CALIFORNIA STATE UNIVERSITY
LONG BEACH
College of Natural Sciences
& Mathematics

College of Natural Sciences and Mathematics

STUDENT RESEARCH SYMPOSIUM

BOOK OF ABSTRACTS

Friday, September 23, 2022

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

Table of Contents

Introduction

Symposium Booklet and Event

Symposium Program

Project Abstracts

California State University, Long Beach

Student Research Symposium

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

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

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

Symposium Booklet and Event

The Student Research Symposium is held in the University Student Union (USU) Friday, September 23, 2022. This event, held by CSULB, College of Natural Sciences and Mathematics is open to undergraduate and graduate participation. The research being presented at this event is from on-campus research and/or from summer research experiences performed at other universities.

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

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

Symposium Program

10:00-10:50am: Check-in and mini fair

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)

1:00-2:00pm: Mini Resource Fair

Coffee will be served in the Alamitos Bay Room at 10:00am.

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

Project Abstracts

INDEX OF ABSTRACTS

*indicates co-presenting

Presenter First Name	Presenter Last Name	Faculty Mentor First Name	Faculty Mentor Last Name	Abstract Number
Adam	Jandga	Thomas	Gredig	1
Adrean	Alva	Michael	Peterson	4
Adren	Blanco	Houng-Wei	Tsai	58
Adrian*	Lopez	Judy	Brusslan	43
Alejandro	Zafra	Jiyeong	Gu	44
Aleksandra*	Brajanovska	Katarzyna	Slowinska	39
Alexander	Avalos	Ummat	Somjee	35
Amber	Simonpietri	Kelly	Young	34
Amir	Omidwar	Michael	Peterson	2
Andrea*	Orozco	Judy	Brusslan	53
Andrew	Harrison Hanson	Judy	Brusslan	45
Andy	Huang	Shahab	Derakhshan	20
Angie	Brulc	Jiyeong	Gu	46
Angus	Fuori	Peter	Ramirez	71
Armando	Reynoso	Thomas	Klaehn	21
Brian	De La Torre	Mason	Zhang	60
Bryan	Skorka	Jason	Schwans	68
Christina	Pantoja	Peter	Ramirez	73
Christy	Nguyen	Dequina	Nicholas	31
Dana	Sakr	Judy	Brusslan	47
Daniel*	Uzunyan	Judy	Brusslan	43
Derek	Bergner	Claudia	Ojeda-Aristizabal	6
Derek	Wingard	Zoltan	Papp	57
Earl*	Givens	Judy	Brusslan	49
Earl	Givens	Peter	Lundquist	72
Elizabeth	Moses	Ashley	Carter	40
Enidh	Padron	Deborah	Fraser	23
Eyas	Alnasser	Julie	Wahlman	36
Fanuel	Mendez	Andreas	Bill	12
Isabel	Villafuerte	Douglas	Pace	70
Ivan	Pelayo	Claudia	Ojeda-Aristizabal	5
Jacob	Weber	Claudia	Ojeda-Aristizabal	8
Jacquelin	Chen	Karen	Casciotti	16
Jade	Sinatra	Deborah	Fraser	30
James*	Koo	Judy	Brusslan	49
Jamie	Albertson	Deborah	Fraser	25
Jasmine	Nguyen	Vasanthy	Narayanaswami	33
Jayde	Zimmerman	Judy	Brusslan	51
Joyce*	Choi	Yuan Yu	Lee	61
Kamaljit	Devi	Young-Seok	Shon	52

Presenter First Name	Presenter Last Name	Faculty Mentor First Name	Faculty Mentor Last Name	Abstract Number
Karel	Aceituno	Eric	Sorin	38
Kasandra	Khiev	Vasanthy	Narayanaswami	29
Kathryn	Morales	Deborah	Fraser	27
Katlyn	Lawrence	Katarzyna	Slowinska	41
Katrina	Jensen	Jason	Schwans	66
Kenta	Kodama	Claudia	Ojeda-Aristizabal	7
Kimberly	Izarraras	Deepali	Bhandari	65
Laura	Abonce	Amanda	Fisher	28
Laura	Tandy	Andreas	Bill	14
Lindsay	Park	Jesse	Dillon	24
Luis*	Gutierrez	Yuan Yu	Lee	61
Lydia*	Smith	Deborah	Fraser	30
Madeleine	Phan	Jackie	Dawson	18
Maria	Maalouf	Alex	Klotz	59
Matt	Acosta	Peter	Ramirez	75
Matthew	Plazola	Enrico	Tapavicza	62
Megan	Dinh	Yuan Yu	Lee	63
Meleia	Vyrak	Jesse	Dillon	26
Michelle	Leon	Kathryn	McCormick	69
Michelle	Smith	Judy	Brusslan	55
Miguel	Garcia	Katarzyna	Slowinska	37
Mikaela	Meitz	Paul	Sun	56
Miontranese	Green	Shu	Yang	15
Miriam	Torrez	Katarzyna	Slowinska	39
Nanthanann	Nuon	Ashley	Carter	42
Nicholas	Cassar	Thomas	Klaehn	19
Patrick	Barfield	Claudia	Ojeda-Aristizabal	10
Ruben*	Tapia	Judy	Brusslan	49
Ryan	Mizukami	Thomas	Gredig	3
Saba	Dalaub	Young Seok	Shon	54
Samantha	Perez	Deepali	Bhandari	67
Samra	Tekle	Thomas	Gredig	13
Serli	Khanbabaei	Jason	Schwans	64
Shanel	Deal	Thomas	Klaehn	17
Shinta	Tanamas	Shahab	Derakhshan	22
Stephanie	Gonzalez	Raisa	Hernandez-Pacheco	48
Sylvia	Chow	Prashanth	Jaikumar	50
Vanessa*	Avila	Judy	Brusslan	53
Vanessa*	Plong	Deborah	Fraser	32
Victor*	Phan	Yuan Yu	Lee	61
Victoria*	Sarkisian	Katarzyna	Slowinska	41
Vinh	Tran	Claudia	Ojeda-Aristizabal	9
Vinh	Tran	Prashanth	Jaikumar	11
Zyrille Chloe*	Abela	Deborah	Fraser	32

1. **Defect Assisted Tunneling Through Different hBN Insulators**

Adam Jandga[1], Zoe Phillips[2], Anthony Harbo-Torres[2], Morgan Hamilton[2], Marzieh Kavand[2], Exekiel Johnston-Halperin[2], Thomas Gredig[1]

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

[2]Department of Physics, Ohio State University, Columbus, OH 43210

Stacked devices based on graphene and hexagonal boron nitride (h-BN) are built to study quantum tunneling. The graphene acts as an electrode to the insulating h-BN. The h-BN is sourced from commercial grade and purified to reduce the number of defects. Graphene is added by mechanical exfoliation with a dry transfer process using a heat transfer microscope. The purpose is to observe the differences in creating the stacks with the two types of h-BN insulators as well as the quantum tunneling data obtained in the experiments with these different stacks. Separately, spin-coated phthalocyanine thin films are prepared and studied with atomic force microscopy towards the goal of building novel stack devices incorporating phthalocyanine thin films.

This project is supported by the NSF Materials Research Science and Engineering Center Grant DMR-2011876 and 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.

2. **Exact Diagonalization Studies of the Fractional Quantum Hall Effect at Filling Factor 5/2 under the Tao-Thouless Limit**

Amir Omidwar, Michael R. Peterson, Ph.D.

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

The main fault behind quantum information processing is quantum decoherence which results in the destruction of encoded quantum information and requires the use of logical q-bits or quantum error correction. An alternative approach is to make the system unaffected by common sources of quantum decoherence which involves the use of topological phases of matter. One candidate topological state is thought to exist in the fractional quantum Hall effect (FQHE) in the half-filled second Landau level (filling factor 5/2). This state is described by the Moore-Read Pfaffian wave function and likely supports physics applicable to topological quantum computing. Theoretically, this is difficult to solve, since the FQHE is a strongly interacting electron problem, and numerical techniques are required. In 2018 Hutzel et al. studied an alternative description of the Pfaffian using purely two-body interaction terms. In this work, we study this alternative approach to the Pfaffian state for a two-dimensional system with periodic boundary conditions such that the topology is equivalent to a torus. We use exact diagonalization to study the ground states of this alternative Pfaffian in the thin-torus limit where the 2D system maps to a 1D electrostatic problem in hopes of gaining a deeper understanding of this important physical state.

3. **Surface Morphology of Thermally Annealed Copper Phthalocyanine Thin Films**

Ryan Mizukami, Thomas Gredig

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

The effects of thermal annealing on post-deposition Copper Phthalocyanine (CuPc) thin films are systematically studied. Several CuPc thin films are concurrently deposited at room temperature and separately annealed in vacuum at temperatures up to 320°C for 30 minutes. Atomic force microscopy images show that the surface morphology changes from small round crystals around 59 nm in diameter to elongated crystals randomly oriented on the surface as the annealing temperature rises. This work demonstrates how the post-annealing procedure can affect structural properties in small molecular thin films.

This material is based upon work supported by the National Science Foundation under Grant No. 2018653 (NSF MRI) and Grant No. 2122199 (NSF PREM).

4. Micromagnetic Modeling

Adrean A. Alva[1], Matt Shmukler[2], Jacob Freyermuth[2], Denis Pelekhov, Ph.D.[2], Mohit Randeria Ph.D.[2], Chris Hammel Ph.D.[2]

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

[2]Department of Physics, The Ohio State University, 191 W Woodruff Ave, Columbus, OH 43210

A program was written in Python to minimize the demagnetizing energy of a system of normalized dipoles in a one-dimensional magnetic structure by iteratively rotating each dipole into the effective demagnetizing field vector at their location to observe magnetic domain formation. Micromagnetic modeling software was used to confirm the analytical relationship of domain wall width as a function of exchange energy and uniaxial anisotropy through numerical simulations.

This project is supported by the NSF Materials Research Science and Engineering Center Grant DMR-2011876 and 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.

5. Electronic Properties of the Type-II Dirac Semimetal $PtTe_2$ Probed Through Angle Resolved Photoemission Spectroscopy (ARPES)

Ivan Pelayo[1], Derek Bergner[1], Warren L Huey[2], Archibald Williams[2], Luca Moreschini[3], Jonathan Denlinger[3], Ziling Deng[2], Wolfgang Windl[2], Alessandra Lanzara[4], Joshua Goldberger[2], Claudia Ojeda-Aristizabal[1]

[1]Physics & Astronomy Department, California State University of Long Beach, Long Beach, CA, 90840

[2]Ohio State University, Columbus, OH, 43210

[3]Lawrence Berkeley National Laboratory, Berkeley, CA, 94720

[4]University of California, Berkeley, Berkeley, CA, 94720

The Dirac equation is a wave equation in quantum mechanics that is used to describe particles moving at speeds close to the speed of light. The equation is used to describe free fermions in high energy collisions taking place inside of particle accelerators. In materials such as $PtTe_2$, particles behave as Dirac fermions. Furthermore, the quasiparticles in $PtTe_2$ do not obey Lorentz invariance, a symmetry that requires physical laws to be independent of the frame of reference in which they are observed. These properties classify $PtTe_2$ as a type-II Dirac semimetal.

The energy-momentum relationships characteristic of type-II Dirac semimetals can be observed through Angle Resolved Photoemission Spectroscopy (ARPES). ARPES is an experiment technique that uses the photoelectric effect to probe the properties of the electrons in a material sample. In ARPES, light of specific energy is shone on a sample at a specific angle (momentum). The light excites the electrons in the sample and causes them to shoot out. The electrons are then caught by experiment instruments, reading their energy and momentum. Conservation of energy and momentum of the light and sample are then used to deduce the properties of the electrons inside of the sample. $PtTe_2$ is a semimetal with a layered two-dimensional structure, making it ideal for ARPES study.

With the help of The Ohio State University's (OSU) sample production of $PtTe_2$ and ARPES experiments at Beamline 4 of the Advanced Light Source (ALS) synchrotron at Berkeley Lab, we have performed ARPES experiments on $PtTe_2$. We have acquired data showing the energy-momentum relation of the electrons in the x-y plane of the crystal. Using light with a wide range of energy has also allowed us to see the momentum of electrons along the z axis of the material. This is crucial to seeing Lorentz invariance violated in electron behavior. We observe linear dispersions (momentum vs energy) in the x-y plane indicative of relativistic charge-carriers, with dependence on momentum along the z-axis. In addition, due to the wide range and high photon energy capabilities at the ALS, features previously unobserved are seen.

Our experiments show novel features not reported in the literature that we hope to better understand through collaboration with condensed matter theorists at OSU. Using the data obtained through experiments, we can help fine-tune the parameters used in calculations to produce models that better describe the electrons inside the $PtTe_2$ crystal structure. Our study is also motivated by our additional experiments on $Cr_xPt_{1-x}Te_2$, a ferromagnet with a similar structure to its parent material, $PtTe_2$. We are currently awaiting further ARPES experiments on $PtTe_2$ and $Cr_xPt_{1-x}Te_2$, with hopes of further characterizing the materials and their exciting properties.

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.

6. Analysis of the Layered Ferromagnet $Cr_xPt_{1-x}Te_2$ through Angle Resolved Photoemission Spectroscopy (ARPES)

Derek Bergner[1], Ivan Pelayo[1], Warren L Huey[2], Archibald Williams[2], Luca Moreschini[3], Jonathan Denlinger[3], Ziling Deng[2], Wolfgang Windl[2], Alessandra Lanzara[4], Joshua Goldberger[2], Claudia Ojeda-Aristizabal[1]

(1) Physics & Astronomy Department, California State University of Long Beach, Long Beach, CA, 90840 (2) Ohio State University, Columbus, OH, 43210 (3) Lawrence Berkeley National Laboratory, Berkeley, CA, 94720 (4) University of California, Berkeley, Berkeley, CA, 94720

In 2004, the Nobel Prize in Physics was given for the discovery of graphene, due to it's unique electronic and thermal properties. Since this discovery there has been much interest in new Dirac materials derived from their multitude of applications to spintronics, quantum computing, and more. Platinum Ditelluride ($PtTe_2$) has been reported to be a Type-II Dirac Semimetal with recent additions to the literature. In conjunction with Ohio State University we have started an investigation on this material. The Goldberger group has newly synthesized random chromium alloys to potentially add magnetism as a tunable feature for this reported Dirac Semimetal. At Cal State Long Beach, using Angle Resolved Photoemission Spectroscopy (ARPES), we have directly probed the valence electronic band structure using the photoelectric effect to unveil characteristics of these materials. Using the Advanced Light Source at the Lawrence Berkeley National Laboratory, we have measured the band structure of $PtTe_2$ and its chromium alloys. We report the band structure under the chromium addition and the survival of the surface state Dirac cones previously reported in literature for $PtTe_2$. It is noted that while Fermi surface features change across the different compounds, we see a preservation of the 6-fold symmetry. We have deposited potassium in-situ on the surface or these $Cr_xPt_{1-x}Te_2$ surfaces to adjust the Fermi energy and peer into the conduction bands to illuminate differences in the different alloys and their amount of chromium replacement. We note that with different linear polarizations of light used in our ARPES experiment, we can contrast the resulting spectra to analyze the orbital character of the band manifolds. In conclusion, we report the band structure of the novel $Cr_xPt_{1-x}Te_2$ series and propose it as a possible material that can be studied for Dirac fermion quantum mechanical phenomena and added to the next generation of electronics.

7. Using Scanning Tunneling Microscopy to Study the Characteristics of Topological Materials

Kenta Kodama[1], Luis Carretero[2], Samra Tekle[1], Joshua Goldberger[3], Jay A. Gupta[2], Claudia Ojeda-Aristizabal[1]

[1]Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840,
[2]Department of Physics, Ohio State University, Colombus, OH 43210, and
[3]Department of Chemistry and Biochemistry, Ohio State University, Colombus, OH 43210

Topological materials have been a widely researched topic in condensed matter physics due to their unique characteristics of retaining exotic properties regardless of disturbances to their physical structure. Here, we study a material called, platinum ditelluride (or $PtTe_2$), which is classified as a Type II Dirac Semimetal. Topological semimetals such as this one have possible practical applications such as energy-efficient electronic components and photovoltaics. As opposed to a regular semimetal that can be converted to either a metal or insulator by either "closing" or "opening" the energy gap between its conduction and valence bands, topological semimetals resist change to their semimetal state. Furthermore, type II Dirac semimetals are characterized by the presence of Dirac points formed by a fourfold overlap of two doubly-degenerate energy bands mapped in momentum space, which also may host a break in Lorentz invariance through their highly tilted Dirac cones. The energy dispersion relations that allow us to observe these natural phenomena can be obtained via scanning tunneling microscopy. By taking advantage of quantum tunneling, we are able to apply a voltage between an extremely sharp conducting tip and a sample of choice while leaving a vacuum gap between the two components. Such a non-invasive and precise method of measurement—due to the extremely narrow width of the tip of the piezoelectric scanner—will give us the ability to probe the characteristics of our topological semimetal with sub-Angstrom precision. The two modes of operation—constant current mode and constant height mode– allow us to obtain both topographic and spectroscopic data from our sample. The constant current mode captures topographic images of our sample by applying a bias voltage between the tip and the sample and maintaining the tunneling current (which is exponentially proportional to the distance between the tip and the sample) via a feedback system while maneuvering the piezoelectric scanner attached to the tip through a desired area. The constant height mode disables the feedback system that controls the tunneling current while maintaining the height of the piezoelectric scanner. We can obtain spectroscopy data from a single atom by sweeping the bias voltage at one location while reading the associated tunneling current values, giving us a plot of the differential conductance of the sample (dI/dV) vs the amount of bias voltage applied to the sample. By combining the capability of the STM and its two modes of operation, we can acquire a direct correlation to the local density of states of the sample as well as a precise mapping of the energy dispersion relations. We are currently obtaining data on $PtTe_2$ in unison via scanning tunneling microscopy, angle resolved photoemission spectroscopy, and transport experiments with the hope of reconciling the conclusions gathered on this unique type of material.

This project is supported in part by the Department of Energy, Office of Basic Energy Sciences under award number DE-SC0018154 and 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.

8. Study of the molecular arrangement of a CuPc/graphene/h-BN heterostructure

Jacob Weber, Francisco Ramirez, Ryan Mizukami, Patrick Barfield, Maya Martinez, Thomas Gredig and Claudia Ojeda-Aristizabal

We study the arrangement of a thin film of planar magnetic molecules of copper-phthalocyanine (CuPc) on a graphene/hexagonal Boron nitride (h-BN) heterostructure. Atomic Force Microscope (AFM) reveals a dissimilar arrangement of the molecules on graphene with respect to its insulating counterpart h-BN, giving evidence of the importance of the interaction between π orbitals from graphene and the Cu-Pc molecules. Our surface characterization informs electronic transport measurements performed on CuPc/graphene/h-BN heterostructures.

Atomic force microscopy imaging was supported by the MRI program of the National Science Foundation under the award number 2018653.

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

Jacob Weber 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.

9. Nanofabrication Techniques to Unveil Exotic Phenomena in Low Dimensional Materials

Vinh Tran[1], Maya Martinez[1], Patrick Barfield[1], Francisco Ramirez[1], Vikram Nagarajan[2], Takashi Taniguchi[3], Kenji Watanabe[3], James Analytis[2], Claudia Ojeda-Aristizabal[1]

1.Department of Physics and Astronomy, California State University, Long Beach, CA, 90840; 2. Department of Physics, University of California, Berkeley, Berkeley, CA 94720 ; 3. National Institute for Materials Science, Japan

Low dimensional materials offer an exciting area for exotic phenomena not realizable in their bulk form. In particular, monolayer alpha-Ruthenium Chloride (α-RuCl3), a Mott insulator, is expected to be a Kitaev-Heisenberg material candidate and Copper-Phthalocyanine (CuPc) is thought to undergo a phase transition to a ferromagnetic state at low temperatures. One method for probing these materials is through Van der Waals heterostructures, where another thin crystal is put into proximity with the original crystal (or molecular thin film) leading to novel properties not exhibited in the constituents separately. Graphene (Gr) on RuCl3 for instance is thought to become strained and due to its higher electron mobility, demonstrate exciting phenomena that might be masked by the insulating nature of RuCl3. In our experiments, the addition of CuPc to a Gr/h-BN (hexagonal Boron-Nitride) heterostructure has had the effect of inversing the sign of the magnetoresistance as well as leading to an asymmetry in the field dependence. Improving the quality of heterostructures is an important task to improve the quality of the electronic transport data and revealing the hidden nature of these materials. In this vein, we present here the various techniques used for fabricating devices including a novel technique utilizing a polymer masking technique in conjunction with electron beam lithography for assisting in constructing heterostructures as well as using hexagonal Boron Nitride (h-BN) as an atomically flat substrate.

Electronic transport measurements were supported by the US Department of Energy, Office of Science, Office of Basic Energy Sciences under award number DE-SC0018154 V.N. was supported by the NSF GRFP, Grant No. DGE 1752814

Crystal growth was supported by the Department of Energy Early Career Program, Office of Basic Energy Sciences, Materials Sciences and Engineering Division, under Contract No. DE-AC02-05CH11231

10. Looking for Signatures of Ground States of the Kitaev-Heisenberg Model in $RuCl_3$

Patrick Barfield[1], Maya Martinez[1], Vinh Tran[1], Vikram Nagarajan[2], James Analytis[2], Claudia Ojeda-Aristizabal[1]

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

2. Department of Physics, University of California Berkeley, Berkeley, CA, 94720

Alpha Ruthenium Chloride (α-$RuCl_3$) is part of a special class of Mott insulators, Kitaev materials, that exhibit strong spin orbit coupling and bond directional exchange interactions. As a result, the Kitaev-Heisenberg model predicts this material to host interesting ground states such as a Quantum Spin Liquid (QSL) with fractionalized excitations making it ideal for applications in topological quantum computing. This work attempts to prove these interesting ground states via electronic transport measurements at low temperatures. We find that electronic transport is dominated by thermally activated transport at high temperatures and Efros-Shklovskii Variable Range Hopping transport at low temperatures down to the zig zag antiferromagnetic ordering transition at 7K. We also demonstrate that this antiferromagnetic ordering is

robust up to fields of 11T out of the plane. Future experiments will explore the effects of a magnetic field in the plane of the sample to hopefully induce the QSL state.

Electronic transport measurements were supported by the US Department of Energy, Office of Science, Office of Basic Energy Sciences under award number DE-SC0018154 V.N. was supported by the NSF GRFP, Grant No. DGE 1752814

Crystal growth was supported by the Department of Energy Early Career Program, Office of Basic Energy Sciences, Materials Sciences and Engineering Division, under Contract No. DE-AC02-05CH11231

11. Characterizing the Core Composition Dependence of *g*-modes in Neutron Stars with Hyperons

Vinh Tran, Prashanth Jaikumar

California State University, Long Beach, CA,

The physics of microscopic interactions at intermediate densities such as in neutron star cores is currently not well understood. As a result, the composition of core matter can range from purely nucleonic (neutrons and protons) matter, to pure quark matter, to hybrid compositions with possible phase transitions and other exotic states. A potential tool to constrain the possible compositions is the g-mode oscillation, a non-radial stellar oscillation whose characteristic frequency, the Brunt-Vaisala frequency, is dependent on two sound speeds in matter and thus the composition of the material itself. Previous work comparing the g-mode frequencies between nucleonic and quark stars demonstrated a stark contrast between the oscillation spectra for the two compositions. We extend this analysis to consider compositions with hyperons, baryons with one or more strange quarks, in the context of relativistic mean field models. We begin by solving for the equation of state and macroscopic properties of the star which involves solving a system of coupled nonlinear equations and a system of nonlinear differential equations using multivariable optimization and RK4 methods. The macroscopic values are then fed into another system of differential equations subject to boundary conditions – an eigenvalue problem whose solutions are the g-mode oscillation frequencies. Our current results indicate that hyperonic stars reach larger oscillation frequencies when compared to stars with only nucleonic matter for a given mass. The dramatic difference supports the previous conclusions that g-modes are highly sensitive to compositional variances with the implication that should we detect g-mode oscillations in neutron stars through gravitational wave detection, we could gain a better understanding of the possible states of matter as well as interactions at these densities.

This project was supported by the National Science Foundation (NSF) Grant PHY-1913693. V.T. is also supported by the CSULB CNSM Richard D. Green Graduate Research Fellowship for 2022-2023.

12. Applied Electromagnetic Field on a Diffusive Superconducting Magnetic Proximity System

Fanuel Mendez[1] and Andreas Bill[1]

[1]Department of Physics & Astronomy, California State University, Long Beach CA 90840

We analyze proximity structures made of adjacent nanoscale-width magnetic and superconducting thin films. We determine pair correlations in the presence of large concentrations of non-magnetic impurities (the diffusive regime). We present the method used to solve the Usadel equations numerically, including a hyperboloid parametrization. We discuss how to incorporate the effects of an externally applied electromagnetic field on the proximity system. The radiation is accounted for in the equations through a position-dependent vector potential in the covariant derivative of the Usadel equations.

We acknowledge support from the Gisela and Wilfried Eckhardt Summer Research Assistantship, the Google/APS Bridge Program Fellowship, and the Sally Casanova Pre-doctoral Program.

13. Imaging Bulk PtTe2 Quantum Material

Samra M. Tekle[1], Luis Rijos Carretero[2], William Koll[2], Jay Gupta Ph.D.[2] ,

[1]Department of Physics and Astronomy, California State University, Long Beach, Long Beach, CA 90840 and [2]The Department of Physics, The Ohio State University, Columbus, OH 43210

2D materials have become significantly more popular in the public eye since the discovery of graphene. 2D materials are crystalline solids that grow by forming monolayers weakly bonded by van der Waals forces. While there are several single elements that are capable of this, there are also several groups of compounds that have this ability. The compound group relevant to this study is the transition metal chalcogenides, or TMDs. One particular TMD is platinum ditelluride ($PtTe_2$) classified as a type II Dirac semimetal. Since it possesses such unique characteristics, most notably the type-II Dirac fermions, it holds a great deal of potential for future research and application. In order to gain an understanding of the surface of $PtTe_2$, a bulk sample was imaged using an atomic force microscope (AFM), and a scanning tunneling microscope (STM).

This project is supported by the NSF Materials Research Science and Engineering Center Grant DMR-2011876 and 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.

14. Clean Superconducting-Magnetic Proximity Systems in an Electromagnetic Field

[1]Laura Tandy, [1]Andreas Bill

[1]Department of Physics and Astronomy, California State University, Long Beach

Long Beach, California 90840

Electrons form bound Cooper pairs with opposite momenta and spin in a conventional superconductor. When these pairs tunnel into an adjacent non-superconducting material the pair correlations survive but decay over a finite distance. The effect is particularly interesting when the material between two superconductors is magnetic and has been studied previously in detail. In this work we investigate the effect of an external applied electromagnetic field on an SFS (superconductor-ferromagnet-superconductor) Josephson junction as a function of various parameters of the system. We present how one introduces the applied field into the formalism using the Peierls substitution and how the Bogoliubov - de Gennes equations for pair correlations are modified.

L.T. was generously funded by the Google Summer Research Assistantship and the Richard D. Green Graduate Research Fellowship.

15. Transfer Learning Methods for Individualized Treatment

1 Miontranese Green, 2 Johnny Rajala, 3 Anthony Wang, 4 Kelly Wentzlof

3 Shu Yang, and 3 Yunshu Zhang

1 California State University, Long Beach

2 University of Maryland, College Park

3 North Carolina State University

4 Indiana University Bloomington

Key Words: Causal Inference, Individualized Treatment Rules, Transfer Learning, Augmented Inverse Probability Weighting, Calibration Weighting, Tree-based Methods

Modern precision medicine aims to utilize real-world data to provide the best treatment for an individual patient. An individualized treatment rule (ITR) maps individual characteristics to a recommended treatment that maximizes the expected outcome of each patient. A problem facing modern medicine is that studies on the effect of treatment are conducted for a source population that may be different from the population of interest. Our research goal is to investigate a transfer learning algorithm to obtain targeted, optimal, and

interpretable ITRs. We develop a calibrated augmented inverse probability weighting (CAIPW) estimator by maximizing the value function for the target population to estimate an optimal ITR. Additionally, we investigate transfer learning methods based on two large medical databases, eICU Collaborative Research Database (eICU-CRD) and Medical Information Mart for Intensive Care III (MIMIC-III), identifying the important covariates, treatment options, and outcomes of interest to estimate the optimal linear and tree-based ITRs for patients with sepsis. This project introduces new techniques for data merging to provide data-driven optimal ITRs, catering to each patient's individual medical needs. These techniques extend beyond medicine, applying to a wide range of areas such as marketing, technology, social services, and education.

16. Assessing Nitrous Oxide Cycling in the Coastal Waters of the Eastern Tropical South Pacific Using Stable Isotopes

Jacquelin Chen, Noah Gluschankoff, Karen Casciotti

Stanford University, Stanford, CA 94305

Nitrous oxide (N_2O) is a climatically relevant greenhouse gas that can be produced in the ocean and emitted to the atmosphere, where it can later lead to ozone depletion. Previous studies show high accumulations of N_2O above the oxygen minimum zone (OMZ) of the Eastern Tropical South Pacific (ETSP), but the relative roles of the microbial pathways that dictate N_2O cycling vary regionally. The purpose of this study is to identify the primary pathways controlling N_2O cycling in the coastal waters of the ETSP. In this study, N_2O concentrations and its isotopes, as well as O_2 concentrations and the isotopic compositions of nitrate and nitrite, were analyzed at three stations between the shallow coastal shelf and the shelf slope along the GEOTRACES GP16 Zonal Transect. Our results demonstrated a rapid decline in O_2 concentrations coinciding with accumulation of N_2O. This N_2O accumulation is estimated to support significant fluxes of N_2O to the atmosphere at our stations. N_2O isotopocule results illustrate intense N_2O cycling, driven by a combination of incomplete denitrification and hybrid N_2O production in the oxycline. In the anoxic waters of the ODZ N_2O isotopes indicate concurrent N_2O production and consumption through changes in $\delta^{15}N^{\alpha}$, $\delta^{18}O$, and $\delta^{15}N^{\beta}$. Overall, N_2O cycling in the coastal ETSP waters appears to be mainly driven by denitrification, with a smaller role from hybrid formation.

This project is supported in part by the National Science Foundation Award #1852022. Critical work was performed by Summer Undergraduate Research in Geoscience and Engineering program student Jacquelin Chen. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Science Foundation.

17. Exploring Neutron Star Binaries Using Einstein Toolkit

Shanel Deal, Thomas Klaehn

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

Neutron stars are created when a supermassive star runs out of fuel causing it to collapse on itself. In this collapse the protons and electrons are crushed together into a neutron. Neutron star mergers are a type of stellar collision where two neutron stars orbit each other closing and start an inspiral due to a gravitational force. Matter in neutron star mergers can reach high densities and temperatures up to one hundred MeV. The merger can lead to a black hole or a more massive neutron star. When a merger forms a hypermassive star this can cause short gamma ray bursts before collapsing into a black hole. Einstein Toolkit is a software platform of computation tools that helps support research in gravitational astrophysics. In our research, we have used the initial equation of state data from the LORENE code in order to simulate the inspiraling of two neutron stars forming a hypermassive neutron star. With this data, we are able to see the emitted gravitational waves of the inspiral and the oscillations in the hypermassive neutron star that was formed. With changing the equations of state for the neutron stars, the gravitational waves of the inspiral and oscillations will be reviewed.

18. Examining levels of social support in a mobile health (mHealth) exercise intervention for cardiometabolic disease based on participant exercise adherence

Madeleine Phan*, Alison Ede, PhD, Hsiang-Ling Teng, PT, PhD, Ayla Donlin, EdD and Jackie Dawson, PhD, California State University, Long Beach, Long Beach, CA

Purpose: Adherence to national physical activity guidelines by Americans is low, potentially due to a lack of social support and accessibility to the internet and mobile health devices. Mobile health (mHealth) exercise interventions may promote increases in physical activity (PA). However, more information is needed on the optimal method for the delivery of mHealth interventions to increase exercise exposure. Thus, a mHealth intervention incorporating increasing levels of social support was implemented to improve exercise exposure in sedentary adults.

Aim/Hypothesis: We aim to evaluate participant exercise dose for a mHealth exercise intervention with different levels of social support based on cumulative exercise exposure defined by heart rate-based intensity, duration, and frequency. We hypothesize that the study group with the highest level of social support (Level 3) will yield greater exercise exposure.

Methods: A total of 84 sedentary (<30 min/week of exercise) adults (33.3 ± 14.0 yr) were randomized (1:1:1) into 1 of 3 groups: Level 1 (n=26) received wearable sensor, social application, and website offering wellness material, Level 2 (n=30) received the same as Level 1 along with pre-recorded exercise videos and weekly emails, and Level 3 (n=28) received the same as Level 1 along with instructor-led videoconference exercise sessions. Level 2 and 3 groups received 35-min high-intensity functional training sessions 3x/wk and were encouraged to perform self-directed physical activity. Level 3 received the most social support as exercise sessions were carried out with real-time instruction, individualized support from the instructor, and exposure to other participants during exercise while Level 2 only received pre-recorded exercise videos. Participants wore a chest strap sensor (Myzone MZ-3) during activity to capture heart rate-based intensity, duration, and frequency. Exercise exposure was evaluated by classifying total minutes of moderate-to-vigorous physical activity (MVPA) under heart rate zones meeting national physical activity guidelines. Target heart rate zones were calculated using the Heart Rate Reserve (HRR) equation of HRR = [(max HR - resting HR) x target zone] + resting HR). Differences between groups were tested using one-way ANOVA with Bonferroni-adjusted t tests in post hoc analyses.

Results: Although Level 3 exercise group had higher cumulative exercise exposure (732 ± 629 min/week; mean ± SE) compared to Level 1 (375 ± 547 min/week) and Level 2 (511 ± 531 min/week), no significant differences were observed between groups ($p>0.05$) for total exercise exposure represented as HRR MVPA.

Conclusion: In a cohort of sedentary adults, implemented levels of increasing social support did not influence significant differences in exercise exposure measured by physical activity levels from HRR zones.

Acknowledgements: This work was supported by the California State University Long Beach College of Health and Human Services and the Maximizing Access to Research Careers (MARC) Undergraduate Student Training in Academic Research (U*STAR) training program funded by NIH Grant # T34 GM008074. The Myzone group provided the MZ-3 trackers and software license.

19. Mean Field Modifications to the Hadron Resonance Gas

Nicholas Cassar, Thomas Klaehn, PhD

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

The Hadron Resonance Gas model (HRG) is a statistical approach to describing the thermodynamic properties of nuclear matter such as what is produced in heavy ion collisions. Each species of hadron within the HRG acts as a non-interacting ideal gas. While this is shown to have good agreement with low temperature Lattice QCD data, the HRG model begins to break down at higher temperatures as well as densities due to chiral symmetry breaking and the QCD phase transition. Additionally, modern data has

shown neutron stars with higher masses than what is possible with an ideal gas model, therefore hinting at the importance of interactions at high densities. We modify the HRG model by adding in medium effects via interactions between all baryons within the gas. The mechanism for these interactions is equivalent to the Walecka model in which particles can exchange sigma and omega mesons. We extend the interactions to all baryons but neglect any interactions between mesons in the HRG. Adding interactions gives coupled gap equations which are solved numerically. The results show an improved fit at low densities for pressure and trace anomaly, as well as the in medium effects onto the baryon masses. In addition, it provides a better mechanism for probing the QCD phase transition than the ideal gas model.

20. Synthesis and Characterization of Novel Light Emitting Materials

Andy Huang[1], Shahab Derakhshan, P.hD[,2] Katarzyna Slowinska, Ph.D[3]

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

White light emitting diodes (w-LED) have applications such as detectors, displays or emergency lighting. The methods to generate the white light use either a blue LED and yellow phosphor, blue LED and several phosphors, or an ultraviolet LED and a blue, green, and red phosphors. The phosphor in a high-power semiconductor-based LED uses more than half of the electrical input power that is converted into heat. This increases the temperature of the phosphors and harms the overall performance of the LED device. The long wavelength is converted to a shorter wavelength, which decreases the overall performance of the systems. The phosphors change color, reduced the luminous efficacy, as well as the lifespan of the w-LED. New series of phosphors were synthesized with the general formula of $Ca_{1-x}Sr_xY_{1-y}M_yGaO_4$ (M = Eu, Tb, Bi), $CaYGa_{1-x}Cr_xO_4$, and $CaY_{1-x}M_xGa_{1-y}Fe_y O_4$ (M = Eu, Tb). The samples were prepared by citric acid sol-gel, followed by conventional high-temperature solid state reactions. The phase formation, phase purity and crystal structure of samples were confirmed by powder X-ray diffraction method. The absorption spectra were determined by Hitachi UH-415 and the photoluminescence spectra were determined by using the Shimadzu RF-5301PC Spectroflouorophotometer. The color tuning by the addition of the isoelectric defects from the trivalent europium and terbium will demonstrate great potential to improve the next generation of w-LED solid-state lighting.

21. Exploring Standard Model Symmetries with Clifford Algebras

Armando Reynoso, Thomas Klaehn

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

The Standard Model(SM) of particle physics underlies our current understanding of fundamental physics where the electromagnetic,weak and strong interactions rise as a consequence of gauge invariance under U(1)xSU(2)xSU(3). Despite the rigorous framework of the SM which allows for extremely accurate predictions, there are open ended questions which are not explained by the SM, such as the Charge-Parity problem in the strong interactions, or the missing explanation behind neutrino masses hinting at physics beyond the Standard Model. Viewing fundamental interactions as invariance under gauge groups, it is then natural to explore different algebraic groups which contain SM properties, yet are algebraic different from U(1)xSU(2)xSU(3) to allow the possibility for physics beyond the SM. We start our investigation under a Clifford algebra Cl(p,q) where we demand a SU(3) Lie algebra resulting in Cl(6,0). Our generators of SU(3) are formed under basis elements of Cl(6,0) allowing us to derive our SU(3) Lie bracket. Further symmetries can be found by recalling that a 4D vector space with a symmetric bilinear form generates the Minkowski metric which we associate with Cl(1,3).Our even subalgebra of Cl(1,3) is then isomorphic to the Pauli algebra Cl(3,0) allowing us to incorporate SU(4) gauge symmetry into Cl(6,0) using a Minkowski basis. The ability to incorporate these SM symmetries into Cl(p,q) proves a useful tool in providing a pathway to further our study of fundamental interactions in terms of Clifford algebras as well as studying symmetries of spacetime.

22. Synthesis, Crystal Structure, and Magnetic Properties of Novel Nickel Ruthenates: $Li_{3+x}Ni_{2-x}RuO_6$

Shinta Tanamas[1], Gemma Goh[2], JoAnna Milam-Guerrero[2], Brent C. Melot[2], Shahab Derakhshan[1]

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

[2] Department of Chemistry, University of Southern California, 3620 McClintock Ave., Los Angeles, California 90089

Antiferromagnetic (AFM) interactions in NaCl structure types have the potential to generate geometric magnetic frustration (GMF) due to its triangular sub lattice. To provide more insight on the structure to property relationship of these systems, a series of Li3+xNi2-xRuO6 (x=1, 0.75, 0.5, 0.25, 0) were implemented. These are adaptations of the Li3Ni2OsO6 and Li4NiOsO6 where the Ni and Os ions resulted in ferrimagnetic transitions. Purposefully replacing the 5d Os ions with the isoelectronic 4d Ru ions were to further understand the role of principle quantum number on resultant magnetism. The Li3+xNi2-xRuO6 series were successfully synthesized in the monoclinic crystal system with a C2/m space group using conventional solid state synthesis. Physical properties were explored through temperature dependent AC and DC magnetic susceptibility, field dependent magnetic susceptibility, heat capacity, electrical conductivity, and Seebeck coefficient measurements.

23. Innate immune protein C1q modulation of endothelial wound healing

Enidh Padron, Mehernaz Haque and Deborah A. Fraser Ph.D

Atherosclerosis is a chronic inflammatory disease that is very common and is a major cause of death in the USA. This disease causes damage to the endothelium that lines blood vessels and leads to infiltration of monocytes/macrophages and low densitylipoproteins (LDL) into the arterial wall. LDL can then become oxidized also known as oxLDL, which is pro-inflammatory. Innate immune protein C1q is known to be produced by macrophages in atherosclerotic lesions, and binds oxLDL. C1q has beneficial effects on macrophage functions but the effect of C1q on endothelial functions in atherosclerosis is not well known. The aim of our study was to test C1q modulation of endothelial migration. We tested the hypothesis that C1q bound to oxLDL will increase endothelial wound healing compared to oxLDL alone. To test this, a wound healing assay was performed. A wound was generated in a confluent culture of human aortic endothelial cells (HAEC) using 3-well culture inserts and a sterile pipette. Cells were treated with oxLDL with and without C1q in 1% serum media and monitored for 24-48 hours using live cell imaging. 10% serum was used as a positive control. The average width of the gap was calculated at different time points for each treatment. Data showed that the presence of C1q substantially increased wound healing, even above levels seen in our positive control. These data suggest C1q may have a beneficial effect on the damaged endothelium in atherosclerosis.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; SC3GM111146 (DF) and R25GM071638 (RISE). The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

24. Effects of Plant Restoration on Microbial Soil Communities in a Sediment-Amended Southern California Salt Marsh

Lindsay Park, Alexis Guardiola, Cecilia Heredia, and Jesse Dillon Ph.D.

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

Salt marshes provide key ecosystem services including biochemical cycling, protecting coastal shorelines and developments from natural disaster, in addition to housing endangered species and diverse microbial communities. Human impacts including urbanization California's coastline and sea level rise has led to loss of over 90% of coastal wetlands. Seal Beach National Wildlife Refuge experimented with marsh restoration by

utilizing sediment amendments to raise the marsh elevation followed by transplantation of native cordgrass, *Spartina foliosa*. These restoration efforts are likely to impact the entire ecosystem including plants, invertebrate animals as well as microorganisms that play key roles in biogeochemical cycling and decomposition in these ecosystems. We hypothesize that sediment amendment and associated vegetation loss has significantly reduced sediment bacterial diversity compared to unamended wetlands (control). The introduction of transplanted *S. foliosa* is expected to increase the bacterial diversity of the soil compared to amended soil without plants and that over time bacterial diversity will more closely resemble the unaltered control marsh. This is currently being investigated using nucleic acid extractions and bacterial 16 S rRNA gene sequencing from all 3 sample sites. We have successfully extracted DNA from samples at 0, 6, and 12 months post transplantation and will use bioinformatic approaches to analyze resulting sequence data. Determining the relationship between marsh vegetation and bacterial community diversity in this marsh is essential for understanding the impacts of sediment amendment and inform future estoration efforts.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers: #5R24GM071628-12 #UL1GM118979 #TL4GM118980 #RL5GM118978.

25. Measuring the Effect of Hyperglycemia on C1q Production in Macrophages.

Jamie Albertson, Michelli Chai, and Deborah A. Fraser, Ph.D.

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

Diabetes is a chronic metabolic disease characterized by the body not being able to lower glucose levels in the blood when elevated. A high blood glucose level is known as hyperglycemia and can lead to inflammation throughout the body. Macrophages play a major role in the pro-inflammatory and anti-inflammatory processes by utilizing their phagocytotic abilities and secreting a protein called C1q. The protein C1q has the potential to initiate cascades that affect inflammation. C1q can do this by binding to a pathogen or damaged cell and promoting inflammation via activation of the classical complement pathway or by dampening inflammation by facilitating clearance of targets through a non-complement role. This study focuses on investigating the effect that hyperglycemia may have on the production of C1q by macrophages. Raw264.7 macrophages were differentially polarized towards M0, M1, and M2, and cultured in high and low glucose media. Pellets and supernatants were harvested to compare C1q expression and production across groups. C1q expression and production will be measured using Western Blot, qPCR, and hemolytic titer techniques. Considering inflammation is a complication within diabetes and C1q has some anti-inflammatory effects in the absence of other complement components, changes in secreted levels of C1q may impact macrophage contributions to this disease.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number SC3GM111146 and the U.S. Department of Education Award P031C160085.

26. Characterization of Ampicillin-Resistant Coliforms from a Southern California Beach and Tidal Channel

Meleia Vyrak, Victor Flores, Jesse Dillon, Ph.D.

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

Increased usage of antibiotics in both humans and livestock has led to increased antibiotic resistance in bacteria. Although not all bacteria that attain antibiotic resistance are harmful, our primary concern focuses on pathogenic bacteria, such as fecal coliforms, that pose significant public health risks. Recent work in our laboratory has shown that fecal coliform bacteria isolated from Southern California beaches displayed a high incidence of ampicillin resistance. We are currently investigating the incidence of ampicillin resistance in bacteria isolated on MacConkey agar from two local waterways (a tidal channel and a beach inside the Long

Beach breakwater). Initial biochemical testing using Simmons Citrate, phenol red broth, and SIM tests indicated that there were diverse bacteria, many of which were not *E. Coli*. Ongoing analyses using 16S rRNA gene sequencing of genomic DNA extracts of isolates will be used to identify the isolates. This project will aid in the identification of potentially hazardous ampicillin-resistant bacteria found in Southern California waterways.

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

27. C1q Modulation of Oxysterols in Macrophage Foam Cells

Kathryn E. Morales, Marc C. Pulanco, and Deborah A. Fraser PhD

Department of Biological Sciences, California State University Long Beach, Long Beach, CA, 90802

Atherosclerosis, or inflammation of the arteries, is caused by plaque accumulation. Under normal conditions, macrophages translocate to the site of plaque formation to clear Low-Density Lipoproteins (LDL) and initiate efficient rates of cholesterol efflux. In cholesterol rich environments, macrophages become overwhelmed with cholesterol, form unstable foam cells, and then undergo apoptosis thereby contributing to plaque formation as debris. Identifying mechanisms of foam cell formation is critical in understanding the progression of this disease. C1q is an innate immune protein best known for its ability to activate complement. However, it can also bind directly to targets in the absence of other complement components and increases removal by phagocytes. We have previously shown that C1q binds oxidized LDL (oxLDL) and regulates inflammation during ingestion by Human Monocyte Derived Macrophage (HMDM) foam cells. C1q also increases Liver X Receptor (LXR) activation in THP-1 macrophages during ingestion of oxLDL. To test the hypothesis that C1q is activating LXR through upregulation of oxysterol ligands, lipidomic analysis by mass spectrometry was performed in unpolarized (M0) HMDM foam cells that ingested oxLDL+/-C1q. C1q increased LXR-activating oxysterols 24-hydroxycholestrol (24-OHC) and 25-hydroxycholestrol (25-OHC) in these cells. C1q-mediated changes to 24- and 25-OHC in M1 (inflammatory) HMDM foam cells are also being investigated. To investigate the molecular mechanism by which C1q affects oxysterol levels in HMDM foam cells, changes in gene expression of oxysterol-modifying enzyme cholesterol 25-hydroxylase (CH25H), LXRa (NR1H3), and LXRb (NR1H2) were measured by qPCR in RNA isolated from M0 and M1 HMDM that ingested oxLDL with and without C1q. Since expression of ABCA1 and ABCG1 are LXR-dependent, we also measured gene expression of ATP binding cassette transporters A1 and G1 (ABCA1 and ABCG1) in HMDM foam cells in response to C1q. Our data shows that CH25H levels significantly increase in M1 activated macrophages compared to M0 macrophages as has been previously reported. Levels of CH25H are also significantly reduced in the presence of oxLDL in M0 and M1 macrophages. In 5 out of 6 donors C1q bound to oxLDL increased levels of CH25H to untreated levels. No substantial changes were measured in LXRa, LXRb, ABCA1, or ABCG1 under any treatment condition. These studies identify a novel role for C1q in modifying oxysterols in macrophages and suggest that one mechanism may be through increased expression of cholesterol 25-hydroxylase. Understanding the mechanisms of action of the immune system in atherosclerosis may help identify novel treatments for this disease.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; NIHT32GM138075(KM) and SC3GM111146 (DF). The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

28. Animal Visitors to Western Hemisphere *Justicia* (Acanthaceae): What does Community Science tell us?

Laura Abonce, Josephine Rodriguez, Amanda Fisher

Biological Sciences, California State University, Long Beach

The mutualistic relationship between plants and their animal pollinators has occurred over millions of years and has led to the evolution of distinct features in both. Western hemisphere *Justicia* (Acanthaceae) species have flowers of different colors, shapes, and sizes that attract animal pollinators. To understand *Justicia*-pollinator interactions in the western hemisphere, we used the community science programs eBird and iNaturalist to find observations of animals visiting open *Justicia* flowers in North and South America. We also created a "*Justicia* Pollinators" iNaturalist project. We identified animal visitors and *Justicia* plants to the species level. On the eBird website, we found 32 observations of hummingbirds visiting *Justicia* flowers, which included 15 hummingbird species visiting 7 *Justicia* species. On the iNaturalist website, we found 60 observations of 6 different animal groups visiting 9 *Justicia* species. Hummingbirds were the most abundant pollinators observed on iNaturalist (24), followed by butterflies (21) and bees (11). Since hummingbirds and butterflies are frequently photographed, we tested for bias in the frequency of community science observations of these visitors to four *Justicia* species compared to observations of visitors to these *Justicia* species from pollination studies. Community science observations allow us to expand the geographic scope of our study, and in combination with observations from carefully planned fieldwork, they contribute to our knowledge of animal visitors to *Justicia* flowers. This study will allow us to analyze the pollinator diversity of western hemisphere *Justicia* species and how their flowers adapt to attract different pollinators.

29. Fluorescence Spectroscopic Analysis of Apolipoprotein AI Reconstituted High Density Lipoprotein

Kasandra Khiev, Kyle Meyer, Vasanthy Narayanaswami Ph.D.

Department of Chemistry and Biochemistry, California State University, Long Beach, 1250 Bellflower Boulevard, Long Beach, CA 90840

High density lipoproteins (HDL) are protein-lipid complexes that aid in cholesterol efflux, a process in which HDL particles interact with ATP-binding cassette transporters ABCA1 and ABCG1 to remove excess cholesterol from macrophages. The major protein on HDL, apolipoprotein AI (apoAI), exists in lipid-free and lipid-bound states. When bound to phospholipids, it contains 10 a-helices (H1-H10) that wrap around the hydrophobic lipid tails. Our goal is to understand how the conformation of apoAI changes during cholesterol efflux. We hypothesize that residues 125-158 (helices H5 and H6) form a disordered loop that can accommodate lipid loading and changes in HDL particle size. To test this hypothesis, an apoAI double-cysteine mutant (L134C/A152C) was designed with cysteines positioned on the loop. The purified protein was labeled with N-(1-pyrene)-maleimide (NPM), a spatially sensitive fluorophore that has a distinct emission at ~460 nm when it is within ~10Å of a neighboring pyrene. The pyrene-labeled apoAI was reconstituted with phospholipids at different phospholipid:protein molar ratios (28:1, 70:1, and 100:1) to generate small (~7.8 nm), medium (~9.6 nm) and large (~10.5 nm) diameter HDL referred to as reconstituted HDL (rHDL). The pyrene-labeled rHDL was incubated with J774.1 macrophages undergoing cholesterol efflux, and fluorescence spectra compared before and after efflux. In the rHDL-bound state, apoAI undergoes conformational reorganization with a significant decrease in excimer emission. The data suggests that the conformational changes accommodate for lipid loading, but more studies are required to obtain further details about the conformational reorganization during lipid loading of HDL.

30. Investigating the Effects of Innate Immune Protein C1q on Autophagy and Inflammasome Activation

Jade Sinatra[1], Lydia Smith[1], Deborah A. Fraser[1]

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

Atherosclerosis is a chronic inflammatory disease that is characterized by lesional macrophage digestion of oxidized low-density lipoproteins (oxLDL). Macrophages release pro-inflammatory cytokines such as IL-1β through activation of the NLRP3 inflammasome, which often leads to exacerbation of inflammation and disease progression. We have previously determined that the innate immune protein C1q plays a protective

role in the early stages of atherosclerosis by modulating and dampening components of the NLRP3 inflammasome. C1q effectively polarizes macrophages toward an anti-inflammatory phenotype, thereby decreasing the secretion of pro-inflammatory cytokine IL-1β. During modified lipoprotein clearance, C1q also facilitates the activation of autophagy markers on macrophages through the natural degradation and recycling of cellular elements. Recently, the activation of autophagy in macrophages has been shown to play a central role in the regulation of the NLRP3 inflammasome by acting in an atheroprotective manner to increase macrophage survival. Using this information, we tested the hypothesis that C1q dampens the inflammasome through activation of autophagy. Human monocyte-derived macrophages (HMDMs) were cultured from whole blood and treated in either the presence or absence of a 3-MA autophagy inhibitor. The cells were then treated with oxLDL +/- C1q, which was followed by a collection of mRNA and cell supernatant. Gene expression of NLRP3 and IL-1β were measured by quantitative PCR, and protein levels of IL-1β were measured using Luminex multiplex assay. Our data confirmed that, as was previously observed, C1q dampened IL-1β gene and protein expression in M1 inflammatory macrophages. However, this C1q-mediated reduction in IL-1β was not seen in the presence of autophagy inhibitor 3-MA. These data suggest that C1q is dampening the inflammasome, at least partially, through the activation of autophagy. This provides a novel mechanism through which C1q may be beneficial in atherosclerosis.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number SC3GM111146 (DF). The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

31. Regulation of Female Reproduction by GLUT1-dependent Glycolysis in Gonadotropes

Christy Nguyen[1]; Sizhe Wang[2]; Rubina Kapadia[2]; Thu Nguyen[2]; and Dequina Nicholas, Ph.D.[2]
California State University, Long Beach, Long Beach, CA[1] and University of California, Irvine, Irvine, CA[2]

Polycystic ovary syndrome (PCOS) is a multi-faceted condition that affects 1 in 10 women of reproductive age. It is the main cause of female infertility and is characterized by increased luteinizing hormone (LH) secretion. However, the mechanisms underlying this increase in LH are not fully understood. Previous research has shown that gonadotrope secretion of LH is supported by glucose metabolism, which is facilitated by glucose transporter 1 (GLUT1). If GLUT1 is an important mediator for LH secretion, then we hypothesize that conditional knockout (KO) of GLUT1 will disrupt gonadotrope glucose metabolism and result in reduced LH secretion. We aim to evaluate the role of gonadotrope glucose metabolism in female reproduction by conditional KO of GLUT1 in gonaotropes in female mice of reproductive age. iGricCre$^{+/+}$GLUT1flox$^{+/+}$ mice will receive intraperitoneal (IP) injections with either Tamoxifen to activate Cre-LoxP recombination or corn oil (control) once daily, every other day for a week. Pituitary dissections will then be performed on the mice to validate KO of GLUT1 by flow cytometry. In preliminary studies, we have successfully identified primary gonadotropes using flow cytometry. Results from our pilot study of GLUT1 KO by tamoxifen induced Cre-loxP recombination also confirmed reduced LH secretion in female mice. This validates our flow cytometry approach and serves as a proof of concept for validating the KO of GLUT1 by flow cytometry. Our next steps are to replicate these results, analyze mice estrous cycle, and measure LH surge.

This project is supported by NIH NICHD Grant #R00 HD098330 (DN) and NIH NIGMS Grant #T34 GM008074 (CN).

32. Investigating the Effects of Innate Immune Protein C1q on Oxidative Phosphorylation Gene Expression in Macrophages

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

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

The innate immune system is responsible for removing targets such as pathogens and damaged self-targets. When targets are present, the immune system responds by activating inflammatory cells such as macrophages.

Though inflammation is essential in removing targets such as foreign pathogens, excessive or inappropriate activation can lead to inflammatory disorders such as atherosclerosis. Innate immune protein C1q plays a role in modulating macrophage responses. When C1q binds to targets such as apoptotic cells or oxidized low density lipoproteins (oxLDL) in the presence of complement proteins, complement activation by C1q increases inflammation. In the absence of other complement proteins, C1q binds to targets and can modulate macrophages towards an anti-inflammatory phenotype (M2 macrophages). Recent RNA sequencing data from our lab suggests bone marrow derived macrophages (BMDM) from wild-type mice express lower levels of multiple genes in oxidative phosphorylation pathways (ox-phos) than C1q-deficient macrophages. We hypothesize that treating macrophages from C1q-deficient mice with C1q will decrease expression of ox-phos genes NDUFC2, UQCRFS1, and COX6B1 and lead to a decrease in superoxide production. To conduct this research, we isolated and cultured BMDM from 4 C1q-deficient mice. The cells were treated with C1q alone, or with oxidized LDL with or without C1q bound. Gene expression was measured through qPCR. Gene expression of NDUFC2, associated with Complex I of the mitochondrial electron transport chain was consistently decreased in the presence of C1q, but not UQCRFS1 (Complex III) or COX6B1 (Complex IV). Since Complex I is associated with superoxide production in macrophages, we used flow cytometry to measure superoxide production in RAW 264.7 murine macrophages using the same C1q treatments. Superoxide production decreased when cells were treated with C1q. The data suggests C1q may affect metabolism in macrophages. This 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. Further investigation will explore C1q-mediated changes in overall oxidative phosphorylation.

Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers SC3GM111146 (DF) and R25GM071638 (RISE). The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. All experiments involving animals were performed with the approval of, and in accordance with, the CSULB IACUC guidelines.

33. Structural and Functional Analysis of *Cavia porcellus* and Human Apolipoprotein E4 to Understand its Role in Amyloidogenesis

Jasmine T. Nguyen, George Celis, Vasanthy Narayanaswami, Ph.D.

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

Amyloid-β (Aβ) peptide aggregation and senile plaque formation are hallmark features of Alzheimer's disease (AD), a neurodegenerative disease characterized by cognitive decline. One of the risk factors for AD is the inheritance of the *APOE* ε4 allele that encodes the protein apolipoprotein E4 (apoE4). Several studies have demonstrated the presence of apoE4 in the amyloid plaques, prompting the question of the role of apoE4 in amyloid plaque formation or amyloidogenesis. Other researchers have suggested that the C-terminal domain of apoE4 plays a role in interaction with lipids, Aβ peptide and other apoE4 molecules to form a tetramer. The current study seeks to understand the structure and function of apoE4 and its role in amyloid formation. Sequence alignment of human apoE4 with apoE from *Cavia porcellus*, guinea pig (GP) shows that the latter is only 281 aa long while the former is 299 aa long. A major difference is that GP apoE has two deletions corresponding to residues 193-197 and 246-252 (in the C-terminal domain) in apoE4. GP apoE was used to understand the role of these residues in apoE4. Recombinant GP apoE was overexpressed, isolated, and purified in *E. coli*. Biophysical studies were carried out with GP apoE and apoE4 to gain understanding of the tertiary fold around these segments of apoE4. 1-anilinonaphthalene-8-sulfonic acid (ANS) fluorescence emission spectra presented a blue shift in GP apoE in relation to apoE4 and apoE3 (a polymorph of apoE4 that is present in a majority of the population), indicating an increased level of protein surface hydrophobicity. We are currently performing trypsin digestion of each wild type apoE to compare resistance to proteolytic degradation. Taken together, understanding structural and functional behavior of GP apoE may offer insights into the mechanistic basis of apoE4's role in AD.

This work was supported by the National Institutes of Health (grant# NIH-GM105561 (VN)), NSF LSAMP Program fellowship (HRD-1826490) (JN) and NIH RISE grant (T32GM138075) (GC).

34. Photoperiod alters ovarian mRNA expression of genes in the retinoic acid pathway

Amber A. Simonpietri, Bingjie Alex Yuan, and Kelly A. Young, Ph.D.

Department of Biological Sciences, California State University Long Beach, Long Beach, CA 90840 1250 Bellflower Blvd, Long Beach, CA 90840

Cyclic ovarian function requires the orchestration of multiple signaling pathways; however, most vertebrate ovaries do not cycle continuously due to seasonal pauses in reproduction. While the endocrine regulation of seasonal ovarian change is well understood, how changes in ovarian function impact other signaling pathways remains unknown. Because the retinoic acid (RA) pathway is involved in ovarian cell proliferation, differentiation, apoptosis, and oocyte maturation, we hypothesized that the genes in the RA pathway would be differentially expressed in ovaries that are cycling, non-functional, and returning to function. To address our hypothesis, we used ovaries from seasonally-breeding Siberian hamsters who were exposed to 16-weeks of long-days (16h light:8h dark; LD; cycling ovaries), or short-days (8L:16D; SD; regressed ovaries), or 16-weeks of SD followed by 2, 4, or 8-weeks post-transfer to LD (PTw2-8; recrudescing ovaries). Real-time PCR expression showed that retinoic acid receptor-γ and retinoid X receptor-β, both of which bind the RA ligand, were present in LD ovaries and decreased significantly with SD exposure. This trend was also seen in the RA signaling process with cellular retinol binding protein 1 (RBP1) and stimulated by retinoic acid gene 6 (STRA6). In contrast, mRNA expression of RA-degrading enzyme (CYP26B1) increased significantly in SD as compared to the LD group, with expression returning to lower LD levels in the recrudescing groups. Our results suggest that the RA signaling pathway is active in cycling Siberian hamster ovaries, with decreases in RA binding concomitant with increases in RA degradation in regressed ovaries, and restoration of RA binding occurring as photo-stimulated ovaries return to function.

35. Hypermetric Scaling of Leg Weapons Both Within- and Across-Species of Leaf-Footed Bugs

Alexander Avalos[1], Ummat Somjee, Ph.D.[2], Joseph J. Dubie, Ph.D.[2]

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

[2]Department of Integrative Biology, The University of Texas at Austin, Austin, TX, 78712

In nature, there are three primary scaling relationships that are observed among animals: isometry (proportional scaling), hypermetric scaling (as body size increases, the trait of interest grows disproportionately larger) and hypometric scaling (as body size increases, the trait of interest grows disproportionately smaller). In general, we find hypermetric scaling relationships between body size and sexually selected traits (e.g., antlers in cervids and the horns of rhinoceros beetles). Studies focusing on this phenomenon typically focus on the within-species scaling and overlook trends in across-species scaling. We studied leaf-footed bugs (Hemiptera: Coreidae) in order to examine two questions: First, how does weapon size scale with body size both within- and across-species? And second, how are exaggerated sexually selected traits maintained? To do so we collected six species from their host plants in the wild and measured their pronotum width (body size metric) and hind-leg width (sexually selected trait of interest; males have enlarged femurs which they use in combat with each other to compete for reproductive opportunities). We conducted microdissections of femoral tracheae and measured their diameter in order to determine if the scaling relationship between trachea size and leg width was a potential morphological explanation for how leaf-footed bugs are able to maintain exaggerated femurs. We found that both within- and across-species, male leaf-footed bugs display a hypermetric scaling relationship between leg width and body size. The opposite was true for female leaf-footed bugs, which displayed a hypometric scaling relationship instead. Preliminary data suggests that the femoral tracheae of males scales with a steeper allometry than in females, however more data must be collected in the future. These findings have broad implications which may be applied to studies of sexually selected traits in other taxa and the mechanisms through which they are maintained.

Funding for this research was provided by the Stengl-Wyer Endowment and dispersed through the UT Austin InSTInCT REU.

36. Progress Towards The Total Synthesis Maceneolignan A

Eyas Alnasser, Julie Wahlman, Ph.D

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

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 5 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.

37. Helical hybrid collagen/cell penetrating peptides as plasmid carrier for mammalian cells.

Miguel Garcia, Katarzyna Slowinska, Ph.D.

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

Nucleic acid delivery is an urgent problem in the emerging field of protein replacement therapy with board applications from administering insulin, treating infectious diseases, gene expression, and cancer therapies. Use of nucleic acids as therapeutic agents has challenges ranging from fast degradation in circulation, high molecular weight, and strong negative charge preventing the passive diffusion across the cellular membrane. Lipid-mediated transfections are used in vitro to overcome these challenges, but this method requires the use of cationic lipids which are toxic, thus cannot be used in vivo. We propose an alternative to this methodology: a carrier based on a hybrid collagen/cell penetrating peptide (CHP) that contains a triple helical domain $(POG)_n$ providing stability to the delivery vehicle and a cell penetrating domain that has positively charged arginine residues allowing diffusion across biological membranes. The electrostatic interaction between the CHP and the DNA allows for complexation to occur that is stabilized with the triple helix formation of the collagen domain. Here we present the study on 3T3 Swiss Mouse fibroblast cells, that were treated with plasmid expressing Green Fluorescent Protein (GFP) carried by either Lipofectamine 2000 (a lipid-mediated transfection reagent) or CHP peptide. The 3T3 culture when treated with lipofectamine as GFP plasmid carrier showed uptake efficiency of 26.13%, measured with flow cytometry. Using the CHP sequence developed in our lab the uptake efficiency of carrier only is over 78%, and in delivering short siRNA (21bp) the functional efficiency is 62% of gene knock down. Future experiments will be focused on determining the efficiency of CHP delivering and releasing functional GFP plasmid and optimizing this process.

38. FMOC Leucine Amino Acid Inhibitors Exemplify Strong Noncovalent Interactions in Complex with Butyrylcholinesterase Enzyme

Karel Aceituno, Jia Mao, Jason Schwans, Ph.D, Eric Sorin, Ph.D

Department of Chemistry and Biochemistry, California State University Long Beach

The formation of amyloid beta plaques is a prominent indicator of the progression of Alzheimer's Disease (AD); this symptom is also associated with overactivity of the butyrylcholinesterase (BChE) enzyme, which hydrolyzes the neurotransmitter acetylcholine, making it a plausible target for the treatment of this neurodegenerative disease. Here, computational methods were used to probe the interactions between the enzyme and inhibitor candidates featuring 9-fluorenylmethyloxycarbonyl (Fmoc). Using Molsoft ICM-Pro software, 10000 docking trials of 12 Fmoc inhibitors were performed, and trials resulting in the most optimal docking scores were examined. The best candidate was Fmoc-Norleucine, consistent with experimental IC_{50} values. Analysis of the best-scoring structures show that the length of the aliphatic R group in inhibitors was most influential on resulting docking scores, as the four inhibitors with the largest side chains (L-Norleucine, D-Norleucine, L-Homoleucine, and D-Homoleucine) had the most favorable docking scores. From visual analyses of the enzyme in complex with these inhibitors, their larger aliphatic groups allowed for more significant π-stacking between Fmoc and peripheral aromatic site residues of BChE, as well as orientation of the terminal carboxylate of inhibitors farther into the enzyme active site near the oxyanion hole and catalytic triad, both of which are hydrogen-rich and thus favor hydrogen bonding interactions. Identification of trends observed in experimental and *in silico* studies provides a better foundation for future design of selective amino acid-based BChE inhibitors.

This project is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number R25GM071638.

39. Development of fluorescence-based sensor for self-assembly of peptide heterotrimers

Aleksandra Brajanovska[1], Miriam Torrez[2], and Katarzyna Slowinska, Ph.D.[2]

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

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

Collagen peptides mimic the structure of collagen and thus are used as models to study properties of collagen. However, collagen forms a triple helix structure that has two chains that are identical and one different, AAB-heterotrimer. Most collagen peptides are designed as homotrimer AAA due to difficulty in controlling self-assembly into a pure heterotrimer. This study aims to develop a sensor that will indicate the formation of a heterotrimer by monitoring the fluorescence signal due to the folding and unfolding of heterotrimers ABB, and ABC models. The fluorescence probe (FITC) is conjugated to the N-terminus of the peptide and the signal is based on the proximity of the probes: strong when they are apart and quenched when they are close. The sequences used in these studies are based on hybrid collagen/cell perpetrating peptide $(POG)_8 – (RRG)_2$ that are used as a model in AAB and ABB assembly. The experimental fluorescence intensity measurements for AAB and BBA trimers are used to confirm the mathematical model for statistical, non-preferential assembly. The model is used to assess preferential self-assembly of the heterotrimer ABC that incorporates the sequence of amino acids that electrostatically guides assembly. Currently, ABC heterotrimer formation can be confirmed only with Circular Dichroism Spectroscopy, but only if helix-to-coil transition temperature of heterotrimer is different than any of the homotrimers. The fluorescence-based sensor has no such limitations.

40. Epidemiological and Demographic Factors, but Not State-Level Restrictions, Influenced State-Level COVID-19 Death Rates in the US During the 2020/21 Flu Season

Elizabeth C. Moses, Ashley Carter, PhD

Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90815

The COVID-19 global pandemic has resulted in numerous deaths in the United States, particularly during a surge matching the 2020/21 flu season (Oct 1 - Mar 31), but death rates varied widely between the states. This variation is due to epidemiological and demographic differences such as population density, age

distributions, obesity rates, and access to medical care. Variation may also have been due to varying degrees of state government restrictions arising from legal mandates such as limiting public and private gatherings, requiring masking in public, and closing schools. We therefore sought to estimate the relative importance of these two factors using data for the 48 continental states. Epidemiological differences were estimated using historical flu death rate data and mandate differences were ranked using a numerical score that was calculated by combining numerous factors, including restrictions of indoor dining, mask requirements, and school closures. Multiple regressions were run to determine the relative effects of these two factors. Without considering flu death rates, states with fewer restrictions had higher COVID-19 death rates, but a multiple regression analysis demonstrated that the historical flu death rate was a highly significant predictor of COVID-19 death rates, while COVID-19 mandates became non-significant. We therefore conclude that much of the variation in state death rates during the 2020/21 flu season was due to the pre-existing combination of epidemiological and demographic factors that influence seasonal flu death rates, while there is little to no evidence that variation in state mandated restrictions influenced the relative COVID-19 death rates. Although actions such as masking, social distancing, and reduction in large indoor gatherings appear to reduce the spread of COVID-19, our analysis suggests that the beneficial effects of these activities likely occurred at the national level through overall societal awareness and federal policies rather than via differences in policies at the state level.

41. Cellular Uptake Optimization of Thermoresponsive Peptide-based Nanocarrier in Flow System

Katlyn Lawrence[1], Victoria Sarkisian[1], Katarzyna Slowinska[1]

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

The most successful treatments for increasing patient survival rates of cancer are chemotherapy and combination therapies involving systemic administration. Unfortunately, these therapies give rise to adverse side effects and exhibit non-selective toxicity to all tissues. This project seeks to contribute to elimination of systemic side effects through investigation of a thermo-responsive delivery system, based on a peptide folding mechanism. The nanocarrier, a short peptide, adopts inactive coil conformation (unfolded) at HIGH (37°C) temperature and a helix conformation (folded) at LOW temperature. Only peptides in a helix conformation can penetrate cell membranes and deliver cargo, in this case a fluorescent tag (Fluorescein, FITC). Achieving proper temperature (15°C) in a targeted area allows for activation of the helix conformation, administering the cargo to cancer cells only, which should result in diminished side effects. Here we present a kinetic approach that mimics blood flow conditions in tumor proximity. Using a syringe pump system, 3T3 cell cultures were exposed to a flow rate of 0.015μL/min, mimicking that of the blood flow rate in capillary veins. Temperature is monitored using an IR camera and the delivery of cargo (FITC) is determined by fluorescent microscopy. Results for this project are underway. Preliminary data indicates that with a proper temperature gradient, we can demonstrate that the rate at which the peptide achieves helix conformation is faster than the blood flow rate of capillary veins, and therefore our method is a promising candidate for selective drug-delivery applications.

42. Unusual mortality rates of various diseases were revealed using a comparative analysis of Asian and European countries.

Nanthanann Nuon and Ashley Carter, Ph.D

Department of Biology, California State University Long Beach, Long Beach, CA 90840

Non-communicable diseases kill 41 million people yearly, equivalent to 71% of all deaths globally (WHO). The statistics of people who died due to these diseases led us to conduct a study comparing patterns of the death rates among different countries for various diseases, including diabetes, breast cancer, tuberculosis, heart disease, and respiratory disease. We are interested in examining the twenty-two developing and developed European and Asian countries with a primary goal of finding interesting patterns and outliers and following up by searching for research studies that explain these patterns. We hypothesize that some

countries will exhibit unusually high or low mortality rates for some disorders and that the causes for this will be known in some cases and unknown in others. To further our studies, we collected data from the World Health Organization to determine the death rates for diseases from 2004-2019, impacting a population size of at least 100000 people. We determined the mean of the standardized death rate and used scatter plots to identify outliers. The outcome shows that countries vary widely in the mortality rate among different diseases, which suggests some countries are doing very well with their public health system, which many contributing factors may influence.

This project is supported by National Institutes of Health NIH R25GM071638.

43. The Role of Two bZIP Transcription Factors in Bolting-Associated Leaf Senescence in *Arabidopsis thaliana*

Daniel Uzunyan, Adrian Lopez, Judy Brusslan

Department of Biological Sciences at California State University, Long Beach, Long Beach, CA, 90840-9502

bZIP34 and *bZIP61* are two genes found within the Bolting-Associated Gene (BAG) leaf senescence gene regulatory network of *Arabidopsis thaliana* published by Hinkley and Brusslan in 2020. The bZIP genes are a family of transcription factors (TF) named for the leucine zipper dimerization domain that follows a basic DNA binding site. The bZIP family of TFs regulate a variety of functions in Arabidopsis such as pathogen defense, light and stress signaling, and seed maturation. Both bZIP34 and bZIP61 have a conserved proline residue in the third heptad in the zipper region that interferes with homodimer formation (Shen et al., 2007). However, both bZIP34 and bZIP61 are able to form heterodimers with TFs other than themselves and may regulate plant development in this form. The bZIP genes play a role in pollen development, with bZIP34 involved in male gametophyte development and maturation. Mutated bZIP34 results in physical changes to gametophytes like irregularly shaped nuclei and disorganized cell walls. However, mutation of bZIP34 is not lethal, and the plants grow to resemble WT (Gibalova et al., 2008). Over the course of this project, we have isolated two *bzip34/bzip61* double mutants and have designed both flanking primers and SYBR qPCR primers to test expression levels of the respective genes in the WT, single, and double mutant plants. The gene regulatory network predicts that bZIP34 and bZIP61 have target genes that are up-regulated (examples being AtHB34, WOX2, ATWRKY45) while also downregulating each other, suggesting there is a regulatory function in leaf senescence shared between these two bZIP TFs. The purpose of the research is to analyze the expression levels of these target genes in single mutant plants along with analyzing the expression level of both bZIP genes and the expression levels of their respective target genes in double mutant plants during bolting-associated leaf senescence.

This project is supported by the National Institute of Health (NIH) Award Number R25GM071638.

Keywords: “Gene Regulatory Network” “Arabidopsis thaliana” “Transcription Factors” “Basic Leucine Zipper Domains” “Leaf Senescence” “Bolting Associated Genes”

44. Modification of Nanosphere Templates for Nanocap and Antidot Magnetic Thin Film Fabrication

Alejandro Zafra, Jiyeong Gu, PhD

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

Curved magnetic thin films, such as nanocap thin films, have been known to show exotic magnetic states that arise from their geometry with possible applications in biomedicine, data storage, and spintronics. This study aims to better understand how magnetic states of nanocap and antidot thin films are affected by parameters such as nanosphere diameter, nanocap shape, and gap between the nanocaps. Closely packed nanosphere templates were modified via reactive ion etching. A 40 nm layer of Fe was deposited to form nanocap thin films. By removing the nanospheres after deposition antidot thin films were also obtained. Scanning electron microscope (SEM) images showed different characteristics of unmodified and modified templates. Cross sectional images of various templates are also obtained cross sectional SEM image via Focused ion beam

etching. Finally, magneto optical Kerr effect magnetic hysteresis loops were measured in both nanocap and antidot regime and compared.

This research was primarily supported by an NSF PREM, under award number DMR-2122199.

45. The Role of The ANAC072 Gene in Leaf Senescence

Andrew P. Harrison Hanson and Judy Brusslan, PhD.

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

Leaf senescence (LS) is the programmed cell death process that is coordinated by a dynamic genetic network. This process is initiated by internal signals to allocate nutrients, the most important being nitrogen, from dying leaves to reproductive organs and growing tissue. Understanding LS may lead to reductions in the use of nitrogen fertilizers. Some senescence-associated genes (SAGs) and bolting-associated genes (BAGs) have been determined to regulate the LS process. This research focuses on *ANAC072 (AT4G27410)*, a transcription factor in the BAG LS gene regulatory network (GRN) proposed in Hinckley et al., 2020. The GRN predicts *ANAC072* is a positive regulator of bolting associated LS with many direct gene targets. The loss of function (LOF) mutation SALK_063576 and the gain of function (GOF) mutant SALK_090148 are being studied to confirm *ANAC72's* role in the GRN. We hypothesize that the GOF mutant will result in the further decrease of down-regulated gene targets and a further increase in up-regulated gene targets, while the opposite is true of the LOF mutant. Genotype analysis has determined the mutants are homozygous for the T-DNA insertions in *ANAC072* with the LOF in the open reading frame and the GOF in the promoter region. Real-time-qPCR measurements show the LOF with a decrease in expression while the GOF has an increase in *ANAC072* expression.

46. Improving Magnetic Domain Images Measured By Magneto Optical Kerr Microscopy Implementing a Rotating Ground Glass Diffuser and Image Processing

Angie N. Brulc, and Jiyeong Gu, Ph.D.

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

Magnetic domain images of magnetic thin films captured using magneto-optical Kerr microscopy with a Helium-Neon Laser can be obscured by different types of interference patterns. One of them is caused by the spatial coherence of the highly coherent laser beam. A rotating ground glass diffuser can be placed in the path of the beam to scatter the light waves so that the constructive interference is reduced. Assembly of a rotating ground glass diffuser was made and integrated into the current MOKE microscopy set up. Images with and without the rotating ground glass are compared. Images are taken at saturation, remanence, and coercivity of the hysteresis loop so that the thin film sample can be viewed at all magnetization stages. To observe the change in magnetic domain images more clearly, images taken at saturation state were used as a background and subtracted from images at other fields. Images taken at saturation state contain a single magnetic domain and, therefore, are ideal to be used as a reference image when the contributions from other sources should be removed. What remains after subtracting the saturation image from an image taken during any point of the hysteresis loop is much clearer. Future steps aimed at improving magneto-optical Kerr microscopy images will be replacing the laser with a less focused and coherent light source, an LED.

47. DNA and RNA Extraction and cDNA synthesis in *Arabidopsis thaliana*

Dana A. Sakr and Judy Brusslan, Ph.D.

Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840-9502

Leaf senescence, the final stage of leaf development, is a molecular procedure that recycles nutrients from older leaves to growing tissues. Leaf senescence is a highly regulated cell death mechanism. Both internal, age-dependent factors and external stresses can cause leaf senescence. For the plant to adopt a suitable response

to environmental change and to enable the plant to recycle nutrients stored in senescing organs, leaf senescence must be strictly regulated. The purpose of this research was to learn to perform the molecular biology protocols used in the Brusslan lab. My hypothesis was that genomic DNA isolated from Arabidopsis could be amplified by PCR, that RNA would not be degraded, and cDNA synthesized from RNA could be amplified by PCR. The methods used were DNAzol for genomic DNA isolation, Trizol for RNA, denaturing gel electrophoresis for RNA, MMLV reverse transcriptase and random hexamers for cDNA synthesis, and PCR with SALK_149506, SALK _091690, SALK_123543, and bHLH112 mRNA primers. I am now able to isolate DNA, RNA and produce cDNA that could be amplified. I now have the skills to begin my own project in the Brusslan lab!

This project is supported by NSF LSAMP Program fellowship (HRD-1826490).

48. Early Life Adversities and Stage-Specific Vulnerability in a Non-Human Primate

Stephanie Joanne Gonzalez[1] and Raisa Hernández-Pacheco[1]

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

Psychosocial and nutritional adversities affect the demographic performance of individuals within populations. However, the impact adverse conditions can have on future survival as well as the developmental and early life exposures generating individual differences in risks of death remain unknown. To quantify the effects of early life adversity and identify the early life stage most vulnerable to such conditions, we analyzed 8,130 individual life histories of Cayo Santiago rhesus macaques over the span of 48 years. We identified four sources of early life ecological and psychosocial adversities during infancy and juvenility: population density, major hurricanes, maternal loss, and the presence of a competing younger sibling, and tested whether these individual factors at each stage compromised later life survival using time-varying Cox proportional hazards models. Following this, we tested the effects of aggregated adversities at each stage on later life survival using a cumulative adversity index and a Cox proportional hazards model. Our analysis shows that sex, maternal loss during infancy, and density at birth are associated to survival past infancy (cumulative model weight = 0.92). Females had a 15.98% reduction in risk at each age (HR=0.84; 95% CI: 0.77, 0.92), relative to males. Increasing density at birth by one individual increased risk at each age by 0.08% (HR=1.00, 95% CI:1.0003,1.0012). Individuals who lost their mothers during infancy had a 70.12% risk increase at each age before reaching five years of age (HR=1.70; 95% CI: 1.24, 2.33), relative to individuals who did not experience this adversity early in life. Once reaching five years of age, such annual risk decreased to 0.51% (HR=1.01, 95% CI: 0.70, 1.44). After controlling for sex-specific differences, an accumulation of one adversity during infancy increased risk by 71.70% at each age until age two but became non-significant afterwards (cumulative model weight = 1.0; HR=1.72; 95% CI:1.46, 2.02). Our findings support early life adversity and cumulative adversity frameworks and suggests that infancy is the most vulnerable early life stage to harsh conditions in rhesus macaques.

This project was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number T32GM138075.

49. Analysis of *ERF022* Transcript Quantification and Identification of ERF22 DNA Binding Targets

James Koo, Earl Givens, Ruben Tapia, Judy Brusslan

Department of Biological Sciences at California State University, Long Beach, Long Beach, CA, 90840-9502

Leaf senescence recycles nutrients such as nitrogen from older leaves to developing tissues. Understanding the regulation of this process will be useful in minimizing the amount of nitrogen fertilizers needed for maximizing agricultural output. A previous study done by Hinckley et al. on the late senescing *hac1* mutant line revealed reduced H3K9ac marks on the transcription factor gene *ERF022* as well as reduced overall expression of *ERF022*, suggesting that *ERF022* is regulated by the HAC1 histone acetyltransferase. Furthermore, an *erf022* mutant line also displayed delayed leaf senescence similar to *hac1*, suggesting that

ERF022 is involved in the regulation of leaf senescence. Studying and characterizing *ERF022* may lead to further understanding of a novel regulator of leaf senescence. Detection and quantification of *ERF022* transcripts has been challenging, and we will report progress in the design and optimization of RT-qPCR primers specific to *ERF022*. To test primer specificity and efficiency, mRNA from high *ERF022* expressing cotyledon tissue was reverse transcribed into cDNA. Despite using high-expressing tissue, it was still difficult to detect *ERF022* transcripts via RT-qPCR, so genomic DNA (gDNA) was also used to determine primer specificity. The expression data acquired was compared to the expression data from Hinckley et al. 2019. Initial primers used were identical to the ones used in the published work. However, these primers showed no difference in amplification between non-template controls (NTCs) and cDNA samples. Six newly designed primers were tested, yet in preliminary tests only two amplified cDNA. One primer amplified cDNA nonspecifically. The other amplified more specifically but had issues with quantitative linearization. Once working primers are identified, those can be used to confirm *ERF022* is associated with regulation of leaf senescence by expression analysis. Next, in order to characterize the role of *ERF022* in bolting and leaf senescence, ChIP-Seq will be performed using an *ERF022-GFP A. thaliana* line to identify DNA binding targets of ERF022. As of now, an *ERF022-GFP* plasmid construct has been successfully produced and transformed into *Agrobacterium tumefaciens*, which was then used to transform an *erf022* mutant *Arabidopsis thaliana* line. Currently, the *ERF022-GFP A. thaliana* T0 seeds are being grown on Murashige and Skoog (MS) media supplemented with BASTA to identify transgenic individuals. Identified transgenic hemizygous seedlings will be grown on soil and self-crossed to make the T1 generation and to isolate a homozygous transgenic T2 line that will be used for ChIP-Seq with an anti-GFP antibody.

This research was supported by:

- NIH Award Number R25GM071638 - RISE to Earl Givens and Ruben Tapia

-CSUPERB: 2022 Faculty-Graduate Student Research Collaboration Program to James Koo

50. Neutron Star Properties using the Zhao-Lattimer Equation of State

Sylvia Chow, Prashanth Jaikumar

Department of Physics and Astronomy, CSULB, Long Beach, CA 90840

Constraining the properties of neutron stars is a key element in specifying the equation of state that describes the state of matter within the interior of the star. By comparing observational data obtained from experiments such as the Laser Interferometer Gravitational-Wave Observatory (LIGO) with the properties predicted by the equation of state, limitations can be set on the equation of state. The Zhao-Lattimer equation of state (ZL EoS) is a relatively recent and flexible formulation of dense nuclear matter that meets several observational constraints on neutron stars. We use a numerical solver for the Tolman-Oppenheimer-Volkoff equations to determine the mass and radius of the star given energy density and pressure data obtained from the ZL EoS. In future, we will vary the parameters within a range to determine their impact on sound speeds and oscillation modes.

This project was supported by NSF Grant PHY 1913693.

51. Examining the Role of TET8-associated Apoplast Vesicles with Leaf Senescence in *Arabidopsis thaliana*

Jayde A. Zimmerman, Benjamin Verboonen, Judy Brusslan, Ph.D.

Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840-9502.

In plants, exosomes are extracellular vesicles formed when multivesicular bodies fuse with the plasma membrane, releasing intraluminal vesicles into the apoplast—the liquid component of the plant cell wall that surrounds the plasma membrane. For this reason, plant exosomes are also termed apoplastic vesicles (AVs). AV membranes are enriched with two biomarkers: PENETRATION 1 (PEN1) and TETRASPANIN 8

(TET8). Both biomarkers were recorded through proteomic analysis, immunoblotting, and via fluorescently tagged protein fusions, the latter study showing the two biomarkers in distinct AV subpopulations. These biomarkers were observed at the site of bacterial, fungal and defense hormone inoculations in Arabidopsis. These findings support PEN1- and TET8- associated AVs as being involved in plant immunity. Transcription factors associated with leaf senescence (LS), can also regulate plant immunity indicating a molecular connection between these two different physiological states. This research contributes to a better understanding of the process of LS, which recycles nitrogen and can lead to lower use of fertilizer in agricultural practices.

Preliminary research suggests that apoplast-resident, TET8 is correlated to LS. *pen1pen3* double mutants display an early LS phenotype, and higher levels of TET8-associated AVs were observed in the *pen1pen3* double mutants during LS. It is not presently known if the enhanced TET8 signal results from compensation for the loss of PEN1, causing the plant to primarily produce TET8-associated AVs, or from the early LS phenotype displayed by the *pen1pen3* double mutant. To provide experimental support for one or both of these two possibilities, we hypothesize that TET8-associated AV abundance positively correlates with LS in well-established early (*jub1*) and delayed (*ore1, ors1, AtNAP)* LS transcription factor mutants (H1). Furthermore, we hypothesize that TET8 signal would be low in both WT and *pen1* young leaves and increase in both at 8 weeks, supporting age related LS causes plants to produce TET8 AVs, and the signal not a result of the loss of PEN1 (H2). Finally, we hypothesized that mutants in genes encoding AV biomarkers (PEN1 and TET8) and one proposed biomarker (TET3), will show a delayed LS phenotype compared to WT (H3).

To test these hypotheses, we verified mutants (*tet3, tet8, ore1, ors1, AtNAP,* and *jub1*) to ensure they contained a T-DNA insertion, disrupting their genomic sequence. Only WT cDNA will be amplified by primers that flank the T-DNA insertion site, indicating the insertion is disrupting full-length mRNA expression. To determine if accelerated LS has a positive relationship with TET8-associated AVs (H1), apoplast fluid was isolated in 8-week-old mutants and TET8 was quantified via immunoblotting. LS was confirmed by quantifying *NIT2* expression and chlorophyll depletion. Results showed an enhanced signal from accelerated LS mutant (*jub1*), however, signals from delayed LS mutants were not as strongly reduced comparison to WT, providing mixed evidence that TET8 may play a role in age related LS. An additional replicate will be performed. To determine if AV abundance increases more rapidly in the *pen1* AV mutant as it ages (H2), apoplast fluid was extracted from *pen1* mutants and WT plants at 4-weeks of age (young) and 8-weeks of age (old) and TET8 was quantified via immunoblotting. One replicate indicated an enhanced TET8-signal in the old *pen1* compared WT and to the young *pen1* and WT. While this western blot indicates increase in TET8-AVs as *pen1* mutants age, the rubisco coomassie gel produced from this replicate made it difficult to decipher if total apoplast protein was isolated correctly. Additional replicates will be performed to verify these findings. Finally, to determine if AV related mutants, *tet3tet8, pen1tet8* double mutants and *pen1tet8tet3* triple mutant, positively correlated with LS (H3), we have obtained a *tet3* mutant, and crossed it with *tet8* to form a *tet3tet8* double mutant. The F_1 from this cross are currently growing. Once verified, we will cross this line to *pen1tet8* to produce a *pen1tet8tet3* triple mutant. We expect *pen1tet8* double mutant and the *tet8tet3* double mutants to show the greatest delay in LS as measured by *NIT2* expression and chlorophyll depletion. We expect *pen1tet8tet3* will show an even more severely delayed LS phenotype since TET3 may also be AV-resident. In conclusion we are working to better understand if enhanced TET8 signals are a result of LS or due to the *pen1* mutation. Thus far, our initial findings suggest that TET8 is higher in the *jub1* accelerated LS mutant (H1) and in older *pen1* mutants (H2), supporting our hypothesis that TET8-associated AVs are positively correlated with LS and with loss of PEN1.

52. Dansyl cadaverine as a prospective fluorophore for silicone systems: Developing a methodology to prepare fluorescent silicone polymer films

Kamaljit Devi and Young-Seok Shon*

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

As the demand for more environmentally friendly alternatives for plastic increases, the push for more silicone-based polymeric products is increasing due to their hydrophobic and temperature-resistant characteristics. Silicone products are widely used in industrial and residential applications, namely as caulking, seals, headsets, medical tubing, and LED lighting to name a few. However, since most silicones are clear when applied, it is harder to detect leaks or tears. One method to circumvent this issue is to introduce a fluorophore into the silicone so that leaks and tears could be detected easily using UV light. Our research targeted the development of chemical and physical methods to homogeneously apply dansyl cadaverine (DC) into the silicone matrix. Preliminary studies showed that the glass slide could be linked with DC when the slides were first immersed in a solution containing tetracarboxylic acid linker, the coupling agent, for a few days. When $SOCl_2$ was additionally introduced to facilitate the covalent bonding, a much lower concentration of relevant functional groups and the lower absorbance of DC were observed. However, when tetracarboxylic acid linker was used for the attachment of DC to PDMS, the linker was found to react with the curing agent preventing the polymeric matrix from curing. Further research indicated that DC can be effectively distributed throughout the matrix through physical means without any linker. This indicated DC can stick to a silicone environment while maintaining fluorescence property on glass slides. Our future work will focus on finding the optimal ratio between DC and silicone while keeping the integrity of the silicone matrix. We will define relevant material property requirements and test new fluorescent silicone polymers to verify the materials properties after modification.

This research is supported by grants from the National Science Foundation (CHE-1954659 and LEAP-CSULB)

53. Analyzing T-DNA insertions in *ERF54* (AT4G28140) and the Role of *ERF54* in the Regulation of Leaf Senescence of *Arabidopsis thaliana*

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

Department of Biological Sciences, California State University Long Beach

Leaf senescence (LS) is a critical developmental process in a plant's fitness. Senescence allows the plant to recycle and relocate nutrients from older leaves to developing tissues. The ability of a plant to transition from the vegetative to reproductive phase, termed bolting in Arabidopsis, and make viable seeds is assisted by relocating nutrients from older leave through senescence. One of the lab's goals is deciphering the molecular connection between bolting and leaf senescence in *Arabidopsis thaliana*. Understanding this molecular connection would potentially allow for the development of plants that can overcome early leaf senescence caused by stress related early phase transition. Earlier findings have shown many genes that change their expression in bolting-associated LS, and these genes were named bolting-associated genes (BAGs). A gene regulatory network connecting BAG transcription factors and their targets was proposed in Hinckley et al. 2020. *ERF054* was found to be a central player in this gene regulatory network of. To further study *ERF054* and its loss of function, we have developed qPCR primers that amplify *ERF54* mRNA. We harvested three different T-DNA insertion mutants; *SAIL-512-B08* located in the exon, *SAIL-73-C12* located in the 3'UTR and *SALK-149506* located in the promoter region. Leaves four and five were harvested at week six and eight to observe if *ERF054* mRNA expression is altered by T-DNA insertion in any of these locations. We expect that expression of *ERF054* will be blocked in the *SAIL-512-B08* line since the T-DNA is interrupting the sole *ERF54* exon.

54. Effects of Surface Ligand Density and Lipid Encapsulation on the Catalytic Activity of Hydrophobic Pd Nanoparticles in Different Solvents

Saba Dalaub and Young-Seok Shon*

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

*Email: ys.shon@csulb.edu

Ligand-capped metal nanoparticles exhibit promising properties as catalysts, because their large surface area to volume ratio allows for high catalytic activity, while their ligands dictate the immediate environment around the catalytic surface allowing for directed catalytic selectivity. Our research group has recently reported the effects of surface ligand density on the catalytic activity and selectivity of Pd nanoparticles (PdNPs) in chloroform. Overall, enhanced catalytic activity for the hydrogenation and/or isomerization of alkenes has been observed for PdNPs with a lower surface ligand density. This poster presents the investigation of catalytic activity and selectivity of PdNPs with different surface ligand density in different surrounding environments that change either the conformational structure of ligands or ligand-substrate interactions. First, colloidal Pd nanoparticles are synthesized using the reversed thiosulfate addition protocol, completing the nucleation-growth of PdNPs before the addition of alkyl thiosulfate ligand; this step is completed using tetraoctylammonium bromide (TOAB), in a way to control the size of PdNPs. Second, the catalytic activity and selectivity of PdNPs with different ligand density are investigated in various solvents. This study confirms the solvent-induced conformational change of surface ligands has a profound influence on the catalytic activity and selectivity of PdNPs. Third, the lipid-nanoparticle assemblies (LNAs) of 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC) lipids and PdNPs with different surface ligand density are prepared using a thin film hydration method. This process produces LNAs with a hydrophobic bilayer region where the hydrophobic PdNP catalysts reside. Fourth, the influence of liposome bilayer embedding on catalytic activity and colloidal stability of these PdNPs is studied. The presence of hydrophobic bilayer allows the facile diffusion of substrates and hydrogen gas molecules near the catalytic sites for the enhanced hydrogenation of alkenes in aqueous environments especially for PdNPs with a lower surface ligand density. The catalysis results of alkene hydrogenation are obtained using ^{1}H NMR and gas chromatography analyses.

This research is supported by a grant from the National Science Foundation (CHE-1954659)

55. The Role of the Transcription Factor *HB34* (AT3G28920) in Leaf Senescence

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

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

Leaf senescence (LS) is the breakdown of proteins and chlorophyll in older leaves that is seen as a yellow discoloration in many plants including *Arabidopsis thaliana*. The gene regulatory network (GRN) is a predicted system of how bolting-associated genes (BAGs) interact and regulate each other. BAGs are expressed when plants transition from their vegetative to their reproductive phase. The transcription factor (TF) *AtHB34* is in the middle of many critical transcription factor targets in the GRN. The network shows that this TF can bind to specific BAG targets to either upregulate or downregulate their expression. It is hypothesized that a mutated *AtHB34* will cause an opposite trend in the GRN where the up-regulated targets will not be up-regulated and the down-regulated targets will not be down-regulated. Many BAGs have been shown to have a positive correlation with LS. It is also hypothesized that *hb34* mutants will delay LS. The two types of LS that will be analyzed are bolting-associated LS and dark-induced LS. Bolting-associated LS looks at the expression of the *NIT2* gene and also the chlorophyll levels by comparing the bolting times of T0 (day of bolting), T4 (four days after bolting), and T12 (twelve days after bolting). Dark-induced LS, on the other hand, only measures chlorophyll levels in a detached leaf that goes through severe carbon starvation. Furthermore, primers will be designed to test the BAG targets to support the GRN. If the TF targets are regulated as shown in the GRN, then *AtHB34* would be a bolting-associated gene that affects LS.

56. Hamiltonian Neural Network Exploration for Electron Particle Tracking

Mikaela Meitz

Currently, in the field of accelerator physics, there is an interest in using machine learning methods for aiding in the design and optimization of charged particle accelerators. The Advance Light Sources (ALS) at the Lawrence Berkeley National Laboratory is a periodic circular accelerator called a synchrotron that emits ultraviolet and soft x-ray beams by accelerating electron bunches nearly as fast as the speed of light. There can also be linear particle accelerators. During the design or upgrade process for these machines, electron particle tracking is needed to ensure the particle dynamics are sufficient for the intended scientific use, but can be computationally expensive. These accelerators are prone to beam instability resulting in particle loss and consequently creating less x-ray brightness. The stability of an electron over thousands of revolutions is important to the performance of the accelerator. If the dynamic aperture, the stability region of phase space in the synchrotron, is too small, then adjustments are made and the process is repeated until a desired result is achieved. Optimizing the dynamic aperture can require doing this tracking several times while iterating the accelerator design. Machine learning methods may alleviate some of the need for these expensive computations by making particle integration faster and easier to parallelize. This research explores electron particle tracking with the use of Hamiltonian Neural Networks. Machine learning based Hamiltonian Neural Networks (HNN) constrains the model learning to obey Hamiltonian mechanics so that the neural network can learn conservation laws from data. We compare the performance of HNN to other machine learning based models.

57. Continued Fraction Solution of the Relativistic Second Order Spin-1/2 Equations

Derek O. Wingard, Zoltan Papp

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

It has been demonstrated that with the correct mapping, the relativistic quantum mechanical Klein-Gordon equation with electromagnetic coupling and an additional short range potential can be solved using conventional non-relativistic methods. This method is extended to the second order relativistic Dirac equation for spin-1/2 particles. Using a similar mapping, the Dirac equation has an infinite tri-diagonal representation in the adjusted Coulomb-Sturmian basis. This allows us to determine the exact Green's function in terms of continued fractions. Then, the eigenvalues are the poles of the Green's functions and the eigenvectors are the corresponding residue.

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

Adren Blanco[a], Darren Leung[a], Junho Lee[a], Yada Treesukosol[b], and Houng-Wei Tsai[a],

Department of Biological Sciences[a] and Department of Psychology[b], California State University Long Beach, Long Beach CA 90840

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.

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

Maria Maalouf[1], Ryan Blair, Ph.D.[2], Alex Klotz, Ph.D.[3]

[1]Physics and Astronomy Department, Mathematics and Statistics Department, California State University, Long Beach, Long Beach, CA 90840

[2]Math Department, University of California, Santa Barbara, Santa Barbara, CA 93106

[3]Physics Department, McGill University, Montréal, QC H3A 0G4, Canada

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). 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.

This work is supported by the National Science Foundation (NSF) under Grant No. 2018653, Grant No. 2117629 (MRI), and 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 (PREM).

60. Expression of Human Chitotriosidase against *Candida albicans*

Brian de la Torre, Glory Nguyen, Howard Terrence, Pablo Rivas, Mason X. Zhang, PhD.

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

Candida albicans is a human commensal fungus that can cause superficial infections, but it has also emerged as the fourth leading cause of nosocomial bloodstream infections. Hematogenously disseminated candidiasis is life-threatening and associated with an extremely high mortality rate despite treatment with currently available antifungal therapies. Therefore, there is an urgent need to develop novel therapeutics to combat this pathogen. Previously, we have developed human recombinant antibodies against *C. albicans* that have been shown to be protective in a mouse model of hematogenously disseminated candidiasis. These antibodies promote opsonophagocytosis, but they do not have a direct fungicidal effect. Our current goal is to identify anti-fungal proteins that can be fused with these anti-*Candida* antibodies as a hybrid protein where the antibody directs the fungicidal protein to *C. albicans* cells for direct killing. This project aimed to construct an expression vector and express recombinant chitotriosidase in bacteria. Chitotriosidase is a human chitinase that breaks down chitin in the fungal cell wall and is therefore expected to be fungicidal. The pET expression system was utilized for recombinant protein expression in *Escherichia coli*. A 6X-HisTagged human chitotriosidase gene (CHIT1) was cloned into the pET28b expression vector. Sanger sequencing and restriction digests were used for construct verification. SDS-PAGE, western blot, and ELISA were performed to confirm CHIT1 expression. DNA sequencing and restriction digests confirmed correct DNA sequence and proper orientation of the chitotriosidase gene in the pET28b expression vector. Recombinant protein was detected in cell lysates by SDS-PAGE. Western blots probed for human chitotriosidase and 6X-HisTag showed bands consistent with predicted protein size. Additionally, cell lysates tested by ELISA were positive for both human chitotriosidase and 6X-HisTag. Taken together, these data suggest the successful expression of recombinant human chitotriosidase in bacteria. This protein will be fused to anti-*Candida*

antibodies to create an antibody-antifungal hybrid protein that may be used as a potential therapeutic for *Candida* infections.

61. DIY - A Low-Cost 3D Printed Molecular Biology-Grade Electrophoresis Device

Joyce Choi[1*], Victor Phan[1*], Kristina Soriano[3*], Luis Gutierrez[1], Roger Lo[3], Ph.D. and Yuan Yu Lee, Ph.D.[1,2]

[1]Department of Biological Sciences, [2]Center for Education in Proteomics Analysis (CEPA),

[3]Department of Chemical Engineering, California State University, Long Beach, Long Beach, CA 90840

Gel electrophoresis is a laboratory technique that is used for the separation and analysis of biological samples based on sizes and charges. However, commercial manufactured gel electrophoresis systems are expensive and require trained personnel to operate, and some are only available for purchase through higher education affiliated institutions. In recent years, 3D printing has become a cost-effective alternative to manufacture equipment and components across various fields of study. Our goal is to develop laboratory equipment possesses (1) low production cost, (2) same or better performance and/or resolution manner, and (3) easy to operate and maintain. First, we upgraded and calibrated our PRUSA 3D printer to print with multi-material filaments and yield high resolution prints for molecular biology analysis purposes. Then, we performed a simultaneous gel electrophoresis experiment with coloring dyes using both our 3D printed gel electrophoresis device and the commercialized ThermoFisher EC Classic gel electrophoresis device to test the functionality of our own designed 3D printed electrophoresis gel device.

First, the coloring dye samples successfully ran through our 3D printed gel electrophoresis device, and we also observed that the dye samples traveled further through the gel in our 3D printed gel box compared to the ThermoFisher EC Classic device. The accuracy of results between both devices were also similar. The most exciting achievement and advantage from our device is the cost; we only spent $15 -$40 USD for production materials, compared to the commercialized device from ThermoFisher that retails for $936.50 - $1142.00 USD. In conclusion, engineering effective 3D printed laboratory equipment could allow for the integration of more hands-on laboratory experiments in non-traditional laboratory settings. Manufacturing a cost-effective alternative instead of purchasing expensive market products could be the first step towards providing accessible educational tools.

This work supported by CSUPERB Curriculum Development Grant Program

* equally contribution to this work

62. Molecular Dynamics of Previtamin D_3 in Phospholipid Membranes

Matthew Plazola, Adam S. Smith, and Enrico Tapavicza

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

The photochemical reactivity of vitamin D derivatives depends on excitation wavelength and chemical environment. This dependency is mainly governed by the conformational flexibility of previtamin D, the central compound in the vitamin D photoequilibrium. To assess the influence of the phospholipid bilayer on natural vitamin D photosynthesis, we studied conformational equilibrium of previtamin D in dipalmitoylphosphatidylcholine (DPPC) phospholipid bilayers using classical molecular dynamics simulations. An accurate description of the torsional potential energy of previtamin D requires a balanced description of steric repulsion and π-orbital conjugation of its central hexatriene unit. To achieve this, we applied a correction map (CMAP) based on density functional theory to the CHARMM generalized force field. To sample the thermodynamic limit of the distribution of conformers, we applied the enhanced sampling methods replica exchange molecular dynamics and the adaptive biasing force sampling techique. Our simulations show that the DPPC bilayer leads to a stabilization of the g+Zg+ conformer, which explains enhancement of thermal sigmatropic [1,7]-hydrogen transfer, forming vitamin D. The latter finding is also consistent with a recent interpretation of spectroscopic results, which showed that the g+Zg+ conformer is

preferred compared to the g-Zg- conformer. Our study is consistent with assumption that the g-Zg- conformer is rather an intermediate species that occurs only shortly after photo-induced ring-opening. In addition, we show that photoinduced ring-opening of 7-dehydrocholesterol leads to a reduction of the order parameter of the membrane. The order parameter of the DPPC/previtamin D system, however, is still larger than for a pure DPPC membrane.

63. A Novel Bisphenol A Binding Site on Estrogen Receptor Beta as a Potential Antagonistic Activity

Megan Dinh[1], and YuanYu Lee Ph.D.[1,2]

[1]Department of Biological Sciences, California State University, Long Beach, Long Beach, CA 90840; [2]Center for Education in Proteomics Analysis (CEPA), California State University, Long Beach, Long Beach, CA, 90840

Estrogen is a group of steroid hormones to promote the development and maintenance of female characteristics of the body through estrogen receptors alpha (ERα)- and beta (ERβ) -mediated gene regulations. Bisphenol A (BPA) is a known endocrine disrupting compound (EDC) because its conformational similarities to estradiol, the most common form of the estrogen steroid hormone for female reproductive development. Previous reports showed that BPA can bind to the ligand binding domain of both ERα or ERβ with either agonistic or antagonistic activity. There are several binding sites found between BPA and ERα but lacking detail information of binding sites between BPA and ERβ. Interestingly, the ERβ protein sequence similarity is high (>93%) between humans, mice and rats, but several amino acids replacements at the ligand binding domain. This research aims to investigate any species-specific novel binding sites between BPA and ERβ, specifically within the ligand binding domain.

To do this, protein-ligand docking simulations were utilized to identify potential binding sites between BPA to ligand binding domains of human or mouse or rat ERβs. First of all, we observed that the protein-ligand docking scores and affinities were consistent between two different docking software - CB Dock and 1-Click docking. However, we observed BPA-human ERβ complex with higher binding affinity compared to mouse and rat ERβ complexes which is consistent with previously published findings. There are ~20 potential BPA binding sites found from all three species ERβs. Surprisingly, a novel binding site Leucine 298 found in the top scoring docking conformations in human, mouse, and rat ERβs-BPA complexes in the nonspecies-specific manner. In this study, we found a novel BPA binding sites on ligand binding domain of ERβ protein across different species for our study are humans, mice, and rats. Our next step is to explore more novel BPA binding sites on different domains of ERβ proteins in species-specific manner.

This work supported by MGSS grant.

64. Synthesis and Biochemical Evaluation of Potential Inhibiting Features of Fmoc-Amino Amide Analogues on Butyrylcholinesterase for the Treatment of Alzheimer's Disease

Serli Khanbabaei, Jason Schwans

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

Alzheimer's Disease (AD) continues to affect millions of people worldwide. While there's no cure for AD, multiple approaches are being developed. One of these approaches involves cholinesterases, enzymes involved in neuronal signaling, which have been a target due to the changes in activity observed in individual with AD. The enzymes hydrolyze the substrate, acetylcholine, a cationic neurotransmitter. Butyrylcholinestrase (BChE) is one of the two major classes of cholinesterases that are found in the parasympathetic nervous system. Previous studies have reported that BChE activity has been upregulated in patients with Alzheimer's disease. Amino acid analogs bearing a 9-fluorenylmethyloxycarbonyl (Fmoc) group serve as selective inhibitors of BChE. Although Fmoc amino acids inhibit BChE, their negatively charged carboxylate group could be unfavorable in binding the enzyme. To test this hypothesis, a series of neutral Fmoc-bearing amino amides are being synthesized and biochemically evaluated. The amino amides are

synthesized one step from the corresponding amino acid, purified, and characterized by NMR. The IC50 and KI values obtained from the enzyme inhibition assays were used to compare the inhibitory efficiency of the amidated Fmoc-amino acid (Leucine in this case) analog to anionic Fmoc-Leu-O^-. Initial results suggest that Fmoc-Leucine-NH_2 is a more potent inhibitor compared to Fmoc-Leucine-O^-, supporting the model that the negative charge is unfavorable in binding the enzyme. Building on these results, a series of amino amides are currently being further investigated for their selectivity, reversibility, and type of inhibition. Fmoc-amino acid scaffolds study parameters important for cholinergic inhibition, serving as potential treatment of AD.

65. Visualization of the Nuclear Localization of the Unfolded Protein Response Sensor ATF6 Using Fluorescence Microscopy

Kimberly Izarraras, Samantha Perez, Aida Husain, Miguel Palma, Deepali Bhandari Ph.D.

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

The endoplasmic reticulum (ER) is a membrane bound organelle in eukaryotic cells with many functions including folding and processing of secretory proteins. Conditions that disrupt the normal function of ER, such as increased insulin production by pancreatic beta cells in type 2 diabetes, generate ER stress. To alleviate this stress, cells trigger a signaling program called the unfolded protein response (UPR). One of the main sensor proteins involved in the UPR is the Activating Transcription Factor 6 (ATF6). Under normal conditions, ATF6 is present in the ER membrane. However, upon UPR induction, ATF6 is transported from ER to the Golgi where its N-terminal fragment (ATF6-N) is proteolytically freed from the membrane. ATF6-N is a transcription factor that upregulates the expression of target genes needed to restore ER function. The goal of this project is to develop a method to visualize ATF6 transport in the cells using fluorescence microscopy. We transfected cells with green fluorescent protein (GFP)-tagged ATF6 to aid in the detection of the subcellular localization of GFP-ATF6 under normal and ER stress conditions. Our method was successful in showing the movement of GFP-ATF6 from the ER to the nucleus within 3h of stress. The optimized protocol developed here will be helpful to study the ATF6 pathway.

This research was supported in part by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; UL1GM118979; TL4GM118980; RL5GM118978. This Research was also supported in part by the U.S. Department of Education under Award Number: P031C160085. Dr. Bhandari's lab is supported by NIH grant # SC3GM139707 and CSUPERB Research Development Grant.

66. Determining the Inhibition Effectiveness of Fmoc-Lys$(CH_3)_3$-O^- in Comparison to Fmoc-Lys-O^- Against Butyrylcholinesterase to Use in Treatments for Alzheimer's Disease

Katrina Jensen, Jason Schwans

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

Alzheimer's disease is one of the leading neurodivergent diseases ailing the elderly with an estimated 6.5 million cases in patients sixty-five or older in the United States alone. To find treatments for this disease, many different inhibitors of butyrylcholinesterase (BChE) were tested. Due to difficulties synthesizing Fmoc-Lys$(CH_3)_3$-O^-, instead of creating the compound in our lab, it was acquired through purchase from a different lab. This compound tested the relative activity difference between Fmoc-Lys-O^- and Fmoc-Lys$(CH_3)_3$-O^-. The experiment used to test the two's relative activity includes comparing the activity of the BChE enzyme in a reaction while using Ellman's reagent. The activity is found using the absorbance versus the time in a spectrophotometer. Prior to enzyme assays, the concentrations of Fmoc-Lys$(CH_3)_3$-O^- and Fmoc-Lys-O^- solutions used in the experiments were determined by UV absorbance. These concentrations were then used to determine the enzyme activity of BChE in the presence of Fmoc-Lys$(CH_3)_3$-O^- versus Fmoc-Lys-O^- at equal concentrations.

67. Detecting Cleavage of the Unfolded Protein Response Sensor ATF6 Using Western Blotting

Samantha Perez, Kimberly Izarraras, Aida Husain, Miguel Palma, Deepali Bhandari Ph.D.

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

Cellular stress response consists of signaling pathways that are activated upon exposure to various stressors including pathogens, extreme temperatures, toxins, oxygen deprivation, and protein misfolding. Stress brought on by protein misfolding in the organelle endoplasmic reticulum (ER) triggers a signaling program called the unfolded protein response (UPR). The activation of the UPR initially aims to restore homeostasis within the ER, but if ER stress is prolonged, the UPR can commit cells to programmed death. One of the main sensor proteins involved in UPR is the activated transcription factor 6 (ATF6). While it is an ER membrane protein, under stress conditions, it translocates to the golgi where its proteolytic cleavage frees the N-terminal fragment (ATF6-N) from the membrane. ATF6-N is a transcription factor that upregulates the expression of target genes needed for stress alleviation. Previous experiments in our lab to study the ATF6 pathway activation encountered challenges due to the lack of a specific ATF6 antibody to detect the N-terminal cleavage. Therefore, my objective was to optimize a method to detect ATF6-N through western blotting. A recombinant 3XFLAG-ATF6 construct was transfected into HeLa cells and the presence of ATF6-N was verified using the anti-FLAG antibody on western blotting. This method allowed the detection of 3XFLAG-ATF6-N and can now be used in the ongoing projects in the lab that focus on the ATF6 pathway.

This research was supported in part by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; UL1GM118979; TL4GM118980; RL5GM118978. This Research was also supported in part by the U.S. Department of Education under Award Number: P031C160085. Dr. Bhandari's lab is supported by NIH grant # SC3GM139707 and CSUPERB Research Development Grant. An additional acknowledgement to the support provided by HSI-STEM.

68. Molecular Mechanisms of Enzymes: Enabling High Throughput Studies of Enzyme Temperature Adaptation

Bryan Skorka, California State University Long Beach

2022 University of California San Francisco Summer Research Training Program

Margaux Pinney, Ph.D.

Department of Biochemistry and Biophysics, University of California San Francisco

Enzymes are the primary functional molecules in cells, providing enormous rate enhancements, specificity, and regulation to the diverse chemical reactions that are necessary for life and demonstrate tremendous potential in industry and medicine. Enzymes, like all biological macromolecules, are the products of evolution: adapting to operate within the complex environment of the organism/cell in specific environments while still keeping the unique properties that enhance chemical reactions. In particular, enzyme structures and functions are sensitive to temperature and adapt and evolve in accordance with the temperature of their environment. At increased temperatures, enzymes evolve greater stability to maintain a folded structure, whereas at decreased temperatures, nearly all chemical reactions necessary for life slow; thus placing evolutionary pressure on cold-adapted enzymes to be more active. Here we investigate the mechanisms of enzyme function and stability through the lens of enzyme temperature adaptation. We take advantage of the model enzyme system adenylate kinase (ADK), focusing on three ADK orthologs from organisms with vastly different optimal growth temperatures (T_{growth}): *Bacillus globisporus* (T_{growth} = 13℃), *Bacillus subtilis* (T_{growth}= 30℃), and *Geobacillus stearothermophilus* (T_{growth} = 55 ℃). Here we investigate the activity and stability adaptation of ADK, with the ultimate goal of identifying the residues and molecular mechanisms that allow cold-adapted ADKs to be more active and warm-adapted ADKs to be more stable.

Special thanks to those who made this work possible including UCSF SRTP, UCSF Sandler Foundation, MARC USTAR, and my fellow lab members of the Pinney Lab.

69. Change of Population of Female Cheetahs in the Serengeti

Michelle Leon, Kathryn McCormick

Department of Mathematics and Statistics, California State University, Long Beach, Long Beach, CA 90840

Factors affecting life and death of ccheetahs in the Serengeti were studied across the span of 20 years in (Durant, 2004). The different factors impacting the species were enviromental, including but not limited to food, predators, sex, and age. We will be looking at how the female cheetah population changes throughout time, with an emphasis on survival rates. The female cheetahs are subcategorized by age: cub, subadult, and adult. We will use a discrete linear dynamical system to generate a formula that can model future population. Our model recovers the conclusion in (Durant ,2004) that the female cheetah population in the Serengeti is decreasing. When taken into consideration that female cheetahs have a higher survival rate than male cheetahs, it leads to the conclusion that the overal cheetah population in the Serengeti is declining. We also analyze the possible variation of the cheetah populations under different cub survival rates.

70. Change to spare: understanding the developmental timing of food-induced plasticity during larval development of the Pacific sand dollar

Isabel Villafuerte, Ariana Lee, and Douglas Pace, Ph.D.

Department of Biological Sciences, California State University, Long Beach, Long Beach, CA, 9084

Phenotypic plasticity is the ability of a single genome to produce many different phenotypes based on environmental interactions and is a critical adaptive response mechanism for animals experiencing climate change. Benthic marine invertebrates require larval recruitment to sustain their adult populations. Larvae of the Pacific sand dollar, Dendraster excentricus, undergo food-induced morphological plasticity where larvae developing in low food concentrations will make longer arms to increase their algal feeding ability. Larvae in high-food conditions will pursue a different morphological growth pattern and make shorter arms which allows energy to be invested into faster development and more rapidly attaining metamorphic competency. This plasticity has only been tested during early development when larvae first attain feeding ability. It is unknown if larvae can switch their growth patterns later in development after feeding has been attained. Such information is essential to understanding the relevance of these responses since food levels fluctuate widely and frequently in coastal marine environments. We tested if low-fed larvae could switch to a high-fed phenotypic growth pattern when switched to high-food availability at successively later times in their development. Our results clearly demonstrated that low-fed larvae maintained the ability to rapidly switch to a high-fed phenotype when given a high-food diet. This rapid response mechanism was maintained throughout all of their larval development. Upon switching low-fed larvae to a high-food diet, we observed a reduction in post-oral arm growth and an increase in midline body length, a response similar to constantly high-fed larvae. The rapid decrease in arm length when switched to a high-food diet suggests that the maintenance of long arms imposes significant energetic demands on larvae. In conjunction with rapid changes in morphology, we also observed that low-fed larvae could quickly achieve metamorphic competency when switched to high food conditions. Overall, our data shows that larvae in natural seawater conditions are likely to express such phenotypic switching capacity where changes in food availability occur frequently. They also highlight the energetic consequences of these morphological changes. Such data is critical for understanding how developing organisms will respond to the rapid environmental changes brought on by climate change and the energetic consequences of these responses.

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

71. Characterizing the Relationship Between HIV-1 Nef, Moesin, and HIV-1 Infection

Angus L. Fuori[1], Peter Ramirez, Ph.D.[2]

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

HIV-1 Nef is a major pathogenicity factor *in vivo*. Clinically, most HIV-positive individuals infected with *nef* defective HIV-1 viruses maintain high CD4+ T-cell counts. Mechanistically, Nef associates with membranes to alter the trafficking patterns of membrane-bound proteins, providing an environment conducive for viral replication and persistence. Cellular targets of Nef include the T cell receptor CD4 and the antigen presenting molecule MHC-I. In both cases, Nef acts as an adaptor molecule, linking both proteins to premature lysosomal degradation. Interestingly, virus particles (virions) expressing Nef are more infectious than virions lacking Nef. The exact reason for this phenotype remains unclear. Recently, we identified several Nef-specific cellular proteins using virion-associated quantitative proteomics. Silencing of these proteins decreased virion infectivity, suggesting these proteins act as "cofactors" required by Nef to enhance infectivity. One of these proteins was Moesin (MSN), a member of the Ezrin Radixin Moesin protein family (ERM). Moesin's function has been shown to have a regulated relationship between the plasma membrane and the actin cytoskeleton, participating in the organization of the actin cytoskeleton as well as membrane protein delivery. Based on our preliminary data, we hypothesize HIV-1 Nef binds to MSN within living cells to enhance viral infectivity and/or viral replication. To address this, we are conducting bi-molecular fluorescence complementation (BiFC). Specifically, we created recombinant plasmids where Nef was fused to the N-terminus of yellow fluorescent protein (YFP) and Moesin to the C-terminus of YFP. If the two proteins interact within a cell, the two YFP halves will come together, generating fluorescence. To visualize and quantify fluorescence, we will analyze cells expressing the two proteins and their conjugated tags via flow cytometry. If Nef and MSN interact, we will conduct both mutagenesis and immunofluorescence studies to determine what protein domains are necessary for interactions and where in the cell this interaction is occurring. Conducting these experiments is imperative for furthering our understanding of the mechanisms of HIV-1 infection, as well as the development of novel therapeutic agents to combat the ongoing HIV/AIDS epidemic.

72. Expressing Esterase/Lipase/Thioesterase 4 (ELT4) associated with the Jasmonic Acid biosynthesis pathway in *Arabidopsis thaliana* plastoglobule

Earl Givens[a], Febri Susanto[bc], Peter Lundquist[b]

[a]Department of Biological Sciences at California State University, Long Beach, Long Beach, CA, 90840, and [b]Department of Biochemistry & Molecular Biology, [c]Molecular Plant Science Program; [b]Plant Resilience Institute at Michigan State University, East Lansing, MI, 48824 USA

A large portion of stress responses are mediated through the plant hormone jasmonic acid. Jasmonic acid production starts at the plastids, before travelling to the peroxisomes, and reaches the end of the pathway within the cytoplasmic domain of the cell. In a chloroplast plastoglobule proteomic analysis from a regulatory kinase deficient knockout line (*abc1-k1k3*) and *jaz* decuple mutant (defective in 10 Jasmonate ZIM domain genes), multiple proteins were identified as differentially accumulated in stress trials that were tied to the jasmonic acid biosynthetic pathway. One upregulated protein was Esterase/Lipase/Thioesterase 4 (ELT4), an uncharacterized protein localized to the plastoglobule. Being the sole ELT family gene localized to the plastoglobule, it is hypothesized that the protein's function is to convert glycerol lipids within the thylakoid membrane into entry molecules for the jasmonic acid biosynthesis pathway under specific stress condition. Through creating a working expression system of this uncharacterized lipase, characterization becomes possible. Being able to express for characterization opens the door to better understanding of the jasmonic acid biosynthesis pathway. Understanding how the plastoglobuli ties into stress responses and the jasmonic acid biosynthesis pathway can lead to better understanding of stress responses overall within plants in future work.

This project is supported by the National Science Foundation (NSF) grant DBI-2149531

Key words: Plastoglobule, ELT4, Jasmonic acid, *Arabidopsis thaliana*, Stress tolerance

73. Characterizing Plasmacytoma Variant Translocation 1 (PVT1) Knockdown as a Therapeutic Target for Human Immunodeficiency Virus (HIV-1) Latency Reversal

Christina Pantoja[1], Peter W. Ramirez, Ph.D.[1]

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

The existence of dormant (i.e. latent) reservoirs within CD4+ T cells remains a significant barrier towards a Human Immunodeficiency Virus type 1 (HIV-1) cure. HIV-1 latency reversal remains a popular method to decrease viral load. The "shock and kill" strategy involves latency reversing agents (LRAs) that can reactivate latent reservoirs but suffers from lack of specificity. Long non-coding RNAs (lncRNAs) represent an alternative and attractive approach for targeting the HIV-1 latent reservoir due to their tissue and cell specificity. LncRNAs are involved in several biological processes including gene transcription and viral pathogenesis. Recently, lncRNAs have been identified to play critical roles in HIV-1 pathogenesis. Specifically, the lncRNA PVT1 was upregulated in two distinct T cell models of HIV-1 latency. We therefore hypothesize that PVT1 regulates HIV-1 latency. To test this hypothesis, we aim to reduce expression of PVT1 using short hairpin RNAs (shRNAs) in a leukemic T cell line (Jurkat) that harbor a latent replication-incompetent HIV-1 genome expressing green fluorescent protein (GFP). To do this, we designed and cloned PVT1 specific shRNAs into a lentiviral vector expressing the puromycin antibiotic resistance gene. We are currently producing PVT1 shRNA lentiviruses, which will be used to infect Jurkat cells. Selection with puromycin will enrich for cells that have been infected. We will validate PVT1 knockdown via quantitative reverse transcription PCR (RT-qPCR). Next, we will analyze latency reversal via measuring GFP expression with flow cytometry. We expect to observe an increase in HIV-1 latency reversal in cells knocked down for PVT1. We will also compare levels of cytokine production, T cell-activation and apoptosis between wildtype and PVT1 knockdown cells. This study is designed as a "proof-of-concept" to characterize PVT1 as a potential target for therapeutic development for HIV-1 latency reversal.

I acknowledge the Bridges to the Doctorate (BTD) program which is supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number T32GM138075.

74. No abstract

75. Characterizing the Interaction Between HIV-1 Nef and the Host Factor Annexin A2.

Francisco M. Acosta[1], Peter W. Ramirez, Ph.D.[1]

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

Human Immunodeficiency Virus type 1 (HIV-1) is the causative agent of acquired immunodeficiency syndrome (AIDS). HIV-1 contains essential genes necessary for host cell entry, genome replication, packaging, assembly, and release of infectious viral particles. HIV-1 also encodes "accessory" genes that modulate host immune responses: *nef*, *vif*, *vpr*, and *vpu*. In particular, HIV-1 Nef is a major pathogenicity factor leading to the progression of AIDS. Nef associates with cellular membranes via a post-translational myristoylation motif, serving as an adaptor protein that hijacks endocytic machinery to disrupt the normal trafficking of membrane-bound host proteins. This leads to an environment conducive for viral replication and persistence. The main targets of Nef include the host proteins CD4, MHC-I, SERINC3 and SERINC5. Interestingly, expression of Nef also leads to a more infectious virus particle (virion). Using quantitative proteomics, we identified several Nef-cofactors that, when inhibited by targeted RNA suppression, significantly decreased HIV-1 virion infectivity. One of these proteins, Annexin A2 (ANXA2), is involved in numerous biological functions including: endocytosis, exocytosis, and membrane dynamics. ANXA2 also plays a significant role during the replication cycle of many RNA viruses. However, whether HIV-1 Nef physically interacts with ANXA2 remains unclear. Based on our preliminary data, we hypothesize HIV-1 Nef binds to ANXA2 within living cells to enhance viral infectivity and/or replication. To test this, we utilized bimolecular fluorescence complementation (BiFC). In this assay, proteins of interest are fused to either the N or C terminus of Venus, a yellow fluorescent protein. Binding of the two proteins generates fluorescence,

validating protein-protein interactions. We fused the N-terminus of Venus (VN) to either wild-type Nef or, as a negative control, a myristoylation mutant incapable of membrane association (Nef-G2A). We also fused the C-terminus of Venus to either ANXA2 or, as a positive control, CD4. These plasmids were transfected into 293T cells either alone or in pairs. We then measured fluorescence 48 hours post-transfection via flow cytometry. Interestingly, we detected strong signals between Nef and CD4 and Nef and ANXA2, but not between Nef-G2A and CD4 or Nef-G2A and ANXA2. This suggests Nef requires membrane association to bind both CD4 and ANXA2. We are now conducting experiments utilizing other Nef mutants to identify protein domains essential for interaction and evaluating whether this interaction is conserved among diverse Nef proteins. We also aim to use immunofluorescence to determine where in the cell this interaction is occurring. These studies will enhance our understanding of HIV-1 biology, potentially leading to the development of novel antiviral therapies.