CALIFORNIA STATE UNIVERSITY
LONG BEACH
College of Natural Sciences
& Mathematics

College of Natural Sciences and Mathematics

STUDENT RESEARCH SYMPOSIUM

BOOK OF ABSTRACTS

Friday, September 22, 2023

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

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California State University, Long Beach

Student Research Symposium

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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 22, 2023. 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

10:30-10:50am: Check-in and research & resource fair (until 1pm)

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 will be served in the Alamitos Bay Room at 10:30am.

Pizza will be served in the Alamitos Bay Room at 11:30am.

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1. **Modeling the Effects of Inducing IL-6 and IL-10 on Breast Cancer Immune Cells Using Differential Network Analysis.**

Camille Wong[1], Konstacja Urbaniak[2], Joao Rodrigues Lima Junior[3], Sergio Branciamore[2], Peter P. Lee[3], Andrei S. Rodin[1]

[1]Department of Computer Engineering and Computer Science, California State University, Long Beach, Long Beach, CA 90840;

[2]Department of Computational and Quantitative Medicine, City of Hope, Duarte, CA 91010; and

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Interleukins (ILs) regulate immune responses and cancer development. IL-10 has a two-faced role in supporting tumor proliferation – most notably in breast cancer (BC). It has pro-inflammatory and immune-suppressive properties that drive cancer cell survival and metastasis.

Another IL, IL-6, is overexpressed in BC patients. High levels of IL-6 and impaired IL-6 signaling have been correlated with worse patient outcomes. IL-10 is known to increase the expression of IL-6, yet an amalgamation of these two cytokines has not been studied.

In this study, we aimed to investigate the effect of IL-6, IL-10, and a combinatory treatment of IL-6 with IL-10 on selected proteins in peripheral blood mononuclear cells (PBMCs) from 17 BC patients and 10 age-matched healthy donors *in silico*. Our hypothesis was that the addition of the interleukins would have a significant effect on the proteins. These proteins are composed of immune cell surface receptors and components of the JAK-STAT signaling pathway. The data was gathered via fluorescence-activated cell sorting (FACS).

Traditionally, similar immuno-oncology experiments focus on a single cytokine. The combination of two cytokines has not yet been performed, and we expect that this coalescence is non-additive, and therefore cannot be realistically approximated by the two single-cytokine experiments.

Nested scatter plot graphs of the data reveal that IL-10 heavily influences pSTAT3, and its expression is dramatically elevated in all three treatments compared to the untreated control group.

In order to contrast (1) BC and healthy PBMCs, and (2) four cytokine treatments (untreated, IL-10, IL-6, IL-10 + IL-6), Bayesian network (BN) probabilistic modeling was performed to see how immune signaling networks are re-wired under different conditions. BNs were constructed using BNOmics software with maxent discretization of the whole complement of distributional data (as opposed to just means). Two additional secondary analyses are being currently carried out: (1) Belief propagation to predict *in silico* how switching the healthy/cancer state would change the rest of the network, and (2) projection to overlap the homologous networks under different conditions, in order to enable the seamless visualization and quantitative assessment of the networks' "re-wiring."

This project is supported by Dr. Ruth and Eugene Roberts and NIH grants U01CA232216 and R01LM013138.

2. **Noise Reduction of Visual Task-Based Functional Magnetic Resonance Imaging using NORDIC**

Simon Galleta, Ru Zhang, Dilmini Wijesinghe, Zhifeng Chen, Danny JJ Wang, Kay Jann

Low signal-to-noise ratio (SNR) prevents high resolution fMRI from precisely locating brain function, hindering the utility prospects for clinical and neuroscientific applications. This work highlights the ability to detect brain activity and the performance of Noise Reduction with Distribution Corrected (NORDIC) PCA to denoise by comparing quantitative evaluations to the standard manufacturer reconstruction for visual task-based high-resolution fMRI datasets.

Ten volunteers (mean age 22/2.977 std, 3 female 7 male) participated in a visual task involving a visual checkerboard block design displayed on an MR compatible screen. The task was run eight times with four tasks being run to collect 1mm isotropic resolution images and the other four runs being run to produce 0.8mm isotropic resolution images. Standard and NORDIC Reconstructed fMRI timeseries were motion realigned and no spatial smoothing was performed. A General Linear Model was used to estimate brain responses to stimuli in each run. One-sample t-statistics across runs for each reconstruction modality revealed significant voxels and consistency. Two regions of interests in the left and right visual cortex for the NORDIC and standard reconstruction data were identified to compute the temporal Signal-to-Noise Ratio (tSNR). To evaluate tSNR differences between different spatial resolution data as well as NORDIC and Standard reconstruction methods, one-way repeated measures analyses of variance (ANOVAs) were conducted.

We observed that tSNR in the 1mm isotropic resolution images higher compared to the 0.8mm images (for Standard: mean difference (Δ)of tSNR=13.2, $p<0.001$, for NORDIC: [Equation]tSNR=3.5, $p=0.37$). Comparing Standard against NORDIC revealed significantly higher tSNR for NORDIC for 1mm isotropic resolution [Equation]tSNR=17.1, $p<0.001$) as well as for 0.8mm isotropic resolution images ([Equation]tSNR=26.8, $p<0.001$). Furthermore, we found higher tSNR in 0.8mm isotropic resolution NORDIC data as compared to the 1mm Standard data [Equation]tSNR=13.6, $p=0.012$).

We demonstrated at at 7T, sub-millimeter detection of brain activity is feasible with sufficient tSNR and statistical significance, and that NORDIC denoising significantly improves the tSNR. Submillimeter spatial resolution fMRI will enable the study of the mesoscale architecture of the human cortex including cortical columns and layers.

3. **Mineral Assemblages in Eskers from Iceland: An Analog for Cold and Wet Environments on Mars.**

Candice L. De Anda[1,2] and Elizabeth B. Rampe[3]

[1]California State University, Long Beach, CA 90815, [2]Lunar and Planetary Institute (USRA), Houston, TX 77058, (candice.deanda01@student.csulb.edu), [3]Astromaterials Research and Exploration Science Division, Houston, TX 77058 (elizabeth.b.rampe@nasa.gov)

Orbital images have revealed several sites with potential esker-like features associated with morphological evidence for glaciers. These candidate eskers have been estimated to be from the mid-to-late Amazonian period (i.e., 110-330 Ma), which would indicate wet-based glaciation recently in Mars' history. This research is focused on examining the mineralogy and composition of the esker sediments to get a better understanding of their make-up and whether they exhibit certain mineralogical signatures that could distinguish them from other similar sedimentological features on

Mars (e.g., inverted channels). Through bulk mineral analysis of eskers of varying exposure ages in a Mars-analog environment, we aim to determine the degree of aqueous alteration experienced by eskers sediments and characterize any mineralogical evolution within eskers with increasing exposure age. This research will ultimately help us piece together more of Mars's geologic history and evolution. X-Ray Diffraction (XRD) was used for quantitative mineralogical analysis of sediments from four eskers of different exposure ages. Bulk sediments were analyzed, and size separates were performed on bulk samples that exhibited relatively high concentrations of X-ray amorphous material to better constrain the source of the amorphous material. A Panalytical X'Pert Pro MPD was used for powder analysis of all samples. The data were analyzed using the program Profex. Each pattern was run with the following crystallographic information files: diopside, quartz, actinolite, chlorite, magnetite, andesine, augite and corundum. The bulk mineralogical data show that all eskers sampled contain abundant plagioclase and clinopyroxene, with the former being the most abundant mineral in every sample. The most apparent mineralogical trend in the samples was a higher concentration of amorphous material in the finer facies of the eskers. There was also a difference in X-ray amorphous content with the exposure age of the eskers. The shortest exposed esker exhibited the highest amount of X-ray amorphous material, and the longest exposed esker exhibited the least amount. Analysis of the size separates from samples with higher concentrations of amorphous material demonstrated that the X-ray amorphous material is concentrated in the fine and medium sand-sized sediment. It is now hypothesized that the X-ray amorphous material is dominantly primary (i.e., volcanic glass) and is not a secondary alteration product. This volcanic glass may have formed through explosive hydro volcanism, from lava-ice or lava-groundwater interactions. The relatively low density of this glass may explain the higher amorphous content in the younger eskers, because as the eskers sit exposed over time, the less dense volcanic glass gets transported by seasonal glacial melt water.

This work was supported by the Lunar and Planetary Institute's (LPI's) 2023 Summer Intern Program in Planetary Science and a Cooperative Agreement between NASA's Science Mission Directorate and the LPI, which is operated by the Universities Space Research Association (USRA), and by NASA Solar System Workings grant 80NSSC21K0908.

4. Clean Proximity Systems in an Electromagnetic Field

Cristian Garcia, Laura Tandy, Andreas Bill

Department of Physics and Astronomy, California State University, Long Beach, California 90840

A Josephson junction is made of a non-superconducting material of nano-scale thickness, sandwiched between two superconducting thin films. In the superconductor electrons bind in pairs with opposite momenta and spin. The non-superconducting material considered here is a magnetic multilayer with a flexible magnetic configuration. We first present the behavior of the electron pairs as they tunnel from one superconductor to the other through the multilayer with various magnetic configurations. We then present the formalism that allows to include the effect of an externally applied time-dependent electromagnetic field on the Josephson junction. We discuss how the junction can be used as a sensor for electromagnetic radiations.

This research was supported by the National Science Foundation CSULB-OSU PREM program under Grant No. 2122199

5. **The Relative Importance of Epidemiological Factors and Governmental Restrictions on COVID-19 Mortality Rates.**

Jo A. Estrada, Elizabeth C. Moses, Ashley J. R. Carter, Ph.D.

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

The global COVID-19 pandemic has been responsible for taking numerous lives, however mortality rates varied greatly between the U.S. states. Many studies have looked at how epidemiological factors and government interventions influenced the spread of the virus, but the relative importance of these two types of factors has not been as widely studied. We investigated which type of factor more heavily influenced the variation in COVID-19 mortality rates between the 48 United States continental states during the 2020/21 flu season. We previously found that epidemiological, economic, and demographic factors played twice as much of a role in COVID-19 mortalities as government interventions at the state-level. We wanted to expand this analysis to the county level by investigating COVID-19 mortality rates across 2304 U.S. counties throughout the 2020/21 flu season. Based on our prior results, we expect to see that flu/pneumonia mortalities and therefore pre-existing epidemiological factors explain COVID-19 mortalities more than government interventions at the county-level. By looking at the differences between counties, we may be able to suggest which specific epidemiological factors are most important to be targeted for intervention to possibly curb future outbreaks.

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

6. **Standard Model Lie Algebras as Complex Clifford Representations**

Armando Reynoso,Thomas Klaehn

Department of Physics and Astronomy, California State University Long Beach, Long Beach, CA 90840

The Standard Model(SM) is currently regarded as our best theoretical framework within our current mathematical and experimental limitations in which microscopic phenomena in elementary particle physics can be understood through Lie algebras. Despite its success in computing with high precision the electromagnetic fine structure constant which quantifies the strength of the electromagnetic interaction using QED(Quantum Electrodynamics) at low energies, or predicting the existence of the Higgs boson which is responsible for assigning mass to the particle spectrum, it remains a mystery in understanding the motives for natures preference in choosing $U(1)_Y \times SU(2)_L \times SU(3)_c$ allowing phenomena such as particle decay as seen in, electromagnetic interaction or the binding of matter. We start our investigation by noting that a Clifford algebra exhibits a Grassmanian structure allowing the ability to perform a Witt decomposition. We show that our decomposition can form a super Lie algebra operator representation allowing us to reason $Cl(4,0)$ as the space which exhibits chiral operator algebras in a complex representation. These findings are useful in opening the doors to various algebras to explore the Standard Model through a different lens.

7. **Examining Cancer Research Effort and its Relation to Cancer Disease Burden in 18 European Countries**

Sophia Manjarrez[1], Ashley Carter[1]

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

Cancer research effort has many ways of being quantified, but publication rates are a means to see the relative effort by researchers focused on potential treatments or discoveries related to certain cancers. It has been established that many cancers see a disproportionate level of funding or effort for their burden in places like the United States or United Kingdom, but do these trends of disproportionate funding exist in the same way across Europe, or do European countries have their own trends? Using previously published cancer publication rates, we compared multiple cancer burden values to see if the rate of publication was in line with cancer burden in 18 European countries. Using the burden values of Disability Adjusted Life Years (DALY), mortalities, and Years of Life Lost (YLL), we were able to calculate relative burden values and compare these to the relative publication rates. These comparisons illustrate when effort and burden values are proportional or when there are discrepancies fueling a mismatch between effort and burden. Our results allow us to make recommendations on how to better distribute research funding.

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

8. **Climate Change Reduces Functional Advantage of Nitrogen-Fixing Forb Species on the Kaibab Plateau**

Emily Fitzpatrick[1] and Karen Haubensak, Ph.D.[2]

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

[2] Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ 86011

Climate change is making droughts in the Southwestern United States more severe, and warmer temperatures inhibit drought recovery due to increased evaporation. There is an overall trend toward decreasing water availability. This has major ramifications for plant species, many of which require specific germination cues and climatic conditions to survive, as well as pollinators that rely on floral resources. As water becomes a more limited resource, this may reduce the functional advantage of N-fixing species. This study compares percent cover data collected in 2005 and 2022 on Fabaceae species in the Kaibab Plateau to evaluate how the changing climate has impacted N-fixing forbs and examine what implications this has for pollinators. The frequency of N-fixing species did not significantly decrease from 2005 to 2022 ($p=0.1271$). The average percent cover of N-fixing species per plot decreased drastically from 2005 to 2022 ($p=0.0224$). This significant decline in the presence of N-fixing species implies a reduction in their abundance and ability to proliferate in 2022 climatic conditions when compared to 2005. This loss of percent cover also indicates a loss of floral resources for pollinators. Going forward, the floral traits and pollinator relationships of N-fixing species will be examined to determine if specific pollinator species or groups are likely to be impacted by these changes.

This project is supported in part by funding from the National Science Foundation Grant 1950421, an REU Site award.

9. Small molecule b-AP15 Induces Integrated Stress Response in Cancer Cell Lines

Anma Arora, Dr. Deepali Bhandari, Ph.D.

Department of Chemistry and Biochemistry, California State University, Long Beach, CA 90840

Small molecule b-AP15 (3,5-bis[(4-Nitrophenyl)methylidene]-1-prop-2-enoylpiperidin-4-one), is widely used as a potent deubiquitinase inhibitor resulting in cell death due to the dysfunction of the ubiquitin-proteasome system. However, recent results from our laboratory have shown that SC66, a compound structurally similar to b-AP15, causes oxidative stress and triggers the Integrated Stress Response (ISR). The ISR is a crucial cellular defense mechanism that enables cells to adapt to adverse conditions. It is triggered by various stressors, including but not limited to viral infections, oxidative stress and nutrient deprivation. One of the hallmarks of ISR is the temporary inhibition of general protein synthesis and selective translation of transcription factors such as activating transcription factor 4 (ATF4) that control gene expression of proteins involved in stress alleviation. Depending on the duration and/or severity of the stress, ISR can also activate pro-apoptotic genes, e.g., the C/EBP-homologous protein (CHOP). Given its structural similarity to SC66 and its potential as a cancer therapeutic, we hypothesized that b-AP15 can also lead to activation of the ISR. To test our hypothesis, we treated two cancer cell lines – HeLa (cervical cancer) and DLD1 (colorectal cancer) with b-AP15 and tested the induction of ISR by immunoblotting the cell lysates for ATF4 and CHOP. Our findings revealed that b-AP15 induced ISR in both cell lines as evident by the detection of ATF4 and CHOP in b-AP15 treated cells as compared to control cells. These results indicate that inhibition of the proteasome is not the sole mechanism of action of b-AP15. Understanding b-AP15-induced ISR and its impact on cell survival will offer mechanistic insights into these compounds which are being considered as therapeutic drugs for cancer treatment.

This project is supported by the NIH-NIGMS grant #SC3GM139707 awarded to D.B. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

10. Investigating *TET* Paralog Gene Expression in *pen1, tet3 and tet8* Mutants

Andrew P. Harrison Hanson, Jayde Zimmerman, and Judy Brusslan, PhD

In plants, the two most studied extracellular vesicles (EVs) are PEN1-associated and TET8-associated EVs. PEN1 and TET8 are both integral membrane proteins with TET8 being a tetraspanin and PEN1 being a syntaxin. These EVs are induced during defense responses indicating they may play a role in pathogen response; however, their function is currently undefined. Our lab has used immunoblots to show that extracellular TET8 is increased in *pen1* mutants, suggesting TET8 may be compensating for the loss of PEN1. My research is aimed at determining if the increase in extracellular TET8 is occurring at the level of transcription. I also wanted to determine if other similar *TET* genes are showing a compensatory mRNA increase in *tet3* and *tet8* mutants. WT, *tet3*, *tet8*, and *pen1* plants were grown for 8 weeks. Leaves 4 and 5 of each plant were harvested, RNA was isolated, cDNA was synthesized, and mRNA expression was measured using real-time qPCR. Results showed that *TET8* mRNA expression is not increased in *pen1* mutant, indicating that the changes occur post-transcriptionally. *TET3*, *TET4*, *TET7*, *TET8*, and *TET9* (the closest paralogs to *TET3* and *TET8*) mRNA expression was measured and did not show any increase in expression in either *tet3* or *tet8*. The results indicate that these paralogs do not compensate for loss of tetraspanins in the *tet3* and *tet8* mutants at the mRNA level.

11. Isoform-specific Roles of Protein Kinase Akt in the Unfolded Protein Response

Anthony Rios[1], Samantha Perez[1], Sebastian Bonca[2], Oshiana Schenkelberg[2], and Deepali Bhandari, PhD[1]

[1]Department of Chemistry and Biochemistry, California State University, Long Beach, Long Beach, CA, 90840 and

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

The Unfolded Protein Response (UPR) is a highly conserved set of eukaryotic signaling pathways that is activated during cellular stress incurred when the endoplasmic reticulum (ER) fails to properly fold and release mature proteins. Many cancers utilize the UPR to maintain cytoprotective signaling while growing under stressful tumor microenvironments. Multiple studies have implicated Akt, a family of three homologous serine/threonine kinases, as a regulator of the UPR and cancer cell viability during ER stress. However, it is not known if UPR regulation is specific to one of the isoforms or a redundant role for the Akt family. The goal of this project is to study specific roles of the Akt isoforms during ER stress. We used a colorectal cancer cell line, DLD1 which expresses only two isoforms of Akt - 1 and 2. To first confirm that Akt regulates UPR in DLD1 cells, we treated cells with a pan-Akt inhibitor and analyzed the cell lysates for UPR specific proteins via western blotting. ER stress was induced with either of the two commonly used stressors – tunicamycin and thapsigargin. Comparison of the response of Akt inhibited cells to ER stressors with that of the uninhibited cells revealed that Akt inhibition significantly lowers the UPR. Our results suggest that both Akt isoforms are activated upon ER stress induction, however, with a more pronounced response for Akt2. Both isoforms also showed localization to the crude mitochondrial and microsomal fractions as determined by subcellular fractionation. Membrane localization was reduced in cells treated with the Akt inhibitor indicating that catalytic activity is important for membrane recruitment. Together, these data suggest that in DLD1 cells both Akt1 and Akt2 may be involved in regulation of ER stress signaling. For our future experiments, we will utilize DLD1 cell lines with single gene knockouts of Akt1 or Akt2 and a double knockout of both genes to investigate the roles of the two isoforms. Akt is of therapeutic interest in cancer treatment with many of its inhibitors currently in clinical trials. The current and future findings of this study will shed light on the unique and redundant roles of Akt isoforms in a signaling pathway active in cancer cells and will potentially contribute to the design of more targeted therapeutics.

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12. Studying ERF022's Role in the Regulation of Leaf Senescence Through Generation of Transgenic ERF022-YFP *Arabidopsis thaliana* Lines

James Koo and Judy Brusslan

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The process of leaf senescence in plants recycles nutrients, such as nitrogen, from older leaves to developing tissues, such as developing fruit and grains. Understanding the regulation of this process can provide insight and innovation into ways to reduce dependency on nitrogen fertilizers and to

maximize crop yield to combat a global food shortage. A previous study done by Hinckley et al. on the late senescing *hac1* mutant line revealed reduced H3K9ac activating marks on the transcription factor (TF) *ERF022* as well as reduced expression of *ERF022*, suggesting that *ERF022* is regulated by the HAC1 histone acetyltransferase. Furthermore, an *erf022* mutant line also displayed delayed leaf senescence, suggesting that ERF022 is involved in the regulation of leaf senescence. Studying and characterizing ERF022 and its role in leaf senescence may lead to further understanding leaf senescence regulation. One way to characterize *ERF022* is through the generation of a *pERF022:ERF022-YFP* transgenic *Arabidopsis thaliana* line, that has high expression of ERF022-YFP, for use in Chromatin Immunoprecipitation (ChIP)-seq to identify the DNA binding targets of the ERF022 TF. An anti-GFP antibody that recognizes YFP will be used to immunoprecipitate ERF022-YFP bound to its chromatin targets during ChIP-seq. Multiple lines of BASTA-resistant transgenic *pERF022:ERF022-YFP Arabidopsis thaliana* lines have been generated via floral dip transformations. Resistance to the BASTA herbicide allows selection of transgenic lines. Further genotyping confirmed the presence of the transgene. Real-time-qPCR was used to show gene expression levels of *pERF022:ERF022-YFP* in T2 transgenic lines. The six highest *pERF022:ERF022-YFP* expressing transgenic lines, that are homozygous for the transgene, will have their seeds harvested. Harvested seeds will be sown and the resulting plants will have their ERF022-YFP expression quantified via Western blotting. In addition to the work on the generation of the transgenic *pERF022:ERF022-YFP* line, the experiment from Hinckley et al was repeated to confirm the late senescence phenotypes associated with the *erf022* mutant.

This project received support from the 2022 Faculty-Graduate Student Research Collaboration Program.

13. Investigating the Mechanism of Action of SC66 – A Small Molecule Modulator of Protein Kinase B

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According to the World Health Organization, cancer is the major cause of death worldwide with approximately 10 million deaths annually, or every one in six deaths. About 40% of all tumor types have aberrations in the signaling pathway involving protein kinase B, more commonly referred to as Akt. Akt plays a pivotal role in regulating numerous critical cellular processes, including growth, metabolism, and survival, all of which are essential for the sustenance of cancer cells. Consequently, Akt inhibitors represent a vital category of anti-tumor agents in the realm of cancer therapy. One such inhibitor, SC66, was discovered from a library of small molecules and was shown to allosterically inactivate Akt as well as promote its degradation. The authors proposed that SC66 binds to the amino-terminal pleckstrin homology (PH) domain, however, this was not experimentally tested. The main objective of this study is to determine whether SC66 interacts with the PH domain of Akt. To do so, we cloned the pleckstrin homology (PH) domain of Akt1 (residues 1-113) with an N-terminal hexa-histidine tag in the pET28a bacterial expression vector and expressed it in codon optimized Rosetta *Escherichia coli* DE3 cells. Based on a previous study, to improve solubility of the recombinant protein, three codons for lysine residues were added to the carboxyl-terminal end of the construct. The protein was partially purified by a single step affinity chromatography using Co^{2+} beads and the fractions were analyzed via staining with instant blue dye and western blotting. Subsequently, we employed fluorescence spectroscopy for the preliminary analysis of the binding between SC66 and the purified PH domain. Results from the fluorimeter

analysis showed a change in the fluorescence intensity of Akt after SC66 was added to the solution suggesting a potential interaction. Our future studies include further purifying the protein using ion-exchange chromatography followed by isothermal calorimetry (ITC) studies to analyze the binding between the PH domain and SC66. The findings from this study will enable a reassessment of prior research findings and their implications regarding SC66 as a potential anti-cancer drug.

14. Assessing the Role of *WRKY57* in Bolting Related Leaf Senescence in *Arabidopsis thaliana*

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Leaf senescence is the successive process in which older leaves mature and then die, indicated by leaf yellowing. This is a critical developmental stage in all plants, including the model species *Arabidopsis thaliana*, and is imperative to the plant's fitness, as nutrients are recycled back into the growing and storage tissues of the plant. The *WRKY* gene family encodes transcription factors that play critical roles in response to abiotic stressors. *WRKY57* gene expression is induced by drought and overexpression of *WRKY57* results in drought tolerance. Our lab is interested in *WRKY57* as it may also be important for the regulation of leaf senescence in response to flowering, termed bolting in *Arabidopsis thaliana*. Our project is to monitor *WRKY57* gene expression after bolting and to isolate *wrky57* T-DNA mutants and determine if they display early senescence. Two T-DNA insertions, SALK_006206 and SALK_076716, localize to the *WRKY57* gene. To identify individuals that were homozygous for mutant alleles, we used PCR primers that spanned the insertion site. Two homozygous individuals were isolated for each T-DNA insertion. These PCR products were then sent for sequencing, after which we designed real-time qPCR primers to quantify *WRKY57* transcripts. The WRKY57-1 primer pair amplified cDNA linearly and was used to quantify transcripts in response to bolting. We found that *WRKY57* gene expression was up-regulated after bolting. We purified, sequenced, and mapped the SALK_006206 allele, which is an intron. We then repeated the process with SALK_076716, which mapped to the promoter region. Next, we will determine if T-DNA insertion lines block *WRKY57* gene expression, or in the case of the promoter insertion, activate *WRKY57* gene expression, and will quantify bolting-associated leaf senescence through loss of chlorophyll and activation of *NIT2* gene expression.

This project is supported in part by the McNair Scholars Program at CSULB (P217A220268).

15. Sodium Salicylate Differentially Regulates the Unfolded Protein Response in a Colorectal Cancer Cell Line

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Acetylsalicylic acid *aka* aspirin is a non-steroidal, anti-inflammatory drug that has been linked to reduced occurrence of many cancers, particularly colorectal cancer. However, the cellular mechanism(s) for this protection remains elusive. Cancer cells have altered metabolic demands due to the hypoxic environment and rapid proliferation rate that can induce proteotoxic or endoplasmic reticulum (ER) stress. During ER stress, cells activate an evolutionarily conserved signaling pathway known as Unfolded Protein Response (UPR). The adaptive UPR signaling has been correlated to acquisition of malignancy and chemoresistance in cancer cells. In addition, UPR signaling has a maladaptive phase that commits cells to apoptosis especially during chronic ER stress. The goal of

this project is to investigate whether aspirin regulates UPR signaling in cancer cells. We treated colorectal cancer cell line DLD1 with sodium salicylate (NaSal), a metabolic derivative of aspirin, and analyzed the expression of various proteins involved in UPR signaling via western blotting. Our results revealed that NaSal differentially regulates different branches of UPR signaling in DLD1 cells. Our data also indicated that the expression level of the chaperone glucose regulated protein of 78kDa (GRP78), a key UPR regulator, was lowered in NaSal-treated cells. Since translocation of GRP78 to the cell surface is positively correlated with the metastatic and chemoresistant potential of cancers, our future directions include determining the level of cell surface GRP78 in NaSal-treated DLD1 cells using immunofluorescence microscopy. Overall, our results indicate that regulation of UPR signaling may be one of the mechanisms underlying the potential chemopreventive actions of aspirin against colorectal cancer cells.

This project is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number T34GM149378-01.

16. Two Class E bZIP Transcription Factors Promote Bolting-Associated Leaf Senescence and May Regulate Response to Abiotic Stressors

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bZIP family proteins are transcription factors (TFs) that regulate stress, phytohormone response, and development, including seed maturation (Shen et al., 2007). They are characterized by a basic leucine-rich zipper domain used to dimerize with the same domain of other bZIP proteins to initiate transcriptional regulation. *bZIP34* and *bZIP61* genes were characterized in a bolting-associated gene regulatory network (GRN) of leaf senescence (LS) predicted by Hinckley and Brusslan in 2020. Their specific role as bolting-associated genes (BAGs) is not well characterized; however, they are predicted to regulate transcription of downstream targets such as *NLP3, WOX2* and *WRKY45*. Additionally, these two sole members of the class E bZIP TF clade have a conserved proline residue in their zipper domain, preventing homodimerization—a characteristic found in most bZIPs (Shen et al., 2007). These two members can form heterodimers with Class I member bZIP51, alluding to one possible mechanism of how they might regulate expression in the BAG network. We have isolated two double mutant (DM) *bzip34 bzip61* plants and have measured the expression of a well-known LS marker *NIT2* during time points T0, T4, and T12 days after bolting. In the wild type (WT) plants, we observed a significant increase in *NIT2* expression between the T0 and T12 time points. However, this expression difference was not seen in both *bzip34 bzip61* DM lines. We will begin another replicate comparing only T0 and T12 to confirm this delayed LS phenotype. Further research involves measuring expression of both *bZIP34 and bZIP61* genes to determine whether the mutant alleles were knock-down or knockout mutants. It is also important for us to measure expression levels of our mutants' target genes to further determine the extent of their role in the proposed GRN. We also hypothesize there is a link between bolting-associated LS and response to abiotic stress. Current research is underway in order to fine-tune various abiotic stress protocols including salt and drought stress to measure the effects our double mutant alleles have on resistance to such stressors.

Keywords: "Gene Regulatory Network" "*Arabidopsis thaliana*" "Transcription Factors" "Basic Leucine Zipper Domains" "Leaf Senescence" "Bolting Associated Genes" "Abiotic Stress"

17. *No abstract assigned*

18. Atmospheric Effects on the Photochemical Hydroacylation of Cyclohexane Carboxaldehyde and Diethyl Maleate

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Modern chemistry focuses on green methods to synthesize the compounds in a more efficient and environmentally friendly manner. In synthesis of many pharmaceutical agents, bioactive molecules containing 1,4-dicarbonyls are utilized as precursors or are present in the target compounds. One means of synthesizing 1,4-dicarbonyls is through hydroacylation, which is an atom efficiency process. Adding the use of photons as clean and traceless reagents applies another Principle of Green Chemistry. Recently, studies have explored using organic photo-initiators for these reactions, instead of heavy, toxic metals, to further reduce environmental harm. A remaining challenge in the hydroacylation reaction is the formation of undesired hydroalkylation products. Since the reaction atmosphere is a known complicating factor in photochemical reactions, we are exploring potential correlation between the reaction atmosphere and hydroalkylation. The gases used in this study are: Air, Nitrogen, Carbon Dioxide, Oxygen, and Argon. The reaction vials were sparged with the desired gases to create the desired atmosphere above and within the reaction. The reactions are run in the EvoluChem™ PhotoRedOx Box to control the wavelength, distance between light source and sample, stirring rate, and maintains room temperature. A preliminary study by a previous group member showed that under Air, Oxygen, Nitrogen, and Carbon Dioxide, there is a high percent conversion rate of the desired acylation product with Air and Oxygen showing the presence of hydroalkylated products. This suggested that an oxidizing environment might be the cause of the byproduct formation. Results from the current study show less hydroalkylation product formation than the prior study suggesting the cause of byproduct formation is more complex than originally thought. The next step of the study will look more closely at the oxidized starting materials as a source of hydroalkylated products in organo-initiated hydroacylation reactions.

19. Validating the Bolting-Associated Leaf Senescence Gene Regulatory Network: Analyzing ERF54 Target Gene Expression

Vanessa Avila, Andrea Orozco, Judy Brusslan, Ph.D.

As the need for food grows, it becomes crucial to enhance sustainable agriculture by maximizing the nutrient efficiency of plants. Leaf senescence (LS) is the last step in the natural development of a plant's life. When a plant is growing, and ready to move from its vegetative to reproductive state, it accumulates nutrients to support flowering. Our lab has observed that vegetative leaves express genes related to leaf senescence when the plant transitions to reproductive growth. Nutrients released by older leaves can fuel flower development. Understanding how formation of reproductive structures signals leaf senescence (LS) can lead to tackling global food security and sustainability due to efficient nutrient recycling. Previously, our lab has proposed a gene regulatory network (GRN) to describe this signaling pathway. At the center of the GRN is the ERF54 transcription factor. It has been proposed that ERF54 interacts with different bolting genes that also impact LS. Previous studies have suggested different target genes that can either be downregulated or upregulated by ERF54. My work aims to determine whether target genes proposed to be regulated by ERF54 show a significant change in expression in an *erf54* mutant. We analyzed the expressions of seven different target genes using real-time qPCR. We found that *FH13* and *AtTic32* showed a significant reduction in gene expression. This data supports the proposed GRN. Additionally, we expected *erf54* mutant to show delayed LS due to its central position in the GRN, however; there was no difference in LS

when comparing to WT when chlorophyll and gene expression were quantified. We hypothesize that *erf53* is a redundant paralog and may be compensating for the loss of ERF54 in the *erf54* mutant. To further define this proposed redundancy, we are analyzing the contribution of ERF53 gene by isolating an *erf53* mutant. I have shown the *erf53* allele harbors a T-DNA insertion in the promoter region and is affecting gene expression. We have isolated and identified a homozygous erf53 line, and crossed *erf54* and *erf53* towards producing *erf54erf53* double mutants. By analyzing gene expression during LS we will be able to confirm the relationship between ERF54 and ERF53. Our research highlights the importance of understanding leaf senescence at the molecular level in pursuit of enhancing agricultural sustainability.

20. Novel Synthetic Methods for Thermoelectric Materials

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Thermoelectric materials are capable of converting heat into electricity and vice versa. Such functionalities allow them to be employed in space missions for remote power generation. For instance, Radioisotope Thermoelectric Generators (RTGs) were the driving force for the Mars rover. One such compound, $La_{3-x}Te_4$, was selected for its efficiency at high temperatures to potentially extend the life expectancy of multi-mission radioisotope thermoelectric generators (MMRTG's) with retained energy. Through collaboration with NASA Jet Propulsion Laboratory, the additive manufacturing of $La_{3-x}Te_4$ was investigated to reduce the production time of thermoelectric legs, lessen material wasted, and manipulate different leg shapes. To synthesize the target material, high temperature solid-state method was employed. The raw material manipulation and heating process were conducted in an inert atmosphere, to avoid formation of side products such as oxides. The products were characterized by powder X-ray diffraction (XRD). Lanthanum and Tellurium containing reagents were first mixed in a mortar and pestle to create a homogenous mixture. The mixture was then hydraulically pressed into a pellet (0.5 g) and placed in a quartz tube under an Argon atmosphere. The sample was then heated under constant inert gas flow. The phase purity was determined by comparing the collected sample's diffraction pattern to that of a reference sample. While the first attempts didn't result in single-phase pure samples, further modifications to the reaction condition (choice of reactants, temperature, and time) improved the quality of the product. The project continues to progress with the utilization of phase pure $La_{3-x}Te_4$ in 3-D printing, heat sintering, and the exploration of its thermoelectric application.

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21. Maternal Inexperience is Associated to a Decreased Social Attention in Rhesus Macaques

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Adverse events early in life can negatively impact health and reduce survival. However, we have yet to understand whether these insults have a transient or enduring effect. Here, we tested associations between individual and cumulative early-life adversity and socio-cognitive health across the lifespan of female and male rhesus macaques (*Macaca mulatta*) at the Cayo Santiago Biological Field Station. We identified early-life adversity retrospectively as nutritional and psychosocial sources of adversity defined by maternal loss, maternal inexperience, a competing younger sibling, high population density, and environmental instability due to a hurricane. To test for associations between socio-cognitive health and cumulative adversity early in life, we estimated a cumulative adversity index by adding up all adversities experienced by individuals. Socio-cognitive health was indexed using negative socioemotional bias tasks and looking time methods. We performed analyses at different life stages to contrast short-term effects of adversity (i.e., infant cognition) with long-term effects (i.e., adult cognition) using linear-mixed effects models. Juvenile rhesus macaques with inexperienced (primiparous) mothers showed less social attention, relative to juveniles with experienced mothers. On average, these affected juveniles looked 1.06 ± 0.472 (SE) seconds less at negative stimuli than juveniles with experienced mothers ($p = 0.03$). However, adult rhesus macaques with primiparous mothers were cognitively similar to other adults. We found no association between socio-cognitive health and any other individual or cumulative early-life adversity. This decreased social attention found in juveniles suggests a lack of ability to assess social cues or maintain social attention. Further studies should address the demographic implications of decreased social attention during developmental ages.

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22. Optical Properties of d-f transition in $CaY_{0.95}M_{0.05}Ga_{0.50}Fe_{0.50}O_4$ (M=Bi, Eu, Tb) and $CaY_{0.95}Tb_{0.05}Cr_{0.05}Ga_{0.95}O_4$.

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White light-emitting diodes (w-LEDs) have applications such as detectors, displays, or emergency lighting. The methods used to generate white light included mixing either a blue LED and yellow phosphor, a blue LED and several phosphors, or an ultraviolet LED and blue, green, and red phosphors. The phosphor in a high-power semiconductor-based LED consumes more than half of the electrical input power, while the remainder is converted into heat. This increased in temperature can harmed the overall performance of the LED device. The long wavelength was converted to a shorter wavelength, leading to a change in the color of the phosphors, a reduction in luminous efficacy, and a decreased in the lifespan of the w-LED. The samples were prepared using citric acid sol-gel synthesis, which involved precursors made from metal ligands. The process to synthesized the gel begins by combining stoichiometric amounts of starting materials and adding citric acid to chelate metal ions. The gel was sintered in an electric furnace and subsequently pressed into a pellet to cluster the fine solid particles. The pellet was crushed in a mortar and pestle and then analyzed using Powder X-Ray Diffraction (P-XRD) to characterize crystalline solids. The absorption spectra were determined using the Hitachi UH-4150, and the photoluminescence spectra were obtained

using the Shimadzu RF-5301PC Spectrofluorophotometer. New series of phosphors were synthesized with the formula in $CaY_{0.95}M_{0.05}Ga_{0.50}Fe_{0.50}O_4$ (M= Bi, Eu, Tb) and $CaY_{0.95}Tb_{0.05}Cr_{0.05}Ga_{0.95}O_4$. The color tuning by the addition of the isoelectric defects from the Tb^{3+}, Eu^{3+}, and Bi^{3+} ions will demonstrate great potential to improve the next generation of w-LED solid-state lighting.

23. Social attention is not associated to fitness in rhesus macaques

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Social attention and cognitive competence are important for among-individual interactions and group dynamics. Accordingly, social attention plays an important role on the evolution of populations. Yet, whether individual social attention affects fitness components, i.e., survival and reproduction, remains unclear. Here, we evaluated associations between social attention and reproductive performance across the adult lifespan. For this, we used experimental cognitive data on social attention based on looking time methods of 642 adult female rhesus macaques (*Macaca mulatta*) living at the Cayo Santiago Biological Field Station. We classified each female into one of three different reproductive stages: gestating, nursing, and failed breeders (i.e., females that gave birth, but whose offspring died prior to the cognitive task), and tested associations with social attention using linear mixed-effects models. Our results showed that social attention declines with age. However, there was no association between reproductive stage and social attention. Our findings point towards the absence of trade-offs between cognitive performance and fitness. Understanding how individual variation in cognitive processing translates into ecological and evolutionary dynamics is key to advancing our knowledge about the emergence of phenotypes driving evolutionary trends across species.

24. Synthesis and Magnetic Properties of NaCl type compounds; A_5OsO_6 (A=Li,Na)

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In antiferromagnetic materials the spins of unpaired electrons are ordered in antiparallel arrangement with respect to their neighbors. In materials composed of triangular sub-lattice of magnetic ions the magnetic constraints cannot be fulfilled simultaneously which results in a phenomenon called geometric magnetic frustration. In ordered NaCl structure type composed of FCC arrangement of cations such triangles are present leading to inability of the magnetic spin interactions to align themselves due to the lattice structure. Alternatively, if all the exchange interactions in triangles are not of the same strength, stronger interactions will dominate the magnetic structure by lifting the competition. Our group has previously studied members that belong to this family with Os ions as the magnetic ion centers. Examples include Li_5OsO_6, Li_4MgOsO_6, Li_3MgOsO_6, $Li_3Ni_2OsO_6$, and Li_4NiOsO_6. The focus of this study is to further our understanding on the effect of crystal structure on geometric magnetic frustration. Na_5OsO_6 was synthesized using conventional solid state synthesis method under specific atmospheric conditions. Stoichiometric amounts of osmium(IV) oxide and sodium oxide were mixed into a homogenous mixture, pelletized, and then placed into an alumina crucible. The crucible was placed into a quartz tube and then into a tube furnace and heated to 300 degrees Celsius under argon gas flow for 12 hours and then under oxygen for another 12 hours at 750 degrees Celsius. This process is repeated

until the sample is in its desirable phase. Powder x-ray diffraction (XRD) is employed in order to characterize the phase purity. Preliminary x-ray data has shown that the compound Na_5OsO_6, is possible to create using conventional solid-state synthesis. To conclude it was possible to synthesize Na_5OsO_6, and future studies will be done in order to understand the magnetic frustration of this compound and derivatives of it.

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25. Metformin and Palmitate Induce Unfolded Protein Response in L6 Rat Myocytes

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Endoplasmic reticulum (ER) is a major organelle in eukaryotic cells which carries out several important functions including protein folding and secretion, lipid metabolism, and Ca^{2+} storage. Any perturbations in its function such as accumulation of misfolded proteins cause ER stress and activate a signaling program called the Unfolded Protein Response (UPR). ER stress and UPR are involved in the pathogenesis of many diseases including cancer and type 2 diabetes (T2D). Typically, to study UPR in an experimental setting, perturbations in ER functions are generated by treating cells in culture with chemicals that interfere with protein folding, calcium homeostasis or the oxidative environment of the ER. Although these chemicals provide valuable mechanistic insights into UPR signaling, there is a need to investigate more physiologically relevant ER stressors. Our lab is interested in using muscle cells as a model system to understand the effect of UPR on insulin signaling. The goals of this project are to – (1) optimize protocols to use palmitate, a free fatty acid found in excess in the plasma of obese individuals, as an ER stressor in muscle cells and (2) study the effect of metformin, the most prescribed medication for T2D, on UPR signaling in muscle cells. We used L6 rat myocytes and treated them with a series of palmitate concentrations exposed for different timepoints. The cell lysates were then analyzed by western blotting to determine the optimum concentration of palmitate and treatment time needed to activate the UPR. Our results showed that 8 hours of exposure to 500 mM palmitate optimally activated the UPR in L6 myocytes. For our second goal, we wished to study if metformin (1,1 dimethyl-biguanide hydrochloride) can reduce palmitate induced UPR in these cells. When we co-treated cells with palmitate and metformin, we did not observe any downregulation of UPR. In fact, we found that high amounts of metformin alone can trigger UPR signaling in L6 myocytes. Interestingly, a recent study has shown metformin to impair muscle volume and function. Together, our data have helped establish a protocol to use palmitate as an ER stressor in L6 cells and shed light on the unexpected role of metformin in causing ER stress in muscle cells. Our future experiments will focus on measuring effect of palmitate and metformin on insulin signaling.

26. Knocking down LXR Receptor in Macrophages using siRNA

Bryan Navarrete, Kerollos Roufael, Daniel Chiu, Kien Pham, and Deborah A. Fraser Ph.D.

27. Using Tfm Mutant Mice to Study the Role of Androgen Receptor in Brain Sexual Dimorphism

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Testosterone acts on androgen receptor proteins (AR) to organize and activate the neural circuits that govern sexual dimorphism in behaviors and other brain functions. Like others, our lab has been using testicular feminized (Tfm) mutant mice to study the role of AR in brain sexual differentiation. Tfm mice express nonfunctional, truncated AR due to a deletion mutation, which shifts the reading frame of *Ar* mRNA and then introduces an early stop codon. Besides the possession of the nipples typical of females and a lack of normal male genitalia, genetically male Tfm mice are reported to display female-like phenotypes in a variety of behaviors and brain morphology. An earlier study observed that AR deficiency in the nervous system abolished sex differences in social behavior and hypothalamic expression of *Oxtr* in adult mice. However, it is unclear if this AR-mediated regulation of *Oxtr* transcription occurs during early organization or during later activation in adulthood. To address this, we are measuring *Oxtr* expression in the hypothalamus of wild-type and Tfm juvenile mice prior to the onset of puberty. If AR is necessary for organizing the sexual differentiation of *Oxtr* expression in the developing brain, we expect to see an increase in hypothalamic *Oxtr* mRNA levels in juvenile wild-type females and Tfm males as compared to wild-type males. Currently, we have collected the hypothalamic samples of Tfm male mice and their wild-type littermates at the age of 21 days. All animals have been genotyped for their sexes and Tfm mutation. In addition, we have re-designed the PCR primers for *Oxtr* and are optimizing the conditions of RT-qPCR for *Oxtr*. We will later conduct RT-qPCR to measure mRNA levels of *Oxtr* in the juvenile mouse hypothalamus.

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28. Investigating the Role of LXR in Macrophage Responses to Innate Immune Protein C1q

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Atherosclerosis is a disease caused by the formed deposits and the buildup plaque from the fatty substances as cholesterol (LDL) in the inner lining of the artery. The buildup plaques cause narrowing and hardening of the artery. Macrophages are a type of white blood cells that uses phagocytosis to remove any damaged or dead cells in the body as well as cholesterol. The excessive engulfing of cholesterol in macrophages leads to apoptosis in the cell. C1q is a protein modulator that can enhance the activation of macrophage phagocytosis and increase its survival in order to remove more cholesterol from the body. Macrophages contain a nuclear liver x receptor (LXR) that works on regulating the macrophage cholesterol efflux. In this study, we are investigating the role of LXR and its subunits (a &b) to understand how it affects the respond of the macrophage cholesterol metabolism in the presence of C1q protein. To do this, we first need to develop methods to knockdown gene expression of the LXR subunits. We predict that macrophages with knocked down LXR will not show any enhancements in survival or cholesterol efflux in the presence of C1q. For this experiment, we used THP-1 monocyte cells that matured to become macrophages using PMA after 24 hours. The cells were then transfected with siRNA targeting LXR a, LXR b or a scrambled negative control with the aid of lipofectamine to deactivate the gene expression of LXR in the macrophage. The samples were harvested after 24 and 48 hours to optimize results. After harvesting,

the RNA was taken from the samples to be purified and isolated to create cDNA which will be used to measure the gene expressions of LXR using qPCR. The predicted results if successful, will show a reduction in the gene expressions of the targeted gene (LXR a or □) that was a result of the knocking down. Finally, the qPCR is still under analysis and if our results match our prediction, we will be able to optimize the experiment and develop methods to knockdown LXR subunits a and b. This tool will then help us understand how C1q activates macrophages through using LXR, which will aid in the process of designing therapies for cholesterol management in patients and treating Atherosclerosis.

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29. Locomotor Activity and Exploratory Behavior in Mice Lacking Androgen Receptor

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Androgen receptor (AR)-mediated androgen actions are necessary for the display of both sexual and aggressive behaviors in male mice, yet to what extent AR is involved in the development and expression of locomotor and exploratory behavior has yet to be established. Here, male mice carrying the testicular feminization mutation (Tfm) in the *Ar* gene (n=17), wild-type male (n=22) and wild-type female (n=21) mice were tested in an open field test to assess the role of the AR in these functions. Behavioral testing was recorded by a video camera mounted above the arena (L69 cm × W52 cm), and subsequently analyzed by computer-assisted tracking. In 15-min sessions, Tfm mice tended to spend less time in the peripheral zone and more time in the center zone compared to wild-type mice. As such, percentage of session time spent in the center was higher for Tfm mice than wild-type controls ($p=0.013$). On the other hand, no significant differences in time spent in the center or periphery, or the percentage were observed between wild-type male and female groups. In addition, Tfm mice traveled a shorter distance than wild-type females ($p=0.003$). Although no sex differences were observed for distance travelled, wild-type females displayed significantly more crossings into the center zones than the two male groups ($p=0.008$). These findings indicate that the behaviors tested in the open field paradigm are not sexually dimorphic, but rather the presence of AR, not testosterone, has a critical role in open field test behaviors.

30. Oxysterol Composition in C1q-deficient and Wild-type Mice.

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Atherosclerosis is a progressive inflammatory disorder that contributes to heart disease. This disease causes buildup of cholesterol and other products forming plaque in the inner lining of the artery which can prevent proper blood flow. Arterial macrophages are responsible for the uptake of cholesterol packaged into Low-Density Lipoprotein (LDL) and regulation of cholesterol removal by efflux. Mechanisms of efflux can be switched on through activation of the nuclear LiverX Receptor (LXR) via oxysterol cholesterol metabolites. Recent findings suggest that the complement protein C1q plays an important role in the modulation of cholesterol metabolism. Preliminary data in the lab

suggests that C1q binds oxidized LDL, and modulates oxysterol formation in macrophages during uptake. We will test the hypothesis that the presence of C1q will increase production of oxysterols, including 25-hydroxycholesterol, during oxLDL uptake. We aim to measure levels of oxysterols in macrophages from wild-type and C1q-deficient mice alone, exposed to soluble exogenously added C1q (±oxLDL), or on a surface coated with immobilized C1q (±oxLDL). This will allow determination if modulation of oxysterols require signal transduction: 1) from within the cell 2) from within an endosome during internalization of a target, or 3) from interactions with a surface receptor. In preliminary experiments to generate bone marrow-derived macrophages (BMDM), cells were obtained from femurs of mice and incubated with media containing MCSF to differentiate into macrophages. After 14 days of culture, flow cytometry was performed to test that the cells correctly expressed the macrophage phenotypic marker, F4/80. Preliminary data show we obtained cells greater than 93% conversion to F4/80+ macrophages. Studies are now ongoing to collect samples of macrophages from wild-type and C1q-deficient mice (±C1q±oxLDL) for lipidomic analysis (at UCSD lipidomic core) to determine oxysterol production. Ultimately, new findings on C1q role in lipid metabolism and its mechanism may provide more insightful information in the progression of atherosclerosis and aiding in the development of novel treatments.

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31. Nitroaromatic Sensing and Photocatalytic Reduction with Carbon Quantum Dots

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Nitroaromatic compounds can be found in water supplies and pose a threat to the environment and human health due to the highly reactive nitro groups that induce free radical formation. The use of Carbon Quantum Dots (CQD) as an eco-friendly, non-toxic, and requiring simple one-step synthesis is being studied for its potential as a nitroaromatic sensor and reducter in water. Two species of CQD were synthesized and used in both sensing and reduction of nitrobenzene and nitrophenol. CQD1 was formed from reactants urea and citric acid, both reactants are non-toxic and therefore favorable. CQD2 is synthesized from tris(2-aminoethyl)amine and citric acid. CQDs are well known for their fluorescent properties and tunable characteristic, which can be quenched via the electron transfer (ET) and therefore signal the presence of the nitroaromatic groups with the use of fluorometry. Once these compounds are detected, the next step is to reduce the nitro groups to less harmful amine groups. Using photocatalysis, the CQDs then served as electron donors to reduce the nitro groups. Since CQD1 and CQD2 are successful nitroaromatic reducers and sensors, further research will include the sensing and quenching of the antibiotic nitrofurantoin and determining the detection limits of each CQD with nitroaromatics.

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32. Investigating the Effects of Innate Immune Protein C1q on Mitochondrial Metabolism in Macrophages

Zyrille Chloe E. Abela, Vanessa R. Plong, and Deborah A. Fraser

Macrophages are phagocytic cells that help remove damaged-self targets from the body. Macrophages also promote inflammation to efficiently remove pathogens. However excessive or inappropriate inflammation in response to self-targets can lead to inflammatory disorders. Innate immune protein C1q binds a variety of foreign and self-targets and modulates macrophage inflammatory responses. We are interested in identifying mechanisms of C1q in modulating macrophage polarization. Our RNA sequencing data identified that bone marrow derived macrophages (BMDM) from wild-type mice have significantly lower levels of a cluster of genes in oxidative phosphorylation pathways (ox-phos) compared to C1q-deficient macrophages. We hypothesize that interaction of C1q with macrophages decreases expression of ox-phos genes NDUFC2, UQCRFS1, and COX6B1 and therefore decreases metabolic activity and superoxide production. To test this, we isolated and cultured BMDM from wild-type or C1q-deficient mice. C1q-deficient BMDM were treated with C1q alone, or with oxidized LDL with or without C1q bound to compare endogenously produced C1q, soluble C1q, and target-bound. We measured gene expression through qPCR. NDUFC2 (Complex I) and COX6B1 (Complex IV) decreased with endogenous C1q. Metabolic activity between C1q-deficient macrophages treated with or without soluble C1q was measured using Seahorse ATP Rate assay. There were no differences between treatments. Since Complex I is associated with superoxide production in macrophages, we measured superoxide production in Raw 264.7 macrophages treated with C1q. Superoxide production significantly decreased in cells treated with soluble C1q. Reduced superoxide production may provide one mechanism by which C1q modulates macrophage polarization towards an M2 phenotype and could provide molecular targets for therapeutic intervention in inflammatory disease.

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33. Engineering *Methylotuvimicrobium buryatense* for Rapid Growth in Low Methane Concentrations

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Nearly 30 percent of global warming can be attributed to methane. Compared to carbon dioxide, methane is over 80 times more potent. By reducing the amount of methane in the atmosphere we can have a greater impact in lowering global warming. Several cytochrome *c* genes in *Methylotuvimicrobium buryatense* have been identified for which function is unknown. We deleted these genes to see if there is a change in growth rate at low methane compared to high. This will provide guidance as to which targets to overexpress in attempts to increase growth rate at low methane. 5GB1 mutant that can grow at lower methane concentration would expand the regions of growth and methane reduction. To do this a zeocin construct was amplified centered between a left and right flank that corresponds to the cytochrome *c* gene of interest. We amplified left, right and zeocin

products via PCR then combined all pieces to form a construct 1,500 bp long. Three different constructs were amplified to delete 3 different gene targets. Each one was electroporated into *M. buryatense* 5GB1. These electroporated strains were then plated on NMS2 medium plates with zeocin. Colonies were then streaked onto new NMS2 plates with zeocin to ensure that these were indeed mutants. Colony PCR will show if the construct was inserted, and sequencing will be carried out to confirm the location and sequence of inserted constructs. So far, one mutant colony was sent for sequencing, but the result was of poor quality and will be redone. The other two electroporated colonies did not show that they had the constructs inserted into them when diagnostic PCR was carried out. Constructs may have failed to insert resulting in death of most colonies. The colonies that did grow may have done so due to degradation in zeocin on the plate failing to eliminate them. It's also possible that the deleted genes were critical for growth of *M. buryatense* 5GB1 leading to cell death. Further replication of these experiments will be done to finalize the results.

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34. Characterization of magnetic switching behavior of Py and SmCo nanocap thin films on the monolayer of nanospheres fabricated by drop-casting method.

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Curved magnetic nanostructures, or curved magnetic thin films, produce exotic magnetic states from geometry-induced anisotropy that lead to interesting magnetic domains. Because of this, curved magnetic thin films have a variety of applications, such as for data storage, spintronics, and biological or chemical sensors. There are various techniques that aim to create close-packed monolayer templates for thin films, and this study focuses on using the slope-assembly method to improve the uniformity for the creation of monolayers and how parameters such as temperature, solution concentrations, angle of incline, and nanosphere diameter can affect both uniformity and their magnetic states. Samples were dried at temperatures ranging from 20-60 degrees Celsius, at angles between 5-50 degrees, and with nanosphere diameters of 200 and 400 nm. A 30 nm layer of Permalloy (Py) or Samarium Cobalt (SmCo) were deposited on samples to produce magnetic thin films. Scanning Electron Microscope (SEM) images show a difference in uniformity when observing the angle at which the nanospheres were left to self-assemble, and also the temperature and solution concentration at which the solution was left to dry. Lastly, magneto optical Kerr effect (MOKE) magnetic hysteresis loops were measured and compared between samples with different parameters and uniformity.

This research was supported by the National Science Foundation Partnership for Research and Education in Materials (PREM) program between California State University, Long Beach and The Ohio State University under Grant No. 2122199.

35. The Role of a Newly-Discovered Gene in the Copper Response of Methane-Consuming Bacteria

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Methanotrophs are microbes that can biologically consume methane, a greenhouse gas. They produce an enzyme known as methane monooxygenase (MMO) that can catalyze the oxidation of methane to methanol, as it has various sites that bind copper (Cu) metal ions to use as a critical

cofactor. We will investigate the impact of Cu on gene regulation in the methanotroph *Methylomonas* sp. str. LW13 through transposon mutagenesis and gene expression analysis. A previous screen has identified genes involved in the control of the expression of MMOs by copper availability, known as the "copper switch". A disrupted *ntrC*-like gene led to uncontrolled expression from the soluble MMO (sMMO) promoter, P_{mmoX}-*xylE*. In the future, we will characterize the *ntrC* gene with reported gene analysis, growth phenotypes, and RNA-sequencing.

We acknowledge startup funding provided to Joseph D. Groom from California State University, Long Beach. We acknowledge Guillermo Perez for technical assistance.

36. Developing a Magnetic Circular Dichroism Measurement System

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The Magneto Optical Kerr Effect refers to the change in the Kerr Angle due to a change in angle when the polarized light is reflected off magnetic materials. Similarly, Magnetic Circular Dichroism (MCD) measures the change in absorption between the right and left polarized light. Using these ideas, we can look at the properties of different PMA materials. In my work I learned how to operate and upgrade an experimental set-up, that uses MCD, to measure and explore these magnetic signals. To learn this system, I measured samples of FGT and measured the hysteresis loop at different temperatures to see how these magnetic signals differ at different temperatures. To upgrade the system we used LabView to get more control over the added motor systems, giving more capabilities in moving the laser and a fast-steering mirror to add microscopy to the system allowing for more than just measuring of magnetic signals. We added these upgrades and were able to get similar results to the original setup with most of the added components working.

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37. New components of the response to lanthanum in methane-consuming bacteria

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Lanthanum (La) is an important metal in the regulation of methanotrophic bacteria, and is the critical cofactor for the XoxF methanol dehydrogenase. There is differential gene activation between the alternative methanol dehydrogenase genes *mxaF* and *xoxF* in the presence of lanthanum. When lanthanum is not present, the MxaY histidine kinase begins a signal cascade that activates the *mxaF* gene and represses the *xoxF* gene. It performs this gene regulation via the action of the MxaZ response regulator. Deletion mutants of both *mxaY* and *mxaZ* genes grow very poorly in the absence of lanthanum, because they can not activate the alternative methanol dehydrogenase MxaF. However, suppressors of Δ*mxaY* and Δ*mxaZ* mutants result in a restoration of growth by somehow re-activating the *mxaF* promoter, as verified by a reporter gene assay. Therefore, my research focuses on how we can isolate these suppressor mutants, test gene expression phenotypes within those suppressors, and identify the causal mutations in undiscovered or known genes. I will then make

deletion and point mutations in "clean" genetic backgrounds to verify their function in the response to lanthanum.

This research is funded by Joseph D. Groom from California State University, Long Beach. We acknowledge Guillermo Perez for technical assistance.

38. CT-based geometric analysis of bicuspid and tricuspid aortic valves in patients with aortic stenosis

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In the aortic valve, there are generally three leaflets, which is why it is called a tricuspid aortic valve (TAV). As an anatomic variation, there are rare cases with only two leaflets, which are called bicuspid aortic valve (BAV). Aortic stenosis (AS) is a common disease that can occur in both TAV and BAV populations, with the narrowing of the aortic valve, leading to valve malfunction. The aim is to characterize differences in geometry between bicuspid and tricuspid aortic valves from patients with AS preoperatively utilizing three softwares: SimVascular, ITK-SNAP, and Solidworks. SimVascular is a vessel modeling software where CT scans are inputted, a path is traced, and then segmented. These segmentations allow for 3D models to be made, such as a 3D model of BAV leaflets. SimVascular was utilized to make ten models for a full cardiac cycle (0-90%) of the leaflets, aorta, left coronary artery and branch, and right coronary artery for both TAV and BAV. Additionally, ITK-SNAP is being utilized as it is more suitable for irregular geometry segmentation, both for leaflets and calcium. As a result, leaflets and calcium are modeled for a full cardiac cycle for both TAV and BAV on ITK-SNAP. Furthermore, calcium buildup can be detrimental as it leads to stiffness of the leaflets, so it is important to notice when and where calcium builds up the most. Solidworks is being utilized to co-register 3D models and take measurements from leaflet geometry. Both TAV and BAV leaflet and calcium models are imported into Solidworks and measured to track leaflet distances. For BAV and TAV leaflets, they are furthest apart during the beginning (0%) of a cardiac cycle, and closest in the middle at 40% according to models from SimVascular and ITK-SNAP. The anticipated outcomes involve characterization of leaflet distances using calcium as a reference point. These results for a full cardiac cycle will be compared for both BAV and TAV patients to preoperatively analyze differences to help predict surgical outcomes.

39. Unraveling the Role of the *Methylomonas* sp. Strain LW13 Copper Switch in Methane Metabolism.

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The anthropogenic release of methane gas into the atmosphere poses a significant threat to Earth's climate stability, as this greenhouse gas contributes to climate change 25-fold more than carbon dioxide per molecule. Technologies for capturing methane include the use of living organisms' metabolisms. Methanotrophic bacteria such as *Methylomonas* sp. strain LW13 sequester methane for its oxidation using a copper-containing enzyme. Different copper concentrations result in drastic gene expression changes in methanotrophs, but little is known about copper uptake or regulatory mechanisms. To characterize the *Methylomonas* response to copper, a DNA construct was created with the reporter gene *xylE* fused to the promoter region of a copper-dependent gene *mmo*R. This

was cloned into a plasmid backbone. The resulting genetic construct will be inserted into the *Methylomonas* genome to assess responsiveness to different copper concentrations in the bacterial growth medium, in different genetic backgrounds. This investigation intends to enlighten *Methylomonas* copper physiology in preparation for future genome editing to characterize and enhance methane recycling.

This project is supported by startup funding provided to Joseph D. Groom from California State University, Long Beach.

40. Toxic Threat - Bisphenol A is Sneaking into Your Everyday Life

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Bisphenol A (BPA) is an industrial chemical that is widely used in the production of plastics and has been found to be an endocrine disruptor. Recent studies have suggested that BPA exposure may influence various bodily processes such as growth, cell repair, fetal development, and reproduction - increasing risk to cancers and other health issues. The aim of this study was to create simple and easy extraction and detection methods to identify BPA in everyday plastic items. These plastic items were soaked in ddH2O under 25℃ for 50 hours or 60 ℃ for 5 minutes and later 4-aminoantipyrine (4-AAP), potassium ferricyanide, and sodium bicarbonate were ultimately used to form a color complex. A spectrophotometer was used to measure the absorbance of each sample and to further analyze the data using a standard curve. The results showed that BPA easily leaches from everyday plastic items and is a toxin to human health and the environment as well. These findings provide simplified procedures to understand BPA exposure and advocate to manufacturers to look for safer alternatives for making plastics.

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41. The Role of Depression and Anxiety on Vaccine Hesitancy During COVID-19

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The Covid-19 pandemic, which first became a global concern in December 2019, has significantly impacted our mental well-being. To understand the impact of the pandemic, the Centers for Disease Control and Prevention (CDC) initiated the Household Pulse Survey (HPS) in April 2020, which included self-reported mental health symptoms in addition to various demographics. Numerous studies have been conducted to determine the demographics most affected by the pandemic, many documenting higher rates of mental health problems such as anxiety or depression during the pandemic. We hypothesized that it might be more difficult for individuals with anxiety and depression to get vaccinated against COVID-19, compared to individuals without. To examine the correlations between anxiety and depression and vaccine hesitancy, we analyzed the Household Pulse Survey (HPS) data, specifically survey waves 22 – 33 (Jan 6 – July 5, 2021), using SPSS. Our results showed that there were consistently lower COVID vaccination rates among people with depression and/or anxiety than among those without. Data also showed that among those not

vaccinated, people with depression and/or anxiety reported a higher percentage of intent to get vaccinated. There is a correlation between vaccination rates and mental health, as individuals with anxiety or depression are less likely to be vaccinated against COVID-19. Despite the correlation, the desire to become vaccinated still exists among individuals with anxiety or depression. Additional research is needed to identify the factors that contribute to vaccine hesitancy among individuals with anxiety or depression. This research can deepen our understanding of how traumatic events can affect various demographics in the United States. By gaining this knowledge, we can further investigate the causes behind these disparities and develop strategies to improve mental health and prevent the spread of disease.

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42. Enzymatic Synthesis of Naphthol-Based Unnatural Amino Acids using Tyrosine Phenol Lyase

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Tyrosine derivatives are unnatural amino acids (UAAs) that are key building blocks for the synthesis of anticancer compounds. Despite their importance in pharmaceutical research, commercial syntheses of tyrosine UAAs require multiple steps and the use of hazardous reagents, prompting a search for alternative, 'green' routes of synthesis. Tyrosine phenol lyase (TPL), isolated from *Citrobacter freundii*, is a pyridoxal-5'-phosphate dependent enzyme which catalyzes the reversible hydrolysis of tyrosine into phenol and ammonium pyruvate. Wild-type TPL has been used to synthesize UAAs, including fluorotyrosines from fluorophenols, but phenols with larger substituents were not efficient substrates. In a separate study, enzyme evolution experiments identified the M288S/F448C TPL double mutant as being able to generate a two-ring naphthol analog. Although the mutations may enlarge the active site and allow the larger naphthol to bind, the catalytic role of the specific side chains in broadening substrate scope was not investigated. To evaluate the structural basis for substrate selectivity, we individually mutated residues 288 and 448 to serine and cysteine, respectively. As these mutations also introduce polar hydrogen bonding groups, alanine mutants were also evaluated to reduce the side chain size, solely. We hypothesized that if opening space in the active site is the structural basis for accommodating the larger substrate, then the alanine mutations should allow synthesis of the larger analog. However, if polar and/or hydrogen bonding capability is important, then the alanine mutants are predicted to be less effective than the M228S, F448C single or double mutants at synthesizing the larger analog. To test this hypothesis, plasmids for the mutants were generated by site-directed mutagenesis and the enzymes were expressed in *E. coli*, purified by affinity chromatography followed by size-exclusion chromatography. Assays with the commonly used substrate, S-(o-nitrophenyl)-L-cysteine (SOPC) showed the enzymes were active. Next, naphthol inhibition was tested to screen if the larger substrate affects enzyme activity. The results showed inhibition of SOPC hydrolysis, and greater inhibition of the mutants relative to wild type suggesting that the single mutations may increase naphthol binding. To evaluate if the enzymes generate a naphthol analog, synthesis assays were conducted and analyzed by High Performance Liquid Chromatography (HPLC). Initial HPLC results show formation of several new peaks in the chromatograms for naphthol analog synthesis reactions with the mutants, and we

are currently isolating and characterizing the products formed. Together, these studies are aimed at furthering our understanding of the structural basis for broadening the substrate scope of TPL and the results may aid in using TPL to generate derivatives for use in pharmaceutical development.

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43. Numerical Methods for Chern Insulators

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In non-interacting 2D systems exhibiting the quantum Hall effect, the relationship between the symmetries of a system and its topological invariants has been established. However, for interacting 2D systems exhibiting the fractional quantum Hall effect, the relationship between the symmetries of the system and its topological invariants remains an active area of research. The Haldane model is the first historical example of a Chern insulator, having a quantum Hall effect without an external magnetic field when its topological invariant, the Chern number, is non-zero. In this work, we conduct numerical calculations of the Chern number for the Haldane model with periodic and twisted boundary conditions. We make use of a specialized Python package QuSpin to reproduce previous results and discuss how the twisted boundary condition method can be extended to interacting systems in future work.

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44. Synthesis and Biochemical Evaluation of Potential Inhibiting Features of Fmoc-L/D-Leu-OCH_3 Ester Analogues on Butyrylcholinesterase and Acetylcholinesterase for The Treatment of Alzheimer's Disease

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Alzheimer's Disease (AD) continues to be a significant global health concern, impacting millions around the world. As there is currently no cure for AD, varying strategies are being explored. Cholinesterases, pivotal in neuronal signaling, have drawn attention due to their altered activity in AD patients. For the two cholinesterases, acetylcholinesterase (AChE) and butyrylcholinesterase (BChE), AChE activity is relatively unchanged with individuals with AD, while BChE activity increases. This higher BChE activity is suggested to deplete the available neurotransmitter acetylcholine, which may lead to decreased neurological function. Based on these observations, BChE inhibitors are sought to elevate the available neurotransmitter and increase neurological function. We previously showed that amino acid analogs with a 9-fluorenylmethyloxycarbonyl (Fmoc) group inhibit BChE. However, the initial compounds contained a negative charge, and the neurotransmitter bears a cationic group. To address this potential limitation, we synthesized and tested neutral Fmoc-amino esters. In addition, initial studies suggested that D stereoisomers may be more potent inhibitors relative to the L stereoisomer. Based on these observations, we hypothesized

that Fmoc-D-amino esters will be more potent inhibitors than previous Fmoc carboxylic acids. The D and L Fmoc-amino esters were synthesized by esterifying the corresponding Fmoc-amino acid using an alcohol and a coupling reagent. The products were purified by silica gel chromatography and characterized by NMR. Enzyme assays were then conducted to measure the relative activity, i.e., the ratio of enzyme activity without and with the compound present. Assays with BChE showed that Fmoc-D-Leu-O- and Fmoc-L-Leu-O- had relative activity values of 0.21 and 0.41, respectively. Initial results for Fmoc-amino esters indicated that the compounds inhibit BChE, and we are currently measuring the relative activities. To evaluate selectivity, we also tested AChE inhibition. Initial tests for Fmoc-esters and amides with both stereoisomers showed relative activity values of 0.9-1.0, suggesting that the compounds tested had little effect on AChE activity. We are also conducting computational docking studies to evaluate potential binding modes and interactions between the ligand and enzyme. These findings support the hypothesis that removing the negative charge is favorable for inhibition, and differences in inhibition exist for the stereoisomers. We are conducting a more extensive exploration of various amino amides, focusing on their selectivity, reversibility, and mode of inhibition. Our objective is to identify factors for inhibition and further explore Fmoc-amino acid scaffolds for the development of potent and selective cholinergic inhibition, potentially forming a viable therapeutic strategy for AD.

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45. Local Magnetic Hysteresis Loop Measurement of SmCo Nanocap Thin Films using Magneto Optical Kerr Effect

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The ability of the magnetic materials to maintain and resist the change of magnetization can differ based on its physical features. Local magnetic characteristics of the material can be investigated by the Magneto-Optical Kerr effect (MOKE). The MOKE occurs when an incident light on a magnetic surface result with an altered polarized reflected light. Curved magnetic surfaces have unique magnetic properties beneficial to fields such as biomedicine and spintronics. Curved surfaces such as nanocaps can contain both in-plane and out-of-plane magnetizations. Using a longitudinal MOKE set up with a HeNe laser, in-plane magnetization of the samples can be measured as a function of external magnetic field. Our prime objective was investigating magnetic switching behaviors at a local level for the nanocap samples with different diameters, thicknesses, and materials. 30 nm thick SmCo nanocap thin films on two different sizes of nanosphere templates were studied in this research. MOKE measurement was performed in various local sections within the same sample. It was successfully shown that the MOKE is a very effective tool for the local magnetic measurement in the area of about hundreds of μm. Average coercivities, from the comparison between SmCo nanocap samples on two different diameters of 1 μm and 200 nm, were different by 3 -4 Oe. When the MOKE hysteresis loops of nanocap samples were compared with flat thin film, flat and curved magnetic surfaces show great distinctions in switching behavior.

This project is supported by the Gisela and Wilfried Eckhardt Endowment for Physics and Astronomy and in part by NSF PREM, under award number DMR-2122199.

46. Understanding the molecular mechanisms of phenotypic plasticity during larval development of Dendraster excentricus

Ahira Diaz, Ethan Nguyen, Sarah Kasem, Ariana Lee, Douglas A. Pace, P.h.D.

Phenotypic plasticity is an organism's capability to produce different phenotypes in response to environmental changes, enabling adaptive responses to changing conditions. Benthic marine invertebrates, like the Pacific sand dollar, *Dendraster excentricus*, have a larval stage which brings significant advantages, such as a greater dispersal potential. Previous studies have observed food-induced plasticity in these larvae, encompassing both morphological and physiological plasticity. The underlying molecular mechanisms are unknown, despite confirming the presence of plasticity. Such information is essential to further understand the importance of these responses in helping larvae survive in heterogeneous coastal environments. This study assessed the plasticity responses the larvae exhibited and aim to investigate the molecular mechanisms that support these adaptations in the future. The results clearly demonstrated that the larvae undergo phenotypic plasticity, with the low-fed larvae possessing longer post-oral arms and the high-fed larvae possessing shorter post-oral arms relative to the mid-body length. Samples from the culture will then be sent for RNA sequencing to examine which genes are undergoing differential expression in low- and high-fed larvae, followed by testing the expression levels through quantitative PCR. Overall, this information will result in a comprehensive understanding of phenotypic plasticity.

47. Computing the Ellipticity Parameter of Highly Magnetized Neutron Stars

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During the initial moments of their formation, neutron stars can be endowed with incredibly strong magnetic fields. In particular, these fields are strong enough to cause deformations in the structure of the neutron star, which can be described by an ellipticity parameter. To further investigate this line of work, the research conducted was focused on modeling the neutron star magnetic field as an axisymmetric magnetic field via vector curl and stream functions. Building off a simplified neutron star profile which treats the stellar density as a simple quadratic function of radial distance from the star's center, a series of calculations were carried out to quantity perturbations of density and pressure due to the poloidal and toroidal (PET) magnetic field, and then applying this calculation to a ratio of moment of inertia calculations. The nature of these two calculations involving a piecewise integrand proved to be rather difficult to perform on the numerical software of Mathematica. To get around this issue, integration using a Monte Carlo technique was attempted on Python. While our results on the ellipticity parameter need further investigation, future work could be dedicated to extending the results of the ellipticity parameter on neutron star models involving more realistic neutron star profiles and multipole fields which are more sophisticated than the PET field used for this research.

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48. Effects of C1q Deletion on Complement Gene Expression in an Aggressive Mouse Model of AD

Enidh V. Padron, Shu-Hui Chu, Tiffany J. Petrisko, Deborah A. Fraser and Andrea J. Tenner

Alzheimer's Disease (AD), a major cause of dementia in the United States of America, is a neaurological disorder that causes synaptic loss and leads to cognitive decline. In AD, β-amyloid plaques and tau tangles form resulting in neurodegeneration and destruction of mental functions and memory. We have previously demonstrated that constitutive deletion of complement initiator C1q reduces pathology and synaptic loss in AD mouse models. In vitro studies have suggested C1q has neuroprotective functions independent of the complement cascade but the effects of C1q deletion on different disease states is not known. The objectives of our study are to determine the effects of global versus microglial-specific C1q expression on AD pathology and neuroinflammation at early and late stages of disease compared to controls.

To test the hypothesis that C1q will modulate the gene expression of downstream complement components C3 and C4, the inflammatory receptor GPR6 and LRP1b which are genes induced in young mice by C1q in response to β−amyloid, a quantitative PCR (QPCR) was performed. RNA was extracted from murine hippocampi samples for both WT, Arctic, and littermates with a microglial or global specific deletion of C1q. Gene expression was measured by QPCR, and the relative expression was calculated by comparison to the housekeeping gene HPRT. Data showed that expression of C4 and C3 were higher in Arctic hippocampi relative to WT. GPR6 and LRP1b genes showed similar gene expression levels between 10-month WT and Arctic which was expected at 10 months of age and was not affected by C1q deletion. C3 were not affected by either adult global or local C1q deletion in Arctic models. However adult global but not microglial C1q deletion at the onset of AD pathology reduced expression of C4 expression at 10 months of age. These data suggest peripheral C1q may be needed for induction of C4 expression. Understanding mechanisms of inflammatory gene induction in AD may help determine future therapeutic targets for this disease.

49. Transition Innovative Cell Therapy for Canavan Disease into Pre-Clinical Stage

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Canavan Disease (CD) is a fatal leukodystrophy caused by the mutation of the aspartoacylase (ASPA) gene. The mutation in the ASPA gene leads to a deficiency in ASPA activity through the accumulation of the substrate N-acetyl-L-aspartate (NAA). Increased levels of NAA causes demyelination and spongy degeneration of the white matter in the brain. There is no standard cure nor treatment for this disease. In a previous study, human iPSC-based cell therapy was introduced into patient iPSC-derived neural progenitor cells (iNPCs) or oligodendrocyte progenitor cells (iOPCs) via lentiviral transduction or TALEN-mediated genetic engineering to generate ASPA iNPC or ASPA iOPC. After stereotactic transplantation into CD mouse models, the engrafted cells were able to rescue major pathological features of CD (Feng et al., 2020). In this study, we aimed to achieve two main aspects. To begin transitioning this study into a clinical study, the surgery procedure was further optimized. Primarily, the targeting accuracy was verified by transplanting GFP-NPC into the mice pup brain. The dosing accuracy was also evaluated. To count cells in the whole brain, Imaris and QuPath (two bioanalysis software's), were tested and compared. The

different dose of cells were then injected to test the surgery procedure. Our second aim, using iOPCs, was to examine cell distribution of iOPCs in the whole brain after transplantation. Using immunofluorescence, we were able to map out the location of the transplanted cells throughout the mice brain after transplantation.

Funding for this internship was made possible by the diligent biological faculty at California State University, Long Beach and the California Institute of Regenerative Medicine (CIRM EDUC2-12638).

50. Characterization and Application of Reconstituted Palladium and Apolipoprotein E3-NT Hybrid Lipid Nanoparticle Complexes as a Potential Drug Delivery System

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Cancer is the second leading cause of death in the US and because of the complexity of this disease, finding a reliable means of treatment that does not involve painful and invasive surgeries or nontargeting therapeutics such as chemotherapy and radiation therapy, has been difficult. In an attempt to address this issue, our group developed a drug-delivery system that utilizes palladium nanoparticles (PdNP) encapsulated in a reconstituted high-density lipoprotein (rHDL) nanodisc (rHDL/PdNP) consisting of a phospholipid bilayer surrounded by the N-terminal domain (residues 1-191) of apolipoprotein E3 (apoE3-NT). Palladium is utilized due to its cytotoxic behavior against tumor cells while also exhibiting well-documented catalytic activity towards hydrogenation and carbon-carbon bond formation via the Suzuki coupling reaction. ApoE3-NT is a high-affinity ligand for the low-density lipoprotein receptor that is overexpressed in cancer cells. ApoE3-NT was overexpressed in *E. coli* and purified by affinity chromatography. PdNPs (5nm) with a core size of 2-3nm were prepared using a modified two-phase Brust Schiffrin method with alkyl thiolate capping ligands (dodecanethiolate generated from sodium S-dodecyl thiosulfate) that confers stability while maintaining catalytic activity.

PdNP parameters such as size, shape, and surface ligand adsorption and density were confirmed via ^{1}H-NMR, UV-Vis spectroscopy, FT-IR, TGA, and TEM. rHDL/PdNP complexes were prepared by co-sonicating apoE3-NT, PdNPs and DMPC thin film, isolated using a dynabead magnetic system, and concentrated using an Amicon ultra filter system. Native PAGE of empty nanodiscs and rHDL/PdNP revealed bands in the range of 250-440 kDa with a Stokes radius of 5.2-6.1 nm. Visual validation of nanodiscs revealed discoidal particles of rHDL and rHDL/PdNP measuring 13.7 $\pm$ 3.9 nm and 14.9 $\pm$ 3.3 nm in diameter, respectively. In preliminary analysis, hydrogenation experiments were performed utilizing rHDL/PdNP, empty rHDL and free PdNPs to assess the catalytic function of rHDL-embedded Pd by monitoring the conversion of 1-octene in the presence of H_2(g) by GC-MS. In control reactions, PdNP produced octane at 4.06 min as the major hydrogenation product as expected; for empty rHDL, the substrate 1-octene, was detected at 3.83 min along with some isomerization products. Interestingly, for rHDL/PdNP, the major product had a retention time of 4.49 min, attributed to cis-2-octene. This suggests that the rHDL/PdNP has the capability of isomerizing the substrate with high stereoselectivity. The next steps involve further analyzing this stereospecific conversion and in parallel, assessing the cellular uptake and cytotoxicity of rHDL/PdNPs with cultured tumor cells. We anticipate that our findings will yield new information

about the catalytic activity of nanodisc-encapsulated PdNP and also provide a novel platform for drug-delivery.

51. AFM investigation of Topological and Physical Properties of the Kinetoplast DNA.

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Kinetoplast DNA (kDNA) is a two-dimensional network of topologically linked DNA molecules found in trypanosome parasites. Studying the kDNA can improve our understanding of polymer physics and their topology, particularly as an example of mechanically interlocked molecular rings (polycatenanes). The mechanisms of stiffness and flexibility within topologically interlocked molecules are not fully understood. In this study, linked-ring structures are extracted from the kinetoplasts by dissolving the networks using the Xhoi enzyme and scanned with an Atomic Force Microscope (AFM). The AFM images are analyzed to measure the persistence length of the DNA polycatenanes by mapping them onto the wormlike chain model. Here, we report on the properties of kinetoplast-derived polycatenanes, including their persistence length.

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Keywords: Polycatenanes, Kinetoplast DNA, Persistence Length

Category Type: Experimental and Theoretical

52. Conformational Analysis of Reconstituted Discoidal and Spherical High Density Lipoprotein Bearing Apolipoprotein E3

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Apolipoprotein E3 (ApoE3) is critical in cholesterol metabolism and a resident of high density lipoproteins (HDL), known as the "good cholesterol". It is a 34-kDa protein consisting of 299 amino acids made up of a series of amphipathic a-helices. ApoE3 exists in lipid-free and lipid-bound states contingent on lipid conditions. Our project aims to understand the conformational changes when apoE3 transitions from lipid-free to lipid-bound reconstituted discoidal - HDL (rHDL(d)) to spherical-HDL (rHDL(s)) states. In this study, we use N-(1-pyrene) maleimide (NPM), a spatially sensitive fluorophore that reports proximity between specified sites. The overall goal is to label single cysteine mutants that were introduced at specific sites on apoE3 (A29C, A62C, A102C, K146C, A216C, A256C). Pyrene labeled proteins will emit a large unstructured band ~ 460nm ('excimer') in the presence of a neighboring pyrene which is ~10Å away. In preliminary studies, K146C/C112S and A216C/C112S apoE were overexpressed in E. coli, isolated, and purified by nickel affinity chromatography. The purified protein was labeled with NPM and reisolated by nickel

affinity column. Fluorescence emission spectra of lipid free pyrene-labeled K146C/C112S and A216C/C112S apoE3 revealed a large excimer around 456 nm, indicative of spatial proximity with single pyrene tags on K146C from a neighboring molecule. Unlabeled and labeled proteins were reconstituted with 1-palmitoyl 2-oleoyl phosphatidylcholine (POPC) and cholesterol in a 5:5:4 mass ratio (phospholipid:cholesterol:protein) to generate lipoprotein complexes and isolated by density gradient ultracentrifugation followed by NATIVE PAGE. We expect the reconstitution protocol to yield discoidal lipoprotein complexes comprised of a bilayer of phospholipids and cholesterol surrounded by two pyrene-labeled apoE in an extended helical conformation like a double-belt. If a larger excimer peak is present, it would be interpreted as NPM in position 146 on two neighboring molecules being proximal to each other and that the two 'belts' are aligned in a parallel in-sync configuration. Future experiments will explore possibilities using other variants and determining proximity relationships in rHDL(s). Together, the results will offer valuable insights into the conformation of apoE3 on discoidal and spherical HDL and provide a basis for understanding the mechanistic role of apoE in HDL metabolism.

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53. Room-temperature Ferrimagnetic Properties of the Thin-Film Organic-Based Material: $V[TCNE]_x$

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Low-loss magnetic materials play an important role in quantum information and spintronics. Traditionally, the ferrimagnetic material *yttrium iron garnet* (*YIG*) has been used due to its narrow linewidth in ferromagnetic resonance (FMR), which indicates low damping losses. However, a magnetic material named *vanadium tetracyanoethylene* ($V[TCNE]_x$) shows promise of being an alternative to *YIG* due to its low damping properties at low temperatures. *YIG* is difficult to integrate with electronic chips due to the need for lattice matching. Organics generally grow well on a variety of substrates. Here, we show the FMR response of $V[TCNE]_x$ for different substrates and growth temperatures towards the goal to create bilayered materials based on phthalocyanine for improving the viability for use in microwave electronic devices and assist the ongoing research of quantum information.

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54. Project Title: Development of Nanodiscs with Apolipoprotein E3 for Enzyme Replacement Therapy of acid sphingomyelinase for the Treatment of Niemann-Pick Disease

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Abstract: Lysosomal storage diseases (LSDs) are a group of inherited metabolic diseases that are characterized by enzyme deficiencies that affect the function of the lysosome. Niemann-Pick disease

types A and B are LSDs that are caused by deficiency of the enzyme, acid sphingomyelinase (ASM), resulting in the toxic buildup of sphingomyelin in the lysosome. Currently, available treatments include bone marrow transplantation, enzyme replacement therapy (ERT) of recombinant ASM (rASM), stem cell and gene therapies, of which ERT offers a viable option. However, current ERT is administered as rASM packaged in liposomes, which lacks specificity and targeting ability. We hypothesize that rASM delivered via reconstituted high-density lipoprotein (rHDL) nanodisc, a bilayer of phospholipids surrounded by apolipoprotein E3 (apoE3) may prove effective in targeting enzyme to the lysosome. rHDL is an ideal platform for the delivery of enzymes while apoE3 is a high-affinity ligand for the low-density lipoprotein receptors (LDLr), which facilitates receptor-mediated endocytosis (RME) where the lipoprotein components are delivered to the lysosomes. We designed two chimeric constructs of ASM with apoE3 LDLr binding N-terminal domain (NT): one bearing ASM (86-622) (construct #1, ~84kDa) with a His tag to facilitate isolation and purification and a second bearing the essential catalytic domain ASM (319-579) (construct #2, ~ 55 kDa). Additionally, we designed two other constructs: one bearing ASM (86-622) with a hexa-His tag at the C-terminal end and a transmembrane peptide at the N-terminal end linked via a flexible linker (construct #3, ~ 64 kDa); and the second bearing ASM (319-579) with similar N and C-terminal addendums (construct #4, ~ 35 kDa). The constructs were inserted in pET20b(+) expression vector, overexpressed in *E. coli* and purified using a Nickel Hi-Trap chelating column. Western blot analysis using anti-His antibody, anti-SMPD-1(ASM) and anti-apoE3 polyclonal antibody confirmed the presence of ASM and apoE at expected molecular weights. The proteins were reconstituted with phospholipids (and apoE3 NT for constructs #3 and #4) by the cholate dialysis method, followed by density gradient ultracentrifugation to isolate lipoprotein particles. Physicochemical characterization using native PAGE revealed formation of large complexes (~600 kDa). Preliminary analysis revealed that all 4 constructs retained robust catalytic activity as measured by a commercially available sphingomyelinase activity assay kit. Subsequently, we will carry out structural characterization of the chimera through fluorescence and circular dichroism spectroscopy and determine cellular uptake and lysosomal localization through fluorescence microscopy. Successful findings of this study may provide a non-invasive, targeted procedure for the delivery of large molecule therapeutic agents to treat LSDs.

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55. Monolayer Thickness Calibration in Copper Phthalocyanine Thin Films

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Nanoscale thin films are essential to a vast array of electronics such as transistors, sensors, and energy storage devices. Achieving monolayer thickness accuracy remains challenging and requires calibration of deposition instruments. We have calibrated a thermal evaporator system to deposit copper phthalocyanine (CuPc) thin films and verified the thicknesses via x-ray diffraction (XRD) and x-ray reflectometry (XRR). The deposition rate is measured with a 6MHz quartz crystal monitor; the quantification is then converted into the z-factor and the tooling factor. Through an iterative process, we determined the values to be 1 and 40-45 respectively. The uncertainty obtained from

optical interference via XRD and XRR measurements is ± 1.01nm. This illustrates the procedure to deposit and analyze reproducible monolayer thin films.

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56. Role of Glycosylation in Maintaining the Structure and Function of Human Apolipoprotein E.

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Human apolipoprotein E (apoE) is a cholesterol transport protein that plays a critical role in cardiovascular disease (CVD) and Alzheimer's disease (AD). The *APOE* gene is polymorphic giving rise to common alleles ε2, ε3 and ε4 corresponding to three isoforms: apoE2, apoE3, apoE4 that differ at their amino acid positions 112 and 158. ApoE2 bears Cys, while apoE4 bear Arg at these positions. ApoE3 bears a Cys at 112 and an Arg at 158. While apoE3 is considered cardioprotective, apoE4 is an established risk factor for AD and CVD. While the molecular basis of this is not understood, it has been reported that apoE4 is more susceptible to proteolytic degradation than apoE3. All three isoforms are composed of an N-terminal and a C-terminal domain linked via a protease-sensitive loop, which contains a glycosylation site at Thr194. We hypothesize that glycosylation confers an isoform-specific protection against proteolytic degradation in apoE. To test this, we compared the behavior of recombinant apoE2, apoE3 and apoE4 expressed in Chinese hamster ovary (CHO) cells with that of apoE expressed in *E. coli*, a bacterial expression system. While CHO cells have the capability to add glycosylated moiety following protein translation, *E. coli* can only synthesize non-glycosylated proteins. CHO cells were transfected with pcDNA 3.1 bearing the coding sequence for apoE2, apoE3 or apoE4 with a His-tag at the N-terminal end to facilitate purification. The synthesized proteins were harvested from the medium and purified by affinity chromatography. In parallel, the isoforms were purified from *E. coli* using the pET20b expression system. SDS-PAGE analysis of the purified proteins reveals a band around ~35 kDa (calculated mass: 35,164 Da) for protein from *E. coli* and ~36 kDa (calculated mas: 36,378 Da) for those from CHO cells. In an alternate approach, apoE from guinea pig (GP) was investigated since sequence alignment reveals that GP apoE is missing residues 193-197, a segment that encompasses the O-glycosylation site, Thr 194. This serves as a naturally occurring apoE variant to test our hypothesis about the role of glycosylation in apoE. SDS-PAGE analysis of GP apoE expressed in *E. coli* revealed a band ~33 kDa (calculated mass: 33,438 Da) and ~33 kDa for those from CHO cells (calculated mass: 33,668 Da). Western blot using monoclonal antibody showed cross reactivity between human and GP apoE. Future studies will include biophysical characterization to determine secondary and tertiary conformation, determination of the glycosylated state of the proteins and limited proteolysis analysis to determine if glycosylation plays a role in protecting the proteins against degradation and functional analysis to investigate the effect of glycosylation on lipid binding. Taken together, the data from our study will yield valuable insight into the role of glycosylation on apoE's role in cholesterol metabolism and in CVD and AD.

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57. Maps Between Operator Algebras

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Our problem was motivated by Raphael Clouatre's article, "Completely Bounded Isomorphisms of Operator Algebras and Similarity to Complete Isometries". One of his main results was: Let A and B be unital operator algebras and φ be a unital completely bounded isomorphism from A to B. If A is also unital completely bounded isomorphic to a C*- algebra or uniform algebra, then there exists a unital complete isometric isomorphism φ' that is similar to φ. Our goal was to show that when A is unital completely bounded isomorphic to the Haagerup tensor product of a C*- algebra and uniform algebra then we get the same conclusion as Clouatre. Our first approach was working with the components of the tensor product individually, we were able to leverage Clouatre's results and the injectivity of the Haagerup tensor product to obtain a unital completely isometric isomorphism between Haagerup tensor products of operator algebras. The problem with this approach is that there isn't a non-trivial way to decompose A into a tensor product of operator algebras. In general, the Haagerup tensor product of two operator algebras is not an operator algebra however it is an operator space and Banach algebra. We were able to show that the conjecture is true for two special cases, the first case is when the C* algebra is finite dimensional and the uniform algebra not proper. The second case is when the C* algebra is finite dimensional and commutative, and the uniform algebra is proper. In the finite dimensional setting the conjecture is true but it is unclear to us whether it is true in the infinite dimensional setting.

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58. Probing the Type-II Dirac Semimetal *PtTe2* through Electronic Transport Measurements at Low Temperatures

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Platinum Ditelluride (PtTe2) is a member of a class of materials called Type II Dirac Semimetals (DSMs) that have low energy fermionic excitations that are governed by the Dirac equation. Most importantly, Dirac fermions in these materials are not constraint by the Lorentz invariance. In view of understanding the electronic properties of random Cr alloys of PtTe2 that are known to be air-stable layered ferromagnets, we present an overview of our TeslatronPT system, preliminary electronic transport measurements at low temperatures of thin PtTe2 crystals, and review data demonstrating lithographic damage to transition metal dichalcogenides materials.

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$PtTe_2$ synthesis was supported by the Center for Emergent Materials, an NSF MRSEC, under award number DMR-2011876.

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59. Surveying Habitat Distribution of Invasive Argentine Ant Populations on Santa Catalina Island.

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The Argentine ant (*Linepithema humile*) is an invasive species to Santa Catalina Island, California, USA, that might have negative ecological effects on the habitat and food sources of the endemic Santa Catalina ornate shrew (*Sorex ornatus willetti*). There is limited information on the population distribution of this invasive ant species, so we hypothesized that Argentine ants appear to disrupt the ecological niche of the endemic shrews, alongside other native species, by outcompeting them. Argentine ant infestations may deprive shrews of resources by consuming their main food source, which includes various insect species. We investigated the geographical distribution of the invasive ants by conducting ant population surveys in common riparian habitats associated with the shrew across Santa Catalina Island in July 2022 and July 2023. Locations included Cottonwood Canyon, Ben Weston, Parsons, Two Harbors, Catalina Harbor, and other canyons, watersheds, beaches, and ridgelines across the entire island. Ants were collected by 50 mL conical tubes with a sucrose-soaked cotton ball placed within two cm of the tube's opening to attract ants. Traps were placed at designated checkpoints approximately 100 m from one another under rocks and/or vegetation for shade, with the cap off, and collected after one hour. The ant traps were set out by 11 AM PST to account for the greatest ant activity. Upon collection at least one hour later, each tube was capped and the GPS location and time were recorded. The captured specimens were brought back to the lab and frozen in a -20°C freezer for at least 30 minutes. Ants were then individually placed under a compound microscope to identify them to species level, and to record their abundance. Population survey results revealed that the Argentine ant population appeared to be prevalent in areas that were known to be associated with the native shrew. The presence of Argentine ant populations in shrew territory suggests that the invasive ant species may be displacing the native shrew and contributing to its endangered status. Further research on the Argentine ant population status in various locations may help us understand the altered distribution and abundance of the shrew.

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60. ARPES signatures of symmetries in the Dirac semimetal PtTe2

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The symmetries in a system dictate the allowed physical phenomena. For a solid crystal, the electronic band structure may display a linear relationship between the electrons' momentum and energy, indicative of unusual phenomena, observed through electron transport experiments. $PtTe_2$ is a layered type-II Dirac semimetal hosting two kinds of linear dispersions; a surface-state Dirac cone present at the surface of the material, and a type-II Dirac cone composed from the bulk electronic states of the material only present at specific out-of-plane momenta. As part of Dr. Ojeda-Aristizabal's research group at CSULB, I will present results from ARPES (angle-resolved photoemission spectroscopy) experiments performed at Berkeley Lab's Advanced Light Source showing these two kinds of linear dispersions in $PtTe_2$ crystals grown by the Goldberger group at The Ohio State University. I will also show how these dispersions hide the symmetries that allow the previously mentioned states to exist, including inversion, mirror, and three-fold rotation symmetries.

ARPES measurements were supported by the US Department of Energy, Office of Science, Office of Basic Energy Sciences under award number DE-SC0018154

$Cr_xPt_{1-x}Te_2$ synthesis was supported by the Center for Emergent Materials, an NSF MRSEC, under award number DMR-2011876.

Ivan Pelayo was supported by the Cal. State. Long Beach and Ohio State University Partnership for Education and Research in Hard and Soft Materials, a National Science Foundation PREM, under Grant No. 2122199.

61. *Urobatis halleri* Strikes Back: 3D Tail Kinematics of the Round Stingray

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Injuries from stingray strikes are commonly experienced by beachgoers as stingray habitat often overlaps with human recreation zones. Southern California is known for its stingray populations and associated human injuries, many of which are caused by Haller's round ray (*Urobatis halleri*), one of the most abundant species of stingrays in Southern California. The severity of injury resulting from a stingray strike can vary greatly and may be influenced by many factors, but the barb's morphology

has the potential to inflict significant tissue damage by motions of both slashing (producing a laceration) and stabbing (producing a puncture wound). Despite the rate at which these encounters occur and the threat they pose, very little is known about the behavior of these stingrays or the biomechanical properties associated with strike events. We wanted to evaluate the kinematics of strike behaviors and describe the velocity and acceleration of the strike, as well as estimating the force that is inflicted by the barb. We used 3D high-speed videography to digitize the strike motion using custom MATLAB software. Strike responses were elicited by trials with a pseudo-cadaveric force application device (FAD). Our strike response data indicated that, despite the more viscous water medium, stingrays produced strike velocities comparable to some terrestrial scorpion species. Our data also indicated that rays escaped most of the time when force was applied to a body region other than its midbody, and were only likely to strike when pinned down at the center of their dorsal surface. These findings can be applied to beach safety measures, materials testing, and injury response.

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62. Dirac Excitations in PtTe2 Probed through Circularly Polarized Light

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Platinum Ditelluride ($PtTe_2$) is a type-II Dirac semimetal that hosts at the bulk type-II Dirac fermions. These type-II Dirac fermions present themselves as tilted conical energy-momenta dispersions in the electronic band structure of $PtTe_2$ i.e., type-II Dirac cones. In addition to the type-II bulk cones, $PtTe_2$ also hosts topologically protected surface states. To study the aforementioned bulk and surface states, we performed angle-resolved photoemission spectroscopy (ARPES) on $PtTe_2$ crystals at the Lawrence Berkeley National Laboratory (LBNL) using circularly polarized light. The circular dichroism (difference in the intensity photoemission using right- and left- circularly polarized light) showed a different behavior for the bulk and surface state cones. The surface cone showed a dichroic signal switching across the Dirac point, indicating its different character from the bulk cone, which did not show a switching. This is consistent with a spin-momentum locking of the electrons in the surface state cone. This proves that even though both the bulk and the surface states are due to band inversions, time-reversal symmetry, and spin-orbit coupling, they have different properties. By successfully distinguishing the bulk and the surface states in $PtTe_2$ via circular dichroism, we are furthering the potential of the material to be a major player in future opto-spintronics applications.

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63. Watch your step!: Stingray Sting Prevention

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Every year off California's coast, there are roughly 2500 people being stung by stingrays, with Seal Beach being among the highest locations of reported injuries. The primary culprit of these injuries is the round stingray (*Urobatis halleri*), which is the one of the common stingrays found within California beaches. The stings administered by these rays create a puncture wound and deliver venom that amplifies the pain received by the victim. They are also sharp enough to penetrate most beach outerwear, including neoprene wetsuits. One preventative measure from getting stung is the "stingray shuffle", an act of shuffling your feet while entering the surf zone. To better understand the forces stingrays generate when striking, sting-resistant (neoprene) material can be created to resist these strikes. With the collaboration of material science engineers, we prototyped neoprene-based footwear to withstand these stingray strikes. We tested the point at which the material failed. The forces we measured that round stingrays generated *in-situ* were less than the point of failure for the material, so we determined that our material was strong enough to withstand most round stingray strikes. By acquiring new knowledge on the striking forces that *U. halleri* can generate, we can continue to improve beachwear that provides protection from stingray strikes.

This project is supported in part by the CSULB Department of Biological Sciences and an anonymous donor.

64. Characterization of Graphene Multilayers Using Witec's Alpha 300R Raman Spectrometer

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Graphene samples were examined using WITec's Alpha 300R Raman Spectrometer with the primary objective of the quantification of layers of graphene and the identification of various impurities. The new confocal Raman imaging instrument at CNSM features variable grating, customizable integration time, live oscilloscope and an automated stage. We found that the resulting high resolution hyperspectral images preserved information of a complete Raman spectrum with every image pixel. By specifying the required spectrums and performing background subtraction, its proprietary software could further enhance the image quality. 3D images could also be created by combining Raman scans with AFM images, in which different chemical compounds are color coded. Ultimately, it serves as a powerful non-destructive tool

for materials characterization and analysis.

65. Insights into carbon cycling between carbonate and wood in Green Lake, NY using sediment microscopy and stable carbon isotope ratios

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Terrestrial inland waters cover only ~2-3% of non-glaciated land surfaces, but they serve an outsized role in the global carbon cycle. The sediment of carbonate-producing lakes is critical in recording the biotic and abiotic pathways carbon is cycled through. Green Lake, NY (FGL) has been studied for its permanently redox-stratified water column, microbial carbonate bioherms and biologically driven annual whiting events that precipitate calcium carbonate. Carbonate encrustations of downed trees ubiquitous to the shorelines of FGL have not been previously described. We sought to study whether the relationship between the carbonate and the wood it precipitates on is genetic or merely coincident. Is the carbon within carbonate encrustations of wood sourced from decomposition of the organic compounds of wood, or is wood merely a growth substrate within the photic zone? We analyzed the crystallographic growth habits of carbonate on the surface and within wood grains. Based on the patterns observed, we hypothesized that carbonate minerals precipitate from the alkaline waters of FGL sourcing remineralized carbon from the heterotrophic decomposition of organic compounds in wood (i.e., cellulose, lignin). If the carbon from the wood is being used by the carbonate, then we expect the $\delta^{13}C$ value of the carbonate will be >-25‰ (bulk sediment organic $\delta^{13}C$ from FGL shoreline) but <-3‰ (value of bulk carbonate). Bulk sediment samples were collected from FGL for isotope analysis of the wood and carbonate. Preliminary results using microscopy showed carbonate growth patterns that may support our hypothesis. Various samples contained carbonate minerals that show a dendritic morphology on the surface of the wood and some contained a preferred crystallographic alignment growing with the wood grain and morphologically mimicked the wood. Future work will include analysis of the bulk C isotope values of the wood and carbonate, as well as analysis of the organic compounds that comprise the partially decomposed woody growth substrates and pristine wood from the same tree species at FGL. A mass balance model will be used to predict the isotope values for the carbonate sourcing its carbon from the wood and compared to measured isotope data in order to better understand how carbon cycling is recorded in the carbonate sediment in FGL.

Research was conducted as part of the GeoPEERS REU at Penn State. This material is based upon work supported by the National Science Foundation under Grant EAR-2050463.

66. Impacts of Urban Heat Islanads on Body Proportions of Small Mammals

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Elevated heat due to the urban heat island effect is a key aspect of urban landscapes and is a stressor to urban wildlife. The biogeographic principle known as Allen's rule predicts that endotherm populations in warmer areas will have relatively larger appendages than those in cooler areas, increasing surface area to volume ratio to better manage body heat. Whether urban populations of small mammals exhibit changes in body proportions consistent with Allen's rule due to the urban heat island effect has not been explored. This study aims to investigate whether urban populations of the eastern grey tree squirrel, *Sciurus carolinensis*, have relatively larger tails, ears, and hind feet

compared to their rural conspecifics. I collected body measurement and locality data for 343 *S. carolinensis* specimens from across the United States and used an urban heat island intensity map to quantify urban heat stress at each specimen location. I used linear regression to investigate the relationships between the relative size of each body part and urban heat island intensity. The analysis revealed that squirrels in urban heat islands do not have significantly different tail, ear, or hind foot lengths compared to rural conspecifics. This study is one of the first examples of using natural history data to investigate urban evolutionary biology, and furthers our understanding of urban heat islands as a stressor to mammals.

Support for this project was generously provided by the CSULB Summer Student Research Assistantship.

67. Tracking Paleodiets using the Stable Isotopes of Feces: A Preliminary Study

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Carbon and nitrogen isotopic values of animal feces were linked to values in food to determine whether significant differences exist among feeding strategies and if they are suitable for use in paleodiet studies. Feces and food from wolves, grizzlies, bison, African painted dogs, chimpanzees and Asian elephants were collected from the Los Angeles and Montana Zoos and subsampled using Biosafety Level 2 protocols. Approximately 0.3mg of dried material was then analyzed on a Costech Elemental Analyzer coupled to a ThermoFinnigan delta-XP isotope ratio mass spectrometer in the Institute for Integrated Research in Materials, Environment and Society (IIRMES). The $\delta^{13}C$ values for both food and feces are the most negative for herbivores and the most positive for carnivores. For the omnivores, the $\delta^{13}C$ values for food had a wider distribution, possibly due to the Omalene pellets, and the spread of values for carnivore feces was the largest. Similar to the $\delta^{13}C$, the $\delta^{15}N$ increases from herbivore to carnivore and the feces are always more enriched than the food. Analysis of bulk feces is the first step in exploring the ability of isotopes in specific organic compounds to track changes in paleodiet. Coprolites (fossil feces) are rare but the degradation products, usually fecal stanols, are ubiquitous in the sedimentary record.

This project is supported in part by the National Science Foundation under Grant NSF-BCS-Archaeometry 2115492.

68. Effects of wildfire disturbance on mammal occupancy in fire-prone ecosystems of California.

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Wildfires have historically been a part of California ecosystems, playing a key role in shaping vegetated landscapes. However, anthropogenic disturbances such as urbanization and climate change are altering fire regimes in the 21st century, posing a growing threat to native flora and fauna. While the effects of wildfire on plant and small mammal communities have been well-studied, little

research has been conducted the post-fire succession of medium to large mammal species. Our project goals were to conduct long-term monitoring of mammal occupancy in recently burned areas of Santa Cruz and Orange County, California, and to determine how occupancy is related to environmental covariates. We collected pre- and post-fire detection data at burned and unburned sites in areas affected by the 2017 Canyon 2 fire, 2020 Silverado fire, and 2020 Bond fire in Orange County, and the 2020 CZU Lightning Complex in the Santa Cruz mountains. To explain variation in site occupancy and recolonization rate, site-level environmental covariates were generated from Landsat 8 OLI raster data. We fit single species autologistic occupancy models to compare occupancy of burned and unburned areas over time. Preliminary results suggest that generalist species (e.g., coyotes) do not display strong preference for burned or unburned sites, while dense vegetation specialists (e.g., gray foxes) displayed an avoidance of recently burned sites. The interspecific variability in post-fire site selection suggests that generalist and disturbance-tolerant species may be more capable of exploiting post-fire resources at early successional stages, creating "winners" and "losers" under shifted fire regimes. Our future directions are to explore post-fire succession of other commonly detected California mammal species (e.g., mountain lions) and determine how their occupancy at burned and unburned sites is related to environmental covariates.

This project is supported in part by the Richard D. Green Graduate Research Fellowship.

69. *No abstract assigned*

70. Rangewide trends in bobcat (Lynx rufus) coat pattern distribution

Kelly Hood, Ted Stankowich, Ph.D.

Coat patterns within the *Lynx* genus can vary widely and are highly heritable, suggesting they are influenced by trends in ecological pressures. Within the bobcat (*Lynx* rufus) range, sympatry (and competitive pressure) with intraguild felids is most concentrated at its northern and southern limits. Their northern range is overlapped by the mid-sized congener Canada lynx (*Lynx canadensis*), and their southern range is bordered by populations of other mid-sized felids like ocelots (*Leopardus pardalis*). I am investigating whether bobcat coat pattern types become more uniform where co-occurrence with other felids is increased and niche partitioning is more advantageous. Over n=530 individual bobcats were scored for coat pattern type (plain, spotted, blotched, rosetted) and compared across competitive densities, geographic location, and landcover types using a multinomial logistic regression model. I expected that in areas with more co-occurring intraguild felid species, specific coat pattern types adapted to a given regional niche (like blotched coats in densely vegetated areas and plain coats in open, drier areas) should occur more uniformly than others. In contrast, where bobcats co-occur less frequently with other intraguild cats, their coat pattern types should vary more.

71. Regulating Image Diversity with Machine Learning

Hansell Perez[1], Shane Grothe[1], Jade Nguyen[1], Rami Allaf[1], Jordan Pringle[1], Nate Mohan[2], Devery J. Rodgers, Ph.D.[3], Matt Montegary[4]

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It is common practice for companies to use imagery when promoting their work and products. Another common practice is for prospective students to navigate a college or university's website to develop a feel for the school as well as to gauge compatibility. From previous research (Rodgers,

2022), the visual representation of African American students is at a disappointing 2%, 1% less than advertised. In her work, Dr. Rodgers manually navigated 510 CSULB College of Education affiliated websites and classified images to determine the level of image diversity present in such websites. This effort is focused on automating the work done by Dr. Rodgers, using machine learning tools, with the goals of reproducing previous work and expanding the idea for use on other websites. With a 2 pronged approach this project sought to 1) develop a web-scraping algorithm that can navigate the College of Education affiliated websites and collect all images displayed in such webpages and 2) implement machine learning tools, such as Facebook AI Research's Detectron2, to automate the image classification process. Python's BeautifulSoup library provides efficient tools for scraping a website and is the foundation of the web-scraping script developed that collected over 200 images from over 700 webpages, an expansion on the 510 websites analyzed by the year 1 effort. This method of data collection reduces the time burden spent on labor hours and helps avoid repetition. The work carried out by this effort can help organizations gauge the levels of diversity promoted by their affiliate websites and could lead to increased awareness in the imagery portrayed.

72. H_2 bubble formation dynamics at Au and Cu surfaces

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Formation and evolution of H_2 gas is important to many electrochemical devices relevant to energy production and storage. H_2 evolution in acidic environment is the dominant process at potentials $\leq$ 0 V vs. RHE. This process is favorable for chemical water splitting; however, it needs to be suppressed during CO_2 reduction or operation of aqueous batteries. Here, we report on electrochemical stress and interfacial capacitance measurements of Au and Cu surfaces during H_2 evolution in different solution conditions. We observe characteristic surface stress responses during H_2 evolution and formation of nanobubbles at Au surfaces. Interestingly, bubble formation rate and dynamics are different between Argon and CO_2 saturated acidic solutions. We explain these variations in the formation of H_2 and CO nanobubbles at Au surfaces by comparing the rates of bubble formation in Argon and CO_2 saturated solutions from the time lapsed images during active bubble formation. We will also discuss the role of solution pH and ion concentration on the bubble formation dynamics.

73. Protein Expression and Purification of Apolipoprotein A-I.

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Human apolipoprotein A-I (apoA-I) is the main protein of high-density lipoprotein (HDL). HDL is a spherical protein-lipid complex that performs reverse cholesterol transport. ApoA-I binds to receptors on the cell membrane and promotes the movement of phospholipids and cholesterol from inside the cell to the outer surface. Once apoA-I reaches the cell's surface, apoA-I lipidation results in formation of HDL. Furthermore, apoA-I has been identified as an antimicrobial protein (AMP). AMPs are an organism's innate defense against fungi, pathogenic bacteria, enveloped parasites, and viruses by targeting cellular membranes. Gaining a greater understanding of how apoA-I interacts with membranes of invading gram-negitive bacteria will provide insight to how the human body combats sepsis. Through recombinant protein expression and purification of human apoA-I via

nickel affinity chromatography and size exclusion chromatography, 18.23 mg of protein was produced which can be used for experimental analysis. Sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE) showed that 10.25 mg of unusable and partially degraded protein was also collected that cannot be used.

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74. Synthesis of 2,3-Disubstituted Tetrahydrofurans from Chiral Allylic Silanes

Kayla Ashton, Martina Pedrina, Julie Wahlman Ph.D.

The ability to synthesize tetrahydrofurans, particularly in an enantioselective form, can aid in the synthesis of bioactive natural products. The aim of this project is to develop complementary reactions to synthesize both 2,3-*cis* and 2,3-*trans* substituted tetrahydrofurans from common allylic silane and aldehyde starting materials. The 2,3-*cis* product is formed via an *intramolecular* condensation/cyclization cascade, while the 2,3-*trans* product is formed via an *intermolecular* Sakurai allylation/cyclization cascade. Our investigations have shown that the reaction scope for the 2,3-*trans* product is more limited, and the reaction procedure is very sensitive to air, moisture, and reagent equivalents. The goal of this project is to investigate and extend the substrate scope of various of aldehydes to ensure that a variety of 2,3-*trans* substituted tetrahydrofurans can be prepared. We have successfully reproduced the Sakurai allylation/cyclization cascade to produce the six-membered ring product (tetrahydropyran), and will investigate new aldehyde starting materials for the synthesis of the five-membered ring product (tetrahydrofuran).

75. Effect of Dimerization of the C-terminal Domain of Apolipoprotein A-I on Lipid Binding.

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Human apolipoprotein A-I (apoA-I) is a major component of high-density lipoprotein (HDL) and is essential for reverse cholesterol transport. This 28 kDa protein has two distinct domains: an α-helical N-terminal (NT) and a less structured C-terminal (CT) domain. The CT domain is responsible for the self-association of apoA-I at concentrations above 0.1 mg/mL and constitutes helix 8, 9, and 10 which are also responsible for lipid binding. The exact role of the CT domain of apoA-I in lipid binding is poorly understood, and understanding how dimerization of the CT domain impacts lipid binding may provide new insight in how apoA-I initiates lipid binding. To understand the specific role of the CT domain in lipid binding, single cysteine mutants (S201C, Q216C, and S231C) located in the three helices of the CT domain (helix 8, 9, and 10) and S25C, located in the NT domain to serve as control, were created through site-directed mutagenesis. Circular dichroism was used to show that the single-cysteine mutants did not affect the structural integrity of apoA-I. SDS-PAGE analysis showed that the mutants formed dimers through disulfide bonding. Lipid binding was assessed with dimyristoylphosphatidylcholine (DMPC) vesicles. Using a 1:2 protein to lipid ratio by weight, apoA-I-induced solubilization of multilamellar vesicles (MLVs) into smaller discoidal particles at 24.1°C was measured. The rate solubilization by apoA-I dimers was determined by monitoring the decrease of light scatter of the MLVs, in which MLVs were converted into discoidal particles. The time required for a 50% decrease in light scatter (t ½) was determined and used as a

measure of lipid binding activity. The t ½ was higher for the CT domain mutants S201C (504 s), Q216C (662 s), and S231C (916 s), whereas the half-life of S25C (168 s) was lower and comparable with that of wild-type apoA-I (196 s). Thus, cysteine mutants located in helix 8 (S201C), helix 9 (Q216C), and helix 10 (S231C) of CT domain showed decreased ability to solubilize DMPC vesicles. This indicates that the disulfide bond in helix 8, 9, or 10 hampered lipid binding as this is a critical region in apoA-I lipid binding.

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76. Progress Towards The Total Synthesis Maceneolignan A

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Natural products are molecules that have been isolated from living organisms, some of which have shown promising use as pharmaceutical agents for the treatment of disease. While some natural products can be readily extracted from natural sources on large scale, the ability to synthesize molecules in the laboratory can improve commercial availability and allow for modification to improve efficacy. Maceneolignan A is a dihydrobenzofuran natural product isolated from the evergreen nutmeg tree *Myristica fragrans* and has been shown to express anti-inflammatory response in human skin cells. While a number of dihydrobenzofuran natural products have been previously synthesized, no syntheses of maceneolignan A have been reported. Most syntheses of dihydrobenzofuran natural products rely on strategies that install the a-aryl moiety at an early stage in the synthetic route. In order to streamline the synthesis of various arylated analogues, we decided to evaluate an alternative synthetic approach to this class of natural products that instead relies on a late-stage cross-coupling reaction to install the a-aryl moiety. This approach, if successful, will allow us to demonstrate the first total synthesis of maceneolignan A and provide the ability to synthesize derivatives through late-stage diversification. We have successfully completed 7 out of 9 total steps of the proposed synthesis and we will be discussing our progress and findings.

This project is supported by faculty start-up funds provided by CNSM.

77. Removal of Affinity Tag from Recombinant Apolipoprotein A-I with Tobacco Etch Virus Protease

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Atherosclerosis is a disease which results from the buildup of fatty deposits in the walls of arteries, causing them to narrow and restrict blood flow to vital organs such as the heart or kidneys. The main precursor to the development of atherosclerosis is hyperlipidemia, a condition in which excess cholesterol is circulating in the bloodstream. High-density lipoproteins (HDLs) are considered atheroprotective due to their ability to remove excess cholesterol from the arteries and deliver them back to the liver for excretion through the reverse cholesterol transport pathway. As a key structural component of HDLs, human apolipoprotein A-I (apoA-I) possesses a unique ability to bind lipids, in turn making it a significant target for protein-based atherosclerosis studies. Affinity tags are

unique engineered short amino acid sequences that can be attached to the N- or C-terminus of a protein, and aid in the process of purifying the recombinantly expressed protein. Human apoA-I has been engineered with a six-histidine affinity tag in the N-terminus, along with a recognition sequence for cleavage of the tag with a protease derived from tobacco etch virus (TEV). The imidazole rings on the six-histidine tag have a strong binding affinity for metal ions, and thus play a critical role in the purification of apoA-I via nickel affinity chromatography. Although this affinity tag is required to isolate the recombinant protein for functional studies, it is unknown whether the tag may potentially interfere with the protein's structure or function. Removal of the affinity tag through a TEV protease digest allows future studies to test apoA-I's lipid-binding and self-association capabilities without potential interference from the tag. However, the efficiency of TEV protease in cleaving the affinity tag from wildtype apoA-I has decreased significantly over one year. SDS-PAGE analysis of TEV digests of apoA-I showed that the protease consistently cleaved approximately half of total protein in 24 hours, indicating a reduction in enzymatic activity. Since auto-cleavage of TEV protease has been reported, long term storage may have impacted the enzyme's stability. Further investigations will be carried out to determine other factors that may contribute to the enzyme's loss of reactivity.

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78. Progress Toward the Synthesis of Maceneoligan A through Metal-Catalyzed Reductive Cross-Coupling Reactions to Synthesize Arylated Dihydrobenzofurans

Maria Joana, Araujo, Dr. Julie Wahlman

Maceneolignan A, a dihydrobenzofuran natural product found in evergreen nutmeg trees, has shown an anti-inflammatory response in human skin cells. The use of a late-stage metal-catalyzed reductive cross-coupling could be a viable option for the first total synthesis of this natural product. This synthetic approach would also be amenable to late-stage diversification in order to prepare synthetic analogs. Here we report our results using a Ni-catalyzed reductive cross-coupling reaction on a model system and discuss our efforts at preparing chiral ligands to develop an asymmetric variation of this cross-coupling reaction. Chiral BOX ligands have been widely used in cross-coupling reactions and will be investigated in future studies.

79. Human Apolipoprotein A-I Self-associates at Low Concentrations

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Human apolipoprotein A-I (apoA-I) is the main protein in high-density lipoproteins (HDL). Transport of cholesterol from peripheral tissues to the liver is mediated by HDL. The protein is composed of two domains, an N-terminal helix bundle and an unstructured C-terminal domain. The C-terminal domain is responsible for lipid binding and mediates self-association in the lipid-free state. ApoA-I in the lipid-free state self-associates, and it has been reported in earlier studies that this process starts at a protein concentration of 0.1 mg/mL. Understanding the molecular details of self-association allows further insight into the functional properties of apoA-I. In order to better understand how apoA-I self-associates, we aimed to determine the concentration where apoA-I begins to self-associate. To determine the extent of apoA-I self-association, wild-type apoA-I was crosslinked with dimethyl suberimidate (DMS) and analyzed by SDS-PAGE and western blots.

Crosslinked apoA-I bands were observed between 58-100 kDa in a concentration range between 0.02 and 1.0 mg/mL, indicating the presence of monomers, dimers, trimers, tetramers, and pentamers. Self-association of apoA-I was verified through pyrene labeling of three single-cysteine mutants: S201C, Q216C, and S231C, all located in the C-terminal domain. The emission fluorescence spectra in a concentration range between 0.02 and 0.2 mg/mL displayed excimer peaks, indicating intermolecular interactions at all protein concentrations. Size-exclusion fast protein liquid chromatography was employed to confirm these observations with wild-type apoA-I. Elution profiles at both concentrations of 0.02 and 0.05 mg/mL indicated the presence of multiple protein species present. These results demonstrate that apoA-I is likely at an equilibrium between a monomer and dimer at low protein concentration, and that higher forms begin occurring at concentrations of 0.1 mg/mL. ApoA-I existing as a dimer at physiological concentrations may be an important intermediate when the protein adopts the lipid bound conformation, forming nascent HDL complexes.

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80. Probing the Properties of CuPc/Graphene/hBN Heterostructures through Electronic Transport Measurements

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Graphene/hBN heterostructures are host to unique electronic transport properties not found in bulk crystals thanks to their reduced dimensionality. Through Magnetotransport measurements, we can probe the quantum interference of electron wave functions that give rise to Weak Localization and Weak Anti-Localization. Additionally, the coupling of CuPc, a metal-organic thin film, along with Graphene/hBN heterostructures, can alter the electronic transport properties due to its nonzero magnetic moment. Depending on experimental conditions, this attribute of CuPc can lead to changes in the magnetoresistance by acting as a magnetic dopant.

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81. Quantifying the Enhancement of Cas9-Mediated Mutagenesis with an *in vivo* RNA-Tethering System

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Plants contain various defense mechanisms against exogenous or aberrant RNA, such as transposable elements and viral RNA. Plants use RNA interference (RNAi), also known as post-transcriptional gene silencing (PTGS), as a defense mechanism to degrade these RNAs. However, transgenic DNA, such as pest-resistant genes, are also sorted into RNAi instead of being translated – making it difficult for desired traits to be expressed. A protein-RNA tethering system was developed to enhance the translation of an endogenous mRNA without triggering PTGS. Subsequently, we attempted to utilize this same RNA-tethering system to enhance translation of Cas9 and improve the CRISPR-Cas9 editing efficiency. We generated several synthetic versions of *Cas9* with various 3' untranslated regions for tethering, and *in vivo* tethered a translation enhancer to the transgenic Cas9 RNA. The preliminary data shows that we can successfully boost Cas9 protein production by tethering a translation enhancer to the transcript. To test whether the increased Cas9 protein production results in increased Cas9-mediated mutagenesis, we utilized allyl alcohol screening assays to quantify the mutation rate at *ADH1*, which is targeted by Cas9, of each transgenic line. We show that with the tethering of a translation enhancing factor, we can improve the Cas9-mediated mutagenesis efficiency.

82. Characterizing interactions between Annexin A2 and SARS-CoV-2 Spike

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative agent of coronavirus disease 2019 (COVID-19), relies on structural proteins (spike (S), envelope (E), matrix (M), and nucleocapsid (N)) to facilitate viral entry, assembly, and release. In particular, the SARS-CoV-2 S protein mediates attachment and entry into target cells by binding to the host cell receptors angiotensin-converting enzyme (ACE2) and transmembrane protease, serine 2 (TMPRSS2). S consists of a trimer composed of a receptor-binding region (Subunit 1 (S1)), a membrane fusion region (Subunit 2 (S2)) and a short cytoplasmic tail. Recently, a proteomic screen identified several host proteins, including Annexin A2 (AnxA2), that bound to the cytoplasmic tail of S. AnxA2 participates in several cellular processes, such as membrane domain organization, exocytosis, and endocytosis, and is also linked to the pathogenesis of several viruses. We therefore hypothesize that AnxA2 binds and recruits S to sites of viral assembly. Using Bi-Molecular Fluorescence Complementation (BiFC), we validated that AnxA2 interacts with full-length S in living cells. We are currently generating S mutants to map the regions required for interaction with AnxA2 and plan to determine where S localizes with AnxA2 using immunofluorescence (IF) assays. We are also creating an AnxA2-knockdown cell line to investigate whether AnxA2 is important for SARS-CoV-2 infectivity. Understanding the role of AnxA2 in SARS-CoV-2 pathogenesis will generate key foundational knowledge that may inform the development of novel therapeutics.

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83. *No abstract assigned*

84. Generating AnnexinA2 (AnxA2) knockout clones in mammalian cells using CRISPR/Cas9

Authors: Ruth Bishay, Angelica Cristobal, Christina Pantoja, Peter W. Ramirez

AnnexinA2 (ANXA2) is a multifunctional host protein associated with a wide range of intracellular functions such as endocytosis, exocytosis, and translational regulation through RNA binding. Many viruses utilize ANXA2 to enhance their viral replication, though the exact mechanisms for this occurs remain unclear. We recently found that ANXA2 interacts with two distinct viral membrane proteins, HIV-1 Nef and SARS-CoV-2 Spike. Therefore, this project focused on using CRISPR/Cas9 technology to create a mammalian cell line lacking ANXA2 to determine the importance of this protein in HIV-1 and SARS-CoV-2 replication. First, guide RNAs (gRNAs) targeting ANXA2 were designed and cloned into a lentiviral vector. We verified successful gRNA insertion via sanger sequencing. Next, we generated lentiviruses by introducing our CRISPR plasmids into a mammalian packaging cell line (HEK 293T cells). We are currently transducing our cell line of interest (HeLa) with the LentiCRISPR viruses and will use the antibiotic Puromycin to select for those cells that have been infected. Finally, we will validate our knockouts by Sanger Sequencing and Immunoblotting, to verify that the ANXA2 DNA sequence has been edited and that ANXA2 protein production is absent. Future studies will use this cell line to determine if ANXA2 is important for HIV-1 and SARS-CoV-2 replication and the intracellular location of the ANXA2/HIV-1 Nef and ANXA2/SARS-CoV-2 Spike interaction. Completing these experiments may inform the development of novel anti-viral therapeutics.

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85. First-Principles Prediction of Wavelength-Dependent Product Quantum Yields of a Second-Generation Molecular Nanomotor.

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Synthetic light-driven motors have promising potential for biomedical applications due to their temporal and spatial control. Applications include light-induced drug delivery[1] and the permeabilization of biological membranes.[2] Nanomotors are comprised of a polycyclic rotator and stator connected by a carbon-carbon double bond that isomerizes upon light irradiation, producing a rotary motion.[3]

To optimize functionality of nanomotors, it is necessary to gain a detailed understanding of the mechanism of action on an atomic level. To this end, we study the dynamics of the photoinduced Z-E isomerization of a light-driven, second-generation molecular nanomotor.[3] We use non-adiabatic molecular dynamics based on time-dependent density functional theory (TDDFT)[4] to predict the wavelength-dependent product quantum yields of Z-E isomerization. Using replica exchange molecular dynamics (REMD)[5] we obtain four different ground state conformers, labeled as aMsE, sMsE, aPuE and sPuE. From the ground state ensemble of structures, 375 were chosen for excited state non-adiabatic dynamics. The wavelength dependent product quantum yield was obtained by dividing the absorption spectrum averaged over the initial structures of the successful trajectories by the average absorption spectrum of the initial structures of all trajectories.[6,7] Spectra were computed

using TDDFT as well as second-order approximate coupled cluster theory (CC2). Preliminary results indicate lower wavelengths are associated with higher quantum yields.

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L. Ribovski, Q. Zhou, J. Chen, B. L. Feringa, P. van Rijn, and I. S. Zuhorn, Chem. Commun. **56**, 8774–8777 (2020)

V. García-López, F. Chen, L. Nilewski, G. Duret, A. Aliyan, A. Kolomeisky, J. Robinson, G. Wang, R. Pal, and J. Tour, Nature **30**, 567-572 (2017)

B. Oruganti, C. Fang, and B. Durbeej, Phys. Chem. Chem. Phys. **17**, 21740-21751 (2015)

E. Tapavicza, A. Meyer, and A. Meyer, Phys. Chem. Chem. Phys. **47**, 20986-20998 (2011)

Y. Sugita and Y. Okamoto, Chem. Phys. Lett. **314**, 141-151 (1999)

E. Tapavicza and T. Thompson, J. Phys. Chem. Lett. ***9***, 4758–4764 (2018)

E. Tapavicza, T. Thompson, K. Redd, and D. Kim, Phys. Chem. Chem. Phys. **20**, 24807-24820 (2018)

86. Determining the role of Annexin A2 in HIV-1 Nef activity

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Human Immunodeficiency Virus type-1 (HIV-1) codes for a series of accessory proteins (Vif, Vpu, Vpr, and Nef) that aid in viral pathogenesis. Nef (negative factor) is a peripheral membrane protein that is expressed early in the HIV-1 replication cycle. Expression of Nef enhances the infectiousness of viral particles (virions). Clinically, Nef is necessary for the progression of AIDS. How Nef creates a more infectious virion and whether this relies on the interaction with specific host proteins is still unclear. Using virion-associated proteomics, we identified candidate "dependency" factors or proteins that Nef utilizes to enhance infectivity. One of these proteins was AnnexinA2 (AnxA2), a membrane-associated protein that participates in several biological functions, including the organization of lipid rafts. These cholesterol-rich membrane microdomains often serve as platforms for viral entry, assembly, and release. Interestingly, AnxA2 has been exploited by several RNA and DNA viruses to aid in viral replication. Our preliminary studies indicate that silencing AnxA2 decreased HIV-1 virion infectivity. Additionally, using Bi-Molecular Fluorescence Complementation (BiFC), we show that Nef physically interacts with AnxA2 within living cells. We therefore hypothesize that AnxA2 mediates the localization of Nef to lipid rafts present on the plasma membrane, enhancing HIV assembly, budding and infectivity. To test this, we are currently validating the Nef/AnxA2 interaction via co-immunoprecipitation (Co-IP) studies and determining how AnxA2 may recruit Nef to sites of viral assembly using immunofluorescence (IF) and cell fractionation assays. Critically, the completion of this work will enhance our understanding of HIV-1 biology and has the potential to inform the development of novel Nef inhibitors

87. *No abstract assigned*

88. Determining whether Moesin is a cellular dependency factor of HIV-1 Nef

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Human Immunodeficiency Virus type 1 (HIV-1) remains a significant global concern. Specifically, HIV-1 codes for various genes that are essential for genome replication, viral assembly, release, and pathogenesis. In particular, the nef gene is a major pathogenicity factor that is necessary for the progression to AIDS. Nef is a membrane-associated protein that acts as an adaptor molecule, disrupting the trafficking of host cellular proteins. Expression of Nef also leads to a more infectious virus particle (virion). However, the exact mechanism by which Nef increases the infectiousness of virions remains ill defined. Using a proteomic approach, we identified host proteins (termed "dependency factors") that Nef utilizes to enhance infectivity. One such protein was Moesin (MSN), which functions in upholding epithelial integrity by regulating modification of the actin cytoskeleton as well as helping carry out cell receptor organization. Silencing of MSN led to a decrease in HIV-1 infectivity. Critically, we also detected an interaction between Nef and MSN within living cells using bi-molecular fluorescence complementation (BiFC). We are currently validating this interaction using co-immunoprecipitation assays (Co-IP). We also plan to create a cell line lacking MSN to characterize whether Nef requires this protein Nef to aid its proviral functions. Collectively, our work will define a novel role of how HIV-1 Nef promotes viral pathogenesis and open new avenues for potential treatment.

89. *DDI Directors and trainees (Aaron Levy, Arlan Aquino, Anais Johnson, Carlos Nava, and Deiya Paul) to advertise program. No abstract.*

90. *DDI Directors and trainees (Aaron Levy, Arlan Aquino, Anais Johnson, Carlos Nava, and Deiya Paul) to advertise program. No abstract.*

91. *No assigned abstract*

92. Electrophoretic Deposition Studies of MIL-88B(Fe) on Functionalized Stainless-Steel Surfaces

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The innovation of polymer-free and non-toxic three-dimensional metal organic frameworks (MOFs) has become increasingly viable with regards to drug delivery and applications for drug eluting stents (DESs) after angioplasty surgery in prevention of late stent thrombosis. Herein, experimentation explores novel approaches to the rapid synthesis of the iron containing MOF MIL-88B(Fe), utilizing a voltaic cell for the electrophoretic deposition (EPD) of Fe trimers in solution with dicarboxylate ligands onto medical grade stainless steel mesh, a common material for DES's. MIL-88B is an ideal MOF candidate for potential stent coatings due to high biocompatibility and excellent drug-absorption capabilities. Experimentation can involve variability in precursor solution concentration of MIL-88B substituents and augmentations to the current applied through the voltaic apparatus, giving rise to a diverse array of crystalline formations at the stainless-steel cathode. First, X-Ray

diffraction analysis (XRD) ascertains the characterization of the crystallized MIL-88B(Fe) on the stainless-steel surface revealed from plotting intensity (counts) against angle (2 theta). Additionally, with the aid of scanning electron microscopy (SEM), surface morphology was monitored for further characterization and determination of variation in thin film uniformity across stainless steel surfaces. Ultimately, this project aims to develop methods for the rapid commercial synthesis of MIL-88B(Fe) using EPD to generate thin film crystallization across stainless steel surfaces, providing a novel drug-delivery system, diverging from commonplace polymer-based DESs, with the intent of advancing atherosclerotic therapeutic strategies worldwide.

93. *No assigned abstract*

94. Subsidence Deformation Patterns in Long Beach due to Groundwater and Petroleum Extraction.

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The Los Angeles basin has been deforming as a result of groundwater and petroleum withdrawal, sediment compaction, fault motion, and seasonal fluctuations related to aquifer recharge. Subsidence in Long Beach was noticed as far back as the 1940's: early tide gauge records indicate up to 4 feet of subsidence in a period of 20 years in the Inner Harbor. Today, fluid is injected as petroleum is withdrawn, in order to prevent subsidence. Deformation is still taking place, it's important to monitor it, given that Long Beach is a coastal city that can be affected by sea level rise. The goal of this project is to use satellite data in Long Beach through phase difference of two images and extract surface information to create interferograms. This is a work in progress, but we will show our preliminary results suggesting some areas of Long Beach that demonstrate subsidence deformation patterns.

95. *No assigned abstract*

96. The Role of the Zinc-Finger Homeodomain Transcription Factor HB34 (AT3G28920) and its Redundant Paralog HB23 (AT5G39760) in Leaf Senescence

Michelle M. Smith & Judy A. Brusslan, Ph. D.

Leaf senescence (LS) is the breakdown of proteins, chlorophyll, and other cellular components in older leaves that is seen as a yellowing in many plants including the model organism *Arabidopsis thaliana*. This breakdown allows nutrients to be re-localized from older leaves to the newer leaves and other growing tissues. LS is associated with expressed senescence-associated genes that are regulated by the transition of a plant from its vegetative to reproductive state, which is termed bolting-associated LS. This type of LS is thought to be triggered from bolting-dependent signals to enhance reproductive development. LS is transcriptionally regulated, and more genetic approaches are needed to better understand these regulatory events. Recently, a gene regulatory network (GRN) was developed by Hinckley & Brusslan (2020) to summarize the direct interactions between transcription factors (TFs) and their targets that regulate LS in older leaves in response to bolting. One of the main focuses in the GRN is the Homeobox Protein 34 (HB34) which has a redundant paralog called HB23. I expect that the TFs HB34 and HB23 are bolting associated genes that regulate LS. Genetic approaches will be used to quantify LS in *hb23*, *hb34*, and *hb23hb34* mutants and to evaluate expression of their target genes as predicted by the GRN. Additionally, the mRNA expressions of the two TFs will also be evaluated in bolting wild type plants. The main importance

of working on LS is to incorporate this understanding into crops to make sure they senescence at the right time. With climate change, crops have been experiencing harsher conditions that cause them to go through LS earlier.

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