CALIFORNIA STATE UNIVERSITY LONG BEACH

College of Natural Sciences and Mathematics

STUDENT RESEARCH SYMPOSIUM

BOOK OF ABSTRACTS

Friday, September 15, 2017

Supported by: Jensen Student Access to Science and Math Center &
College of Natural Sciences and Mathematics

Table of Contents

California State University Long Beach

Student Research Symposium

Funding support for this event provided in part by:
College of Natural Sciences and Mathematics, CSULB
Jensen SAS Center and G2 Lab
National Science Foundation (NSF)
National Institutes of Health (NIH)

A Special Thanks to: Our Research Program Faculty Mentors, Jensen Student Access to Science and Mathematics Center, G2 Computer Lab, Academic Advising Center, Peer Mentors, Department of Psychology, University Student Union, Papa John's Pizza, Leon Wood, Daniel Ames, Lane Olsen-Cooper, Margaret Karteron, Brent Scheiwe, Dr. Barbara Taylor (Associate Dean of College of Natural Sciences and Mathematics), Dr. Krzysztof Slowinski (Associate Dean of College of Natural Sciences and Mathematics), and Dr. Curtis Bennett (Dean of College of Natural Sciences and Mathematics).

Without their support throughout the year, this event would not be possible.

Symposium Booklet and Event

The Student Research Symposium is held in the University Student Union (USU) Friday, September 15th, 2017. This event, held by CSULB, College of Natural Sciences and Mathematics is open to undergraduate and graduate participation. The research being presented at this event is from on-campus research and/or from summer research experiences performed at other universities.

The symposium provides an opportunity for students to write abstracts, produce posters, and present research findings thereby bringing scientific and non-scientific communities together to share in ideas and discoveries. Students, staff, faculty, administrators, and community members attend this event and enrich the experience of all participants. If this is your first time attending a symposium, feel free to walk around and ask the students questions about their research experience. We encourage any questions you may have about the research presented today. Thank you for attending our event.

The abstracts provided in this booklet are original works of students in our programs. Each abstract is included alphabetically by first author's first name.

Symposium Program

10:00-11:00am: Student Research Opportunities Presentation

Chantra Nhien, MPH

Vasanthy Narayanaswami, Ph.D.

10:50-11:00am: Poster Session 1 Set Up

11:00-11:55am: Poster Session 1 (Odd Abstracts)

11:55-12:05pm: Poster Session 2 Set Up

12:05-1:00pm: Poster Session 2 (Even Abstracts)

Coffee and orange juice will be served at 11:00am.

Pizza will be served at 11:30am.

****Presenters**, *please go to the Alamitos Bay Room for pizza.*

****Guests**, *please go to the back of the ballroom for pizza.*

Project Abstracts

INDEX OF ABSTRACTS

Presenter	Faculty Mentor	Abstract #
Gregory Kouris	Dr. Deepali Bhandari	17
Hannah Garfin and Carolina Contresas	Dr. Amanda Fisher	94
Helen Dinh	Dr. Ashlyn Spring	82
Hoang Dang	Dr. Valerie Schmidt	76
Ilse Arciga, Youstina Makary, and Karla Soto	Dr. Elizabeth Eldon	18
Itzel Gutierrez	Dr. Bryan Rourke	19
Ivan Salladay-Perez	Dr. Douglas Pace	21
Jaime Cordova	Dr. Dustin E. Schones	96
Jamie Gleason	Dr. Stephen Mezyk	25
Jason Chetsawang	Dr. Douglas Pace	27
Jean-Baptiste Faure and Carlos Lima	Dr. Michael Peterson	28
Jennifer Ramirez	Dr. Jason Schwans	64
Jennifer Vinh	Dr. Jesse Dillon	29
Jessica Layne Wewers	Dr. Ehsan Barjasteh	31
Jordan Ngo	Dr. Deepali Bhandari	84
Jorge Alfaro	Dr. Erika Holland	35
Joshua Corona	Dr. Thomas Gredig	37
Joshua Arias and Emily Do	Dr. Amanda Fisher	39
Joshua Razon	Dr. Kevin Sinchak	41
Josue Rodriguez and Amirari Diego	Dr. Claudia Ojeda-Aristizabal	43
Justin Rodriguez	Dr. Jesse Dillon	45
Kara Wiggin	Dr. Erika Holland	47
Katherine Henson	Dr. Ashley Carter	49
Kathleen Leon	Dr. Kelly Young	16
Kathy Vo	Dr. Theodore Stankowich	51
Keana Tang	Dr. Amanda Fisher	53
Kenneth Rodriguez	Dr. Enrico Tapavicza	55
Kevin Vargas	Dr. Young-Seok Shon	48
Landon Watts	Dr. Stephen Mezyk	57
Layla Ramos	Dr. Houng-wei Tsai	59
Leslie Tram	Dr. Lisa Klig	38
Lupita Lopez	Dr. Brian Livingston	78
Makenna Rivers	Dr. William Pedersen	66
Marc Pulanco	Dr. Deborah Fraser	61
Maria Rivera	Dr. Lisa Klig	58
Marielle Cardenas Valdez	Dr. Judy Brusslan	63
Martha Guerrero	Dr. Michael Schramm	86
Michael Chin	Dr. Fangyuan Tian	68
Michael Lanoye	Dr. Prashanth Jaikumar	65
Michael Toledano	Dr. Lisa Klig	40

Presenter	Faculty Mentor	Abstract #
Naomy Marrufo	Dr. Claudia Ojeda-Aristizabal	88
Nathaniel Morrison	Dr. Thomas Gredig	30
Nicole Lopez	Dr. Theodore Stankowich	70
Nicolette Schuko	Dr. Erika Holland	69
Nina Miller	Dr. Prashanth Jaikumar	71
Noor Osman	Dr. Lisa Klig	60
Patricia Leyva	Dr. Judy Brusslan	73
Peter Joseph Santiago	Dr. Hadi Tavassol	75
Peter Nguyen	Dr. Deepali Bhandari	77
Phillippe Ly	Dr. Ken Nakayama / Dr. Jason Schwans	79
Raphael Monroy	Dr. Prashanth Jaikumar	81
Reema Tomina	Dr. Kevin Sinchak	20
Robert Comito	Dr. Amanda Fisher	83
Ronnie Bourland	Dr. Lijuan Li	98
Rosanna Calderon	Dr. Deepali Bhandari	85
Ryan Reno	Dr. Claudia Ojeda-Aristizabal	87
Santos Fuentes	Dr. Thomas Gredig	89
Sharity Ondrejik	Dr. Kevin Sinchak	91
Shiva Nilakantan	Dr. Enrico Tapavicza	117
Sierra Coleman and Asusena Figueroa	Dr. Amanda Fisher	93
Stanley Nguyen	Dr. Renaud Berlemont	95
Stephanie Araiza	Dr. Shahab Derakshan	50
Stephanie Leal	Dr. Deepali Bhandari	97
Tam Ho	Dr. Michael Schramm	80
Teodora Nedic	Dr. Michael Schramm	99
Terence Baker	Dr. Jiyeong Gu	101
Tina Nguyen	Dr. Vasanthy Narayanaswami	100
Travis Thompson	Dr. Enrico Tapavicza	103
Vera Yangildina	Dr. Deepali Bhandari	105
Vladislav Larionov and Nicholas Werner	Dr. Andreas Bill	107
Wade Shipley	Dr. Ehsan Barjasteh	109
Will Hinckley	Dr. Judy Brusslan	111
William Ryan Sueme	Dr. Schramm	113
Xavier Martinez	Dr. Eric Sorin	115

1. **Peptide-supported Organometallic Catalysts for Dual Transformations in Aqueous Media**

Cristobal Morfin and Katarzyna Slowinska, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Green chemistry principles are often difficult to accomplish in catalytic transformations. Here we propose to employ collagen-mimetic peptides (CMPs) as a support for organometallic catalysts that can achieve high yields in simultaneous dual transformation reactions (Suzuki Miyuara coupling and allylic substitution), while also eliminating costly solvents and by-products. The CMPs allow for well-defined spatial separation of the immobilized catalysts thus will sterically improve selectivity of dual transformations. while also eliminating costly solvents and by-products. Kinetic analysis of products, will be performed using Gas Chromatography with mass spectrometry detector (GC/MS) Both reactions' participation in the dual transformation will be characterized individually, before simultaneous dual transformations reactions are performed. The chromatograms, green chemistry metrics, catalytic turnover rates, and the efficiency of our heterogeneous catalyst system will be determined.

This project is supported in part by the RISE Fellowship (NIH 2R25GM071638-09A1).

2. **No Abstract**

3. **Characterizing the Role of a Putative Calcium Binding Protein (CBP2) in *Toxoplasma gondii* during the Bloodstream Stage**

Dalia Sandoval Olmos, Imara Meepe, Jason Chetsawang and Douglas A. Pace, Ph.D.
Department of Biological Sciences, California State University Long Beach, Long Beach, 90840

The intracellular protozoan parasite, *Toxoplasma gondii*, is one of the most successful parasites on Earth. It infects almost one third of the world's population and is related to the malaria parasite. While it is known that *T. gondii* has a strict dependence on cytosolic calcium oscillations for initiating host cell invasion, the precise mechanisms of such regulation remains obscure. In this study, a gene encoding a putative calcium-binding protein, CBP2, was characterized in order to understand its role in regulating cytosolic calcium concentration during the virulent, bloodstream stage of the parasite. Indirect immunofluorescent assays show that CBP2 is localized in the apical cytoplasm of the parasite during the extracellular stage. Genetic over-expression mutants were developed and the role of CPB2 was investigated. Preliminary results from Giemsa invasion experiments determined that CBP2 overexpression results in greater invasion efficiency (ANOVA, $P < 0.01$) compared with parental control parasite lines. Future experiments will focus on using CRISPR/Cas9 genetic manipulation to knockout CPB2, providing further information on its role in calcium regulation and parasite virulence. Ultimately, this study will aid in the development of a potential novel drug target (calcium-binding proteins) by which to combat this highly ubiquitous parasite.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02, NIH (SCORE, SC3) awarded to Dr. Pace (1SC3GM121223-01).

4. Preliminary Results on the Condensation Reactions of 2-Formylbenzoic Acid with Arenes Catalyzed by Brønsted Superacids

Billy N. Nguyen, Thomas H. Swihart, and Eric R. Marinez, Ph. D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Boron trifluoride (BF_3) combines with water readily and forms the stable BF_3 monohydrate (BF_3-H_2O) complex which has been shown to be superacidic. Many of the reactions BF_3 monohydrate catalyzes is by superelectrophilic activation, the further protonation of non-bonding electron pairs of a monocation that lead to dications which are substantially more reactive than their parent monocation. We are currently comparing the reactivity of BF_3 monohydrate with trifluoromethanesulfonic acid (triflic acid), the superacid of choice for studying superacid catalyzed reactions that proceed by superelectrophilic activation. This study will compare the reactivity of 2-formylbenzoic acid with arenes catalyzed by either BF_3 monohydrate or triflic acid. BF_3 monohydrate selectively produces 3-aryl phthalides, compounds that possess a variety of biological activities that include antibacterial activity and the ability to bind to specific human chemokine receptors that the HIV virus uses to gain entry into target cells. In comparison, the stronger triflic acid can further condense 3-aryl phthalides with arenes to produce 10-phenyl anthrones. Analogs to these derivatives have been studied as organic near infrared dyes that have received interest in applications such as high-contrast bioimaging, optical recording, near-Infrared (NIR) photography, and solar cell.

5. Predicting Metagenomics for Glycoside Hydrolases

Darrian Talamantes and Renaud Berlemont
Department of Biological Sciences, California State University Long Beach, Long Beach, California, 90840

The systematic analysis of sequenced bacterial genomes has revealed the phylogenetic conservatism and the distribution of genes for polysaccharide deconstruction and multidomain/activity glycoside hydrolases in bacteria. More recently, the characterization of sequenced metagenomes revealed the diversity of these sequences in environmental microbial communities. However, as many studies focus on 16S rRNA sequence, little information regarding the potential for polysaccharide processing can be collected from these samples. Here, using a comprehensive understanding of the GH distribution in sequenced microbial genomes, we created a predictive algorithm aimed at inferring the distribution of GH families in taxonomically resolved microbial communities. Briefly, "GH-pred" normalizes environmental dataset(s), identifies the taxonomic groups, and pulls samples randomly from a lookup table with the distribution of GH in specified taxa using the identified taxonomic groups as a reference. This custom database contains information for 44,946 GHs targeting cellulose, xylan and chitin distributed in 11,953 sequenced bacterial genomes. This process is performed three times in order to account for within taxa variation. Finally, GH-pred extracts the median values of every GH. GH-pred was tested with characterized metagenomes and 16SrRNA amplicon libraries. We tested the accuracy and consistency by comparing *in silico* prediction to pre-characterized metagenomes. GH-pred was found to be 96.7% consistent between its prediction for 16S rRNA data and Whole Genome Shotgun (WGS) data predictions. Finally, we ran GH-pred on 16S rRNA sequences pulled from characterized WGS datasets and compared the output with the actual distribution of identified GHs in the samples. GH-pred was found to be 71.9% accurate. In the future, GH-pred will provide a way to estimate the functional properties of a population without sequencing the entire microbiome, thus reducing the cost associated with sequencing. In addition, GH-pred can be applied to predict the distribution of GH sequences in taxonomically resolved microbial communities (e.g., 16S rRNA libraries) collected in the pre-metagenomics era. This program can save many researchers money and time.

Funding: National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers R25GM071638 (D.T), 8UL1GM118979-02 (R.B.) and by CSU Program for Research and Education in Biotechnology (CSUPERB) under award number GF00631142 (R.B.).

6. A Study of GNΦ1, Hypersaline Halorubrum Virus.

Brandon Quintana[1], Shereen Sabet[2], Ph.D., Jesse Dillon, Ph.D.[2]
[1]Long Beach City College, Long Beach, CA
[2]Department of Biological Sciences, California State University Long Beach

Our current study is focusing on reviving and growing more of a hypersaline virus, GNΦ1, that infects *Halorubrum* host cells. We have grown the halovirus through spot plate assays, processed the plaques, filtered, and concentrated the virus sample to approximately a 1 mL solution. This process will be repeated multiple times. Once we attain a desirable titer as determined through plaque assays, we can then sequence its genome and test its physiochemical tolerances. This includes testing the virus in different salinities (0% - 35%), temperatures (-80°C - 80°C), and pHs (pH 2 - 11). So far we have successfully brought back GNΦ1 from extinction and are continuing to grow more of the virus.

This research was supported in part by NIGMS Bridges to the Baccalaureate Grant 5R25GM50089-17 and College of Natural Sciences and Mathematics, CSULB.

7. Androgenic Regulation of Sexually Dimorphic SFSWAP Expression in the Developing Mouse Hippocampus

Edward Kim, John Quitiquit, and Houng-Wei Tsai
Department of Biological Sciences, California State University Long Beach, Long Beach, CA 90840

Sexual differentiation is a critical development process that creates sex differences in brain structure and function. During late embryonic stage and on the day of birth, the developing testes secrete testosterone to masculinize the male brain by activation of androgen receptors (AR). For example, testicular feminized mutation (Tfm) male mice lacking functional AR display feminized brain structure in the hypothalamus and impaired male sexual behavior. Beyond the hypothalamus, sex differences are also noticed in the hippocampus, a brain region regulating complex cognitive function. Testosterone exerts extensive influence on its structure and function, but the molecular mechanism underlying sexual dimorphism in the hippocampus remains unclear. To address this, we have profiled expression of splicing factor, suppressor of white-apricot homolog (SFSWAP) in the developing brains of male and female mice, and have observed that on postnatal day 21 (PN21), female mice contain more SFSWAP-expressing cells in the CA1 of their hippocampus than males. Since AR is highly expressed in the hippocampus, we hypothesized that *AR might play a critical role in down-regulation of SFSWAP expression in the male CA1 during early development*. To test my hypothesis, we collected the whole brains from wild-type male, wild-type female, and Tfm males at PN21. The brains were immediately post-fixed in 4% paraformaldehyde, sectioned, and stained for SFSWAP using immunohistochemistry. After cover-slipped, the tissue sections were analyzed for SFSWAP-immunoreactive cells in the CA1 of the hippocampus. Our preliminary results show that females (7.072 ± 0.186 cells/1000 μm^2) have more SFSWAP expressing cells than males (6.121 ± 0.469 cells/1000 μm^2) while no difference in SFSWAP expression is observed between female and Tfm (6.963 ± 0.264 cells/1000 μm^2) (n=3 per group, P= 0.034). Our finding suggests that AR may downregulate SFSWAP expression, resulting in differential spliced variants of its target genes in the mouse hippocampus between the sexes.

This work was supported by the National Institutes of Health SC3 Grant, GM102051.

8. No Abstract

9. Design and Development of a Motorized Test-bed for Ultrasound Inspection

Edwin Grajeda, Roger Contreras, and Surajit Roy, Ph.D.
Department Mechanical and Aerospace Engineering Department, California State University, Long Beach.

Structural Health Monitoring (SHM) aims to understand the behavior of a structure and its well-being through observation. It is important to understand the structure's current state in order to determine if it is safe to use. One critical component of SHM is in-situ characterization and evaluation of material properties. This project uses non-destructive testing techniques to analyze material properties. The objective is to design and develop a motorized test-bed for ultrasonic inspection. A piezoelectric transducer is used to perform characterization of structural material. However, a mounting system for the transducer and a platform that will have two degrees of freedom are designed. The mounting system comprises of a belt system, modelled after the Core XY belt System. Two stepper motors are used to physically drive the belts, which are controlled by an Arduino Uno microcontroller.

10. Do Changes in Cytosine Methylation Affect CMR-SURG *UGT78D1* Expression?

Charidan L. Jackson and Judy A. Brusslan, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840-9502.

Leaf senescence is the final stage of leaf development in which nutrients are mobilized from older leaves to growing and storage organs of the plant. Efficient leaf senescence is essential for high crop yields. 5-methyl cytosine methylation, a form of epigenetic modification, can activate or repress transcription depending on its location. In the promoter, increased cytosine methylation is associated with the inhibition of mRNA expression; therefore, a decrease in promoter cytosine methylation is associated with activation of transcription. Dimethylation of histone H3 at lysine 9 (H3K9me2) is a histone modification associated with transcriptional silencing that is often accompanied by cytosine methylation. A negative correlation between cytosine methylation and *UGT78D1* gene expression was observed as leaves age in *Arabidopsis thaliana*. For this reason, *UGT78D1* may be a cytosine methylation regulated-senescence up-regulated gene (CMR-SURG). We will use mutant lines *ros1-1* and *suvh4* to verify the relationship between cytosine methylation, *UGT78D1* mRNA expression, and leaf senescence. ROS1-1 is a cytosine demethylase, therefore the *ros1-1* mutant will have increased cytosine methylation when compared to wild type. SUVH4 is responsible for histone H3 dimethylation at lysine 9 (K9), therefore the *suvh4* mutant will have decreased H3K9me2 and cytosine methylation when compared to wild type. *Arabidopsis thaliana* leaf 7 tissue will be collected at 28d, 35d, 42d, and 49d, and genomic DNA will be isolated and subject to bisulfite treatment to measure cytosine methylation. RNA will also be isolated to measure *UGT78D1* and the reference *ACT*2 mRNA levels. We hypothesize that *suvh4* with low cytosine methylation will show higher *UGT78D1* expression while *ros1-1* with increased cytosine methylation will show reduced *UGT78D1* expression. These results would support a cause and effect relationship between the loss of promoter cytosine methylation and mRNA induction during leaf senescence. This study will help further our molecular understanding of the regulation of senescence.
Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638 which funds the Research Initiative for Scientific Enrichment (RISE) program at CSULB. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

11. No Abstract

12. Signaling of Leaf Senescence in *Arabidopsis thaliana*

Ciairra J. Riley and Judy Brusslan, Ph.D.
Department of Biological Sciences, California State University Long Beach, Long Beach, CA 90840-9502

Leaf senescence is observed when plants lose their green pigmentation and nutrients are recycled from older to newer leaves and developing tissue. *RLP7* (receptor-like protein 7) is a K4-SURG, a gene that has an increase in mRNA levels accompanied by an increase in the H3K4me3 activating histone mark as the plant ages. These marked genes may have an important function during senescence. In previous research, *RLP7* was observed to be highly expressed at the start of senescence (Wang et al., 2008); it is hypothesized that it signals the plant to undergo senescence, and this project aims to determine if RLP7 is a positive regulator of leaf senescence. Two T-DNA insertions (SALK_123145 and SALK_030269) were isolated to disrupt *RLP7*, and genomic and preliminary gene expression analysis demonstrate that SALK_123145 is a null allele while SALK_030269 is a knock-down allele. SALK_123145 showed no amplification with flanking and downstream primers, while SALK_030269 showed no amplification with flanking primers, but light amplification with downstream primers. The null allele was evaluated for senescence by measuring chlorophyll degradation and gene expression during senescence, and were compared to wild-type to determine if there are any significant differences.

13. Woolly Apple Aphid Performance on Apple of Varying Resistant Traits

Emmanuel Cuevas[1,2] and Paul Nabity, Ph.D.[3]
[1]CEPCEB REU Site: Research Experiences for Undergraduates in Next Generation Plant Biology;
[2]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840
[3]Department of Botany and Plant Sciences, University of California, Riverside, Riverside, CA 92521

The Woolly Apple Aphid (WAA), *Eriosoma Lanigerum* is native to North America but has spread to all the apple growing regions across the world. Apple trees are the WAA secondary host where it feeds on wounds, axils, and roots of the tree, and reduces nutrient movement in the tree, leading to reduced quality and number of apples. It is important to understand how the WAA infests various apple trees because apples are a major crop around the world. In this study, we assessed the survivorship of the WAA on various apple genotypes that differ in their predicted resistance traits. It was initially hypothesized that two of the four genotypes would be susceptible to the WAA based on the genetics of each genotype previously analyzed. Bare-root plants were established in a greenhouse, and then transferred to an environmentally controlled (ambient sunlight; 75.58°C ± 0.11) insectary to assess survival rates. Each of four different genotypes were initially infested with ten first instar WAA. Re-infestations with up to 10 aphids occurred every other day to measure experimental error. After eight days, no further re-infestations were performed and survival through time was assessed up to 13 days. We observed that all genotypes provided a significant level of resistance to WAA, resulting in mortality from 60-90%. One genotype reduced survival more than the other three genotypes ($\bar{x}$=94%, P=0.005). Future studies should characterize the traits that underlie the resistant phenotype; however, the most resistant genotype shows great potential as a rootstock to deter the WAA.

This work was supported by the National Science Foundation REU grant 141297 to the UC-Riverside Center for Plant Cell Biology

14. Characterization of GIV-GRP78 Interaction During Endoplasmic Reticulum Stress

Clariss Limso, Jordan Ngo, Stephanie Leal, and Deepali Bhandari, Ph.D.Department of Chemistry and Biochemistry, California State University, Long Beach, 1250 Bellflower Boulevard, Long Beach, California 90840

Endoplasmic Reticulum (ER) stress occurs when there is an accumulation of misfolded proteins in the ER. Cells facing ER stress initially attempt to restore cellular homeostasis, but if the stress becomes chronic and homeostasis is not achieved within a reasonable timeframe, cells initiate programmed cell death. Cancer cells are able to withstand and overcome ER stress better than regular cells. One of the key factors to promote cancer cell survival during ER stress is overexpression of the chaperone GRP78 (Glucose Regulated Protein 78 kD). Although it is regarded as an ER lumenal protein, recent studies have shown that when overexpressed GRP78 can translocate to other cellular locations including the cell surface. Expression of GRP78 on the cell surface has been shown to activate cytoprotective signals, however the mechanism by which it does so remains elusive. Our laboratory has recently identified GIV (Gα-Interacting Vesicle associated protein) - a known enhancer of the pro-survival Akt signaling - as a novel binding partner of GRP78. This finding led us to hypothesize that this interaction may be the missing link in understanding the mechanism by which cell surface GRP78 leads to the activation of the Akt pathway. Because GIV and GRP78 are normally localized in different cellular compartments, it is important to identify the sub-cellular location of this interaction. To look at their subcellular localization, cell lysates of HeLa cells treated with Tunicamycin (an ER stress inducer) were fractionated using two different approaches - differential centrifugation and sequential fractionation - and analyzed by western blotting. Our results show that GIV is present in both membrane and cytosolic fractions during normal as well as ER stress conditions. GRP78, on the other hand, is in the membrane fraction under normal cellular conditions, but appears in the cytosolic fraction when cells are ER stressed. Using cell-surface biotinylation experiments, we determined that the cell surface expression of GRP78 is reduced in cells depleted in GIV. Finally, we also confirmed that the interaction between GIV and GRP78 is direct by performing *in vitro* GST pull-down assays with both proteins expressed and purified from bacterial cells. Taken together, our results show that during ER stress GIV and GRP78 can potentially interact in the cytosol and that this interaction may facilitate cell surface expression of GRP78.

This research was supported in part by the BUILD program - National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02 and by the NIH MARC program – National Institutes of Health under Award number: T34GM008074. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

15. Complement protein C1q modulates chemokine gene expression in macrophage foam cells

Emmeline L. Cosman, Ayla Manughian-Peter, and Deborah A. Fraser, Ph.D.
Department of Biological Sciences, California State University Long Beach, CA 90840

Atherosclerosis is an inflammatory disease that resulting in an accumulation of macrophages in the arterial wall. Disease progression is caused by the ingestion of low- density lipoproteins (LDL), generating foam cells and the formation of plaque. Apoptosis is triggered by the accumulation of oxLDL and other cytokines, which plays a role in the development of lesions and plaque. C1q is an anti-inflammatory factor of the classical complement cascade that reduces atherosclerosis by improving macrophage foam cell survival through the opsonization of C1q, increasing phagocytosis in foam cells. Chemokines play an important role in atherosclerotic disease by sending leukocytes to the inflammatory site. Chemokines are proteins that immune cells release to bring other immune cells into the affected area by inducing chemotaxis on neighboring cells, activating neutrophils, macrophages, and T cells. C1q alters chemokine gene expression, and the goal of this study is to investigate C1q modulation of chemokine levels in human monocyte derived macrophages (HMDM). To further investigate this study, M1-polarized HMDM were treated with 10 μg/mL oxLDL along with another treatment of oxLDL with 75 μg/mL of C1q, and isolated RNA was used to run quantitative PCR.

16. Exploring the Ovarian Transcriptome During Photostimulated Recrudescence in Siberian Hamsters

Kathleen Leon[1], Jon D. Hennebold[2,3], Suzanne S. Fei[4], and Kelly A. Young[1]
[1]Department of Biological Sciences, California State University Long Beach, Long Beach, CA 90840.
[2]Division of Reproductive & Developmental Sciences, Oregon National Primate Research Center, Beaverton, OR 97006; [3]Department of Obstetrics & Gynecology, Oregon Health & Science University, Portland, OR 97239.
[3]Biostatistics & Bioinformatics Unit, Oregon National Primate Research Center, Oregon Health & Science University, Portland, OR 97006.

To offset the energetic expense of reproductive activity, individuals often breed only during seasons that optimize parent and offspring survival. In Siberian hamsters, exposure to short days (SD, 8h of light: 16h of dark) for 14 weeks reduces reproductive function centrally by decreasing gonadotropin secretion. Subsequent transfer of photoinhibited hamsters to stimulatory long days (LD, 16L:8D) promotes FSH release leading to ovarian recrudescence. Although differences between SD and LD ovaries have been investigated; a systematic investigation of the mechanisms that restore folliculogenesis during recrudescence has not been conducted. Our aim was to analyze the transcriptome of Siberian hamsters across photoperiod groups to identify potentially novel signaling factors that contribute to photostimulated restoration of ovarian function. Adult hamsters were assigned to one of four photoperiod groups for 14-16 weeks: LD to maintain ovarian cyclicity; SD to induce ovarian regression; or post transfer (PT), where females housed in SD for 14 weeks were transferred to LD for two days (PTd2) or one week (PTw1) to reflect photostimulated ovaries prior to (PTd2) and following (PTw1) the return of systemic FSH. Ovarian RNA was extracted and the samples (n=4/group) were sent to the Massively Parallel Sequencing Shared Resource Core at OHSU for creation of RNA-sequencing libraries and the short read sequencing Illumina assays to map and quantify ovarian transcriptomes. Alignment using SNAP, DESeq2 normalization and differential expression analysis was then performed. Ovarian and uterine masses, plasma FSH, and numbers of antral follicles and corpora lutea were decreased in SD as compared to LD females ($p<0.05$). When reads were aligned to the mouse genome, 18,548 genes were sufficiently quantified. Most of the significant changes were noted between functional LD ovaries and regressed SD ovaries. When normalized counts for select genes were confirmed via ANOVA followed by Newman Keuls post hoc tests, four patterns emerged. Many genes showed the expected pattern of high expression in LD ovaries, with significant declines in expression in the SD, PTd2, and PTw1 groups, including: Bcar1, Sept5, Rap1, Crispld2, Igfbp3, and Adamts1. A second pattern where expression was high in LD, declined in SD ovaries, but then was restored in PT ovaries also emerged, including: Inhb, Tubb4a, Susd1, and Dhh. Another pattern where gene expression in SD, PTd2, and PTw1 groups was increased as compared to LD, included: Bmx, Dcn, Aqp9, and Cyp27a1. Finally, a fourth pattern where expression increased in SD ovaries as compared to lower levels in LD and PT groups was noted, including Lgr5, Hey1, Fgl2, and Ltb. Not only do these results provide an overall map of ovary function during recrudescence, they also provide a large number of novel genes that may prove to be key intra-ovarian regulators in the resumption of ovarian activity.

This research was supported by the National Institutes of Health: R25GM071638-RISE undergraduate (KL) and 1SC3GM116696-SCORE (KAY).

17. Expression and Purification of Recombinant Cyclin Dependent Kinase 5 from Inclusion Bodies

Gregory Kouris[1] and Deepali Bhandari[2], Ph.D.
[1]College of Engineering, [2]College of Natural Sciences and Mathematics
California State University Long Beach, Long Beach, CA 90840

Cyclin-dependent kinase 5 (CDK5) is a proline-directed serine/threonine kinase which plays an important role in many key cellular processes. Dysregulation of CDK5 activity has been implicated in several pathologies including cancer, diabetes and neurodegeneration. Therefore, investigation of mechanisms regulating CDK5 activity is important to understand the pathological basis of diseases associated with CDK5. Recent results from our laboratory have suggested that CDK5 may be regulating itself via autophosphorylation. To study CDK5 autophosphorylation further, we need to express and purify recombinant His6-CDK5 and its cognate activator, p35 from bacteria. Initial attempts to purify the CDK5-p35 complex showed that majority of it was sequestered in the inclusion bodies. The goal of my project is to isolate and purify CDK5 from inclusion bodies. To this end, we first tested the type (Urea or Guanidinium chloride) and concentration (1M-4M) of the denaturant to use for isolating the proteins from inclusion bodies. The CDK5-p35 complex was then purified using Co^{2+}-NTA affinity chromatography. The purified complex retains its activity as confirmed by performing a kinase assay. Our current and future goals include optimization of the protocols to increase the protein yield further.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health

18. The Effects of a High Fat Diet on Developmental Timing and Lifespan in *Drosophila melanogaster*

Ilse Arciga, Karla Soto Sauza, Youstina Makary, and Elizabeth Eldon, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840-9502

Approximately 36% of the adult population in the United States is considered to be obese, meaning that more than one-third of adults are likely to suffer from obesity-related illnesses such as diabetes, atherosclerosis, heart disease, high blood pressure and sleep disorders. Many of these diseases are common and preventable causes of death in the United States. Obesity and its related illnesses continue to increase in the United States. *Drosophila melanogaster* was used in this study as a model organism to examine how a high-fat diet affects lifespan, as well as developmental timing in distinguishable stages. *Drosophila melanogaster* is an ideal model organism to study the effects of obesity due to its ease of breeding and maintenance, easily trackable developmental stages, and short lifespan. The *Drosophila melanogaster's* short lifespan makes it an ideal organism for multigenerational studies, allowing us to monitor the developmental effects of a high-fat diet on the resulting offspring. We hypothesize that *Drosophila melanogaster* raised on a high-fat diet will exhibit symptoms of obesity such as decreased lifespan and high levels of stored lipid, and differences in developmental timing. These effects may be observed over multiple generations, and in progeny of high-fat parents, which are raised on normal food. 1st generation and 20th generation *Drosophila melanogaster* were raised on control and high fat diets and were monitored daily for their lifespan and developmental progress. Our results indicate that a high fat diet does affect the lifespan of *Drosophila melanogaster* and continues to affect them over multiple generations. We expect developmental timing to also be affected by the media on which *Drosophila melanogaster* are reared.

This research was supported in part by NIGMS Bridges to the Baccalaureate Grant 5R25GM50089-17.

19. Myosin Heavy Chain Isoforms in the Heart and Pectoralis of Avian Species

Itzel Gutierrez, Kelsey Condell, and Bryan Rourke, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Powered flight in vertebrates requires different muscle performance characteristics than does terrestrial locomotion. We analyzed myosin isoform expression in fresh tissues of interesting bird species, and from amino acid sequence information deposited in GenBank. The literature and description of myosin proteins in birds is confusing, technically incorrect in many instances, and generally not standardized in protocol or nomenclature. For fresh samples, we included easily obtainable species such as chicken and duck, as well as an assortment of birds that were either migratory or resident to Alaska. The Alaska species include raptors, shorebirds, powerful flyers, and amphibious birds. The fresh samples were analyzed by SDS PAGE protein electrophoresis, which reveals the number of myosin isoforms in flight, leg, and heart muscle. However, positive identification of these proteins is hampered by differential migration of isoforms on a species-specific basis. We therefore sequenced the amino acids of various avian muscles, and have identified several novel isoforms. We also refute several incorrect descriptions of avian flight muscle physiology. This protein identification was carried out against a molecular phylogeny of all known avian myosin isoforms. We have identified many sequences that were mis-named in GenBank, and we have used this phylogeny to putatively identify our new isoforms from fresh bird samples. We hypothesize that birds with different flight abilities will express different (MyHC) isoforms. It had been stated in literature that slow myosin, typical of terrestrial aerobic activity, was not included in flight muscle. We however found that avian species contain 4 myosin isoforms in their pectoralis which in which include fast type 2a, 2x, embryonic as well as the slow-twitch isoforms. Past studies have only concluded that expression of fast type 2a and embryonic so the discovery of MyHC 2x and slow-twitch isoforms was novel and notable. We have many exciting flight muscle datasets that can now be accurately determined.

This project is supported in part by Office of Research and Sponsored Projects, CSULB.

20. SERMS TAMOXIFEN AND ICI 182,780 RAPID FACILITATION OF LORDOSIS VIA GPER IS MEDIATED BY THE ORPHANIN FQ-OPIOID RECEPTOR-LIKE RECEPTOR-1 SYSTEM

Reema Tominna, Sima Chokr, Nathan Long, and Kevin Sinchak, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach 90840

In the female rat, sexual receptivity (lordosis) can be facilitated by sequential activation of estrogen receptor-α (ERα) and G protein-coupled estrogen receptor-1 (GPER; aka GPR30). Estradiol benzoate (2 μg; EB) initially activates β-endorphin (β-END) neurons in the arcuate nucleus of the hypothalamus (ARH) that project to the medial preoptic nucleus (MPN) to activate μ-opioid receptors (MOP), which inhibits lordosis. Activation of the orphanin FQ-opioid receptor-like receptor-1 (OFQ/N-ORL-1) system facilitates lordosis via inhibition of β-END. Our previous studies showed that GPER are expressed in 85.7% of ARH OFQ/N neurons. Infusion of non-esterified 17β-estradiol (E2) into the ARH 47.5 hours after EB treatment rapidly reduces MPN MOP activation and facilitates lordosis within 30 minutes. We have previously shown that E2 acts through GPER on OFQ/N neurons to release OFQ/N and facilitate lordosis. SERM therapies tamoxifen (TAM) and ICI 182,780 (ICI) are ERα/β antagonists but in many cases exacerbate tumor growth via GPER activation. Like E2, TAM and ICI signal through GPER to facilitate lordosis and deactivate MPN MOP. Therefore, we tested the hypothesis that TAM or ICI infusion in the ARH of an EB-primed OVX rat rapidly deactivates MPN MOP and facilitates lordosis via activation of the OFQ/N-ORL-1 system. As expected, ARH infusion of TAM or ICI 47.5 hours after EB priming facilitated sexual receptivity within 30 minutes. Further, pretreatment with UFP-101, an ORL-1 selective antagonist, blocked TAM and ICI facilitation of sexual receptivity. These data indicate that, like E2, TAM and ICI signal through a GPER dependent pathway that induces the release of OFQ/N that reduce β-END neurotransmission. Since GPER are expressed in ARH OFQ/N neurons, GPER signaling appears to directly regulate ARH OFQ/N release that activates ORL-1 to inhibit β-END neurotransmission, which facilitates lordosis.

This project was supported by Award Number RO1HD058638 from the Eunice Kennedy Shriver National Institutes of Child Health & Human Development, Research Initiative for Science Enhancement (RISE) GM07163 at CSULB, BUILD 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118979-02 at CSULB, The Doris A. Howell foundation, and HOGAR.

21. No Abstract

22. A Cooperative Crystallization Strategy For Entrapment Of Metal Clusters On A Kagome Platform

Andy Dinh, Xiang Zhao, Ph.D., and Xianhui Bu, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, CA 90840

Porous materials have the ability to adsorb gaseous molecules, which can be utilized to store volatile fuels or recapture pollutants such as carbon dioxide. The extent to which gaseous molecules can adhere to the material is correlated with the material's surface area. Through the concept of pores space portioning, this project sought to attach cobalt metal dimers to the pore surfaces of a metal-organic framework (MOF) consisting of indium, triazole (trz), and benzenetricarboxylic acid (btc). This attachment will tune the surface area of the crystal, providing additional area for interaction with gaseous molecules. We determined a viable synthesis condition and characterized the crystal for purity and structure. The stability and gas adsorption are being studied. Through X-ray diffraction, we determined the crystal to have a hexagonal prism structure with unit cell of a = 22.1783 (64) Å, b = 22.1783 (64) Å, c = 20.5420 (59) Å, Alpha = 90°, Beta = 90°, Gamma = 120°. The main building block for this MOF is the zigzag chain composed of a group of 3 indium atoms linked by 4 carboxyl and 2 oxygen. Each group of 3 is connected to another group by 3 molecules of triazole. The chains are attached and aligned parallel to the others by btc. Our data showed cobalt metal dimers held onto the surface of the hexagonal pores through 2 nitrogen from trz and 2 carboxyl from btc. The successful attachment of cobalt to the pores increases the crystal's overall surface area. Results from additional testing will quantitatively determine the gas affinity of the MOF system. Data obtained from this experiment could help drive the development of fuel storage and carbon sequestration as well as providing a greater insight on MOF-gas interaction.

This project is supported by the Undergraduate Education Program of the W. M. Keck Foundation. This research is supported in part by the CSULB Department of Chemistry and Biochemistry, CSULB-LSAMP through the (National Science Foundation) under Grant #HRD-1302873, and the Chancellor's Office of the California State University. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation or the Chancellor's Office of the CSU.

23. Screen Development to Analyze Interactions of *18-wheeler* Gene Mutations and X-Linked Chromosome Deficiencies

Jacquelyn Villalba, Anel Molina, Karen Ixcoy, and Elizabeth Eldon, Ph. D
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

The *18-wheeler* gene found in *Drosophila melanogaster* directs epithelial cell migration during development. Previous work has demonstrated that homozygous *18-wheeler* mutant embryos have abnormal salivary glands. *Drosophila* salivary glands are an excellent model for mammalian organ development. To identify genes that interact with *18-wheeler* during epithelial organ development we take advantage of the observation that an embryo heterozygous both for *18-wheeler* and for a gene that interacts with *18-wheeler* will produce defective salivary glands. We are systematically searching the X-chromosome for interacting genes using a collection of 93 X-chromosome-linked deficiencies (*Df(1)*). Together these deficiencies delete 2,288 of the 2,331 euchromatic genes on the X-chromosome (98.1%). To obtain embryos that are heterozygous for both *18-wheeler* and an X-linked deficiency, males carrying an *18-wheeler* mutation and a green fluorescent protein (GFP) reporter expressed in salivary glands (stock 84-1) are mated with females heterozygous for an X-linked deficiency. Their other X-chromosome is a GFP-expressing "balancer". Control embryos are obtained by using males that are wild type at the *18-wheeler* locus, but still carry the GFP salivary gland reporter (stock 15-1). Embryos are collected, fixed, and subjected to immunocytochemistry to detect GFP, which is expressed in the salivary glands of the *18-wheeler; Df(1)* embryos. If the mutations interact, salivary gland morphogenesis will be abnormal. Defects include, but are not limited to, glands lengthening, shortening, or migrating asymmetrically. *Df(1)BSC719* (stock 26571) show no gene interaction, since wild type glands are observed in both the 15-1 and 84-1 heterozygous embryos. *Df(1)BSC644* (stock 25734) shows a genetic interaction, but not in the manner predicted. When crossed to the *18-wheeler* mutant, wild type glands are observed, but when crossed to wild type *18-wheeler*, the glands are shorter. This suggests that the deficiency causes a defect in gland morphogenesis that is rescued by reducing the dosage of the 18-Wheeler protein. Further work will examine the genes within *Df(1)BSC644* in more detail by ordering flies with smaller deficiencies within that deficiency to narrow down the location of gene responsible for the defect in morphogenesis.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980; 8RL5GM118978-02.

24. Using Metal Organic Framework Film as a Drug-Eluting Stent Coating

Angela Bui and Fangyuan Tian, Ph.D.
Department of Chemistry & Biochemistry, California State University Long Beach, Long Beach, CA, United States.

One of the leading causes of deaths within the United States are coronary heart diseases, such as thrombosis and restenosis. Clinically tested drug eluting stents filled with immunosuppressive drugs have been shown to reduce these symptoms. However, the problem with the commercial stents is the polymer coatings with hypersensitivity reactions, late stent thrombosis, and block of nearby endothelial tissues. Our research focuses on the replacement of the polymer coating on stainless steel stents, as well as studying its drug-loading capabilities. In our lab we demonstrate an alternative to the polymer coating with a non-toxic Fe containing metal-organic framework (Fe-MIL-88). One of the greatest benefits to using this compound, in addition to its non-toxicity, its chemical bonding to the metal surface unlike the physical adsorption of the polymer-based coatings. In the preliminary studies. we use gold as the metal substrate to build the Fe-MOF on. Firstly, we functionalize the gold surface with carboxylate anchoring groups, specifically 16-Mercaptohexadecanoic acid (MHDA). Next, we select our Fe-MIL-88 then directly coat the surface using a liquid epitaxial submersion technique. To confirm each modification of the gold surface we characterized the film with infrared spectroscopy and quartz crystal microbalance (QCM). To study the drug loading and eluting capabilities of Fe-MIL-88, the MOF film was prepared on a QCM sensor. We then gradually introduce the MOF to a solution of ibuprofen. Using the QCM we were able to measure its mass change. In order to study the drug release kinetics we utilized the surface plasmon resonance (SPR). Our research is aimed in increasing the understanding of MOF thin film applications and its contribution in drug delivery systems.

This project is funded in part by RISE and by the National Institute of Health Grant 2R25GM071638-09A1

25. Radical-induced Degradation of Estrogenic Steroids in Wastewaters

Jamie M. Gleason and Stephen P. Mezyk, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840.

The presence of trace chemical contaminants remaining after traditional wastewater remediation processes remains a major concern. Amongst the most important pharmaceutical contaminants in wastewater are trace levels of estrogenic steroids. These contaminants are causing concern due to their reproductive impacts on both aquatic organisms and humans. As such, the elimination of remaining steroidal activity through an advanced oxidation process (AOP) treatment is being considered by wastewater utilities. The AOP utilizes highly reactive radical species that react with, and ultimately, mineralize chemical contaminants. In order to fully understand the chemistry of these radical reactions occurring within the AOP, allowing for optimization of eliminating steroid activity, second order rate constants for four estrogenic steroids and progesterone with a suite of important AOP radicals were quantified in this study using an electron pulse radiolysis system at the University of Notre Dame. These steroids were found to react relatively quickly with species such as the hydroxyl radical, for example, the reaction of dissolved estradiol with the hydroxyl radical has a second order rate constant of 2.7×10^{10} $M^{-1}s^{-1}$. These kinetic data allow for mechanistic insight into the oxidative processes occurring, as well as providing the valuable data required for the AOP optimization needed to completely remove all estrogenic steroid activity found in treated real-world waters.

26. Structural Characterization of Perovskite/YBCO/Perovskite Thin Films

Anh Nguyen[2], Hao Zhang[1], John Y. T. Wei.[1,3], and Thomas Gredig[2]
[1]Department of Physics, University of Toronto, Toronto, M5S1A7, Canada
[2]Department of Physics & Astronomy, California State University, Long Beach, Long Beach, CA 90840
[3]Canadian Institute for Advanced Research, Toronto, M5G1Z8, Canada

Four perovskite/YBCO/perovskite trilayer thin films were grown by pulsed laser deposition. The thickness of each layer is determined separately using x-ray reflectivity and analyzed with the simulation software GenX. The YBCO thickness is found either 5 or 6 ML and 9 and 11ML. From x-ray diffractometry, we observe the YBCO(001) peaks and determine the c-lattice parameter, which is 11.66 Å for YBCO on LCMO. The c-lattice parameter for $YBaCu_3O_{7-\delta}$ grown on LNO is slightly less, around 11.60 Å with larger uncertainty. This value indicates optimal doping and small δ values. The $SrTiO_3$ substrate peaks show prominently at the expected positions for a pseudo-cubic unit cell of 3.905 Å. The thickness of YBCO layer plays an important role for the critical temperature of the superconductor. To distinguish strain effects from magnetic effects, ferromagnetic LCMO and paramagnetic LNO are used. Both LCMO/YBCO/LCMO and LNO/YBCO/YBCO trilayers have a similar strong reduction of T_c when decreasing the thickness of YBCO. The results also indicate that the heteroepitaxial strain plays an important role in the suppression of superconductivity.

This project is supported by NSERC, CFI-OIT, the Canadian Institute for Advanced Research, and the Keck Energy Materials Program.

27. Over-expression of a putative Calcium-Binding Protein (TgCBP1) results in loss of invasion efficiency in the human parasite, *Toxoplasma gondii*.

Jason Chetsawang, Imara Meepe, Dalia Sandoval and Douglas A. Pace, Ph.D.
Department of Biological Sciences, California State University Long Beach

Toxoplasma gondii is an Apicomplexan eukaryotic parasite that can invade mammals and avian species. It belongs to the same phylum as *Plasmodium falciparum*, the causative agent of malaria. *T. gondii* is known to cause toxoplasmosis in fetuses and the immunocompromised. *T. gondii* dependence on calcium (Ca^{2+}) during host cell invasion processes such as motility, microneme secretion, and conoid extrusion has been established. Despite the known importance of Ca^{2+}, the mechanisms that *T. gondii* employs to regulate this critical signaling cation are still unknown. This study focuses on the role of a putative calcium binding protein (TgCBP1) that is highly expressed during the lytic cycle of *T. gondii*. We hypothesize that manipulation of the expression of TgCBP1 will result in an alteration of invasion efficiency and other traits central to the lytic cycle due to its interference on Ca^{2+} regulation. A mutant parasite was generated using an epitope-tagged ectopic expression vector. Over-expression (OE) levels were confirmed with immunofluorescence and western blotting techniques. Experiments employing the use of Giemsa counterstaining were done to determine short-term invasion, a step of the lytic cycle in which a single parasite invades a cell and creates a parasitophorous vacuole (PV) to replicate in. Short-term assays, measured by the number of PVs per nuclei, demonstrated a significant diminishment in invasion efficiency of TgCBP1-OE mutants relative to parental control. These results suggest that TgCBP1 is critical for invasion. Future research will focus on the overall lytic cycle, or long-term invasion, through plaque assays. In addition, we will be phenotyping subclones of TgCBP1-OE mutants, examining the immediate role of this protein on real-time calcium regulation, and generating a knockout mutant using CRISPR/Cas9 gene editing. This study will help further elucidate the biological mechanisms and pathways that *T. gondii* and other Apicomplexan parasites rely on for host cell invasion.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02;8RL5GM118978-02. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. NIH (SCORE, SC3) awarded to Dr. Pace (1SC3GM121223-01).

28. Determining Magnetic Exchange Interactions through Density-Functional-Theory

Jean-Baptiste Faure[1], Carlos Lima[1], Tyler Salners[1,3], Michael R.Peterson, Ph.D.[1], Shahab Derakhshan, Ph.D.[2]

[1] Department of Physics and Astronomy, California State University, Long Beach, 1250 Bellflower Blvd., Long Beach, California 90840

[2] Department of Chemistry and Biochemistry, California State University, Long Beach, 1250 Bellflower Blvd., Long Beach, California 90840

[3]Department of Physics, University of Illinois at Urbana-Champagne, 1110 West Green St., Urbana, Illinois61801-3003

The study of energy materials is important in the development of novel energy production and storage methods and helps meet a global technological need. In recent years, transition metal oxides with potentially frustrated magnetic interactions have been of keen interest. Interestingly, frustrated magnets have the potential to produce exotic phases known as quantum spin liquids with additional potential applications in quantum computing. A method for calculating and theoretically understanding the magnetic properties of a material is to first determine the underlying electronic structure and from that construct an accurate effective physical model. Here we describe a technique of mapping density-functional-theory (DFT) ground state energies to a theoretical spin model, i.e., the Heisenberg model [Son, et al., Inorg. Chem 2011, 50, 9400-9405]. After determining the magnetic exchange parameters of the Heisenberg model of a particular material, important physical properties can be calculated in the framework of statistical mechanics. As an application we apply this technique to a novel spin-1 Osmate, Li_4MgOsO_6 .

This project is partly supported by the Undergraduate Education Program of the W. M. Keck Foundation, and the National Science Foundation under grant number DMR-1508290

29. The Bactericidal Effect of Sodium Hypochlorite and Hypochlorous Acid on *Enterococcus faecalis* Model Oral Biofilms

Jennifer Vinh[1], Austin VanDusen DDS[2], Stephen Chan DDS[2,] and Jesse Dillon, Ph.D.[1]
[1]Department of Biological Sciences, California State University, Long Beach
[2]Veteran's Affair Long Beach Endodontic Program, VA Long Beach Medical Center

Infections found in endodontic practices are commonly caused by an excess growth of bacteria. These bacteria form biofilms, which are often highly resistant to treatment. Although both eradication and irrigation are used to treat oral infections, the latter is more commonly used. Because of its ability to dissolve tissue, sodium hypochlorite (NaOCl) or 'bleach' is the most widely used treatment. However, the usage of NaOCl against mature biofilms, can result in damage to patient tissues. Hypochlorous acid (HOCl) is less cytotoxic, however its efficacy against oral biofilms is not known. *Enterococcus faecalis* are common in endodontic infections due to their ability to thrive in diverse environmental conditions, including nutrient-deprived environments, thus, preventing the usage of less potent irrigants. The purpose of this study is to compare the effect of sodium hypochlorite and hypochlorous acid (HOCl) on a 3-week-old *E. faecalis* biofilm. *E. faecalis* was grown anaerobically on hydroxyapatite (HA) discs coated with bovine dermal collagen I for three weeks in order to develop a mature biofilm. These biofilms were treated with either a 0.25% NaOCl or 5% HOCl Carr solution for 10, 20, and 30 seconds. The cells were stained with a live/dead stain (LIVE/DEAD® BacLight™ Bacterial Viability Kit L-7012) and then visualized using a confocal laser scanning microscope (Olympus IX-81). The percentage of live and dead cells were quantified via image analysis software. At the concentrations used, HOCl had kill rates 14.2% and 10.1% higher than NaOCl for 10 and 20 second intervals, but not for the 30 second treatment. The comparable results suggest that HOCl is an effective irrigant for *E. faecalis* biofilms and could be applied to clinical situations, given its lower cytotoxicity.

This research was supported by NIH Award Number R25GM071638 through the RISE program and NIH Award Numbers 8UL1GM118979-02, 8TL4GM118980-02, and 8RL5GM118978-02 through the BUILD Program.

30. Precision with Which Lambert's Law Can Be Used to Inexpensively Determine Thin Film Thickness.

Nathaniel J. Morrison and Thomas Gredig, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, CA 90840

Phthalocyanine thin film thickness affects the properties of the film in numerous applications. Typically, x-ray diffraction is used to determine the thickness of films in the sub-micrometer range. However, the x-ray measurements are complex, expensive, and, especially when the surface of the film is not smooth, can be inaccurate. Separate methods to measure the thickness of extremely thin films need to be used to ensure accuracy. Lambert's Law, which states that the thickness of a material is proportional to the natural logarithm of the amount of light it transmits divided by the amount of light it absorbs, could provide such a method, provided it can be used to accurately and precisely determine the thickness of thin films. To this end, the amount of light absorbed and transmitted by multiple films consisting of phthalocyanine on glass substrates were measured and used to calculate the thickness of the phthalocyanine. In this method, laser light passes through a variable beam attenuator and illuminates a photodetector. The voltage that develops is measured to determine the incident light levels. A thin film is then placed between the attenuator and the photodetector. At low light intensities, the transmission intensity is linear with the laser light intensity and a material-specific constant can be calibrated using a known sample. The setup is inexpensive and fairly consistent results across samples of the same materials are found. This suggests that the method may be a viable, quick, and inexpensive way to determine the thickness of thin films in the sub-nanometer length scale.

This research was supported by the W. M. Keck Foundation.

31. Optimization of Graphene Extraction and Infusion of Polyamide Nylon Fibers (PA-12)

Jessica Wewers and Ehsan Barjasteh Ph. D.
Department of Chemical/Mechanical and Aerospace Engineering, California State University, Long Beach, Long Beach, CA 90840.

Graphene, a 2-D, carbon allotrope, had been enthusiastically studied since its dimensional discoveries at the University of Manchester in 2004. The focus of it attraction is due to its many potential applications and highly desirable physical properties. Mass preparation of graphene thus far has been successful utilizing various techniques. The technique explored during this project was the liquid-phase exfoliation method of graphite to extract graphene. By implementing Hansen Solubility Parameters, this method has the potential to be quite simple, green and an inexpensive way to produce graphene. A frequent problem of using graphene for infusion into the fabric is their tendency to form accumulative blockages (aka agglomerates), minimizing optimal surface coverage during the coating process. While the HSP method using acetone and water does give a high quality of graphene dispersion in the solvent, its application in fabric infusion process has not been explored yet. Another approach, known as the 'Interfacial Trapping' method, also addresses this difficulty by creating an area for graphite/ graphene layers to reside (between two immiscible solvents). Therefore, this project will combine methods of HSP and interfacial using acetone, water and hexane to verify the hypothesis that this combination will result in an increase of graphene infusion into the fabric and thus enhance the PA12 surface conductivity.

This research was supported in part by LSAMP.

32. Oxygen Evolution Catalysis by Complex Oxides

Charles Bloed, Jiam Vuong, Hadi Tavassol, Ph.D., and Shahab Derakhshan, Ph.D.
California State University Long Beach, College of Natural Sciences and Mathematics
Long Beach, CA 90840

In this work, we will present our results on catalytic properties of complex oxides, i.e. perovskites and brownmillerites toward oxygen evolution reaction (OER), a key component of renewable energy devices. Catalysts based on precious metals such as RuO_2 and IrO_2 exhibit the highest activity, while lack of stability, high overpotenitals and cost are main obstacles in their application [1]. Complex oxides present an intriguing class of materials with high tunability of structure and property [2,3]. We focus on perovskites and brownmillerites with similar compositions. We employ novel solid state and gas phase synthesis methods to rationally design complex oxides with varying electronic properties and oxygen vacancies. A combination of physical characterization and electrochemical methods are then employed to investigate the interplay of these effects and OER catalysis. We are particularly interested in the effect of the ordering of the oxygen deficiencies on catalytic activity. We will present the results of our laser spectroscopy analysis of chemomechanics of oxygen interactions and its dependence on ordering of the oxygen deficiencies in model perovskite and brownmillerite systems.

References:

[1]WE, S. Electrocatalysis by Oxides Attempt at a Unifying Approach. J. Electroanal. Chem. Interfacial Electrochem. 1980, 111, 125−131
[2]Goodenough, J. B. Covalency Criterion for Localized vs Collective Electrons in Oxides with the Perovskite Structure. J. Appl. Phys. 1966, 37, 1415−&.
[3]J. Suntivich, May, K. J., Gasteiger, H. A., Goodenough, J. B., and Shao-Horn, Y., "A Perovskite Oxide Optimized for Oxygen Evolution Catalysis from Molecular Orbital Principles", *Science*, vol. 334, no. 6061, pp. 1383 - 1385, 2011.
[4]F. M. Figueiredo, J. R. Frade, and F. M. B. Marques, "Electrical and electrochemical behaviour of LaCoO3−)+La2(Zr,Y)2O7- based electrode materials," Solid State Ionics, vol. 118, no. 1-2, pp. 81–87, 1999.

33. No Abstract

34. Generation of Organoids from Human Neural Stem Cells and from Patient-derived Glioblastoma Cells

Alejandra Velazquez Ojeda, Blake Brewster, Christine E. Brown, Karen S. Aboody, Margarita Gutova*, and Michael E. Barish*
CIRM Bridges to Stem Cell Research Scholar, CSU Long Beach
*Co-senior authors
Departments of Developmental and Stem Cell Biology, and Hematology/HCT, City of Hope Beckman Research Institute and Medical Center

Three dimensional cultures *in vitro* that form self-assembling structures termed organoids that are reminiscent of their source tissue have emerged as a valuable technique in fundamental/translational medical science. We are interested in using this preparation to study cellular process of brain and brain tumor development and progression. Here we describe using L-myc immortalized human neural stem cells (NSCs; LM-NSC008) to initiate organoid cultures in Matrigel. Grown in appropriate media with gentle circular mixing, neural and brain tumor organoids survive without signs of necrosis for over two months. We explored temporal and spatial expression of markers of neural lineage in organoids initiated with LM-NSC008 neural progenitor cells. We also compared development of these cerebral organoids with organoids containing both LM-NSC008 cells and patient-derived glioblastoma (GBM) cells (PBT017), initially established at 1:1 ratio, to probe consequences of exposure of GBM cells on normal neural cell progenitors. To date we have probed expression of Sox2 (pluripotent stem cells), nestin (neural stem/progenitor cells), β-tubulin type III (Tuj1 antibody; early differentiated neurons), glial fibrillary acidic protein (GFAP; reactive astrocytes and GBM cells), Frizzled9 (Wnt5a receptor; presumptive hippocampus), FoxG1 (presumptive frontal cortex), p-Vimentin (radial glia), carbonic anhydrase IX (CA-IX) and HIF1α (hypoxia). Over time, LM-NSC008 organoids expanded and increasingly expressed markers of neural differentiation while maintaining neural progenitor cell populations. In older organoids, we observed regions of circumferential and radial orientation. Mixed LM-NSC008 + PBT017 cell organoids also became highly heterogeneous, apparently expressing neural differentiation markers in different patterns as compared with organoids with no PBT017 cells. Together, these data suggest that three-dimensional organoids are capable of recapitulating neural tissue development, and can be a useful tool for examining reciprocal NSC-GBM interactions. In a separate study not presented here, we have also examined growth of patient-derived GBM cells in organoid cultures, and suggest that GBM organoids may provide a physiologically-relevant platform for preclinical in vitro evaluation of nascent therapies for patients with GBM.

This project was supported by funding from CIRM Grant EDUC2-08383

35. Measuring Changes of Prolactin Expression by Gene Regulator DREAM (Downstream Regulator Element Antagonist Modulator) in Response to Exposures of PCBs95 and Triclosan

Jorge Alfaro and Erika Holland, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Cellular calcium (Ca^{2+}) plays a critical role in the function of endocrine pituitary cells, including cellular depolarization, internal protein: protein interactions and regulation of gene expression. Two protein channels that contribute to Ca^{2+} homeostasis in pituitary cells are the ryanodine receptor (RyR), a Ca^{2+} release channel imbedded in the sarco/endoplasmic reticulum of a cell, and L-type voltage-gate calcium channels (CaV1), which regulate Ca^{2+} entry upon cellular depolarization. Environmental pollutants such as non-coplanar polychlorinated biphenyls (ncPCBs) and triclosan (TCS) can alter RyR and CaV1 signaling, causing cellular Ca^{2+} signaling disruption (CSD). Disruption of RyR and CaV1 channels is associated with neurodegenerative diseases, and altered cardiac and skeletal muscle contraction. The cellular events contributing to these pollutant-based impacts are currently not fully understood, but are likely diverse considering that Ca^{2+} is involved in such a wide array of signaling pathways. My project investigates whether CSD, caused by the ncPCB, PCB95, and triclosan, may alter transcription of genes regulated by the Ca^{2+} dependent transcriptional repressor known as DREAM (downstream regulator element antagonist modulator). I will use a growth hormone secreting cell line (GH3) from the anterior pituitary to measure the impact of contaminant exposure on the expression of prolactin (PRL), which is known to be regulated by DREAM. Cells will be exposed to several concentrations of PCB95 or triclosan, for up to 24 hours and mRNA levels of PRL will be measured using qPCR. This work will help extend our knowledge of pollutant induced CSD by ncPCBs, triclosan and other compounds with structural similarity, such as the flame retardant tetrabromobisphenol A or polybrominated diphenyl ethers. Together, this work can determine whether CSD can contribute to DREAM regulated expression, where DREAM is found in cerebral neurons, the pancreas, pituitary and thyroid gland with implications in endocrine and cognitive health.

This project is supported in part by CSU Program for Education and Research in Biotechnology New Investigator Research Grant (CPO 15-51842) and the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980; 8RL5GM118978-02

36. Inositol Effects on Hyperglycemia and Obesity in *Drosophila melanogaster*

Angelina Flores, LongThy Nguyen, Elizabeth Eldon, Ph.D., and Lisa Klig, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Myo-inositol is a six-carbon sugar alcohol that is known as a precursor for phosphatidylinositol (PI), a cell membrane phospholipid. It is also involved in the phosphoinositide signaling pathway, which is essential for the regulation of cellular functions. *Myo*-inositol has been implicated in diseases and complications such as hyperglycemia, diabetes, and obesity – all of which are a major threat especially within the United States. This study focuses on these diseases by utilizing the model organism *Drosophila melanogaster*, also known as the fruit fly. The high sucrose diet used in the experiments induced obesity and hyperglycemia. Larvae grown on this semi-defined food had an obese-like phenotype that was demonstrated in a float buoyancy assay. Increasing the inositol concentration of this semi-defined food reduces the number of obese-like larvae. The deletion of the inositol synthase gene, or MIPS, also caused an obese-like phenotype. Since density is a function of both weight and size (volume) these buoyancy experiments were furthered with a preliminary evaluation of the density of the larvae. This study also addresses hyperglycemia by measuring the glucose content within the hemolymph of the larvae. High sucrose increases the levels of glucose in the hemolymph, while inositol supplementation reduces the hemolymph glucose. The lack of the MIPS gene results in elevated glucose within the hemolymph. These studies should contribute to a better understanding of inositol's role in diseases such as obesity, hyperglycemia, and diabetes.

This project is supported in part by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638 and CSULB RS114.

37. Phthalocyanine Growth Dependence on Gold Substrate Roughnesses

Joshua Corona and Thomas Gredig, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

The growth of copper phthalocyanine (CuPc) in the form of thin films is studied on top of metal substrates with different roughnesses. Phthalocyanine thin films grow different molecular stacking configurations either on insulator or metal surfaces. In this study, the roughness of the metal surface is modified through either a chromium seed layer or the thickness of the metal, which is gold. The Gold thickness is varied by depositing 0 nm – 30 nm on top of Chromium-adhesion layer. One control sample has CuPc deposited directly onto the Silicon substrate. The growth of the phthalocyanine is studied via x-ray diffraction (XRD) and x-ray reflectivity (XRR). From XRD, the crystallinity, roughness, and thickness are determined. Increasing the Gold thickness resulted in rougher surfaces, such that the CuPc (200) crystal peak disappeared. This indicates that CuPc is partially lying on thin, smooth gold surfaces, and oriented differently on the thicker, rougher surfaces. XRR gives better data at grazing angles, of 1 - 10° 2θ. The oscillations confirm the smooth surface at 5 nm of Gold thickness.

38. The Role of Microglia in Traumatic Brain Injuries in Mouse Models and Human iPSC-derived 3D Cerebral Organoids

Leslie Tram[1], Krystal Carta.[2], Diane Su.[2], Eric Gold.[2] and Brian Cummings, Ph.D.[2]
[1]Department of Biological Sciences, California State University Long Beach
[2]Institute for Memory Impairments and Neurological Disorders, University of California-Irvine

Traumatic brain injury (TBI) is the leading cause of death and disability in the young population with an estimate of 1.7 million Americans affected yearly. Previous studies have shown that there is a strong association between TBI and Alzheimer's Disease (AD), suggesting that repeated concussions can lead to formation of amyloid25plaques and neurofibrillary tangles. Our lab is probing the link between TBI and AD by studying the role of microglia, which carry out innate immune responses such as neuroinflammation following TBI. Microglia have been shown to be both neurotoxic and neuroprotective after TBI. Their phagocytic activity can rescue neurons from degeneration by sequestering foreign bodies that penetrate the brain. Microglia are also the source of proteins that are upregulated in both post TBI and AD including b–amyloid precursor protein(b-APP) and g-secretase, resulting in higher Ab production. As well, the complement system has been implicated in CNS disorders whereby an imbalance in complement proteins could result in increased phagocytic activity by macrophages. I am studying the role of microglia in TBI to determine whether neuroinflammation influences the development of AD neuropathology. It was hypothesized that injured groups in all models would have significantly higher microglial counts in comparison to controls due to a rapid neuroinflammatory response that occurs following TBI. To test this, we measured microglia post TBI in 3 different models (3D-cerebral organoids generated from induced pluripotent human derived stem cells with different ApoE genotypes, repeated mild TBI (rmTBI) in mice, and a cortical contusion injury (CCI) in complement C3 knockout (KO)mice). Analysis of microglia quantified by Iba1 immunohistochemistry revealed a significant increase in microglia between the sham cerebral organoids compared to injured. In addition, there was a significant increase in microglia in the hippocampi of mice who received rmTBI compared to uninjured mice 6 months post TBI. Lastly, there was a significant increase in the microglia levels in C3 wild type vs KO brains 6 weeks post TBI, indicating that C3 does play a role in microglial activation. In conclusion, we show that rmTBI is responsible for microglial activation and that microglial activity is regulated by C3. We show that there was a trend for increases in microglia between control/sham compared to injured 3D cerebral organoids post long term TBI, indicating microglial degeneration after a certain period. Future studies will examine the correlation between microglia and the development of AD pathology following rmTBI in mice carrying the tau gene or the human b-APP gene.

This project was supported by funding from CIRM Grant EDUC2-08383.

39. Transcriptome-based phylogeny of the plant family Acanthaceae

Joshua D. Arias, Emily Do, and Amanda Fisher
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90804

Acanthaceae is a diverse, widespread, and ecologically important tropical plant family with approximately 4000 species, many of which have striking floral displays. The family includes *Justicia* (ca. 400 spp.) and *Ruellia* (ca. 300 spp.), genera that have both had species radiations in the new world tropics. Knowing the closest relatives to these genera will help in our understanding of these radiations in an evolutionary context. The likely candidates are in the BAWN clade, an acronym for the subfamilies Barlerieae, Andrographideae, Whitfieldieae and the genus *Neuracanthus*. Our goal is to estimate a nuclear-based phylogeny of Acanthaceae to test which lineage is most closely related to *Justicia* + *Ruellia*. We hypothesize that a nuclear-based phylogeny of Acanthaceae will resolve areas of low support in the BAWN clade, allowing for a more comprehensive understanding of relationships within Acanthaceae. Complementary DNA libraries of seven Acanthaceae species were created using the Breath Adapter Directional sequencing method, and sequenced with Illumina HiSeq 4000. The seven newly sequenced species and publicly available sequence data for four additional species were assembled from cleaned reads using Trinity (v2.4.0). The 11 transcriptomes were analyzed using OrthoFinder (v1.1.8) to identify orthologous loci and infer a preliminary phylogenetic tree. OrthoFinder identified 26,457 orthologous genes, 25 of which had a single copy across all sampled species. Our preliminary tree conflicts with the previously published chloroplast tree in that the BAWN clade is paraphyletic, placing *Justicia* + *Ruellia* sister to *Andrographis* + *Whitfieldia*. We also prepared stained slides of transverse leaf sections from representative species in the BAWN clade and describe differences in their leaf anatomy that may be systematically relevant. This research will inform future systematic and character evolution studies of Acanthaceae that will contribute to our understanding of diversity in the family.

This project is supported in part by the National Institutes of Health Award #R25GM071638 and A. Fisher's start-up funds provided by the state of California.

40. Targeted therapy for breast cancer bone metastases using mRNA engineered mesenchymal stem cells: a promising treatment.

Michael Toledano[2], Aude Ségaliny[1], Leanne Hildebrand[1], Jason Cheng[1], Michael Liao[1], Dongxu Liu[3], Jaedu Cho[3], Lizhi Sun[4], Gultekin Gulsen[4], and Weian Zhao[1]

[1]Department of Pharmaceutical Sciences, Sue and Bill Gross Stem Cell Research Center, University of California, Irvine, Irvine, CA, 92697

[2]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

[3]Department of Biomedical Engineering, University of California, Irvine, Irvine, CA, 92697

[4]Henri Sameuli School of Engineering, University of California, Irvine, Irvine, CA, 92697

Mesenchymal stem cells (MSCs) appear to be an ideal vehicle for drug delivery to bone metastases due to their natural tendency to home to the bone marrow and their ability to localize into and integrate within the tumor niche. In addition, they are easy to handle, readily available in sufficient numbers, and they lack major immunogenicity. When used as a platform for the delivery of treatment to a tumor region, they exert strong therapeutic activity within 7 days after transplantation, and leave little or no residual presence when their therapeutic lifespan is exceeded. Their safety has been demonstrated in hundreds of studies and in a multiplicity of treatment modalities. In our study, we used a simple mRNA transfection to simultaneously amplify the MSCs' natural homing tendencies to bone metastases and deliver on site a therapeutic combination treatment designed to prevent both the tumor progression and the osteolysis which is one of the most damaging and debilitating consequences of bone metastases. We demonstrated that our mRNA transfection utilizing a well-characterized prodrug conversion system induces MSCs to secrete a cytosine deaminase that successfully converts 5-fluorocytosine, the pro-drug, into the metabolically active 5-fluorouracil; we demonstrated that the mRNA transfection of PSGL-1 and FUT-7, a pair of selectin ligands, significantly increases homing of MSCs to targeted regions; we demonstrated that the non-TRAIL-binding osteoprotegerin variant reduces osteoclast maturation in tumor regions; and finally we demonstrated that the entire clinical package of mRNA-transfected MSCs is effective as a viable therapy for bone metastases in our animal model.

Funded by CIRM grant EDUC2-08383 and NIH grant 1DP2CA195763

41. Progesterone Receptor, Src Family Kinase, and Dopamine D1 Receptor Colocalization in Arcuate Nucleus β-Endorphin Neurons.

Joshua Razon, Nasir Khan, Monica Eskander, Timbora Chuon, and Kevin Sinchak, Ph.D.
Department of Biological Sciences, California State University, Long Beach, CA 90840

A priming dose of estradiol benzoate (EB) inhibits sexual receptivity (lordosis) in ovariectomized (OVX) rats through activation of β-endorphin (β-END) neurons in the arcuate nucleus of the hypothalamus (ARH). These β-END neurons, which project to the medial preoptic nucleus (MPN), then cause the activation and internalization of μ-opioid receptors (MOP) to inhibit lordosis. EB upregulates the expression of progesterone receptor (PGR) necessary for facilitation of lordosis. EB priming with sequential progesterone leads to the deactivation of ARH β-END and consequently the deactivation of MPN MOP to facilitate lordosis. Previous behavioral studies have shown EB priming and subsequent progesterone to facilitate lordosis within 30 minutes. The rapid effects of progesterone indicate that extranuclear receptor signaling is involved to facilitate lordosis. These effects are mediated by PGR complexing and signaling through Src. Previous studies confirmed, through western blot analysis and co-immunoprecipitation the presence of PGR, Src, and PGR-Src complexes in cytoplasm and membrane cellular fractions of the ARH. This PGR-Src complex is interdependent on dopamine receptor (D1) signaling to facilitate sexual receptivity. Dopamine receptor has been shown to signal through Src as well as interact with progesterone receptors through ligand independent mechanisms. We hypothesize that PGR, Src, and D1 are co-expressed on ARH β-END neurons and their signaling converges interdependently to facilitate lordosis. To test this, both double-label and triple-label immunohistochemistry were performed. Double-label immunohistochemistry shows positive immunostaining of PGR, Src, and D1 colocalized on ARH β-END neurons. Further, triple-label immunohistochemistry shows colocalization of PGR, Src, and D1 on β-END neurons at the level of the ARH. The data supports the interdependent signaling of PGR, Src, and D1 to facilitate lordosis.

This project is supported in part by Award Number RO1HD05638 Eunice Kennedy Shriver National Institutes of Child Health & Human Development.

42. The role of correlated electrons in thermoelectric properties of filled skutterudites

A. Cortez[1], D. Cheikh[2, 3], K. E. Star [2], K. Lee [2], J.P. Fleurial[2], and S. Bux[2], and S. Derakhshan[1]

[1]Department of Chemistry and Biochemistry, California State University, Long Beach, 1250 Bellflower Boulevard, Long Beach, California 90840, United States.

[2]Thermal Energy Conversion Research and Advancement, Jet Propulsion Laboratory 4800 Oak Grove Drive, Pasadena, CA 91109, USA.

[3]Department of Materials Science and Engineering, University of California Los Angeles, 410 Westwood Plaza, Los Angeles, CA 90095.

Filled skutterudites have attracted a great deal of interests due to their ability to host various physical properties. They have shown to be promising thermoelectrics, heavy- fermion compounds, and superconductors and also exhibit various phenomena such as metal– insulator transition. Their general formula is A_yBX_3 where *B* is typically a group eight or group nine transition metal ion and *X* is a pnictogen, which forms X_4^{4-} polyatomic ions. Accordingly, these materials are placed in the class of zintl phases and are generally expected to obey the electron precise formulae [1]. Electronic properties of these materials show strong dependency to their constituent elements along with the electron count scheme. The maximum value of y in the filled variants is equal to 1. Selection of *y* value is critically important as it simultaneously affects the charge carrier density and the lattice thermal conductivity. Due to the charge balance the attempts to fill $CoSb_3$ base compound has resulted in $y_{max} \sim 0.3$ thus far by high pressure synthesis method which has resulted in an enhanced zT of ~1.06 at 863K [2]. To increase La occupancy, partial replacement of Co^{3+} by Fe^{2+} ions have been already formulated. This approach has proven to be effective in optimizing the transport properties of the material. Here we report on our recent work on heavy element transition metal doped analogs of the materials. More diffused *d* orbitals of *4d* and *5d* metals compared to those of *3d* elements along with their stronger spin-orbit coupling is expected to improve the effective mass of charge carriers in favor of enhanced Seebeck coefficient. TE properties of these novel variants will be presented.

The research reported in the paper has in part been supported by the W. M. Keck Foundation through the Keck Energy Materials Program (KEMP) at CSULB.

References:

H. Luo, J. W. Krizan, L. Muechler, N. Haldolaarachchige, T. Klimczuk, W. Xie, M. K. Fuccillo, C. Felser and R. J. Cava, A large family of filled skutterudites stabilized by electron count, *Nat. Commun.* **(**2015). DOI: 10.1038/ncomms7489

C. Chen, L. Zhang, J. Li, F. Yu, D. Yu, Y. Tian, and B. Xu; Enhanced thermoelectric performance of lanthanum filled $CoSb_3$ synthesized under high pressure, *J. Alloys Compd.* **699** (2017) 751–755. DOI: 10.1016/j.jallcom.2016.12.425.

43. Experimental Techniques for Low Temperature Electronic Transport Measurements

Josue Rodriguez[1]*, Amirari Diego[1]*, Ryan Reno[1],Francisco Ramirez[1], Jared Lara[1] and Claudia Ojeda-Aristizabal, Ph.D.[2]
[1]Department of Physics, California State University, Long Beach, Long Beach, CA 90840.
[2]Ph.D. Physics, Université Paris-sud XI, Orsay France (2010).
*A. D. and J. R. contributed equally to this work

Low temperature electron transport measurements can be used to probe exotic physics in two dimensional materials. Such experiments require sophisticated sample fabrication, the integration of the samples into microelectronic devices and a cryogenic temperatures to execute measurements. The Nanoelectronics Group has mounted new equipment for this purpose, including a lithography system to draw circuits at the nano-scale and a closed cycle cryostat free of liquid cryogens to perform electronic transport at low temperatures and in magnetic fields up to 12 Tesla. Materials to be studied present novel phenomena derived from the interplay of electronic correlations and spin-orbit coupling. Preliminary sample fabrication will be presented using the new nanolithography system installed on the CNSM scanning electron microscope, as well as the procedure to create a nano pattern using the Nanometer Pattern Generation System developed by J. Nabity. Details on the setup and testing of the closed cycle cryostat will be presented, including the fabrication of a breakout box that allows performing measurements on samples sensitive to electrostatic discharges.

44. Lipid-Encapsulated Hydrophobic Palladium Nanoparticles for Biphasic Catalysis of Olefins in Water

Dominick Ortega, Tuan Trinh, and Young-Seok Shon, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840.

Despite the availability of many water-soluble organometallic and nanoparticulate catalysts, the direct application of water-soluble catalysts for the reaction of immiscible and hydrophobic substrates has been hindered by the low solubility of nonpolar reactants in water. Our research group has shown that alkanethiolate-capped palladium nanoparticles (PdNP) exhibit excellent catalytic activity and selectivity for hydrogenation of unsaturated compounds in organic solvents. This PdNP was synthesized using the thiosulfate protocol using sodium S-dodecylthiosulfate as ligand precursor. The purpose of this study is to examine the catalytic activity of PdNP encapsulated in phosphatidylcholine (PC) lipids in water. After the lipid assembly of PdNP with PC in dichloromethane, the solvent was removed under vacuum and the hybrid was hydrated with phosphate buffered saline (PBS) solution. The resulting lipid-PdNP hybrids dissolved in water were characterized by UV-vis spectroscopy and transmission electron microscopy (TEM). During the catalysis reaction, the micellar characteristics of lipid-PdNP hybrid would allow the hydrophobic substrate such as 1-octene to momentarily enter the hydrophobic region of the catalysts with adequate stirring force. After the reaction, the resulting products from bi-phasic system were subsequently extracted with organic solvents and analyzed using ^{1}H NMR spectroscopy. The results suggested that the transformation of 1-octene to octane could be completed within 1 h of catalysis reaction under atmospheric pressure and at room temperature. The recycling tests of catalysts indicated that the aqueous phase containing the lipid-PdNP hybrids could be reused multiple times with only small decreases in the overall reaction rate.

This project is supported by the National Institute of General Medical Science (#SC3GM089562).

45. Characterization of GNΦ2, a *Halorubrum* virus: one-step growth curve

Justin O. Rodriguez, Shereen Sabet, Ph.D., and Jesse G. Dillon, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Prior studies of extremophiles cultured from habitats such as hot springs and hypersaline ponds have resulted in important biotechnological and industrial applications. However, much is still unknown about the biological diversity of halophilic microbes (e.g. bacteria, archaea) and even less is known about the viruses that infect these microorganisms. Thus, research on extreme halophilic viruses may yield important breakthroughs for biotechnological and industrial applications. A key first step is to characterize the growth of halophilic viruses in relation to their host. Research in our lab is currently being done with an extreme halophilic virus, called GNΦ2, using its haloarchaeal (*Halorubrum*) host, named P12. We are currently investigating the growth cycle of GNΦ2. When host cell lysis occurs, we predict GNΦ2's growth to increase exponentially in a one-step curve while P12's growth will decrease. Before attempting to infect our host cells, the correct multiplicity of infection (MOI) was determined. Uninfected and infected culture bottles were monitored for 72 hours with optical density (OD) readings taken every 6 hours to record P12 growth activity, while, infected cells were sampled to perform a plaque assay, determining the virus' titer at each time-point. Preliminary experiments showed unexpected results, indicating an asynchronous infection. I will repeat the experiment with modifications to synchronize the infection in order to gain more accurate data. Understanding how GNΦ2 proliferates is crucial to understanding its biology.

This project is supported by the Research Initiative for Scientific Enhancement (RISE) (NIH 2R25GM071638-09A1).

46. Synthesis Characterization and Physical Properties of Novel NaCl Type Transition Metal Oxides

G. T. Tran[1], L. Lawson[1], T. Gredig, Ph.D.[2], and S. Derakhshan, Ph.D.[1*]
[1]Department of Chemistry and Biochemistry, California State University, Long Beach, CA 90840-9507
[2]Department of Physics and Astronomy, California State University, Long Beach, CA 90840-9505

Heavy element transition metal oxides with ordered rock salt structure type have attracted a great deal of interest due to their potential in exhibiting geometric magnetic frustration. [1-2] This phenomenon takes place when the spin constraints cannot be fulfilled simultaneously. Our group recently discovered and characterized Li_4NiOsO_6, and $Li_3Ni_2OsO_6$ where the interactions between 3d and 5d paramagnetic ions resulted in ferrimagnetic ground state. In an effort to expand our knowledge in such interactions and investigate the role of spin quantum numbers in resultant magnetism, we successfully synthesized Li_4FeOsO_6 and Li_4FeReO_6 by conventional solid-state method. The crystal structure was determined, employing powder X-ray diffraction technique. These compounds crystallize in monoclinic space group *C2/m* and are isostructural with Li_4NiOsO_6. Temperature dependent magnetic susceptibility data reveals a broad maximum, which is indicative of short-range, low-dimensional antiferromagnetic transition.

The research reported in the paper has in part been supported by NSF Award #160181 and the W. M. Keck Foundation through the Keck Energy Materials and Education Program (KEMP) at CSU Long Beach.

References:

[1]P-H. T. Nguyen, M. Kemei, M. S. Tan, S. Derakhshan., Synthesis, crystal structure and magnetic properties of the two polymorphs of novel *S=1* osmate; Li_4MgOsO_6, J. Solid State Chem., **242**, (2016), DOI: 10.1016/j.jssc.2016.01.025.
[2]P-H T.Nguyen, *F.* Ramezanipour, J. E. Greedan, L.M.D. Cranswick, S. Derakhshan**,** Synthesis, Crystal Structure, and Magnetic Properties of $Li_3Mg_2OsO_6$, a Geometrically Frustrated Osmium(V) Oxide with an Ordered Rock Salt Structure: Comparison with Isostructural $Li_3Mg_2RuO_6$, Inorg. Chem., **51**, (2012), 11493-11499, DOI: 10.1021/ic3013377.

47. Methods for Detecting the Prevalence of Microplastic Pollution Surrounding the Highly Urbanized Area of Long Beach, CA

Kara J. Wiggin and Erika B. Holland, Ph.D.
Department of Biological Sciences, California State University at Long Beach, Long Beach, CA 90840

Plastic production has drastically increased over the last 60 years, and consequently so have the levels of marine plastic pollution, largely attributed to mismanaged waste and litter. New research demonstrates a vast prevalence of smaller plastic particles in the marine environment, known as microplastics (<5 mm in size). Microplastic pollution presents an increasing concern as these smaller sizes can be consumed by lower trophic species vital to the bottom of the food chain. Even though recent studies have shown that invertebrate zooplankton can eat plastic particles from 1μm to 30 μm, common sampling protocols only sample plastic greater than 333 μm, a common plankton net size. Thus questions remain regarding the exact sizes and quantities of microplastics prevalent in the environment. To address this data gap, the presence of microplastics sized between 1 and 500 μm will be assessed in the Long Beach Harbor, the San Gabriel River, and the Los Angeles River (CA; USA), three areas with highly urbanized surroundings. Microplastics were quantified in 20 L surface water grab samples and particles size fractionated through sieves of various pore sizes. Particles present on each sieve were subject to hydrogen peroxide in order to isolate plastics from organics, and the remaining plastic particles quantified and categorized under 40x-200x magnification. In preliminary assessments, the San Gabriel River revealed a potential 609 microplastic particles in 20 L, and the Los Angeles River revealed a potential 2,359 microplastic particles in 20 L. The majority of particles present in the water samples from both rivers were microfibers. This project will help establish a standard processing protocol for microplastic quantification to include sizes below 500 μm, helping to better understand the risk that small microplastics pose to invertebrate zooplankton.

This project is supported by the COAST Graduate Student Research Grant, the Reish Research Grant in Marine Biology and the SCTC Marine Biology Foundation Grant.

48. Synthesis of Alkanethiolate-Capped Palladium Nanoparticles Through Reversed Alkyl Thiosulfate Addition to Control Core Size & Vary Surface Ligand Density.

Kevin M. Vargas, Khin Aye San, and Young-Seok Shon, Ph.D.
Keck Energy Materials Program and Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840.

Ligand-capped metal nanoparticles exhibit promising properties as catalysts. Its large surface to volume ratio allow for high catalytic activity, while its ligands dictate the immediate environment around the catalytic surface, allowing for directed catalytic selectivity. Alkanethiolate-capped palladium nanoparticles (PdNP) have previously been synthesized using a modified Brust-Schiffrin synthesis (thiosulfate method), in which the nanoparticle core size is established during alkyl thiosulfate passivation followed by sodium borohydride ($NaBH_4$) reduction and nanoparticle formation. This resulted in PdNP with smaller cores having higher surface ligand density and PdNP with larger cores having lower surface ligand density. To directly study the effects of surface ligand density on catalytic activity, PdNP with similar core sizes, yet different surface ligand density were synthesized using reversed alkyl thiosulfate addition method. In this method, $NaBH_4$ is added before the alkyl thiosulfate and the core size of PdNP is established during the temporary passivation of Pd nucleation by borohydride and tetraoctylammonium bromide (TOAB), allowing for nucleation to reach completion. Various molar equivalents of alkyl thiosulfate are then added, causing the replacement of borohydride and TOAB and the formation of alkanethiolate-capped PdNP. The resulting nanoparticles were characterized by ^1H NMR, UV-vis spectroscopy, infrared spectroscopy (IR), thermogravimetric analysis (TGA), and transmission electron microscopy (TEM). Future directions involve assaying the synthesized PdNP of varying surface ligand density for catalytic activity with a library of substrates and subjecting to kinetic studies. Successful optimization of the reversed thiosulfate method would allow researchers valuable control over ligand-capped metal nanoparticle synthesis.

This project is supported by the Undergraduate Education Program of the W. M. Keck Foundation and the National Institute of General Medical Science (#SC3GM089562).

49. Effect of Previous Exposure to a Female of a Single Phenotype on Subsequent Male Mate Choice in *Drosophila melanogaster*

Katherine E. Henson and Ashley J.R. Carter, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

A prevalent paradigm in sexual selection theory is Bateman's principle of a "choosy female" and "promiscuous male," leading to male mate choice being deemed inconsequential. However, male choice may play a larger role in sexual selection than previously thought. We examined male choice in *Drosophila melanogaster* by observing relative preference for certain phenotypes by males after differing initial exposure treatments. Virgin male wild type *D. melanogaster* individuals were exposed to a female that was wild type, yellow, or ebony. Later, the same males were allowed to choose between three females differing in phenotype: two thereby having novel phenotypes and one having the phenotype already encountered. Males showed a significant preference for novel phenotypes, with the familiar phenotype being the least preferred ($p=0.0175$). This evidence supports a process by which males aim to increase genetic diversity among offspring by mating with phenotypically diverse females when given the opportunity.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

50. Novel Phosphors for Solid-State Lighting Devices

Stephanie Araiza, Katarzyna Slowinska Ph.D.[1] and Shahab Derakhshan Ph.D.[1]
[1]Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach CA, 90840

A Phosphor material is a substance that emits light through the process of luminescence. Inorganic solids may show luminescence when a host material is doped with impurities referred to as activators. These activators are essentially a light emitting center within the host material, and can be stimulated with a variety of sources, such as light, heat, current and mechanical pressure. One of the most common types of activators are inner transition metal ions, which utilize high energy electromagnetic radiation to achieve luminescence. Currently, there is a large drive to utilize these materials for solid state lighting which have many advantages over ubiquitous incandescent and fluorescent sources. Some advantages to solid-state lighting include improved efficiency, decreased toxicity, thermal stability, spectral tunability, and better color rendering. The novel phosphors were created by starting with host lattice $CaYGaO_4$[1]. The system belongs to the olivine family and crystallizes in the orthorhombic *Pmna* space group. $CaYGaO_4$ exhibits full cationic ordering, which is a different structural feature from all reported silicate and germate olivines. The host lattice contains three independent cationic positions, each of which gives rise to a different chemical environment. Edge shared CaO_6^{10-} octahedra form infinite chains along the *b*-axis, corner shared YO_6^{9-} octahedra form puckered layers perpendicular to the a-axis and GaO_4^{5-} tetrahedra fill the spaces between the octahedra. The parent compound was doped with various lanthanide ions in the yttrium position up to ten percent. The samples were synthesized via sol-gel technique, using the appropriate nitrates and carbonates with water as the solvent and citric acid as the binder. The reactions were monitored by powder X-ray diffraction technique. Absorption, excitation and emission spectra were measured using fluorescence and diffuse reflectance. Europium and Terbium were successfully doped into the system up to ten percent. All excitation spectra were found to lie within the UV range and emission colors varied from green to orange, depending on the activator. Future work for this project includes doping of cerium and erbium ions and the partial replacement of oxygen with nitrogen. Finally, different combinations of activator ions will be doped into the parent compound to create a white light emitting material.

References:

Clark, R.; Zhu, S.J.; Zheng, S.-T.; Bu, X.; Derakhshan, S. *Journal of Alloys and Compounds*. 2014, *616,* 340-344.

This research was supported by the NSF DMR RUI Award #1601811. This research was also supported by W.M. Keck Foundation through the Keck Materials Energy Program (KEMP) at CSULB.

51. Effects of Mammalian Aposematic Pattern Variation on Predator Response.

Kathy Vo and Theodore Stankowich, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Bold, contrasting coloration causes aposematic individuals to stand out in their environment and be easily distinguished from more palatable prey. The degree to which aposematic coloration makes prey defenses easy for predators to learn, recognize, and remember is important because more effective learning reduces mistaken attacks. While we know a great deal about predator learning and the evolution of aposematism in avian predators on aposematic invertebrates, mammalian predators and aposematic mammalian prey have been mostly ignored. Coyotes (*Canis latrans*), ubiquitous mammalian predators, overlap in range with and are potential predators of striped skunks (*Mephitis mephitis*), an aposematic prey animal found widely across North America. In order to determine how contrast intensity and pattern structure influence the speed of avoidance learning in canid predators we are initially conditioning captive coyotes to attack brown benign, baited prey models and subsequently presenting them with noxious spraying prey models that vary in pattern structure and contrast intensity. Differences in the latency to attack or interact with the novel spraying models is compared with respect to the contrast intensity and pattern structure of the model. Past research shows that coyotes can easily learn to avoid attacking black-and-white prey models and can generalize this avoidance to models with greater amounts of white (high contrast) but not to models with greater amounts of black (low or no contrast). Preliminary findings suggest that coyote subjects demonstrate greater latency to attack all black-and-white (maximum contrast) models, regardless of pattern structure, compared to the black-and-gray (minimal contrast) model. If supported by further data, these early results may explain the consistent use of black and white coloration, but large variation in pattern structure, exhibited by skunks in the continental United States.

This project is supported in part by Bennett Kayser, as well as the National Institutes of Health Grant 2R25GM071638-09A1.

52. Effects of Electromagnetic Radiation on a Proximity System

Alberto J. Garcia[1], Luis Leal[1,2], Andreas Bill, Ph.D.[1]
[1]Department of Physics & Astronomy, California State University, Long Beach, Long Beach, CA, 90804
[2]Department of Physics and Astronomy, University of Rochester, Rochester, NY, 14627-0171

We analyze superconducting-magnetic hybrid structures made of inhomogeneous magnetic film and a superconducting thin film (S/F). In previous work done by the group, we determined pair correlations in the diffusive regime (in the presence of large concentration of non-magnetic impurities). More recently, we also started working on the opposite, clean limit and wrote a code to solve the Bogoliubov-de Gennes (BdG) to compare pair correlations in the two limiting cases. In this work, we continue the study of pair correlations in the clean limit and incorporate the effects of an externally applied electromagnetic radiation. The applied field can be modeled as a slow-varying plane wave with a fixed but arbitrary frequency incident on the system at a certain angle. We implement the effects of the radiation using the Peierl's substitution to include a time-dependent vector potential in the tight-binding model Hamiltonian. The Peierl's substitution modifies the hopping parameter by introducing a phase that describes the added perturbation. We present the method and discuss how the electromagnetic radiation affects the pair correlations in a superconducting-magnetic proximity system.

We gratefully acknowledge support from the National Science Foundation under grant DMR-1309341. A.J.G. thanks the Office of Research and Sponsored Programs (ORSP) for the summer support through the Summer Research Scholarship.

53. No Abstract

54. Neural Stem Cell-Mediated Approach to Treat Advanced Cervical Cancer

Angela D. Hoang[1], Revathi Tirughana[2] , Soraya Aramburo[2], Linda Flores[2], Asma Abdul Majid[2] , Karen S. Aboody[2]
[1]California State University, Long Beach, Long Beach, CA
[2]Research Institute & City of Hope, Duarte, CA

Cervical cancer is the fourth most common cancer among women worldwide. Detection at an early stage has a favorable prognosis; however this disease can often go unnoticed. As the stage of cancer progresses, fewer treatment options are available. At advanced stages, standard of care treatment is limited to platinum-based combination chemotherapy and clinical trials. However, response rates to second-line therapy diminish if the cancer persists, often leading to an incurable disease (Recurrent disease 5-year survival rate <5%). For that reason, there is a crucial need for an effective therapeutic approach to treat advanced cervical cancer. Neural stem cells (NSCs) have been shown to be inherently tumor tropic to numerous tumor models. For that reason, NSCs can be utilized to selectively target many different solid tumors and deliver various therapeutic agents. Our lab has established a well-characterized and non-immunogenic human neural stem cell line that is currently being tested in three Phase 1 clinical trials. For this study, we aim to identify an NSC-mediated approach to deliver therapeutic payloads to cervical cancer cells. We have conducted *in vitro* tumor tropic studies with NSCs to cervical cancer cell lines (HeLa, SiHa, C-33A) as well as *in vivo* NSC biodistribution studies. Simultaneously, we are testing the therapeutic efficacy of two NSC-mediated treatments that are currently being evaluated in other cancer models. One approach is the prodrug/enzyme therapy in which NSCs will secrete an enzyme to convert a prodrug into its highly active metabolite form at tumor sites. Another approach is utilizing NSCs as cell carriers to deliver the oncolytic adenovirus CRAd-S-pk7 to tumor sites. NSCs are capable of overcoming viral delivery hurdles and can release infectious CRAd-S-pk7 progeny capable of inducing cancer cell death. CRAd-S-pk7 is a conditionally replication-competent adenovirus consisting of two genetic modifications which (i) Promote viral entry into target cells and (ii) Prevent viral replication in the absence of the survivin promoter, a gene that is over-expressed in many cancers. By showing *in vitro* and *in vivo* NSC tumor tropism as well as therapeutic efficacy of two different NSC-mediated approaches *in vitro*, our next step is to demonstrate therapeutic efficacy of these treatments *in vivo*. Our long term goal is to propose a novel approach to treating advanced cervical cancer while minimizing toxicity to normal tissue in patients. This project was supported by funding from CIRM Grant EDUC2-08383.

Keywords: Neural stem cells, Cancer, Targeted therapy

55. Photochemical Reactivity and Reaction Mechanisms of 1,4-Cyclohexadiene: A Theoretical Approach

Kenneth Rodriguez and Enrico Tapavicza , Ph.D.
Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach CA, 90840

Organic photochemical reactions are ubiquitous in biological systems, such as vitamin D formation and retinal isomerization, and have medical implications, such as photodynamic therapy and drug-induced photosensitivity. From these instances, the photochemistry has been extensively studied, however the details of their mechanisms are largely unknown. In a previous study, our lab had accurately described several bond breaks of 1,3-cyclohexadiene (1,3-CHD), a molecule that performs a photoinduced ring-opening reaction akin to the photosynthesis of vitamin D. This was accomplished by studying the excited state dynamics using *ab initio* molecular dynamics based on linear response time-dependent density functional theory surface hopping methods (LR-TDDFT-SH). Our goal is to extend this study using 1,4-cyclohexadiene (1,4-CHD) to better understand the fundamental mechanisms in organic photochemistry, particularly the photochemical behavior of double bonds. So far, our results show that when the excited state dynamics of 1,4-CHD proceeded to the ground state, the molecule was mainly unreactive, however the formation of either 1,3-CHD or bicyclo[3.1.0]hexane can occur. Unlike previous findings of 1,3-CHD, in which a relatively high percentage of simulations resulted in ring-opening reactions, the simulations for 1,4-CHD indicate that the high degree of symmetry of the molecule may be responsible for limiting the available photoinduced reaction pathways.

Acknowledgements: This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Key Words: Cyclohexa-1,4-diene, organic photochemistry, ab initio, molecular dynamics

56. Relative abundance of *Myo*-inositol-3-phosphate Synthase Transcripts (MIPS) in *Drosophila melanogaster.*

Diana Machado, Mya Walker, ED Eldon, Ph.D., and LS Klig, Ph.D.
Department of Biological Sciences, California State University Long Beach, Long Beach, CA 90840

Myo-inositol is a six-carbon sugar alcohol that is essential as a precursor of the phosphoinositide signaling pathway, and aids in cellular metabolism and osmoregulation. Alterations of *myo*-inositol metabolism has been implicated in a number of disease processes, including bipolar disorders, Type II diabetes, female infertility due to polycystic ovary syndrome, and male infertility due to sperm motility disorders. Inositol is obtained three ways: transport from the environment, breakdown of inositol-containing macromolecules, and synthesis from glucose-6-phosphate diverted from glycolysis or produced by the pentose phosphate pathway. Inositol synthesis is catalyzed by *myo*-inositol-3-phosphate synthase (MIPS), which is a homotetramer in most organisms. In *Drosophila melanogaster,* post-transcriptional processing of the MIPS mRNA produces at least three isoforms: the canonical 1.8kb transcript comprised of five exons in sequential order, a 1.4kb, exon-shuffled transcript with a fragment of the second exon translocated to the 5' end of the transcript, and a 1.1kb transcript entirely lacking the second exon (Jackson, 2015). These three isoforms were observed in RT-PCR experiments and confirmed by sequencing. Each of these transcripts contain open reading frames, the largest (1.8 kb) encodes the established 62 kDa MIPS protein, while the 1.4 kb and 1.1 kb encode the same 35 kDa protein. Additionally, the 1.4 kb transcript encodes two small proteins (2.7 and 1.9 kDa). Preliminary qPCR experiments reveal differences in the relative abundance of these three transcripts in larvae, pupae, and adults. There are no obvious differences in the levels of these transcripts, however, between males and females at any given stage. These studies contribute to understanding the regulation of inositol synthesis in eukaryotes by characterizing an element of post-transcriptional control of MIPS gene expression.

This project was supported in part by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638.
This project was supported by funds from CSULB Academic Affairs (RS114).

57. Trichloramine reactivity with amino acids under wastewater treatment conditions

Landon Watts[1], Stephen Mezyk, Ph.D.[2], Jamie Gleason[3], and Kenneth P. Ishida[4]
[1]BUILD student at California State University Long Beach.
[2]Professor, Physical/Environmental Chemistry at California State University Long Beach.
[3]MARC U STAR student at California State University Long Beach.
[4]Research Chemist, Orange County Water District, Fountain Valley, CA

The Orange County Water District uses an Advanced Oxidation process (AOP) as the final step in their extended treatment of wastewater. In this process, hydrogen peroxide (H_2O_2) is photolyzed by UV light, yielding hydroxyl radicals (OH) that destroy any chemical contaminants that remain after their primary, secondary, microfiltration and reverse osmosis processes. The optimal use of a UV/H_2O_2 AOP depends on having minimal loss of the ·OH radicals to other wastewater chemicals. One particular problematic group of species in the AOP are the chloramines, NH_2Cl, $NHCl_2$, and NCl_3. which are deliberately generated in the wastewater train to prevent biofouling of the RO membranes. These chloramines significantly interfere with the wastewater remediation chemistry by directly absorbing UV light which decreases the ·OH radicals produced. In addition to this, chloramines thermally react with organic chemicals to produce toxic halogenated byproducts. The focus of this study was to establish the importance of the latter pathway, to determine NCl_3 thermal reactivity with a suite of deprotonated amino acids at a pH of approximately 12. Absolute temperature-dependent rate constants for these reactions were determined from the decrease of NCl_3 absorbance at 336 nm using a stopped-flow spectrophotometer. Correlations between amino acid structure and NCl_3 reactivity were also attempted in order to gain insight into their importance under AOP conditions.

58. Bone Morphogenetic Protein 4 and Cyclopamine-KAAD Together Enhance Choroid Plexus Epithelial Fate in Modified Mouse Embryonic Stem Cell Cultures

Maria Rivera[1], Brett Johnson[2], and Edwin Monuki[2]
[1]Department of Biological Sciences, California State University, Long Beach
[2]Department of Pathology and Laboratory Medicine, University of California of Irvine

The choroid plexus of the brain contains epithelial cells (CPECs) that are vital to brain health by producing the cerebrospinal fluid (CSF) and by creating the blood-CSF barrier. These CPEC functions diminish during normal aging and at an accelerated rate in neurological disorders such as Alzheimer's disease. The ability to generate and maintain CPECs should therefore enable many clinical applications, providing material for cell transplants and for screening of drugs that might benefit CSF production and the blood-CSF barrier. However, these possibilities are hampered by the currently inefficient expansion of CPECs in culture. Previous work in the Monuki lab determined that bone morphogenetic protein 4 (BMP4) is sufficient to induce CPECs in a mouse embryonic stem cell (mESC) culture system involving cell aggregates, but the efficiency of derivation was quite low and CPEC induction plateaued even at high BMP4 concentrations. In the present study, we investigated a modified mESC culture system in which aggregated mESC-derived neural progenitor cells were dissociated to form monolayers to allow for uniform exposure to BMP4 with or without the sonic hedgehog pathway inhibitor cyclopamine-KAAD (Cyc). Using RT-qPCR to detect the expression of CPEC markers, as well as fluorescence from a transthyretin (TTR) reporter, we found that the monolayer system resulted in efficient derivation of CPECs, and this effect was enhanced further by Cyc, with peak effects at 15 nM. Notably, the expression of the thyroxine carrier TTR increased about 30,000-fold upon addition of BMP4, with a further 64-fold enhancement by 15 nM Cyc, and the expression of the water pump aquaporin 1 increased by about 1000-fold with BMP4, and another 10-fold with 15 nM Cyc. Also, the expression of a number of other genes associated with CPECs, Msh homeobox 1 (MSX1), claudin 1 (CLDN1), claudin-2 (CLN2), and LIM homeobox transcription factor 1 alpha (LMX1a), were significantly upregulated. Therefore, a combination of BMP4 and cyclopamine-KAAD in monolayer systems may greatly facilitate the production of CPECs for clinical applications.

59. Sexually Dimorphic Expression of Calbindin Neurons in the Cerebral Cortex of the Developing Mouse Brain

Layla Ramos, Regina Henson, and Houng-Wei Tsai
Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach, CA

Calbindin-D28K, a calcium binding protein, is a biomarker for sexually dimorphic neuronal populations in the rodent brain, with more calbindin-expressing cells in the preoptic area (POA) and the bed nucleus of the stria terminalis (BNST), two regions intimately connected with the control of male sexual behavior, of male mice than in females [McCarthy, 2001]. This sex difference in the number of calbindin-immunoreactive (ir) neurons has been shown to be regulated by perinatal exposure to testosterone (T) partially via activation of androgen receptor (AR) [Bodo, 2008]. A recent study reported that sex differences in social and anxiety-like behaviors as well as gene expression in the amygdala and prefrontal cortex were eliminated in calbindin-knockout mice, indicating that sexual dimorphism in calbindin expression and function might be present and similarly regulated by AR in non-reproductive brain regions as well [Harris, 2016]. To test our hypothesis, we used immunohistochemistry to detect calbindin-ir neurons in the forebrains of testicular feminized (Tfm) mice, lacking functional AR, and their wild-type littermates around pre-pubescence. We first observed that calbindin is widely expressed in a variety of brain regions, including the cerebral cortex, amygdala, and hippocampus. Next, we found more calbindin-containing cells in the primary motor cortex (M1), however not entorhinal cortex, of wild-type female mice than males, and Tfm males show female-like number of calbindin-ir neurons. Preliminary analysis of the amygdala and hippocampus indicates that calbindin is expression is ubiquitous, however a sex difference in those areas has not yet been determined. Our preliminary data support a critical role for the AR in establishing brain sexual dimorphism in calbindin expression during early development as well as its links to non-reproductive neural function.

Bodo, Cristian, and Emilie F. Rissman. "The Androgen Receptor is Selectively Involved in Organization of Sexually Dimorphic Social Behaviors in Mice." *Endocrinology* 149.8 (2008): 4142-50. Print.
Harris, Erin P., et al. "Calbindin Knockout Alters Sex-Specific Regulation of Behavior and Gene Expression in Amygdala and Prefrontal Cortex." *Endocrinology* 157.5 (2016): 1967-79. Print.
Sickel, M. J., and M. M. McCarthy. "Calbindin-D28k Immunoreactivity is a Marker for a Subdivision of the Sexually Dimorphic Nucleus of the Preoptic Area of the Rat: Developmental Profile and Gonadal Steroid Modulation." *Journal of neuroendocrinology* 12.5 (2000): 397. Print.

60. Using CRISPR to Create Models of Epilepsy in Human iPSCs

Noor Osman[1], Olga Safrina, Ph.D.[2], Charlesice Hawkins[2], Martin Smith, Ph.D.[2], Diane O'Dowd, Ph.D.[2]

[1]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840
[2]Department of Developmental and Cell Biology, University of California Irvine, Irvine, CA 92617

Epilepsy is a class of neurological disorders that is characterized by recurrent seizures. These seizures result from an abnormal increase in the firing of sodium-dependent action potentials in excitatory neurons in the brain. Some forms of epilepsy are caused by mutations in ion channel genes that are important in regulating action potential firing. The SCN1A gene, which codes for the alpha subunit of the voltage-gated sodium channel Nav1.1, is a hotspot for mutations that cause epilepsy. However it is not known whether different mutations in this gene affect sodium channels in similar or distinct ways to cause epilepsy. Currently our lab is interested in two specific amino acid locations in the gene. The first is 1648 because there are two known mutations at this site that cause two different types of epilepsy. One mutation changes the arginine to a histidine (R1648H) and causes genetic epilepsy with febrile seizures plus (GEFS+), a relatively mild disorder that results in fever induced seizures past 6 years of age. However, when arginine is changed to cysteine (R1648C), this causes Dravet Syndrome (DS), a much more severe type of epilepsy that includes developmental and social cognitive defects. One of my projects has been to use CRISPR/Cas9 gene editing technology to insert the R1648C or R1648H mutations into human induced pluripotent stem cells. Co-transfection of a plasmid and a repair template were used to introduce one of the two point mutations in stem cells from an individual without a neurological disorder. We have already generated 2 positive cell lines for R1648C. Total homology-directed repair success was 11%, but the efficiency was 2% for clones that contain the mutation and no other modifications. We are in process of generating cell lines with R1648H mutation. The second position we are currently interested in is 1270. We are now using the same gene editing strategy to correct the mutation in this location by changing threonine to lysine in a GEFS+ patient cell line. We have identified one positive clone to date that carries the wild type amino acid at 1270. The next step is to differentiate the mutant iPSC lines into neurons to evaluate how these mutations affects sodium channel function and the ability to fire action potentials.

This project was funded by CIRM grant EDUC2-08383.

61. Complement Protein C1q Modulates Macrophage Foam Cell Lipidome

Marc C. Pulanco and Deborah A. Fraser, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Lipid-filled macrophages, termed foam cells are a hallmark of Atherosclerosis. As atherosclerosis progresses, foam cells may undergo apoptosis and necrosis releasing pro-inflammatory cytokines, proteases, and free radicals that lead to plaque rupture. Therefore, the survival of these macrophage foam cells is vital to plaque stability. Complement protein C1q is an important recognition protein of the innate immune response. Recent studies suggest that C1q plays a protective role in early atherosclerosis. C1q directly opsonizes targets including modified low-density lipoproteins (LDL) resulting in increased macrophage foam cell phagocytosis, survival, and efflux. Since cholesterol efflux and survival are often associated with activation of the liver X receptor pathway in macrophages, we investigated modulation of LXR activity by C1q. THP-1 cells, a human monocyte cell line, were differentiated into macrophages before treatment with medium or highly oxidized LDL (MoxLDL or HoxLDL) with or without C1q. LXR activation was measured in cells transfected with an LXR-luciferase reporter gene construct using luminometry. Preliminary data shows that after 3 and 24 hours, C1q significantly increases LXR activation in macrophages ingesting highly oxidized LDL. To determine the potential lipid species involved in activation of the LXR, we performed lipidomic analysis by mass spectrometry. These data suggest that C1q alters the production and secretion of specific LXR-activating oxysterols/cholesterol intermediates such as 24-, 25-hydroxycholesterol and desmosterol. To investigate the change in lipid production, we performed RT-qPCR to measure gene expression of lipid-modifying enzymes that produce LXR-activating lipids. C1q significantly increases gene expression of Cholesterol 25-hydroxylase, the enzyme that generates 25-OHC. The presented data supports the protective role of C1q in decelerating atherosclerosis by modulating the macrophage lipidome to promote macrophage foam cell survival.

This project is supported in part by the National Institute of General Medical Sciences, National Institutes of Health under Award Numbers SC3GM111146 and 8UL1GM118979-02 (to D.A.F.), and 2R25GM071638-09A1 (to M.C.P.)

62. Enzymatic Synthesis of a Naphthol Analog of Tyrosine

Christian E. Loo, Vannalyn C. Abille, and Jason P. Schwans, Ph.D.
Department of Chemistry and Biochemistry California State University Long Beach, Long Beach, CA 90840

Modified amino acids such as fluorescent amino acids are powerful tools for biochemical studies, as the compounds can introduce fluorescent probes for imaging, attach biomolecules of interest through chemical modification, and systematically perturb the chemical properties of amino acids within proteins. A naphthol analog of tyrosine was previously suggested as a useful tool for studying protein structure and function. The naphthol group introduces a fluorescent moiety with minimal structural perturbation relative to several aromatic amino acids. Although the amino acid was previously made by chemical synthesis, this approach consisted of four steps and limited the quantities available for biochemical studies. Tyrosine phenol lyase (TPL), an enzyme that assembles tyrosine from phenol, pyruvate, and ammonium acetate, has been used to generate fluorosubstituted tyrosines; we previously used this enzyme to generate fluoro- and cholorotyrosines. Building on these experiments, we postulated that the enzyme could be used to generate the naphthol-containing amino acid in one enzymatic step. To test this hypothesis, we recombinantly expressed and purified *Citrobacter freundii* TPL. A challenge in the bioorganic synthesis of unnatural amino acids is that reactions are generally performed in water, but the reagents used in the reactions often have limited solubility in water. Methanol has previously been used to enhance reagent solubility, but it was found to decrease enzyme activity. To overcome this challenge, a battery of cosolvents was evaluated using kinetics assays to identify solvents that increase the solubility of the starting materials without significantly affecting enzyme activity. A series of alcohols, diols, and common cosolvents such as DMSO were tested. The enzyme was shown to be the least sensitive to ethylene glycol, while low concentrations of ethanol or isopropanol decreased activity. Next, enzymatic synthesis of the amino acid was monitored by HPLC, and reactions showed the formation of a new compound. Following ion-exchange chromatography and solid phase extraction, NMR analysis of the product was consistent with the formation of the naphthol-containing amino acid. Initial yields were relatively low (<50%) and we are now optimizing the conditions for the enzymatic synthesis. Together, the results suggest that TPL can enzymatically synthesize a naphthol-containing amino acid in one step. This method expands the range of potential biochemical tools synthesized by TPL and provides the foundation for the use of this enzyme in the synthesis of polycyclic compounds.

Acknowledgements: This work was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award numbers RL5GM118978 and T34GM008074. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

63. Indole Glucosinolate Biosynthesis Effects on Developmental Leaf Senescence in *Arabidopsis thaliana*

Marielle Cardenas Valdez and Judy A. Brusslan, Ph.D.
Department of Biological Sciences, California State University, Long Beach, 1250 Bellflower Blvd. Long Beach, CA 9084-9502

Leaf senescence is the ultimate stage of leaf development in which nutrients are recycled and reallocated to newly developing organs. In a pivotal study, gene ontology analysis was performed on a group of Senescence-Upregulated Genes (SURGs), which revealed an enrichment for indole glucosinolate synthesis genes, suggesting these genes are involved in senescence. Indole glucosinolates (IG) are secondary metabolites, which are present in the Brassicaceae plant family, possess protective properties against herbivory and fungal infections. We have shown that inhibition of IG synthesis at the beginning of the pathway results in premature senescence, however blocking this portion of the pathway can lead to loss of other metabolites as well. Recent data demonstrated that an IG transport double mutant *pen1/pen3* exhibited premature leaf senescence implicating the IG metabolites as playing a protective role. In this study, it is hypothesized that the presence of the IG biosynthetic pathway provides a protective role against premature leaf senescence. Furthermore, we intend to identify the major IG metabolites that play this protective role. The IG biosynthetic pathway will be investigated through mutant lines for biosynthesis gene families CYP81F & IGMT, transport genes PEN1 &PEN3, regulatory genes MYB51 & MYC2, and signaling gene MPK3. The progression of senescence will be analyzed in homozygous mutant plants, compared to *Arabidopsis thaliana* wild-type (WT) plants. Relative gene expression will quantified with RT-qPCR at specific time points as leaves undergo senescence. Spectrophotometric analysis of total leaf chlorophyll content will be performed to quantify the rate of leaf senescence. Compared to WT plants, early senescence is expected in mutant lines containing a disrupted gene that is essential for the synthesis of the critical IG metabolites. Similarly, such mutant lines are expected to exhibit lower levels of chlorophyll content, higher expression of SURGs, and lower expression of Senescence-Downregulated Genes (SDRGs) at an earlier time point than WT plants.

This project is supported by the National Institutes of Health (NIH) Grant SC3GM113810 awarded to Dr. Judy A. Brusslan.

64. Developing Human Hsp70 Variants to Counter Neurodegeneration

Jennifer Ramirez[1], Ipsita Subudhi[2], and James Shorter, Ph.D.[2]
[1]Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840
[2]Department of Biochemistry and Biophysics, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, PA 19104

Heat Shock Protein 70, or Hsp70s, are universally conserved chaperones that act as part of the metazoan disaggregase system (MDS). They assist in a variety of activities, including folding new proteins and refolding misfolded proteins and aggregates. Various neurodegenerative diseases are associated with protein misfolding, such as TDP43 and FUS in amyotrophic lateral sclerosis (ALS) and α synuclein in Parkinson's disease (PD). Previous work in the lab has revealed several variants in the yeast homolog of Hsp70 that can rescue disease-mediated toxicity from α synuclein and TDP43. Here, the human homolog Hsp72 was mutated at homologous residues and tested against a yeast proteinopathy model to find enhanced disaggregase activity. Through this model, we identified variants that showed the ability to rescue α synuclein- and TDP43-mediated toxicity. Future studies will involve testing additional variants that display stronger rescue than those previously identified. Thus, engineered Hsp72 variants could potentially serve as therapeutics for neurodegenerative diseases.

This project was supported by the MARC program, funded by the NIGMS, NIH T34GM008074; and the NIGMS, NIH under Award Numbers: UL1GM118979 and RL5GM118978, Penn BGS (Biomedical Graduate Studies), and Penn ORDT (Office of Research and Diversity Training).

65. General Relativistic Methods for Gravitational Wave Frequencies of Neutron Stars

Michael Lanoye, Benjamin Diaz, and Prashanth Jaikumar, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Neutron Stars are expected to be a prominent source of gravitational waves. Once we have determined the spacetime oscillations at the surface of the star we can project it out into space and determine the gravitational waves that could be detected here on Earth. We compute the general structure of a neutron star by using a polytropic Equation of State. We determine the surface of the star precisely using a variation of the Tolman-Oppenheimer-Volkoff (TOV) equations based on enthalpy. We then calculate the spacetime oscillations of the star at its surface in order to determine the gravitational waves that it will emit. The surface variables that are needed to determine the oscillation modes are found by solving a system of 4 coupled linear differential equations. These equations project the solution at the center of the star using the Runge-Kutta computational method out to the surface.

This project is supported in part by National Science Foundation Grant PHY-1608959.

66. Protecting one's own: The moderating effect of sensitivity to in-group criticism on ruminative displaced aggression towards In-group and Out-group targets

Makenna L. Rivers, Christopher A. Gunderson, Tatiana Avila, and William C. Pedersen. Ph.D.
Department of Psychology, California State University Long Beach, Long Beach, CA 90840

We constantly see examples of intergroup violence in our world. One major aspect of intergroup aggression is group-based retribution, wherein an in-group member seeks revenge against any out-group member even if that individual was not involved in an initial provocation. Such an incident would constitute an act of displaced aggression (i.e., "taking it out" on an innocent individual). The degree to which this happens, however, is presumably influenced by a person's sensitivity to assaults against their in-group. The current study investigated the impact of sensitivity to in-group criticism on ruminative displaced aggression towards both in-group and out-group targets. It was hypothesized that displaced aggression would be higher towards out-group targets only when individuals are high in sensitivity to in-group criticism. To test this hypothesis, participants (n=99) from California State University, Long Beach (CSULB) were recruited. Participants completed a premeasure at the beginning of the semester in which one item assessed sensitivity to in-group criticism ("It really makes me angry when others criticize CSULB"). During the experimental session, participants were first provoked by an out-group member from another university who insulted their performance on an academic task and disparaged CSULB students. Next, participants were allowed to ruminate about these comments. Participants then completed a displaced aggression measure in which they indicated the amount of time either an innocent in-group or out-group member would need to place their hand in painfully cold ice water. Consistent with expectations, results indicated that sensitivity to in-group criticism moderated ruminative displaced aggression towards target type (b=6.07, p=.041). Specifically, displaced aggression towards in-group and out-group targets did not differ when sensitivity was low (p=.61) but did differ when sensitivity was at mean (p=.005) or high (p<.001) levels. Contrary to predictions, however, the directionality of this effect did not indicate that displaced aggression towards out-groups increased as a function of sensitivity to in-group criticism. Instead, further analyses revealed that as participants' sensitivity to in-group criticism increased they became less aggressive towards fellow in-group members (b=-4.92, p=.034). These observations suggest that higher levels of sensitivity to in-group criticism resulted in more favorable and protective actions towards fellow in-group members in the face of an out-group provocation. These findings enhance our understanding of the dynamics of real world intergroup violence. Implications of this research for reducing intergroup aggression will be discussed.

67. No Abstract

68. Title: ZIF-8 for the Remediation of Dye-Contaminated Effluent

Michael Chin and Fangyuan Tian, Ph.D.
Department of Chemistry & Biochemistry, California State University Long Beach, Long Beach, CA 90840

Metal-Organic Frameworks (MOFs) are an interface between the organic and inorganic sectors, consisting of a metal ion coordinated to organic linkers forming a framework. These frameworks have been of interest because of their numerous applications in catalysis, gas separation, and drug delivery. One class of MOF Zeolitic Imidazolate Frameworks (ZIFs), has substantial stability and hydrophobic properties that make them ideal for aqueous separations. We have been working on removing organic dyes from effluent waste by incorporation of the target dye molecules into the porous ZIF because of the toxic effects these dyes can have on biological systems. In this study, we have chosen ZIF-8 for removing organic dye in aqueous because of its excellent thermal and chemical stability, relatively simple synthetic method, in addition to its intrinsic surface defects for coordinating with organic molecules. ZIF-8 is a framework of zinc tetrahedrally coordinated by imidazolate rings with negatively charged surface defects, such as hydroxide and amine groups. We hypothesize ZIF-8 will conjugate to organic dyes via a Schiff-base bond, thus remove contaminants in aqueous phase with greater efficiency than traditional methods that use TiO_2. To verify our hypothesis, we have first successfully synthesized ZIF-8 nanoparticles as confirmed by X-ray powder diffraction and infrared spectroscopy studies. Subsequently, solutions of Rhodamine B and Methylene Blue were prepared and investigated for degradation in control (Milli-Q water), TiO_2, and ZIF-8 environments using UV-Vis spectroscopy. We noticed that the absorbance of both Rhodamine B and Methylene Blue dyes decreased by 60% after mixing with ZIF-8 nanoparticles for less than 1 minute. Additionally, when the dye solutions were passed through a ZIF-8 embedded HPLC filter the absorbance of the filtered solution dropped noticeably as much as 63%. Preliminary results showed ZIF-8 is effective and efficient in removing both Rhodamine B and Methylene Blue dyes in solution by soaking and membrane filtering methods. Our future studies include mechanism simulation by density functional calculations and membrane fabrication to improve the efficiency of organic dye separation in aqueous solution.

This project is supported in part by National Institutes of General Medical Science Grant #T34GM008074 and the Undergraduate Education Grant Program of the W. M. Keck Foundation.

69. Pollutant-Induced Changes in Ca^{2+} Channels Alter Gene Transcription

Schuko, Nicolette, Javier J. Lepe, Deepali Bhandari, Ph.D., Douglas A. Pace, Ph.D., and Erika B. Holland, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA, 90840

Several environmental pollutants, including polychlorinated biphenyl (PCB) congeners and triclosan, are capable of causing Ca^{2+} signal disruption (CSD) by altering the activity of the ryanodine receptor (RyR) or the L-type voltage gated Ca^{2+} channels (CaV1). These two channels are important to countless physiological processes, but the extent to which CSD through these channels contributes to altered cellular pathways is currently unclear. We investigated whether CSD, caused by cellular exposure to PCBs and triclosan, can cause changes in gene transcription as regulated by the Ca^{2+} -sensitive transcriptional repressor DREAM (downstream regulator element antagonistic modulator). This research utilized the GT1-7 hypothalamic neuronal cell line and the TαT1 thyrotrophic cell line to measure whether CSD alters transcription of gonadotropin releasing hormone (GnRH) or thyroid-stimulating hormone (TSH), respectively. Cells were exposed to varying concentrations of each pollutant for multiple time periods, and GnRH and TSH levels assessed using qPCR. GT1-7 cell exposures to the potent RyR activator PCB 95 did not lead to changes in GnRH mRNA expression, which was supported by low RyR basal gene expression in the cell line. Exposure of GT1-7 cells to triclosan decreased GnRH transcription in a dose-dependent manner. Triclosan is known to inhibit CaV1 channels leading to decreased Ca^{2+} entry into the cell. When intracellular Ca^{2+} concentrations are decreased, DREAM remains bound to DNA, repressing transcription. DREAM is important to proper functionality of the digestive system, central nervous system, and skeletal and cardiac muscle, and it has been tied to pain reception, learning and memory and thyroid-gland health. This work will help address whether CSD is contributing to such alterations by altering DREAM-mediated transcription.

This research is supported in part by Southern California Society of Environmental Toxicology and Chemistry.

70. Correlated Evolution of Antlers and Tusks in Cervids

Nicole Lopez and Theodore Stankowich, Ph.D.
Department of Biological Sciences, California State University, Long Beach, CA, 90840

Tusks are mostly seen on smaller ungulates and used primarily as sexual weapons, whereas larger ungulates lack tusks but instead possess antlers, used as a visual display of social status. There are two Genera of deer that have both antlers and tusks: Muntiacus and Elaphodus. In muntjacs, all fights are preceded by a "dominance display", typically performed by the dominant male, resulting with the subordinate male's withdrawal. A gradual increase in the influence of this display may have led to the reduction in size of tusks and eventual evolution of complex, large antlers due to the rarity of fighting. My project will study the correlation between antlers and tusks in relation to overall body size and other ecological factors. I hypothesize that as body size increases, then relative size of tusks will decrease and the relative length of antlers will increase. Antler and tusk data on several species of cervids has been collected from the museum specimens. I will use this data to try and prove the correlation by using phylogenetic generalized least squares tests, which are regression type tests that take species relatedness into account. Our preliminary studies suggest as the species move from closed to open habitats, from solitary to group living lifestyles, and from small to large body sizes there is a significant trend of tusk size decrease and antler size increase. I will also examine the effects of environmental and social factors, such as habitat type and fighting style, on the evolution of these traits. The significance of the question is that it would help contribute to our understanding of the selective forces that led to the transition between small solitary tusked deer and large social/polygynous antlered deer.

71. Nuclear Fusion in the Deuterated Cores of Inflated Hot Jupiters

Nina M. Miller and Prashanth Jaikumar, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840.

We explore the possibility of Deuterium (D) fusion at the core mantle interface of giant exoplanets as a mechanism to explain the observed heat excess. Deuterium fusion in the interior of giant planets is screened by electronic as well as ionic effects. While the electronic screening is mild, the ionic screening can increase the fusion rate by several orders of magnitude. We focus on including this ionic screening effect by means of a theoretical calculation of the reactivity, and present results for this quantity across a range of temperatures typical of the core of Hot Jupiters. Based on these results, we conclude that under suitable conditions, screened D fusion along with core erosion could explain the excess heat of sub-Jupiter mass exoplanets.

72. Screen Development to Analyze Interactions of *18-wheeler* Gene Mutations and X-Linked Chromosome Deficiencies

Jackie Villalba, Anel Molina, Karen Ixcoy, and Elizabeth Eldon, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

The *18-wheeler* gene found in *Drosophila melanogaster* directs epithelial cell migration during development. Previous work has demonstrated that homozygous *18-wheeler* mutant embryos have abnormal salivary glands. *Drosophila* salivary glands are an excellent model for mammalian organ development. To identify genes that interact with *18-wheeler* during epithelial organ development we take advantage of the observation that an embryo heterozygous both for *18-wheeler* and for a gene that interacts with *18-wheeler* will produce defective salivary glands. We are systematically searching the X-chromosome for interacting genes using a collection of 93 X-chromosome-linked deficiencies (*Df(1)*). Together these deficiencies delete 2,288 of the 2,331 euchromatic genes on the X-chromosome (98.1%). To obtain embryos that are heterozygous for both *18-wheeler* and an X-linked deficiency, males carrying an *18-wheeler* mutation and a green fluorescent protein (GFP) reporter expressed in salivary glands (stock 84-1) are mated with females heterozygous for an X-linked deficiency. Their other X-chromosome is a GFP-expressing "balancer". Control embryos are obtained by using males that are wild type at the *18-wheeler* locus, but still carry the GFP salivary gland reporter (stock 15-1). Embryos are collected, fixed, and subjected to immunocytochemistry to detect GFP, which is expressed in the salivary glands of the *18-wheeler; Df(1)* embryos. If the mutations interact, salivary gland morphogenesis will be abnormal. Defects include, but are not limited to, glands lengthening, shortening, or migrating asymmetrically. *Df(1)BSC719* (stock 26571) show no gene interaction, since wild type glands are observed in both the 15-1 and 84-1 heterozygous embryos. *Df(1)BSC644* (stock 25734) shows a genetic interaction, but not in the manner predicted. When crossed to the *18-wheeler* mutant, wild type glands are observed, but when crossed to wild type *18-wheeler*, the glands are shorter. This suggests that the deficiency causes a defect in gland morphogenesis that is rescued by reducing the dosage of the 18-Wheeler protein. Further work will examine the genes within *Df(1)BSC644* in more detail by ordering flies with smaller deficiencies within that deficiency to narrow down the location of gene responsible for the defect in morphogenesis.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980; 8RL5GM118978-02.

73. Genetic analysis of three negative regulators of leaf senescence, *WRKY54*, *WRKY58* and *WRKY70*, in *Arabidopsis thaliana*.

Patricia Leyva and Dr. Judy A. Brusslan, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA. 90840-9502

Leaf senescence is a degradation process that recycles the nutrients in older leaves of a plant. The visible manifestation of leaf senescence is when the green leaves turn yellow/brown. In the model plant organism, *Arabidopsis thaliana*, a network of transcription factor (TF) genes, many from the *WRKY* TF family, play key roles regulating leaf senescence. It has been previously shown that *wrky54* and *wrky70* mutants show an acceleration of leaf senescence indicating they work as negative regulators. Transcription factor *WRKY58* was also discovered to work as negative regulator of leaf senescence in our lab. The additive effect of these three WRKY transcription genes will be tested by analyzing the senescence phenotypes of wild type, single, double and triple mutants. All three double mutant combinations were isolated through PCR analysis of genomic DNA. A parental cross was made between the *wrky70/wrky54* and *wrky54/wrky58* double mutants. The F_1 progeny are expected to be *wrky54* homozygous and heterozygous for *wrky58* and *wrky70*. These F_1 plants will self-fertilize to produce F_2 seeds. These seeds will be grown and PCR analysis will be used to isolate a triple mutant, *wrky70/wrky54/wrky58*. Triple mutants should comprise $1/16^{th}$ of the progeny. Once double and triple mutants are confirmed, senescence phenotypes will be measured, these include expression of senescence up-regulated genes and the rate of chlorophyll loss. If the genes are additive, the triple mutants will show a faster rate of senescence than single, double and wild type plants.

Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638 through California State University Long Beach Research Initiative for Scientific Enhancement (RISE) program.

74. Providing Academic Services for Students With a Constraint Optimization Model

Diana Gonzalez and Jen-Mei Chang
Department of Mathematics and Statistics, California State University, Long Beach, Long Beach, CA 90840-1001

There are many resources for students to aid in academic success. With so many resources available, students are unable to deem what is most appropriate for them. Decision aids have been successful in the medical field for helping patients make well-informed decisions. This idea was adapted to help students at Cal State Long Beach make well-informed decisions for choosing resources to help them succeed. A survey was developed by analyzing data gathered from survey responses to Noel Levitz questionnaires. The method of factor analysis was employed to determine which questions from the Noel Levitz survey provided new information. The new (and validated) survey consisting of 14 questions is significantly shorter compared to the original questionnaires (75 and 35 questions) and saves 13 minutes.

This project is supported in part by the California State University, Long Beach ORSP 2017 Student Summer Research Assistantship Project.

75. Sustainable Energy Storage in Chemical Bonds

Peter Santiago, Stephanie Araiza, and Hadi Tavassol, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, CA 90840

Energy storage is vital to the development of renewable energy systems. Our lab is working toward identifying abundant electrocatalysts for storing renewable energies in hydrogen bonds, through the hydrogen evolution reaction (HER, $2\ H^+ + 2\ e^- \rightarrow H_2$), due to their light weight and high energy storage capacity. Electrocatalysts allow for reactions to be accelerated without altering the chemical composition. Platinum, a precious metal, is an efficient HER catalyst. However, due to its inflated cost, we investigate two transition metal dichalcogenides (TMD), molybdenum disulfide (MoS_2) and molybdenum diselenide ($MoSe_2$), as cheaper alternatives. MoS_2 has been shown to be active for HER. MoS_2 has an asymmetric layered structure, while the location and mechanism of HER catalysis remain unknown. It is believed that the active sites are on the edges rather than the basal planes of MoS_2. We report on our investigation on the properties of MoS_2 edge sites and basal planes using Raman microscopy and *in-situ* chemomechanics.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health

76. Photocycloadditions of Electronically Unbiased Alkenes Using a Transition Metal Catalyst

Hoang Dang[1], Daniel M. Flores[2], and Valerie Schmidt, Ph.D.[2]
[1]Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840 and
[2]Department of Chemistry and Biochemistry, University of California, San Diego, La Jolla, CA 92093

Cycloadditions are an incredibly powerful mode of reactivity that has been utilized by synthetic chemists for generations. Thermally allowed [4+2] cycloadditions, which occur via a concerted movement of electrons, result in useful cyclohexenes that can be further modified but often require high temperatures and functionalized conditions. Currently, little is known regarding the use of photochemistry to make cycloadditions of thermally allowed but minimally functionalized systems occur via stepwise radical bond formation. Here, we propose the use of light-absorbing metal complexes to facilitate [4+2] diene-olefin photocycloadditions. A series of nitrogen-tethered diene-alkene substrates were synthesized and were coordinated together by Copper(I) into a photocatalytic system, which was subjected to a UV light setup. UV-C irradiation resulted in decomposition of substrates and thus reaction conditions will be modified to allow for the isolation of a product and ultimately to selectively synthesize [4+2] cycloadditive products. This method for stepwise rather than concerted addition may help to circumvent the limitations of and is fundamentally different from traditional methods. Success in developing this strategy can lead to the advancement of other complex reactions such as [2+2+2] cycloadditions, intermolecular cycloadditions, and [2+2] dimerizations.

This project is supported in part by the University of California, San Diego Summer Training Academy for Research Success (STARS) program.

77. GIV/Girdin Mediates Cell Survival during Endoplasmic Reticulum Stress

Peter Nguyen, Rosanna Calderon, Yoanna Rodriguez, Deepali Bhandari Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Endoplasmic reticulum (ER) stress is a form of cellular stress that is experienced both under normal physiological conditions such as in professional secretory cells and disease states such as cancer, diabetes and neuro-degeneration. Upon facing ER stress, cells initially try to restore normal function by activating a conserved signaling pathway called the Unfolded Protein Response (UPR). However, if the stress is overwhelming and cells are not able to recover within a reasonable time frame, the UPR ultimately commits cells to apoptosis. How cells make this life-or-death decision remains an exciting yet poorly understood phenomenon. Here, we show that GIV (**G**α-**I**nteracting **V**esicle associated protein aka Girdin), a multimodular signaling protein, helps promote cell survival during ER stress via activation of the Akt pathway. HeLa cells treated with various ER stressors activate the Akt pathway and this activation is significantly diminished upon shRNA-mediated depletion of GIV. Furthermore, GIV-depleted cells show an increase in levels of C/EBP homologous protein (CHOP - a pro-apoptotic transcription factor) and a significant decrease in cell survival during ER stress. Together, these findings suggest that GIV may play an important role in helping cells survive ER stress in HeLa cells.

This project is supported by the NIH grant # GM121246 (DB) and in part by the NIGMS Award # R25GM071638 (RC and YR). The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

78. The Skeletal Proteome of *Eucidaris tribuloides* Test and Spines

Lupita S. Lopez, Rachel L. Flores and Brian T. Livingston, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach CA 90840

The skeletal proteomes of *Strongylocentrotus purpuratus* test, spine, tooth and larval skeleton have been determined and revealed that the prominent proteins were a family of spicule matrix proteins and MSP130. We have recently characterized the skeletal proteomes of two adult brittle stars and the sea star *Patiria miniata*. Surprisingly, we did not find either spicule matrix proteins or MSP130 occluded in the mineralized tissue. We have identified a number of other proteins that are conserved among all of these echinoderm groups. In order to understand the evolution of the proteins involved in echinoderm skeleton formation, we have characterized the test and spine proteome of the cidaroid urchin *Eucidaris tribuloides*. *E. tribuloides*, considered a "primitive" sea urchin, displays undiversified morphology from the ancestral form, allowing us to further explore the evolution of these skeletal proteins in a sea urchin evolutionarily distant from *S. purpuratus*. Proteins were isolated from mineralized tissue in *E. tribuloides* and peptide sequences were obtained using LC/MS/MS. Using the NCBI protein database the proteins isolated were characterized. We have found C-type lectin proteins in the skeleton homologous to the spicule matrix proteins, but they lack the extensive repetitive domains. The cidaroid urchin also contains MSP130 homologues in the skeleton. The relationship between these proteins and those identified in other echinoderms has been determined. We also compare the overall proteomes of *E. tribuloides* to other echinoderms. Additionally, we have characterized the proteins present in the insoluble material that appears during skeletal protein isolations. We find most of the proteins present in the soluble fraction, as well as some additional proteins. *E. tribuloides* spines are pigmented, and the pigment segregates entirely to the insoluble fraction. We discuss what this analysis tells us about skeleton formation in echinoderms.

This project is supported by National Institute Health grants 5UL1GM118979-04; 5TL4GM118980-04; 5RL5GM118978-04

79. Monovalent Organophosphorus Inhibitors of Butyrylcholinesterase: The Substitution of Oxygen by Sulfur Atoms and their Effects on Inhibition

Phillippe Ly, Trina Tran, Nicholas Nieto, Karlo Artiga, Jason Schwans, Ph.D., and Kensaku Nakayama, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

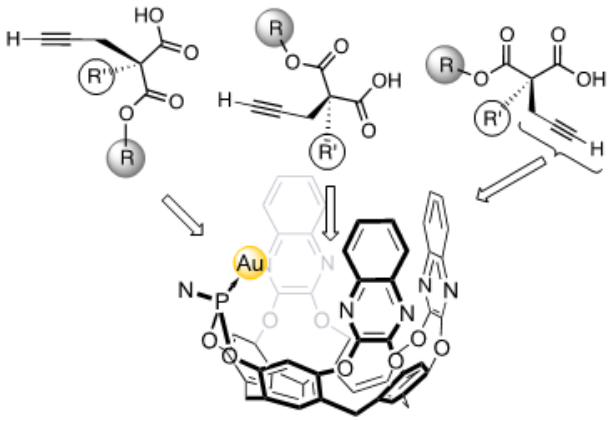
The Alzheimer's Association estimates that 5.6 million Americans are currently affected by Alzherimer's Disease (AD) and is projected to increase to nearly 16 million by 2050. Based on the cholinergic hypothesis, the characteristic decline in cognition is attributed to the dysfunction of acetylcholine-containing neurons. The presence of butylrylcholinesterase (BuChE) has been shown to increase significantly over time as AD progresses. Organophosphorous compounds have been shown to be selective inhibitors of this nonspecific cholinesterase. It has been previously shown that a single substitution of an oxygen atom by a sulfur atom significantly increases the inhibitory effect of a monovalent organophosphate by nearly 50-fold, measured by the K_i (inhibition constant) value. We are making progress on synthesizing a library of compounds with specific oxygen-sulfur substitution(s) in different positions on the phosphate group. In one planned synthesis scheme, a mixture of butanethiol and sodium hydride is added in excess to a solution of 4-nitrophenyl phosphorodichloridate to yield a sulfur-disubstituted precursor. The product of the initial reaction provides a versatile precursor, as further reactions with: 1) an alcohol yield a disubstituted product, or 2) an alkylthiol generates a trisubstituted compound. *In vitro* enzymatic activity assays with BuChE from equine serum have been completed for several oxygen- and sulfur-substituted compounds and will be conducted to determine the K_i of each new analogue. Additional studies to evaluate the specificity of each inhibitor and to determine if they are a reversible or irreversible inhibitor will be performed. Together, these experiments determine if and how position and number of substitutions affects inhibition, allowing us to exploit this property to design new inhibitors with better inhibitory properties.

This project is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638. The content is solely the responsibility of the author and does not necessarily represent the official views of the National Institutes of Health.

80. Supramolecular Catalysis Using Gold Cavitands

Tam Ho and Michael P. Schramm, Ph.D
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840.

Natural receptors such as enzyme with inwardly directed functional group serve as well-organized chemical catalysts. New supramolecular cavitands that contain inwardly directed functional groups have also yielded specialized transformations and trapping of reactive intermediates. However, broad reaching catalysts has not been possible until now. A newly reported 3-wall Au cavitand could provide new opportunities for supramolecular catalysis and the study of reactive intermediates. In our study, we use a variety of intramolecular reactions to explore the effect of the cavitands on chemical reactivity. Alkyne-acids with different spectator groups are expected to result in differential catalyst behavior. Using a variety of substrates will allow us to identify new trends and limitations on cyclization reactions. These results will give insight into how cavitands can be used towards new chemical challenges.



This work is supported by NSF (RUI CHE-1708937) and NSF (MRI CHE-1337559). The content is solely the responsibility of the authors and does not necessarily represent the views of the National Science Foundation.

81. The Effect of Superfluidity on the Oscillation Modes of Compact Stars.

Raphael Monroy and Prashanth Jaikumar, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840.

A neutron star is a star consisting largely of neutrons, created in the later stages of a massive star's life cycle. The state of matter in the interior of the star is unknown. According to theoretical models, the conditions of the neutron star favor the creation of a "neutron superfluid", a special type of fluid that has zero viscosity. While the superfluid is not directly observable, it affects the overall structure of the star. This in turn affects the oscillation modes - the resonant frequencies that the star vibrates at. By performing a numerical calculation on the theoretical model, we can predict the spectrum of neutron star oscillation modes. Though the modes cannot be observed with current technology, increasing the sensitivity of the Laser Interferometer Gravitational-Wave Observatory (LIGO) could allow us to compared calculated modes with observations to determine a realistic model of the interior of neutron stars.

This project is supported by the National Science Foundation under grant PHY-1608959.

82. Tissue-Specific loss of Smn and its effect on the Immune Response of Drosophila Melanogaster

Helen Dinh, Dominique Brown, Ashlyn Spring, Ph.D., and Greg Matera, Ph.D.
Department of Biology, University of North Carolina Chapel Hill, Chapel Hill, NC 27599

Spinal muscular atrophy (SMA) is a neurodegenerative disease that is characterized by neuromuscular junction reduction, muscle atrophy and early death. This disease is primarily caused by mutations in human *survival motor neuron 1 (SMN)* gene. Previous studies have shown that SMN protein has a role in regulating the biogenesis of small nuclear ribonucleoproteins (snRNPs), which comprise the spliceosome. Further research has shown that SMN protein has specific tissue function, but its relevancy to SMA pathology is poorly understood. In our research, we use the model organism *Drosophila melanogaster,* which has a similar immune system to humans, to address the tissue-specificity of Smn in immune system activation. To evaluate the immune response of larvae, adult fly survival rate, and larvae mobility, three assays were used respectively: melanotic mass scoring assay, viability assay, and larval locomotion assay. Results from melanotic mass scoring assays suggests that there may be a specific role of Smn protein in immune-related tissues. However, further experiments are needed to support these results.

83. Phylogeny of the Genus *Barleria* (Acanthaceae)

Robert Comito and Amanda Fisher, Ph.D.
Department of Biological Sciences, California State University Long Beach, 1250 Bellflower Blvd, Long Beach, CA, 90840-9502

Against the backdrop of a global extinction crisis fueled by rampant ecosystem destruction and the increasingly severe effects of climate change, the need to understand and conserve biodiversity is greater than ever. One approach in this endeavor is to use molecular systematics to study the evolutionary history of organisms. *Barleria* is a genus of approximately 300 species in the family Acanthaceae. Species of *Barleria* are widely distributed across the tropics, with variable habit, vegetative, and reproductive morphologies. Previous morphological studies have subdivided the genus into two subgenera and seven sections, but these groupings have come under scrutiny in light of molecular analyses based upon chloroplast loci and the nuclear locus nrITS. The aim of this study is to uncover the relationships in the genus through a phylogenetic analysis that includes many species of *Barleria* and is based on comparisons of many nuclear loci. We will generate single nucleotide polymorphisms data using RAD-seq and next-generation sequencing. We hypothesize that the RAD-seq phylogeny will corroborate the chloroplast and nrITS tree. Sampling will include at least 130 species, subspecies and varieties from within the genus, including representatives from each putative subgenus and section, as well as five to ten outgroups from other closely related genera in Acanthaceae. Currently over 120 samples have been obtained and are now being assessed for quality. We will prepare and sequence RAD-seq libraries. Then, we will process sequence data *de novo*, assemble RAD-seq fragments using the PyRAD program, and align sequences using Geneious. From those alignments, we will use RAxML to estimate a phylogenetic tree and generate bootstrap values to assess confidence in each clade. We expect substantial overlap with the previous chloroplast and nrITS tree. Alternatively, inheritance patterns of nuclear and chloroplast loci may differ, and lineage sorting effects may persist, so we may see conflict between the trees, which we will assess with a Shimodaira-Hasegawa test for significance. This study will assess the monophyly of the genus *Barleria* and proposed subgeneric taxa, and will more broadly inform our understanding of diversity and evolution in Acanthaceae.

This project is supported in part by the National Institutes of Health through RISE (NIH 2R25GM071638-09A1) and Fisher's start-up funds provided by the state of California.

84. Characterization of a novel interaction between GIV and GRP78

Jordan Ngo, Peter Nguyen, and Deepali Bhandari, Ph.D.
Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach, CA, 90840

Endoplasmic Reticulum (ER) stress occurs when there is an accumulation of misfolded proteins in the ER. Cells facing ER stress initially attempt to restore cellular homeostasis, but if the stress becomes chronic and homeostasis is not achieved within a reasonable timeframe, cells initiate programmed cell death. Cancer cells are known to be able to withstand and overcome ER stress better than regular cells. One of the key factors to promote cancer cell survival during ER stress is overexpression of the chaperone Glucose Regulated Protein 78 kDa (GRP78). Expression level of GRP78 positively correlates with levels of cytoprotective signals and chemoresistance, however the mechanism by which it does so remains elusive. Our laboratory has recently identified Gα-Interacting Vesicle associated protein (GIV) - a known enhancer of the pro-survival Akt signaling - as a novel binding partner of GRP78 via mass spectrometric analysis. This finding led us to hypothesize that this interaction may be the missing link in understanding the mechanism by which GRP78 leads to the activation of the Akt pathway. Here, we have confirmed and characterized the GIV-GRP78 interaction further using *in cellulo* and *in vitro* binding assays. Using *in cellulo* GST pull-down assays, we show that the carboxyl-terminal domain of GIV (GIV-CT) is sufficient to pull-down GRP78 from cellular lysates and that this binding increases upon induction of ER stress. To confirm that the two proteins can interact directly without the assistance of another protein, we expressed and purified GST-tagged GRP78 and His_6-tagged GIV-CT from bacterial lysates using affinity chromatography. The *in vitro* binding assays confirmed that GRP78 and GIV-CT can interact directly. Using these assays, we also confirmed that GRP78 binds to GIV-CT via its C-terminal substrate-binding domain. Together, our results show that GRP78 interacts with GIV in an ER stress dependent manner. This interaction may potentially be important to endow cancer cells with viability in the face of ER stress. Our current and future experiments are directed toward understanding how this interaction enhances pro-survival signaling in cancer cells experiencing ER stress.

85. GIV/Girdin Mediates Cell Survival during Endoplasmic Reticulum Stress

Rosanna Calderon, Peter Nguyen, Yoanna Rodriguez, and Deepali Bhandari Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Endoplasmic reticulum (ER) stress is a form of cellular stress that is experienced both under normal physiological conditions such as in professional secretory cells and disease states such as cancer, diabetes and neuro-degeneration. Upon facing ER stress, cells initially try to restore normal function by activating a conserved signaling pathway called the Unfolded Protein Response (UPR). However, if the stress is overwhelming and cells are not able to recover within a reasonable time frame, the UPR ultimately commits cells to apoptosis. How cells make this life-or-death decision remains an exciting yet poorly understood phenomenon. Here, we show that GIV (**G**α-**I**nteracting **V**esicle associated protein aka Girdin), a multimodular signaling protein, helps promote cell survival during ER stress via activation of the Akt pathway. HeLa cells treated with various ER stressors activate the Akt pathway and this activation is significantly diminished upon shRNA-mediated depletion of GIV. Furthermore, GIV-depleted cells show an increase in levels of C/EBP homologous protein (CHOP - a pro-apoptotic transcription factor) and a significant decrease in cell survival during ER stress. Together, these findings suggest that GIV may play an important role in helping cells survive ER stress.

This project is supported by the NIH grant # GM121246 (DB) and in part by the NIGMS Award # R25GM071638 (RC and YR). The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

86. Synthesis of Membrane Transporters: Calix[4]arene Tetra Phosphonic Acid

Martha Guerrero and Michael P. Schramm, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840.

The delivery of small molecules across biological membranes has been a long-standing challenge to medicinal chemistry. Often, *in vitro* active drugs are challenged by an impenetrable cell membrane. Our lab has proven that host-guest chemistry, using synthetic receptors, can effectively transport drugs and drug-like molecules across 3-phase liquid membranes, as well as vesicle bilayers. Calixarene species containing ionizable groups were capable of transporting several payloads and proved to be moderate extractors and weak binders. Calix[4]arene tetra phosphonic acid, a lipid soluble receptor that can recognize and bind to drug-like molecules modified with a variety of handles, has been synthesized and will be utilized to investigate the transport of complex drugs in biological systems.

This research project is supported by NIH/NIGMS MARC U*STAR Grant Number T34GM008074.

87. Using Python to Automate Experiments and Provide Real-Time Data Visualization

Ryan Reno and Claudia Ojeda-Aristizabal, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Low temperature electron transport on low dimensional nanomaterials are ruled by quantum effects. To accurately observe these effects, precise and repeatable experimental parameters must be used. An example of this is resistance of a graphene device as a function of temperature. Recording data from sensors by hand as both parameters change introduces uncertainty in their correlation. We present a method using the Python programming language and open source libraries to control measurement devices and a closed-circuit cryostat with superconducting magnet to automate an experiment and data acquisition. We also present an implementation of a library which provides a web-based interface to interactively visualize incoming data from multiple sensors in real time. Using these tools, we have developed experiments can be automated with a high level of repeatability and incoming data can be interpreted as the experiment unfolds.

This project is supported in part by a Department of Energy grant.

88. Simulating and Predicting NASA ICON Explorer Results

Naomy Marrufo, Carmina Cruz, Colin Triplett, Thomas Immel, Tori Fae, Astrid Maute
University of California Berkeley, Berkeley, CA

As part of the Ionospheric Connection Explorer (ICON) mission, the Space Sciences Laboratory runs a model of the near-Earth space environment, fed by recently collected data from several different sources. The model simulations will consist of electrodynamic interactions of the thermosphere and ionosphere. The Thermosphere Ionosphere Electrodynamics General Circulation Model (TIEGCM) will also incorporate data from the mission while it is in flight. ICON will address what causes changes in the ionosphere, how large-scale atmospheric waves control it at low latitudes, and how ion-neutral coupling processes respond to increases in solar forcing and geomagnetic activity. Specifically, TIEGCM will be used to see how large-scale waves control the ionosphere at low latitudes, while other numerical models will be used to analyze the alterations in the ionosphere and the coupling processes. With this, ICON will understand the physical connection between the Earth and the space environment. Before the launch in November 2017, this modeling environment needs to be set up and tested, to run automatically when new data are downloaded, and produce summary plots of its different data fields. These include parameters as specific as the height of the ionospheric peak around the planet, to its density, or the total abundance of plasma around the planet. The neutral atmospheric parameters such as the zonal wind, the zonal mean zonal wind, the abundance of oxygen vs the abundance of nitrogen, etc. can also be plotted. TIEGCM-ICON will use the resulting electric fields and currents from dynamo effect calculations to calculate the plasma dynamics. The largest geomagnetic storm occurred during Memorial Day weekend 2017 from May 27th, 2017 to May 29th,2017. This kind of event is a focus for the ICON mission, in measuring the competing effects of terrestrial and solar drivers of space weather. The ICON mission flies in 2017, but the mission already has the capability to simulate storms like the one that occurred during Memorial Day weekend at the Space Sciences Laboratory (SSL). This is because models are used to provide a broader picture of events of which ICON can only see part. The recent storm allows us to test the interfaces that provide the data from repositories to the models that run at SSL and the models to see how well they simulate the storm effects. Further, these simulations provide a capability to provide simulated Level 2 data products (geophysical data on geographic coordinates) for the instrument suite that was running through that weekend in its final test. Our simulations showed a general pattern of increased temperatures and increased velocities during the storm. As the orbit is limited models such as TIEGCM-ICON will be used to provide a full picture of the ionosphere. The simulations ran proved the models' data to be accurate.

89. Characterization of bithermally deposited iron phthalocyanine thin films

Santos Fuentes and Thomas Gredig, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach CA 90840

Metallo-phthalocyanine thin films are best known for applications based on their optical and electronic properties. Yet, recently, interesting magnetic properties have been found in iron phthalocyanine thin films. The grain size of iron phthalocyanine increases as the deposition temperature increases. These larger grain sizes also have larger coercivities. We expand this idea and grow iron phthalocyanine thin films via thermal evaporation in two stages. Each layer of iron phthalocyanine is grown at a different temperature. Measurements of grain sizes of the top layer are taken using Atomic Force Microscopy imaging, and the magnetic properties of the thin film are observed using the Vibrating Sample Magnetometer option on the Physical Property Measurement System. The early results suggest the top layer's growth is influenced by the bottom layer. Both the shape and size of the hysteresis loop are influenced with these heterostructures.

This research was supported by the W. M.Keck Foundation.

90. Graphene Coated Polyamide Fibers Embedded in Collagen Composite for Cardiovascular Patch Applications

Alejandra Juarez Rojas[1] and David A. Stout, Ph.D.[2,3]
[1]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840, [2]Department of Mechanical and Aerospace Engineering, California State University, Long Beach, Long Beach CA 90840, and [3]Department of Biomedical Engineering, California State University, Long Beach, Long Beach CA 90840

Cardiovascular disease (CVD) is one of the leading causes of death in the United States and worldwide. In recent years, various techniques have been developed to promote heart cell growth around dead tissue after a heart attack and reduce the high probability of another occurrence with minimal positive results. Past research has proved that collagen-like materials make excellent scaffolds due to its porous property allowing cells like cardiomyocytes to adhere and proliferate; however, there is a lack of conductivity which the heart requires for contraction and proper blood flow. The exploration of nanotechnology in cardiovascular applications for the promotion of heart cell regeneration has not been thoroughly investigated. Therefore, we present a simple solution proof-of-concept method of creating an innovative nano-cardiovascular patch to assist with stem-cell regeneration. By creating a biocompatible collagen scaffold, embedded with graphene coated fibers that are conductive and biodegradable, we have observed that the use of graphene has not negatively impacted cardiomyocytes growth and in turn increased stimulation of stem-cell tissue regeneration. To test the conductivity properties of graphene, collagen composites were stimulated using a multichannel stimulator designed to mimic signals given in the native heart environment. The proliferation and adhesion rate of the cardiomyocytes were then tested at time intervals of 24, 48, and 96 hours and compared to control to see if there was a significant increase in cells due to the embedding of graphene in collagen composites. To validate the biocompatibility of graphene within the collagen, in vitro cell adhesion, proliferation, and mechanical characteristics were examined, through different forms of cell staining and microscopy: epifluorescence, confocal, and scanning electron microscope. This proof-of-concept method presents a novel technique of using graphene coated yarn embedded in collagen, to deliver an alternative method in combating extended CVD infirmities. Our research will conceivably reduce the progression of individuals living with cardiovascular disease, using a non-invasive medical approach through regrowing healthy heart tissue.

This project is supported in part by NIH Grant 2R25GM071638-09A1.

91. Src Family Kinase Signaling Mediates Neuroprogesterone Induction of the Luteinizing Hormone Surge

Sharity Ondrejik[1], Timbora Chuon[1], Paul Micevych[2], and Kevin Sinchak, Ph.D.[1]
[1]Department of Biological Sciences, California State University, Long Beach, CA 90840
[2]Laboratory of Neuroendocrinology, Brain Research Institute & Dept of Neurobiology, David Geffen School of Medicine at UCLA, Los Angeles, CA

Estrogen positive feedback is regulated by astrocyte-neuronal interactions. Estradiol induces neuroprogesterone (neuroP) synthesis in hypothalamic astrocytes and upregulates progesterone receptors (PGR) in kisspeptin (kiss1) neurons of the rostral periventricular region of the third ventricle (RP3V). NeuroP then stimulates kiss1 expression and release onto the GnRH neuron to mediate induction of the estradiol-induced LH surge. In vitro models of RP3V kiss1 neurons demonstrate that PGR signaling requires Src activation. Based on this, we tested the hypothesis that neuroP induction of the LH surge is mediated by PGR-Src signaling. First, we established PGR and Src co-expression in the RP3V using immunohistochemistry on tissue from ovariectomized (ovx) rats treated with oil or estradiol benzoate (EB, 2μg). Estradiol upregulated the number of cells expressing either PGR or Src in the RP3V and the percentage of PGR and Src co-expression when compared with oil controls. In the second experiment, we tested the hypothesis that Src activation will trigger the LH surge in ovx/adrenalectomized rats primed with 2μg EB. Three groups of animals received two sequential infusions into the RP3V. The first administered infusion, given 51.5 hours after EB, was either DMSO or the Src antagonist (PP2; 50 nmol). We then administered a subsequent dose of Src agonist (Src Family Activator; 50 nmol) or DMSO 15 minutes later. Two hours later, rats were anesthetized and trunk blood and brains were collected. Animals infused with Src Family Activator demonstrated significantly higher concentrations of serum LH compared to DMSO controls, and PP2 blocked the increase in LH concentrations by Src activator. In the last experiment, animals were primed with 50μg EB, inducing neuroP, which triggers the LH surge. For three consecutive days, PP2 (50 nmol) was injected into the DBB to inhibit Src activity. Blocking Src with attenuated LH surge. Taken together, these results indicate that PGR and Src are colocalized in the RP3V, and neuroP may be activating a membrane associated PGR-Src complex to trigger the LH surge as predicted from in vitro experiments.

This project is in part supported by Award Number R01HD042635 (PEM) RO1HD058638 (KS) from the Eunice Kennedy Shriver National Institutes of Child Health & Human Development, Research Initiative for Science Enhancement (RISE) GM07163 at CSULB.

92. Mathematical Modeling of Environmental Crime Using Level Set Methods

D. Tonne[1], A. L. Bertozzi[2], S. Osher[2], D. J. Arnold[2], D. Fernandez[2], R. Jia[2], C. Parkinson[2], and Y. Yaniv[3]
[1]Department of Mathematics, California State University, Long Beach, Long Beach, CA 90840
[2]Department of Mathematics, University of California Los Angeles, Los Angeles, CA 90095
[3]Department of Mathematics, University of Maryland College Park, College Park, MD 20742

We conceive and analyze a new mathematical model for environmental crime in protected national parks. We model the movement of environmental criminals (or extractors) as if they form a front which propagates from the edge of a protected area towards the center using the level set method. Application of level set method allows for arbitrary geometry and spatial heterogeneity; vast improvements on the previous model which relied on symmetry and spatial homogeneity to simplify the problem. In order to incorporate the efforts of law enforcement agencies in patrolling the area, we devise a novel method by which to calculate the expected profit for any extractor. Using this and given a patrol strategy, we can predict which portions of the protected area will be affected by environmental crime and which will remain pristine. We apply our methods in several scenarios and discuss the effect that different patrol strategies have on environmental crime. This new model allows us to predict the effect of environmental crime without the spatial limitation of previous models.

This research was supported by funding from the National Geospatial-Intelligence Agency under NGA NURI grant HM02101410003.

93. Vascular Plants of Pleasants Peak, Cleveland National Forest, California

Sierra Coleman, Asusena Figueroa, Keana Tang, and Amanda Fisher, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Pleasants Peak is in the Santa Ana Mountains of Cleveland National Forest in Southern California. The area contains a large outcropping of serpentine-derived soils that are high in magnesium and heavy metals and low in calcium, nitrogen, potassium, and phosphorus. These soils are poor substrate for most plants. During the spring and summer of 2017 we surveyed the vascular plants of the peak and surrounding area to generate a list of the taxa found in this area and to better understand plant tolerance to serpentine soil in Southern California. We also visited herbaria to identify historic collections from the area and prepared a checklist of the plants that have been documented there. The plants of the area are generally coastal sage scrub, with several striking stands of knobcone pine (*Pinus attenuata*) and Coulter's pine *(Pinus coulteri*). We confirmed 70 native and 10 non-native taxa documented with herbarium vouchers and 61 additional sighted, but unvouchered taxa. Shrubs are the dominant cover on Pleasants Peak and due to evolutionary convergence of their leaves and short flowering seasons, identification to species can be difficult. We created a visual guide to the vegetative characteristics of 17 common shrubs to help identify them to species. Pleasants Peak has an unusual flora, mainly drawn from the coastal sage scrub community, but incorporating species typically found in Northern California, such as knob-cone pine.

This project was funded by Fisher's start-up funds provided by the state of California.

94. Morphological Variation in Sierra Lodgepole Pines (*Pinus contorta* ssp. *murrayana*)

Carolina Contreras, Hannah Garfin, and Amanda Fisher, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Lodgepole pine (*Pinus contorta*) is composed of three subspecies, of which *P. contorta* ssp. *murrayana* is the most common in California. This subspecies is found throughout the Sierra Nevada Mountains, in the Southern California Transverse Ranges, and extending into Northern Baja California. In Southern California it has been documented in the San Bernardino, San Jacinto, and San Gabriel Mountains. We hypothesize that there are morphological differences between the Sierra Nevada and Southern California populations of lodgepole pine caused by reproductive isolation. We sampled populations of *P. contorta* ssp. *murrayana* across its range in the Sierra Nevadas and in the San Bernardinos of Southern California for 26 characters from 74 individuals to test if there are morphological differences between the Sierra Nevada and Southern California populations. We found significant differences between several characteristics, but the effect sizes tended to be small. We also used species niche modeling to estimate differences in the climate variables important to the distribution of lodgepoles in the Sierra Nevada and Southern California. We found that Southern California lodgepoles are found in hotter, but not necessarily drier locations than lodgepoles in the Sierra Nevada. MaxEnt projections predict that different climate variables influence the distribution of suitable lodgepole habitat in Southern California and the Sierra Nevada. Southern California lodgepole habitat is driven by precipitation and temperature in the summer and winter. Sierra Nevada lodgepole habitat is driven by daily and yearly temperature oscillations and precipitation during the winter. We found morphological differences between the Sierra Nevada and Southern California lodgepole pine populations that may be related to differences in climate. Additional Southern California and Baja California populations will be included to further test this hypothesis.

This project is supported by Fisher start-up funds provided by the state of California.

95. Water content of the environment influences Glycoside Hydrolase architecture and distribution.

Stanley Nguyen and Renaud Berlemont, Ph.D.
Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840

Glycoside hydrolases (GHs) produced by microbes are involved in the breakdown of polysaccharides (e.g., cellulose, chitin, starch, xylan) in the environment and are important enzymes for biotechnology (e.g., biofuel, mammal nutrition). Across ecosystems, the distribution of GH enzymes matches the carbohydrate supply. GHs are sometimes associated with accessory non-catalytic domains such as carbohydrate binding modules (CBMs) aimed at anchoring the catalytic domains (i.e., GHs) to their substrate. These multi-domain enzymes display reduced diffusion and improved catalytic efficiency, however it has been shown in vitro that when water availability decreases, the catalytic benefit associated with CBMs decreases. Here we tested the effect of the ecosystem type, based on the moisture level, on the frequency of CBM-associated GHs, using a custom bioinformatic approach and publically accessible metagenomes. We developed a custom bioinformatic pipeline aimed at identifying GH and CBM domains in publicly accessible short read (n=1,000 datasets) and assembled (n=450 datasets) metagenomes corresponding to 4 broadly defined ecosystems. Then we compared the ratio of CBMs to GHs (short reads) and identified the multi-domain architecture of GHs and CBMs (assembled metagenomes), across environments. In environments with high water content, the substrate specific CBM/GH ratio ($CBM_{cellulose}/GH_{cellulose}$) was higher than in environments with low water content. This suggests that the carbohydrate supply has a strong effect on GH distribution whereas the water content strongly affects the multi-domain architecture of enzymes involved in carbohydrate processing. Finally, mining assembled metagenomes for multi-domain GHs highlighted the diversity of protein architecture and helped identify new proteins potentially interesting for biofuel industries.

96. Type 2 Diabetes and PI3K/Akt/mTOR: A Potential Role in Triple Negative Breast Cancer

Jaime Cordova[1,2], Parijat Senapati, Ph.D.[2], and Dustin E. Schones, Ph.D.[2]
[1]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840
[2]Department of Diabetes Complications and Metabolism, Beckman Research Institute of City of Hope, Duarte, CA 91010

Women of color have a higher prevalence of obesity and Type 2 diabetes than women of European descent. Women of color also tend to have a higher prevalence of triple negative breast cancer (TNBC), an aggressive molecular subtype of breast cancer, originating from basal breast cells, which are characterized by the lack of HER2, estrogen and progesterone receptors. During the early stages of diabetes, the functionality of the insulin receptor begins to decrease resulting in elevated glucose levels. Due to the heightened glucose levels, the pancreas begins to secrete an increasing amount of insulin, eventually leading to hyperinsulinemia. Insulin has been demonstrated to activate the PI3K/Akt/mTOR pathway; phosphorylated-mTOR, the active form of mTOR, has been shown to be more prevalent in TNBC than in non-TNBC breast cancer subtypes. The PI3K/Akt/mTOR pathway activates the biogenesis of mitochondria. Heightened mitochondrial activity leads to an increase in intermediates for acetyl-CoA production. Increased acetyl-CoA levels provide more substrates for nuclear acetyltransferases to acetylate histone lysine residues. In this study, we hypothesize that hyperinsulinemia contributes to altered histone acetylation via the PI3K/Akt/mTOR pathway. Using the MDA-MB-231 TNBC cell line, we demonstrate the role of the pathway in nuclear histone acetylation using specific inhibitors of the pathway. We assess protein expression and activity, after inhibition, via western blots. This assessment can contribute to determining if the PI3K/Akt/mTOR pathway can act as a target for treatment in patients who are affected by both TNBC and Type 2 Diabetes.

This project was supported by a grant from the National Cancer Institute (R01CA220693), the National Cancer Institute's Continuing Umbrella of Research Experience (CURE) Program, and by the Eugene and Ruth Roberts Summer Student Academy.

97. No Abstract

98. No Abstract

99. Gold Cavitands: New Selection Rules for Alkyne Cyclization

Teodora Nedic and Michael P. Schramm, Ph.D.
Department of Chemistry and Biochemistry, California State University-Long Beach, Long Beach, CA 90840

Gold cavitands and their applications to furthering the understanding of natural enzymatic processes have been a great interest in our lab. Using cavitands with gold functional groups, we expect to find new chemical transformations of small molecules as well as a better understanding of their properties. The experiments are designed to test the cavitand's performance. The substrate we will be working with contains a carboxylic acid and an alkyne and, upon the influence of the cavitand, we question as to whether it will form a 5-membered or a 6-membered ring. Various analogs of this substrate will be synthesized using basic organic chemistry techniques and will all be tested against the cavitand. We anticipate that the cavitands will behave differently depending on how a given substrate probes the cavitand interior. The results will further our understanding of both gold cavitands and, on a grandeur scale, how enzymes behave with their substrates.

This project is supported in part by RISE (NIH 2R25GM071638-09A1), NSF RUI (CHE 1708937)

100. Investigating the Transendothelial Transport of Apolipoproteins

Tina Nguyen , Siobanth Cruz and Vasanthy Narayanaswami, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach CA 90840

Despite the vast amount of literature that indicates low plasma levels of high density lipoproteins-cholesterol (HDL-C) is a risk factor for cardiovascular disease (CVD) the last decade has seen a paradigm shift in the concept that it may not be HDL-C levels *per se* but the functionality of HDL that is a determining factor in CVD. The inverse correlation between plasma HDL-C levels and CVD risk has been questioned since numerous studies show that neither pharmacological nor genetic intervention to increase HDL-C levels lowered the risk for CVD. Thus, there is a need to understand the role of HDL in CVD from a mechanistic perspective and understand structure-function relationships in HDL. HDL are large lipid-protein complexes with proteins such as apolipoprotein (apo) AI and apoE3 being important components and players in cholesterol transport. The overarching goal of our lab is to understand HDL transcytosis as it traverses across the endothelial layer lining the arterial intima and to investigate possible structural and functional alterations to the HDL as a consequence of transcytosis. In the current project, we tested the hypothesis that apoAI and apoE3 undergo transcytosis in either the lipid-free or lipid-associated state. To address this issue, primary bovine aortic endothelial cells (BAOEC) were grown to confluence on Transwell inserts, establishing tight junctions and achieving a transelectrical resistance of ~ 9 Ohms. Recombinant apoAI and apoE3 bearing a hexa-His tag were over-expressed in *E. coli*, and purified by affinity chromatography. Both proteins were complexed with 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC) by the cholate dialysis method yielding discoidal reconstituted HDL (rHDL) particles. BAOEC were treated with lipid-free or rHDL-associated apoAI or apoE3 on the apical side (representing the vasculature side) for 24 h. The conditioned medium from the basolateral side (representing the sub-endothelial intima side) was incubated with cobalt-coated Dynabeads to capture apoAI or apoE3. Lipid-free apoAI, but not apoE3, appeared on the basolateral side of BAOEC as revealed by Western blot analysis using anti-His tag antibody. However, both proteins appeared on the basolateral side when added in the rHDL-associated state. Further, preliminary mass spectrometric analysis of apoAI recovered from the basolateral side revealed that lipid-free apoAI was oxidatively modified during the transcytosis process; however, apoAI in the rHDL-associated state was protected against oxidative modification. Further studies will focus on identifying the precise sites and nature of modification, other protein or lipid components acquired by rHDL during transcytosis and alterations in the functional status of the HDL. The long-term goal is to identify direct relationship between structure/composition and the atheroprotective effect of HDL.

This project was supported by grants from the National Institutes of Health #GM105561 (to VN) and by the 2017 CSULB Student Summer Research Award from the Academic Affairs and the Office of Research & Sponsored Programs (to TN).

101. Atomic Force Microscopy of Nanosphere patterned Cobalt Thin films

Terence Baker, Alexander Beach, Jiyeong Gu, Ph.D., Chuhee Kwon, Ph.D.
1250 Bellflower Blvd, Long Beach, CA 90840
California State University Long Beach

Nanosphere lithography is a viable method of pulling out a material's full potential in the field of material science. Of the two samples that were analyzed during this study one had nanospheres deposited on a subtrate and the other had material deposited on it after lithography and then had the nanospheres removed. Through Atomic Force Microscopy (AFM) and Magnetic Force Microscopy (MFM) it is possible for scientists to thoroughly study materials that have been fabricated using nanosphere lithography at the nanoscale. The first images that were collected were from a platinum coated calibration grid that was 1 μm x 1 μm. Multiple images were taken during the calibration process but the final image shows the scanner is correctly calibrated within the specified error range. During the calibration process a MFM calibration scan was taken as well using a magnetic stripe, the magnetic domain and the direction of the magnetic field along the plane of the thin film was observed from the magnetic stripe. Images of 25 nm – 30 nm thick cobalt thin films patterned with nanosphere sizes of 200 nm and 600 nm and the nanospheres removed were taken. These samples had the indent of the nanospheres left behind with the deposited cobalt around it. The other samples had nanospheres of size 930 nm and were scanned at 10 μm x 10 μm in size, it was fabricated using the Langmuir-Blodgett method. The future plan is to make scans of freshly made permalloy and cobalt samples with larger sized nanospheres ranging from 900 nm - 1000 nm and the same thickness as before. These samples will have the nanopatterned structure still intact as well as a thin layer of material deposited over that structure. After AFM scans are obtained, MFM scans can be made from the nanostructured material to obtain the magnetic characteristics of the sample.

This project was supported by FY2016/2017 Small Faculty Grant as well as the summer Scholarship Fund

102. Investigating Large Area Deposition of Densely Packed Polystyrene Nanospheres.

Alexander Beach, Terence Baker, Chuhee Kwon, PhD., Jiyeong Gu, Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Nanosphere lithography is the process of creating close packed monolayers of nanospheres as a substrate mask, which can be used to created ordered long range nanostructures with interesting optical and magnetic properties. Three different methods for creating densely packed monolayers of polystyrene nanospheres were attempted in this study; drop-casting, Langmuir film deposition, and vertical evaporation. Langmuir film deposition yielded the largest areas of densely packed monolayers, up to 1mm by 0.5mm. Drop coating is an easier and quicker approach, but has created smaller monolayer areas approximately 10μm by 10μm. and the samples do not dry fully on their own after several days in an open room. Vertical evaporation samples had similar results to drop casting samples, small monolayer areas, and large areas of unevaporated liquid. Langmuir films are the most promising option investigated, but there are many parameters that must be controlled. In the future samples will be created while varying solution temperature, subphase cleanliness, compression time, subphase surface pressure, and other paramters. Once a sample with a suitable monolayer area is created, the sample will be sputter coated in conductive material to investigate the magnetic properties of the surface using magnetic force microscopy and through the magneto-optical Kerr effect.

This project was supported by FY2016/2017 Small Faculty Grant from California State University Long Beach, and the Margaret Heeb Summer Research Scholarship awarded by the Department of Physics and Astronomy at California State University Long Beach.

103. Excited State Dynamics of Tachysterol Investigated by Non-Adiabatic Molecular Dynamics

Travis Thompson[1] and Enrico Tapavicza, Ph.D.[2]
[1]Department of Physics and Astrophysics, California State University, Long Beach, Long Beach, CA, 90804
[2]Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA, 90804

Tachysterol is an important factor in the vitamin D photo equilibrium. Although it has long been known that Tachysterol and its derivatives have several biological functions in the body, its photochemical reactivity and role in the photochemical equilibrium of vitamin D is not well understood. To sample the equilibrium of its conformers, we carry out replica-exchange molecular dynamics. Based on the generated Boltzmann ensemble, we simulate its absorption spectrum and address its photochemical reactivity by real time non-adiabatic dynamics based on time-dependent density functional theory. We find four main ground state rotamers. Tachysterol's broad absorption spectrum arises from a superposition of contributions from the ground state rotamers. We see a strong dependency of reaction channels on the dihedral angle conformation. Only cis-E-cis rotamers have been found to produce previtamin D via double bond isomerization. Tachysterol's large extinction coefficient and low previtamin D quantum yield suggest that it plays a major role in the quenching of previtamin D production upon extended sun expose.

104. Alternative Splicing of *Mapt* Exon 10 in the Developing Mouse Cortex and Hippocampus

Allyson Milla, Michael Franklin, and Houng-Wei Tsai, Ph.D.
Department of Biological Sciences, California State University of Long Beach, Long Beach, CA 908040

Microtubule associated protein, tau (*Mapt*), binds to and organizes microtubules to form and maintain the neuronal axon. Exon 10 of this gene encodes the second of four microtubule-binding domains (MBDs). The alternative splicing of *Mapt* exon 10 generates two isoforms: exon 10^- mRNA produces 3-repeat (3R) tau with three MBDs, and exon 10^+ mRNA produces 4-repeat (4R) tau with four MBDs. Mutations that affect splicing of exon 10 have been linked to frontotemporal dementia (FTDP) and other neurodegenerative disorders. Splicing factor, suppressor of white-apricot homolog (*Sfswap*) is a gene that codes for an alternative splicing regulator that inhibits the inclusion of *Mapt* exon 10 in the final form of mRNA. We have previously found that in the mouse cortex/hippocampus, *Sfswap* mRNA levels decreased with age during early development. Thus, we hypothesized that there would be an age-dependent increase in the inclusion of *Mapt* exon 10 occurring in the developing mouse cortex/hippocampus. To test our hypothesis, we used reverse transcription with polymerase chain reaction (RT-PCR) and quantitative polymerase chain reaction (RT-qPCR) to characterize and measure the levels of 3R- and 4R-tau mRNA in the cortex/hippocampus of male and female C57BL/6J mice collected on the day of birth (PN0), 7 (PN7), 14 (PN14), and 21 (PN21) days after birth (N=8 per sex per age). First, using RT-PCR, we observed that regardless of sex, PN0 mice expressed only 3R-tau mRNA and PN7 animals generated equal amounts of 3R- and 4R-tau mRNA in their cortex/hippocampus, while only 4R-tau mRNA was produced at PN14 and PN21. Next, we used RT-qPCR to quantify relative expression of 4R-tau mRNA. Consistent with the PCR data, 4R-tau levels were very low at PN0, and the ratios of 4R-tau mRNA vs. total tau increased with age ($p<0.05$). Overall, our data demonstrate that the splicing of *Mapt* exon 10 is age-dependent in the developing mouse cortex/hippocampus, possibly due to down-regulation of *Sfswap*.

References:

https://ghr.nlm.nih.gov/gene/MAPT#conditions
www.premierbiosoft.com/tech_notes/gene-splicing.html
Journal of Neurochemistry. *Tau exon 10, whose missplicing causes frontotemporal dementia, is regulated by an intricate interplay of cis elements and trans factors.* Junning Wang, et al. (2004)
Molecular Neurodegeneration. *Tau exon 10 alternative splicing and tauopathies.* Fei Liu and Cheng-Xin Gong. (2008)
GMR *Potential Hippocampal genes and pathways involved in Alzheimer's disease: a bioinformatic analysis.* L.Zhang, et al. (2015)

105. Expression and Detection of Purified Protein Complexes: CDK5-p25/CDK5-p35

Vera Yangildina[1], Amy Tran[2], and Deepali Bhandari, Ph.D.[3]
[1]Department of Chemical Engineering, California State University, Long Beach, Long Beach, CA 90840
[2] Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840
[3]Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Cyclin dependent kinase 5 (CDK5) is a serine/threonine kinase. Its activation requires interaction with its cognate activator p35 or p25 (a truncated product of p35). While p35 has a short half-life, p25 is a very stable protein in mammalian cells. To test if this is also the case in bacterial cells, we co-expressed CDK5 and p35 as well as CDK5-p25 in E. coli SoluBL21 cells. The goal of my summer project was to use Western blotting to detect the protein complexes in samples generated by another student in the lab. The proteins were purified using Ni2+-NTA affinity chromatography and analyzed by Western blotting to confirm the presence of the protein complexes. Our results showed that p25 is more stable than p35 in bacteria as well. My current and future goals include performing the kinase assay to determine if these complexes are catalytically active.

This project is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers: 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02.

106. Using the Aerobic Enzyme, Citrate Synthase, to Understand Biogeographic Dispersal Potential in Echinoid Echinoderm Larvae

A. Pouv, A. Ohanian, T. Tran and D. A. Pace, PhD.
Department of Biological Sciences, California State University Long Beach, Long Beach, CA 90840.

Temperature is a primary determinant of biogeographic distribution in animals due to its overwhelming influence on biochemical processes. This study explores the possibility that habitat ranges of adult echinoids are linked to temperature sensitivity of critical metabolic enzymes during the planktotrophic larval stage. Echinoid larvae depend on the Krebs Cycle for the generation of ATP to fuel growth and development. The thermal performance of the regulatory Krebs Cycle enzyme, citrate synthase (CS), was determined in several echinoid larvae with the following thermal habitat ranges: *Dendraster excentricus* (2-28˚C), *Strongylocentrotus purpuratus* (2-24˚C), *Strongylocentrotus fragilis* (0-10˚C), and *Centrostephanus coronatus* (12-30˚C). *In vitro* analysis of CS activity and temperature sensitivity (from 5-35˚C) was determined for 10-day old larvae of each species, reared at 16˚C (except *S. Fragilis,* reared at 9˚C) and fed Rhodomonas algae at a concentration of 10,000 cells/mL. Temperature sensitivity was assessed through Q_{10} calculations and determination of activation energy through Arrhenius breakpoint analysis. As indicated by Q_{10} analysis, *D. excentricus* was the most sensitive to temperature, especially at colder temperatures. *S. fragilis* exhibited a peak temperature sensitivity at 15-20˚C and *S. purpuratus* was relatively insensitive to temperature except at the coldest extreme. *D. excentricus* did not exhibit any discrete change in activation energy throughout the temperature range, in concordance with its broad habitat temperature range. *S. fragilis* and *S. purpuratus* displayed discrete shifts in activation energy at 15˚C and 20˚C, respectively, matching their relative differences in habitat temperature ranges. The results of this study help to understand how thermal dependence of early life-history metabolic pathways has ramifications for dispersal potential of planktotrophic larvae of benthic marine organisms. This information is important for understanding biogeographic distributions and population dynamics of marine organisms.

Key Words: Citrate Synthase, Enzymatic Temperature Sensitivity, Echinoderm

Acknowledgement: Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number RL5GM118978. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

107. CPU and GPU Parallelization in Python for Calculating Properties of Graphene Multilayers

Vladislav Larionov, Nicholas Werner, Andreas Bill Ph.D.
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Graphene (a two-dimensional honeycomb lattice of Carbon atoms) was shown to display a wealth of interesting physical properties (unusual elasticity, optical and electronic properties, etc.). We are interested in studying how electronic properties change when stacking individual graphene sheets on top of each other. This represents a major numerical challenge due to the computation time required. For accurate results, we expect a large grid of computation points will be required per layer, and as the number of layers increases the calculation time grows to a point where it is no longer feasible. To perform the calculation for each point sequentially (for example as a function of frequency or momentum) would lead to a computation time of many days to a few weeks to complete. We explored techniques for reducing execution time using the multiprocessing features of Python. We devised a method to split computation among each available CPU core, which gave us a speed gain approximately linear with the number of CPU cores. We also considered an alternate form of parallelization for Python using OpenCl, which allowed us to use the GPU capabilities of our research computers. We present the result of our analysis and what physical properties can now be calculated with the parallelized code.

We gratefully acknowledge support from the National Science Foundation under grant DMR-1309341.

108. No Abstract

109. Effects of the Melting Temperature of Polyamide Veils as Interleaving Materials in Carbon-Fiber Composites

Wade Shipley, Tejas Reddy, and Ehsan Barjasteh, Ph. D, Department of Chemical and Mechanical Engineering, California State University Long Beach, Long Beach CA 90840

Carbon-fiber composites are increasingly employed in the aerospace and automotive industries owing to their lightweight and excellent mechanical properties. However, this class of material, when subjected to out-of-plane loads, is often susceptible to an internal damage in the form of delamination that can severely reduce its load bearing capacity. Several toughening methods including the implementation of thermoplastic materials are used to increase the damage tolerance of the polymer-matrix composites. In particular, non-woven thermoplastic veils, when used as interleaving materials between the plies in a composite structure, is extremely efficient at improving the interlaminar (delamination) fracture toughness and impact-resistance of composites. In addition, the toughening of the polymer matrix, if not adversely affecting the manufacturing process, can result in an increase in the toughness-related properties of composite laminates such as the resistance to micro-cracking under thermal-cycling conditions.

In this study, the effects of matrix toughening and interleaving of the composites with non-woven Polyamide (PA) veils on the Interlaminar Fracture Toughness (ILFT) of Carbon-fiber/Benzoxazine composites are investigated. Formulated Benzoxazine (BZ) resins in non-toughened and toughened variants along with several non-woven PA veils with different melt temperatures are used to manufacture composite laminates through the Vacuum-Assisted Resin Transfer Molding (VARTM) process. The ILFT of composites is measured by obtaining the resistance to crack propagation in the interlayer under tensile forces (Mode-I ILFT) or shear forces (Mode-II ILFT). The critical strain energy release rate (G_c) recorded during interlaminar fracture gives a measure of the ILFT of a composite.

The laminates interleaved with the PA veils show an increase of nearly 50% for the Mode-I crack Initiation (G_{Ic} *initiation*), regardless of the melt temperature of the PA veils. The Mode-I crack propagation (G_{Ic} *propagation*) of the laminate increases by using the PA veils with melt temperatures lower than the cure temperature of the BZ resin.

In the Mode-II ILFT (G_{IIc}) tests, the laminates interleaved with the PA veils show a significant impact on the G_{IIc} values, as increases of nearly 170% are observed. A strong correlation between PA melt temperatures and the G_{IIc} values is noted. The greatest G_{IIc} values are noted when the melt temperature of the PA veil is greater than the cure temperature of the BZ resin.

The matrix toughness plays a significant role in affecting the G_{Ic} values. The laminates manufactured with the toughened BZ resin result in the greatest increase in the G_{Ic} values. In contrary, the use of the toughened BZ resin does not result in an improvement in the G_{IIc} values.

This project is funded in part by NIH grant number R25GM071638

110. Purification of the CDK5-p35 complex from *E. coli* SoluBL21-DE3 cells

Amy Tran and Deepali Bhandari, Ph.D.
Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach, CA

Protein phosphorylation, a reversible modification, plays a central regulatory role in various cellular processes, such as proliferation, differentiation, migration etc. Thus, over- or under-activation of kinases (the enzymes that carry out phosphorylation) can result in various pathologies. Cyclin-dependent kinase 5 (CDK5) is a proline-directed serine/threonine kinase whose over-activation has been implicated in multiple diseases such as neurodegeneration, cancer, and type II diabetes. Thus it is important to understand how CDK5 activity is regulated. In order to do so, we need to be able to express and purify recombinant CDK5. We cloned CDK5 and its cognate activator p35 in pET-DUET expression vector. When we co-expressed the CDK5-p35 complex in *E. coli* BL21-DE3 cells, majority of the complex was insoluble and aggregated into inclusion bodies. Our attempts to make the complex more soluble by changing induction and expression conditions (lower temperature, decreased time of induction and lower amount of inducer) did not succeed. We then switched to SoluBL21-DE3 cells, a variant of *E. coli* BL21-DE3 cells specifically designed to increase protein expression in the soluble fraction. We found that expression in SoluBL21-DE3 cells did increase the yield of the protein complex in the soluble fraction. We purified the complex using Ni^{2+}-NTA affinity chromatography and tested its activity using an *in vitro* kinase assay. Together, our results suggest that SoluBL21-DE3 cells improved the solubility of the CDK5-p35 complex and that the complex purified from these cells is active. Our current and future goals include scaling up the expression and optimizing the purification protocol.

111. Determining the Molecular Connection between the Timing of Flowering and Leaf Senescence in *Arabidopsis thaliana*.

Will Hinckley and Judy Brusslan, Ph.D.
Department of Biological Sciences, California State University, Long Beach, 1250 Bellflower Blvd., Long Beach, CA 90840-9502

Higher order *atx* (*Arabidopsis* trithorax) mutant plants display an additive phenotype. We have shown that homozygous triple mutants (*atx1,atx3,atx4*) bolt and senesce earlier than double mutant combinations, which in turn bolt and senesce earlier than single mutants and wildtype. ATX enzymes are recruited to trimethylate lysine 4 of histone H3 (H3K4me3), a histone tail mark associated with active gene expression. RNA-seq and ChIP-seq data demonstrated that 319 of 1,450 senescence upregulated genes gain the H3K4me3 mark and these genes are predicted to play important regulatory roles in senescence. We hypothesize that flowering and senescence are connected at the molecular level by regulatory genes that are up- or down-regulated at the time of flowering. RNA-seq is being used to identify regulatory genes that change expression in early flowering and early senescing *atx* triple mutants. Two sibling triple mutant lines were be grown alongside wildtype. A set of plants from each triple mutant genotype were marked for use based on bolting on a similar date to ensure plants are at the same developmental age. When the largest set of developmentally similar bolts emerged, a BrAD-seq (RNA-seq) time-course experiment was performed in two-day increments using vegetative WT of the same age as the control. RNA-seq data will be analyzed by Short Time-series Expression Miner (STEM) to cluster genes with increasing or decreasing expression in the triple mutants but not in wildtype plants. Clusters will be interrogated for genes known to influence flowering or with transcription factor domains. T-DNA insertions into these genes will be studied to determine if these genes contribute to the coordination of the timing between flowering and senescence.

This work was supported by NIH SC3GM113810 awarded to Dr. Judy Brusslan and NIH R25GM071638 which funds the Research Initiative for Scientific Enrichment (RISE) program at CSULB.

112. The Role of Lysine 52 and 54 in the Stability of Apolipophorin III

Angela B. Tran, Kriti Shah, and Paul M.M. Weers, Ph.D.
Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Apolipophorin III (apoLp-III) is an 18 kDa exchangeable apolipoprotein found in insects. ApoLp-III is often used as a model due to the availability of the three-dimensional structure of the protein, which helps understanding lipid transport processes. The protein contains eight lysine residues, some of which may help to maintain the structure of the protein. . Previous experiments showed that the double mutant K52/54Q greatly reduced the stability of the protein. It is hypothesized that one of these lysine residues forms a salt bridge with glutamate or aspartate residues to stabilize the protein. In order to identify which lysine is involved in maintaining protein stability, attempts were made to create two single lysine mutants at position 52 or 54. Through site-directed mutagenesis the K54Q mutant was produced, however, several attempts to create the K52Q mutant were unsuccessful. New sets of primers were designed, which resulted in the successful mutation at position 52. Both mutant proteins, K52Q-apoLp-III and K54Q-apoLp-III, were expressed in *E. coli*, and after purification the structure of the proteins will be assessed using circular dichroism to determine the helical content and stability of the protein. This will shed light on the role of lysine residues play in the structure and function of apolipoproteins, and can help to understand their role in cardiovascular disease.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02; GM089564.

113. Biomimetic Bis Gold Supramolecular Catalysts

William Ryan Sueme and Michael P. Schramm Ph.D.
Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach, CA

The synthesis and use of biomimetic molecules is an important and ever expanding field of study in chemistry and biochemistry. In nature enzymes will often possess multiple active sites capable of performing several chemo and regio-selective transformations on a variety of substrates. We have previously demonstrated the ability to use supramolecular catalysts modeled after natural enzymes with multiple active sites to catalyze the dimerization of alkynes using a double gold motif.

We expand on this result using resorcinarene based bis gold phosphoramadite supramolecular catalysts. We will prepare several variations of this superamolecular catalyst. The size of the aromatic "walls" attached to the resorcinarene scaffolds surround the active site, their size and chemical characteristics should play some role in catalysis. Our newly prepared supramolecular biomimetic catalysts will enable testing to determine how altering the chemical and steric properties of the catalyst affects the yield of dimerization reactions. The information provided by this study will allow for the generation of new catalysts for industrial and academic uses, further our understanding of gold as a transition metal catalyst, and provide insight into deep cavitand catalyst synthesis and capabilities.

This work is supported by NSF (RUI CHE-1708937) and NSF (MRI CHE-1337559). The content is solely the responsibility of the authors and does not necessarily represent the views of the National Science Foundation.

114. Kinetic modeling of DTPA (diethylenetriaminepentaacetic acid): The aqueous actinide holdback reagent in nuclear waste reprocessing

Anneka J. Miller, Kristian Larsson, Ph.D., Stephen P. Mezyk, Ph.D.
Department of Chemistry and Biochemistry, California State University at Long Beach, Long Beach, CA, 90840.

The reprocessing of spent nuclear fuel from power reactors is usually achieved by sequential solvent-extraction steps. The used fuel bundle is initially dissolved in concentrated HNO_3/HF, resulting in a highly-acidic (4 – 6 M) solution containing most of the metals in the periodic table. The first separation step is the extraction of the fuel uranium, plus the fission products plutonium and neptunium, from this acidic mixture into an organic medium. This allows these metals to be re-used for new fuels. In general, the remaining aqueous phase is then discarded in a repository. However, in order to reduce the long-term heat load in repositories an additional extraction step to remove the minor actinides (americium and curium) is often performed. Again, a solvent extraction system is typically used where the lanthanides are extracted into an organic phase, leaving these two minor actinides in the aqueous phase. In order to facilitate this separation the ligand DTPA (diethylenetriaminepentaacetic acid) is often used as an actinide "holdback" reagent in the acidic aqueous phase. However, this ligand is not perfectly selective; and DTPA will also complex the lanthanides that need to be extracted into the organic phase. Our work focused on understanding the formation rate of DTPA complexing to lanthanides. These kinetics have been previously determined using ligand-displacement techniques based on complexed dye molecules; however, we have found this to significantly underestimate the actual rate constants. To accurately determine these rates, we have used the direct luminescence of the lanthanide europium when it binds to DTPA. This gave us the exact information on europium's formation constant, which was then was used to determine the relative formation constants for the other lanthanides. Additionally, we determined the exchange rate of the different lanthanides between the complexes through three experiments. A large difference in both rate and equilibrium conditions for the different lanthanides was found, and will be reported here. Further studies will include organic phase kinetic reactions and the combination of these studies to model the mixing of organic and aqueous phases which must include the interface transfer of metals. The combination of these three domains will allow us to model the solvent extraction process and properly elucidate external impacts from solution buffers and the effects of radiation.

115. Building the infrastructure to Collect and Monitor Massive Molecular Dynamics Simulations via Worldwide Distributed Computing

Xavier Martinez[1] and Eric J. Sorin, Ph.D.[2,*]
Department of [1]Computer Engineering & Computer Science and [2]Chemistry & Biochemistry, California State University Long Beach, Long Beach, California 90840, United States

Physical and virtual installation of Folding@Home (F@H) Work Servers (WS) was performed to allow for the collection of parallel all-atom Molecular Dynamics (MD) simulations. Following installation of multi-terabyte RAID storage arrays, the Debian 9 OS was installed on two high-performance WSs, where the F@H WS software was then installed. Network configuration procedures, such as port control; remote access authorization; and networked data redundancy, were performed and tested. Following successful server configuration, simulation projects were distributed to the F@H network of approximately 400,000 processors worldwide, with each of our WSs collecting approximately 10 μs of sampling per day. Herein, we describe a streamlined procedure for hosting CPU intensive MD projects, as well as a system for hosting a password authenticated, outward-facing web platform to visualize incoming data in real-time. Our use of the latest web technologies, such as the Python-based Django and Django REST back-end frameworks; Google's AngularJS; and the Relational Database Management System MySQL, placed our platform on top of a fast and scalable architecture for monitoring terabytes of data. These technical efforts have allowed us to begin collection of massive MD simulations to probe the inhibition of Butyrylcholinesterase by an ensemble of potential drugs, and to visualize attributes from this dynamic data set on the fly. This work will fully support new projects of this nature, including studies of collagen structure as a function of glycine point-mutation, relevant to myriad human health issues, and the folding and function of RNA pseudoknots and riboswitches of varying size and structure.

XM acknowledges support from the RISE program at CSULB and NIH (Award Number R25GM071638)

116. No Abstract

117. An Investigation of Replica Exchange Molecular Dynamics and Absorption Spectra of Molecules in Smog

Adam Smith[1], Mary Caitlin Jordan[1], Shiva Nilakantan[2], Enrico Tapavicza, Ph.D[1]
[1]Department of Chemistry and Biochemistry, California State University Long Beach, Long Beach, CA 90840 and
[2]College of Engineering, California State University Long Beach, Long Beach, CA 90840.

Smog is a type of air pollutant that is visible to the human eye. Atmospheric aerosols are suspensions of solid and/or liquid particulates which can be found in smog. Reaction mechanisms have been proposed for the formation of Major Gas- and Aerosol-Phase products by the use of High-Resolution Mass Spectroscopy[1]. In this study the ground state and excited state dynamics of one of these molecules, an imine dimer with an M/Z 145, was performed using the quantum chemistry package TURBOMOLE[2] to better understand the behavior of the molecule in a photochemical setting. Replica Exchange Molecular Dynamics (REMD) consists of running and switching four simultaneous dynamics calculations of the same molecule at temperatures of 300, 600, 900, and 1200 K. Two REMD simulations were performed in order to provide a quantum mechanical canonical ensemble. An absorption spectrum was generated by averaging the spectra of 250 structures from both REMD simulations and visualized using MATLAB[3].

[1]David O. De Haan. Department of Chemistry and Biochemistry, University of San Diego, 5998 Alcala Park, San Diego CA 92110 USA
[2]TURBOMOLE V6.2 2010, a development of University of Karlsruhe and Forschungszentrum Karlsruhe GmbH, 1989-2007, TURBOMOLE GmbH, since 2007; available from http://www.turbomole.com
[3]MATLAB and Statistics Toolbox Release 2012b, The MathWorks, Inc., Natick, Massachusetts, United States.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; 8UL1GM118979-02; 8TL4GM118980-02; 8RL5GM118978-02.

118. General Relativistic Methods for Gravitational Wave Frequencies of Neutron Stars

Michael Lanoye, Benjamin Diaz, and Prashanth Jaikumar, Ph.D
Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840

Neutron Stars are expected to be a prominent source of gravitational waves. Once we have determined the spacetime oscillations at the surface of the star we can project it out into space and determine the gravitational waves that could be detected here on Earth. We compute the general structure of a neutron star by using a polytropic Equation of State. We determine the surface of the star precisely using a variation of the Tolman-Oppenheimer-Volkoff (TOV) equations based on enthalpy. We then calculate the spacetime oscillations of the star at its surface in order to determine the gravitational waves that it will emit. The surface variables that are needed to determine the oscillation modes are found by solving a system of 4 coupled linear differential equations. These equations project the solution at the center of the star using the Runge-Kutta computational method out to the surface.

This project is supported in part by National Science Foundation Grant PHY-1608959.

119. No Abstract

120. Synthesis and Characterization of Esters of Fmoc-Amino Acids as Potential Butyrylcholinesterase Inhibitors

Bianca Y. Pingul[1], Jennifer Ramirez[2], and Jason P. Schwans, Ph.D.[2]
[1]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840 and [2]Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA 90840

Neurodegenerative diseases such as Alzheimer's disease is the sixth leading cause of death in the United States and affects 5.5 million Americans. While cures for this disease have not yet been discovered, several pharmaceuticals are available to alleviate symptoms. These compounds typically target the cholinesterases, acetylcholinesterase (AChE) and/or butyrylcholinesterase (BChE). In patients with Alzheimer's disease (AD), AChE activity is relatively unaffected, while BChE activity increases leading to a depletion of the neurotransmitter, acetylcholine. The decrease of acetylcholine has been suggested to contribute to the dementia observed in patients with AD. Thus, inhibitors of BChE are sought in the treatment of AD. We previously found Fmoc-amino acids selectively inhibit BChE leading to a potential new class of cholinesterase inhibitors. While the role of the amino acid side chain was explored, the effects of modifying the carboxylate group were not explored. Specifically, the enzyme binds the cationic substrate, acetylcholine, but the Fmoc-amino acids are anionic. We postulated Fmoc-amino acid esters may be more potent inhibitors, as the ester ablates the negative charge and introduces the ability to increase steric bulk and subsequently increase van der Waals interactions. To test this model, Fmoc-amino acids were esterified using EEDQ (N-Ethoxycarbonyl-2-ethoxy-1,2-dihydroquinoline), purified by chromatography, and characterized by NMR. Although removing charge may lead to better inhibitors, it is expected to decrease aqueous solubility. The solubility limits for the Fmoc-containing esters were evaluated using UV-Vis absorbance measurements. Initial results suggest the esters may be more potent inhibitors compared to the Fmoc-amino acid, but are limited by solubility. We are now investigating additional esters bearing cationic groups to enhance solubility. These results may guide the design of new Fmoc-containing compounds that specifically and effectively inhibit BChE.

This project is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers R25GM071638, UL1GM118979, TL4GM118980, RL5GM118978, and T34 GM008074. The content is solely the responsibility of the author and does not necessarily represent the official views of the National Institutes of Health.