

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The project aimed to develop an analytical method for measuring the critical micelle concentration (CMC) of sodium dioctyl sulfosuccinate (AOT). In a two-solvent system of hexane (nonpolar), the main solvent, and tetrahydrofuran (THF, polar), the minor solvent, reverse AOT micelles were prepared. The formation of micelles was monitored using the fluorometric probe Coumarin-120 (C-120). Studies with varied AOT concentrations were performed to encompass a wide range of values, which included the known CMC of AOT. A solvatochromic blue shift of emission maxima was observed indicating encapsulation of the fluorophore due to increased polarity in the core of the micelles. From the emission maxima of the probe, the experimental CMC of AOT was determined. It was concluded that the experiment was not precise due to a high relative standard deviation (30%). However, the percent error of the average experimental CMC (4.5%) indicated accuracy of the data. It was also concluded that the method needed further modification in order to precisely determine the experimental CMC of AOT in hexane.

INVESTIGATING THE COMPLEXES OF RHODANINE WITH NOBLE METALS

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In our recent publication, we have reported a template free green synthesis of nano-micro spheres of polyrhodanine with copper salt. These nanospheres have positive charge localized over its backbone and we have experimented successful degradation of methyl orange dye to about 80% within 3 hrs with polyrhodanine microspheres. These high-quality conducting polymers with metal nanoparticles have interesting applications like catalysis, sensors, colored films and memory devices. In addition, these composite materials have unique properties of electrical conductivity, environmental and thermal stability, and protection against corrosion of metals in aqueous medium. They behave as biosensors and can transfer electric changes and serve as immobilizing matrices for biochemical reactions.

We are now investigating complexes of Noble metals (Au, Pd) with Rhodanine and studying their morphology via Infra-red (IR) spectroscopy, SEM (Scanning Electron Microscopy) and TEM (Transmission Electron Microscopy) analysis. Rhodanine-Pd complexes analyzed via IR and UV-vis spectroscopy shows great resemblance to the complexes formed from Rhodanine and Cu. SEM analysis displays spherical structures of the product same as that observed for Rhodanine-Cu complexes. In this presentation, Rhodanine-Noble metal complexes and their role in the polymerization of Rhodanine and in the extraction of azo dyes/heavy metals from waste water will be presented.

MMPs, TIMPs AND ACTIVATORS

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Matrix Metalloproteinases (MMPs), are zinc-dependent endopeptidase that are capable of degrading all kinds of extracellular matrix proteins and can process a number of bioactive molecules. MMPs have been targets for the development of therapeutics to modulate their activities in the diseases like cancer, wound healing etc. Our lab has discovered exogenous activators to an active form of a collagenase (MMP-1). Here, we are studying effects of activators, tissue inhibitors of metalloproteinases (TIMPs), and reducing agents on the activities of MMPs. Our results indicate that these molecules can modulate the binding of each other.

COMPUTATIONAL INVESTIGATION OF CURCUMIN IN GASEOUS STATE AND DIFFERENT ORGANIC SOLVENT USING QUANTUM MECHANICS AND SEMI-EMPIRICAL METHODS

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The compound investigated with computational chemistry calculations was “Curcumin” which is an organic compound, it consists of two benzene rings, two ketonic oxygens and two trans-hydroxyl groups attached to it. Curcumin is found in turmeric root and is a relative of ginger. Computational investigation shows that the semi-

empirical methods AM1 (Austin model 1 method) and PM3 (Parametric Method 3) give approximate values of heat of formation, molecular energy, molecular orbitals and difference in molecular energy levels between Highest Occupied Molecular Orbitals (HOMO), Lowest Unoccupied Molecular Orbitals (LUMO), and the vibrational frequencies of curcumin. Same approximation in values is found in calculations run with HF (Hartree-Fock) and DFT (Density Functional Theory) methods which include basis set like Basic, Routine and Accurate. Computational results of curcumin were also obtained in different solvents like water, methanol and cyclohexane. Analysis of dipole moment values in different solvents shows that the semi-empirical method: AM1 and PM3 were in agreement with each other. Same results were observed for HF and DFT methods. Calculations of molecular orbitals energy, detail structure of HOMO and LUMO were obtained and some investigations were done to determine the site of reactivity for an electrophilic attack by metals like Al (III), Fe (III) and Cu (II). Mullikan charges obtained from computational results predict that the oxygen atom is the reactive side in curcumin molecule for an electrophilic attack. To determine the role of aluminum in Alzheimer Disease, curcumin-aluminum complex was studied. It was the ketone oxygen where aluminum forms the complex-ligand. Curcumin to aluminum was 2:1. Aluminum (III) Curcumin Complex was formed and the computational results were successful with quantum mechanics methods because the values for heat of formation were in agreement with experimental results.

A NEW SEQUENCE OF TEACHING LABORATORY EXPERIMENTS THAT UTILIZE A 60MHZ BENCHTOP NMR SPECTROMETER IN ORGANIC CHEMISTRY COURSES

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The recent development of relatively inexpensive benchtop NMR spectrometers has allowed the inclusion of hands-on experience of this important technique into many undergraduate teaching laboratories. However, because of the low field strength of their magnets, the spectra obtained from benchtop NMR spectrometers have broad peaks and, consequently, often poor peak separation making their interpretation difficult for all but the simplest molecules.

We have developed new experiments for our organic laboratory courses, based around the high-yield syntheses of a series of diimine compounds, all of which give clear 60 MHz ^1H (and 15 MHz ^{13}C) NMR spectra. The spectra of these compounds show both characteristic chemical shifts for the functional groups present and unambiguous coupling patterns. Students can, therefore, obtain NMR spectra from their own samples and then determine the molecular structure of their products.

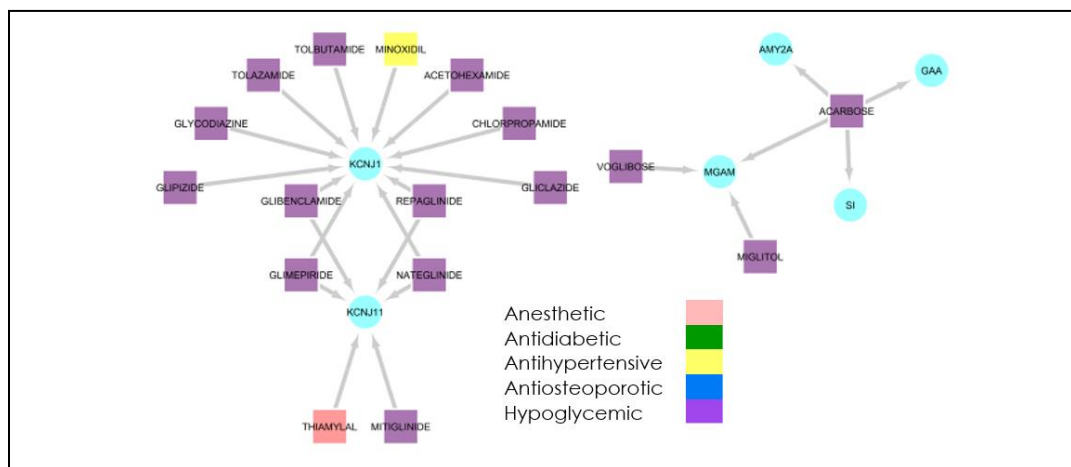
Our poster will give experimental details of the preparation of the diimine compounds and show their ^1H and ^{13}C NMR spectra obtained on a 60 MHz benchtop NMR spectrometer. The elucidation of the compounds' molecular structures from these spectra will be fully described.

METHODOLOGIES FOR ANALYZING BIOLOGICAL NETWORKS WITH A FOCUS ON DRUG-DRUG INTERACTIONS, DRUG-DISEASE ASSOCIATIONS, AND CHEMICAL-DISEASE ASSOCIATIONS

ARIEL EIGHMEY (MCC) *Φ

Ariel Eighmey Dr. Sutapa Ghosh and Dr. Phalguni Ghosh
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The molecules in a biological system interact with each other and form molecular complexes, modules or pathways that carry out various biological functions. High-throughput research techniques have generated enormous amounts of data on many biological networks. The challenge now is to interpret the big volume of data and extract relevant information that could be of used to improve healthcare and pharmaceuticals. Online repositories, such as KEGG, Reactome, STRING and many more host a massive amount of data that can be readily represented as a network and then analyzed. Cytoscape is a free software platform that allows the investigation and visualization of integrated diverse networks. It is adaptable and expandable with over 300 applications that can be incorporated for numerous research requirements. Using Cytoscape to study biological networks, begins with building a combined network for the topic of interest and mapping the curated network for analysis. Being able to visualize combined and curated data allows the researcher to understand and evaluate targeted information that would otherwise be cluttered in multiple massive networks. In this study, we have looked at drug-drug interaction networks and drug-disease associations networks. Specifically, we have analyzed and built networks showing (a) single protein molecule being targeted different classes of drugs (b) same drug interacting with multiple (c) chemical-disease associations (d) drug-disease associations amongst common drugs for pain and cancer. These biological networks display the potential cross-reaction between drugs and give a visual representation of the side effects of some common drugs.



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DECORATIVE SOLAR CELLS

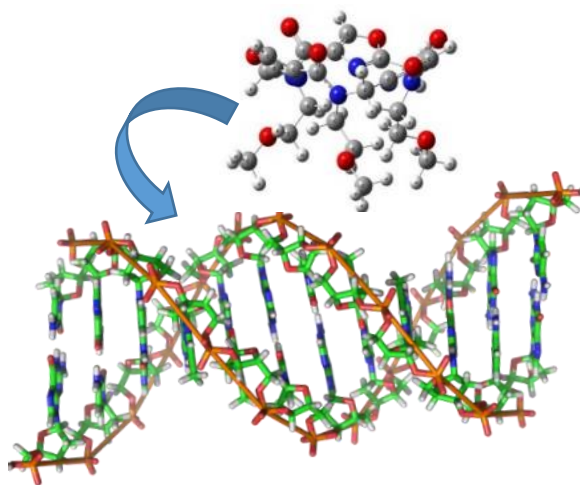
Raghad Nofal and Dr. Jonathan Foley
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The design of decorative solar cells that have color in the visible part of the spectrum while maintaining high efficiency and low cost facilitates the integration of PV technology directly into commercial and residential buildings. Here, we will describe a different designs of decorative solar cell applications, such as perovskite and silicon solar cells, whose decorative appearance derives from multi-layered coatings. We will use WPTherml, a software package developed at William Paterson University for designing materials with tailored optical and thermal emission properties, to characterize and design these coatings. We will investigate the impact of structure on both the appearance and efficiency of decorative solar cell by adding or removing different layers of nanostructure with different thickness using scalable, inexpensive material coatings.

PEPTOID MACROCYCLES AS POTENTIAL ANTICANCER AGENTS: THE ROLE OF IONS IN CONFORMATIONAL EQUILIBRIUM

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Dr. Yana Kholod Kosenkov and Dr. Dmitri Kosenkov
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In the field of cancer research, the toxicity of anti-cancer drugs is an urgent problem. Ligands, which are small organic molecules, have been proposed as potential anti-cancer drugs, since they bind to DNA macromolecules in telomeres to inhibit tumor growth. The cytotoxicity of these potential drugs is estimated based on the selectivity of their binding to specific DNA conformations. The current research focuses theoretically modeling ligands that have shown promise as anti-cancer drugs with low toxicity. Specifically, various oxazole and thiazole peptoid macrocycles are being considered. Different molecules belonging to this class, depending on their structure and substituents, bind in an extremely selective fashion to certain DNA forms, like the double-helix, parallel, anti-parallel, G-quadruplex, and mixed-type hybrid structures. Such oxazole/thiazole-based macrocycles can be chosen for optimal binding to these specific DNA conformations, and therefore, the subsequent targeted inhibition of telomerase in cancer cells.



To study conformational equilibrium in those designated sets of oxazole and thiazole peptoid macrocycles and to explore effects from the surroundings, focusing on the role of cations, a computational chemistry study has been conducted. Initially, a comprehensive sampling of various conformations for the predetermined oxazole/thiazole-

based macrocycles was performed. Low energy conformations have been located for neutral peptoid macrocycle molecules as well as for their complexes with one and two sodium ions. The simulations have been conducted in solution to replicate the effects of the environment. It has been determined that sodium ions stabilize certain conformations significantly. Furthermore, we anticipate that the inclusion of cations in our ongoing examination of ligand-DNA binding will promote strong affinity of the ligands under study to DNA molecules.

THERMOELECTRIC GENERATORS: A PROTOTYPE AND COMPUTER MODEL

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The work presented here has two components: experimental thermoelectric prototype and a computer model written in Comsol Multiphysics to model and optimize the prototype. Thermoelectric materials use heat energy as input and give off electric energy as output. The effect is called the Seebeck effect. The reverse effect, using electric energy to extract heat is called the Peltier effect. The goal of the prototype is to test the Seebeck effect in a bismuth telluride array of semiconductor blocks electrically connected in series. The Computer model and the Prototype match very well in both water cooled and not cooled set-ups. The voltage generated goes up by at least a factor of three if the TEG is cooled efficiently. Thermoelectrics are an environmentally clean and efficient way to harvest waste heat and turn it into electricity.

MODELING IMPACT OF INTERMOLECULAR INTERACTIONS OF LPG— ALCOHOL MIXTURES ON STABILITY OF PHYLLOSILICATES: TOWARDS IMPROVEMENT OF DRILLING FLUIDS

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Dr. Dmytro Kosenkov and Dr. Yana Kholod
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American Chemical Society – Petroleum Research Fund; Research Corporation for
Science Advancement – Cottrell Scholar Award; Monmouth University School of Science

In recent years of fracking, the issue of borehole failures from shale instability has been increasing. Shale instability is caused by intermolecular interactions of polar water-based drilling fluids with shale minerals. Identifying this issue, it was proposed to use liquefied petroleum gas (LPG) based drilling fluids in fracking. LPG is a mixture of propane, butane, and other nonpolar components that can be safely recovered from the borehole. This project aims to solve issues of shale instability by improving a waterless fracking method that uses LPG-alcohol mixtures instead of water-based drilling fluids. Using computational chemistry methods, such as density function theory (DFT) and fragment molecular orbital theory (FMO) intermolecular interactions between components of LPG mixtures and phyllosilicates that create shale instability are identified and analyzed. These non-covalent interactions include Coulomb electrostatic, polarization, exchange-repulsion, and dispersion. Bulk steric factors that impact LPGphilosilicate interactions are also taken into consideration. By using quantum DFT calculations, optimum configurations of the molecules separately and bound in the gas-phase are predicted. Performing an FMO investigation of the optimized LPG-based mixtures and phyllosilicate crystals will allow us to understand which intermolecular interactions are most prevalent in these systems. If successful, it may be possible to integrate the results into the field of fracking to solve the issue of borehole failures from shale instability and to provide a safe waterless drilling fluid.

MULTI-LAYER STRUCTURE OPTIMIZATION USING WPTHERML

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The Design of materials with tailored thermal radiation properties is a key challenge for a number of renewable energy and energy efficiency applications. We will describe a computational materials design engine to help in the design of multi-layer nanostructures for a variety of thermal energy applications, named Wptherml. Wptherml can make an impact including Solar Thermophotovoltaics (STPV), Passive cooling, and efficiency incandescent lighting. These applications are important in highly efficient energy production and energy savings. In addition to materials design we will describe how Wptherml can be used to optimize structure design. We will present results demonstrating the merits and ease of use of this computational software.

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