2023

UC RIVERSIDE

RISE & MARC

SUMMER SYMPOSIUM

AUGUST 30, 2023

MARC U*

UC RIVERSIDE RISE
SUMMER RESEARCH IN SCIENCE & ENGINEERING

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CONGRATULATIONS AND WELCOME

The Research in Science & Engineering (RISE) is a 10-week summer research program designed for rising sophomores, juniors, incoming transfers, and seniors. Participants work under the supervision of a faculty mentor on a cutting-edge research project. The program features faculty mentoring, professional development opportunities, immersive experience in the UCR research community, and an undergraduate symposium.

Students deepen their own scientific knowledge while creating new knowledge related to their individual research project. The primary objectives of RISE are:

1. **Shaping undergraduate students' research and professional identity**
2. **Enhancing scientific communication and literacy**
3. **Attaining foundational research skills and knowledge**
4. **Developing a sense of belonging within UC Riverside**

The College of Natural and Agricultural Sciences (CNAS) mission is "To transform lives through discovery, communication, translation, application, and preservation of knowledge." The RISE program is an important part of our mission as it engages our students in the process of scientific discovery and development.

Through support from generous donors and institutional financial commitments to undergraduate research, CNAS celebrates thirteen years of RISE. We would like to especially thank:

The Campbell Family
The Munshi Family
The Whitehead Family
The Leonard Family
The Gray Family

This year's summer undergraduate research symposium is co-hosted with MARC. The goal of the Maximizing Access to Research Careers (MARC) research training program is to develop a diverse pool of undergraduates who complete their baccalaureate degree, and transition into and complete biomedical, research-focused higher degree programs (e.g., Ph.D. or M.D./Ph.D.). This research opportunity provides support to eligible, domestic institutions to develop and implement effective, evidence-informed approaches to biomedical training and mentoring that will keep pace with the rapid evolution of the research enterprise.

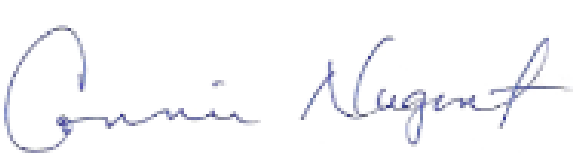
CONGRATULATIONS AND WELCOME

CNAS RISE and UCR's MARC Program are working alongside other partners dedicated to increasing access and diversifying the undergraduate research and graduate school pipeline.

This year's symposium partners includes:

CNAS Learning Communities Scholars
CNAS Summer Bridge To Research (SBTR)
California Alliance for Minority Participation (CAMP)
Dynamic Genome Summer Scholars (DGSS)
Digital Agricultural Fellowship (DAF)
Faculty Sponsored Program - Dr. Dawn Nagel (NSF Grant)
Faculty Sponsored Program- Dr. John Franchak (NSF Grant)
Faculty Sponsored Program - Dr. Viji Santhakumar (AES Bridge Program)
Faculty Sponsored Program - Dr. Jessica Purcell (Six Legs Program)
Maximizing Access to Research Careers (MARC)
Riverside Community College Bridges 2 Baccalaureate (RCC-B2B) Program
USDA NIFA Antimicrobial Resistance in Agriculture (AMR in AGRI)

We congratulate all of the 111 students for their dedication, commitment, and hard work over the past 10 weeks. We thank all faculty-mentors, research scientists, graduate students, undergraduates and other staff personnel for helping us make this a successful program. We hope that this has been a rewarding experience for you as you continue on your academic journey and we look forward to watching you succeed in your future professional aspirations. It has been our pleasure to work with each of you and we want to say congratulations on your special day!



Dean of Student Academic Affairs
College of Natural & Agricultural Sciences (CNAS)

Professor of Biochemistry
Program Director of MARC Program

Assistant Director of Student Success Programs
College of Natural & Agricultural Sciences (CNAS)

Administrative Director of MARC Program

PARTICIPATING PROGRAMS

CNAS Scholars

The mission of CNAS Scholars is to provide tools and support for our students to graduate from UC Riverside with competitive grades, personal development, and enriched educational experiences. We do this by providing our first-year participants with supplemental instruction, peer support, faculty exposure, research opportunities, a year-long cohort experience, and guaranteed seats within their math and science courses. Following their completion of our program, we offer additional success offerings, such as summer research, job opportunities and sophomore support programs. Our ultimate goal is for our students to become successful and compassionate leaders who will provide our larger communities with life-changing knowledge and service.

Summer Bridge to Research

The CNAS Summer Bridge to Research Program is a paid ten-week, full-time research experience for first-time incoming community college transfer students admitted for the Fall quarter to one of the 17 academic majors housed in the College of Natural and Agricultural Sciences [CNAS]. The program is aimed at supporting underrepresented student populations in the Science, Technology, Engineering, and Mathematics [STEM] fields. The program aims to increase the number of students transferring into the STEM fields and improve their success and retention in the university.

PARTICIPATING PROGRAMS

Faculty Sponsored Research

Our goal is to provide mentored research experiences to transfer students from underrepresented groups to enhance recruitment and retention in STEM. Students have the opportunity to continue their research projects through graduation. This program is funded by an NSF-CAREER grant. - Dr. Dawn Nagel

The Perception, Action, & Development Lab is directed by Dr. John Franchak in the UC Riverside Department of Psychology. Dr. Franchak advises students in the Developmental and Cognition and Cognitive Neuroscience areas of the Psychology Department. The lab's research is funded by grants from the National Science Foundation and James S. McDonnell Foundation. - Dr. John Franchak

Our goal is to provide mentored summer research experience in the area of epilepsy to students from underrepresented groups to enhance recruitment and retention in the epilepsy field. Students have the opportunity to continue their research projects through graduation. This program is funded by an American Epilepsy Society BRIDGE (Broadening Representation and Inclusion by Growing Diversity and Equity) grant. -Dr. Viji Santhakumar

CAMP Scholars

The California Alliance for Minority Participation (CAMP) program in funded by NSF and was established at UCR in 1994, and works to encourage underrepresented students in the STEM fields to successfully complete undergraduate science degrees and further pursue their studies at the graduate and professional level. -Dr. Brandon Brown

PARTICIPATING PROGRAMS

USDA-NIFA Antimicrobial

Using a series of greenhouse and outdoor (larger-scale) experiments, we are quantifying the dissemination of antibiotics and antimicrobial resistance determinants (ARDs), e.g., antibiotic resistance genes (ARGs), antibiotic resistant bacteria (ARB), and mobile genetic elements (MGEs), within the wastewater/manure–soil–plant–animal (earthworm) continuum. Understanding these pathways is of critical importance in assessing the potential for antimicrobial resistance to spread through food chains. Once these pathways are more clearly understood, the use of biochar application to soil as a strategy for mitigating the dissemination of antibiotic compounds and antibiotic resistance within the agricultural system will be assessed. The research results will be considered within an assessment framework for better understanding the potential risks of antimicrobial resistance within food chains. - Dr. Daniel Ashworth

Our goal is to provide undergraduate student research opportunities on this USDA-NIFA funded project on the dissemination of antimicrobial resistance in agricultural food chain during the reuse of treated municipal wastewater. - Dr. Yujie Men

Dynamic Genome Summer Scholars

The Dynamic Genome Summer Scholar (DGSS) program for first year UCR students seeks to immerse students in plant biology research and introduce them to careers in biotechnology beyond the bench. The students learn to conduct research and develop molecular biology skills. In addition, the students complete a team project where they develop a business plan to market a hypothetical solution for a threat to a California crop. DGSS is funded by the Neil and Rochelle Campbell Presidential Chair, Campbell & Wessler Endowment, and the NSF. - Dr. Jim Burnette

PARTICIPATING PROGRAMS

MARC

The goal of the Maximizing Access to Research Careers (MARC) research training program is to develop a diverse pool of undergraduates who complete their baccalaureate degree, and transition into and complete biomedical, research-focused higher degree programs (e.g., Ph.D. or M.D./Ph.D.). This research opportunity provides support to eligible, domestic institutions to develop and implement effective, evidence-informed approaches to biomedical training and mentoring that will keep pace with the rapid evolution of the research enterprise. - Rebecca Brown

Digital Agricultural Fellowship

The Digital Agriculture Fellowship (DAF) aims to support the future workforce of digital agriculture. In collaboration with UC Riverside's Research in Science and Engineering program, undergraduate students at participating campuses can apply to join the 15-month long program. The DAF includes: paid and mentored student-led research, participation in student clubs, externship opportunities, and networking opportunities. A major purpose of DAF is to provide Fellows with career-building opportunities and to support awareness of digital agriculture as a career option. The program is supported by the USDA National Institute of Food and Agriculture, as part of the "Artificial Intelligence for Sustainable Agriculture" project. - Dr. Elia Scudiero, Dr. Noel Salunga, and Samantha Lemus

PARTICIPATING PROGRAMS

Six Legs

This program is a partnership between four institutions in Southern California's Inland Empire (UC Riverside, Moreno Valley College, Riverside City College, and Norco College). Our short-term goals are twofold:

1. We will provide research-based learning opportunities in combination with information about relevant careers to community college and university students.
2. For interested students in their junior and senior years at UC Riverside, we will offer intensive training and funded internship opportunities, in order to prepare participants for post-graduate opportunities. Participants will also contribute to educational events for K-12 and community college students.

Ultimately, we hope to enhance educational opportunities for participants and increase students' familiarity with alternative career paths. We aspire to provide a clear pathway, including opportunities for development of specialized skills, for students interested in careers in the agricultural sciences.
Funding Provided by USDA NIFA - Dr. Jessica Purcell

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Yongtao Cui
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Alberto Reyes
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Amanda Arrieta
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Andrea Pearson
Andrew Yee
Angel Pulido
Annette Mercado-Sanchez
Arsema Araya
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Sonika Khare
Sophia Zhou
Steve Zhang
Taewon Yoo
Tina Coley
Tina Fathibitaraf
Valerie Gonzalez
Victoria Batiz
Wesley Hur
Yousef Abdelkadous
Yuna Aguilar
Zoey Pilling

SCHEDULE

SYMPOSIUM SCHEDULE

MORNING

8:00 AM - 8:30 AM - Registration & Refreshments

8:30 AM -8:40 AM - Welcome & Opening Remarks (Opening Speaker: Dean Stefano Vidussi, PhD)

8:40 AM - 9:40 AM - Oral Session 1

9:40 AM - 9:50 AM -BREAK

9:50 AM - 10:50 AM - Oral Session 2

10:50 AM - 11:00 AM - BREAK

11:00 AM - 12:00 PM - Poster Session 1

12:00 PM - 12:45 PM - LUNCH

AFTERNOON

12:45 PM - 1:45 PM - Oral Session 3

1:45 PM - 2:00 PM - BREAK

2:00 PM - 3:00 PM - Poster Session 2

3:00 PM - 3:05 PM -BREAK

3:05 PM - 3:50 PM - Oral Session 4

3:50 PM - 4:00 PM - Closing Remarks & Certificates

ORAL PRESENTERS

ORAL SESSION 1
(8:40 AM - 9:40 AM)

Moderator:
Dr. Jessica Purcell

Yousef Abdelkadous
Kassem Issa
Dae Kim
Snigdha Maddula
Shruti Nemlekar
Grace Wang
Steve Zhang

ORAL SESSION 2
(9:50 AM - 10:50 AM)

Moderator:
Dr. Dawn Nagel

Yuna Aguilar
Amanda Arrieta
Cynthia De Leon
Rami Koudsi
Kawon Pyo
Sierra Rupp
Taewon Yoo

ORAL SESSION 3
(12:45 PM - 1:45 PM)

Moderator:
Dr. Viji Santhakumar

Jonah Frazier
Emmanuel Green
Sonika Khare
MJ Olivia
Gayatri Raut
Harry Stoltz
DG Scholar Group

ORAL SESSION 4
(3:05 PM - 3:50 PM)

Moderator:
Dr. Ernest Martinez

Shayne Cruz
David Grant
Alma Luquin
Lisa Martinez
Gabriela Mota Orozco
Cori Zuvia

POSTER PRESENTERS

POSTER SESSION 1

11:00 AM - 12:00 PM

Dana Aghahassan
Melissa Arellano
Andrea Barajas
Victoria Batiz
Manuel Bostock
Desmond Cairo
Renee Cheung
Harrison Chow
Tina Conley
Evelyn Dibos
Natalie Dinh
Edward Duong
Tina Fathibitaraf
Cynthia Franco Gonzalez
Valerie Gonzalez
Jimmy Gu
Lance Hiew
Dylan Huang
Wesley Hur
Firdouz Hussain
Cassandra Irahola
Paul Isaac
Mahibah Jamal
Isabel Kang
Elizabeth King
Pilar Lara
Ricky Le
Linlin Liu
Jorge Lomeli-Prieto
Azariah Lopez
Naran Luvsanravdan
Elijah Muro
Joshua Nghiem
Natalie Nguyen
Mari Nolasco
Christopher Nouneh
Nicole Ormeno
Andrea Pearson
Zoey Pilling
Angel Pulido
Emilio Rivas
Adrian Salas
Patricia Sanchez
Simarpal Singh
Abby Sond
Mabel Tan
Ideen Tayebi
Ohnmar Thwin
Michael Vitarella
Matthew Wang
Jonathan Wu
Andrew Yee

POSTER PRESENTERS

POSTER SESSION 2
2:00 PM - 3:00 PM

Isabella Aguilar
Joshua Alexis
Arsema Araya
Shaylyn Blackburn
Lily Caplon-Guin
Noah Cecilio
Diego Chavez
Eric Cheang
Rumaan Cheema
Renee Cheung
Hannah Dela Cruz
Natalie Dinh
Tina Fathibitaraf
Michael Ghaly
Jimmy Gu
Cassetty Habib
Bryan Hernandez
Isaiah Hernandez
Lance Hiew
Wesley Hur
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Cassadnra Irahola
Mahibah Jamal
Jacob Jauregui
Nicholas Jimenez
Bethany Johnson
Elizabeth King
Gabriel Livas
Matthew Lui
Annette Mercado-Sanchez
Quintin Meyers
Gregroy Mikol
Maheshwaran Natarajan
Kealani Nelson
Natalie Nguyen
Christopher Nouneh
Nicole Ormeno
Noel Perez
Reyna Quinonez
Gayatri Raut
Jorge Recarte
Alberto Reyes
Daniel Reyes Alcaron
Esmeralda Rivera
Ashley Ruvalcaba
Alissa Salas
Abby Sond
Casey Souder
Ime Stevenson
John Tate
Clemente Villafana
Michael Vitarella
Nam Vu
Andrew Yee
Sophia Zhou

ABSTRACTS

ORAL SESSION 1

SCINTILLATOR USE IN CALORIMETER FOR ELECTRON-ION COLLIDER

Yousef Abdelkadous, Miguel Rodriguez, and Miguel Arratia
Department of Physics and Astronomy, UC Riverside

The Electron-Ion Collider (EIC) is a large, high energy, collider of electron and ion beams to study the quarks, sub-particles in protons and neutrons, and gluons, the bonds that hold quarks together. A high-granularity calorimeter insert has been proposed for the new Electron-Ion Collider (EIC) as a sub detector to be used in the collider. This calorimeter is based on plastic scintillators with silicon photomultiplier (SiPM). Effectiveness of this detector depends on the granularity, the scale of detail in describing information of particles detected, and light yield, the amount of light produced and detected due to the particles. To ensure maximum effectiveness of granularity and light yield, different shapes of scintillators were tested with cosmic-rays and a radiation source, Strontium-90. Each scintillator was polished, painted white on the sides, and annealed to ensure effectiveness during testing. While we are still in the testing phase, we expect our results to indicate a scintillator shape that achieves higher light yield. With this scintillator technology applied to the EIC, future advancements in theoretical quantum physics, medicine, and technology are expected.

ORGANIC HYDROPEROXIDES DETECTED DURING MULTIPHASE AGING OF ORGANIC AEROSOLS

Kassem Issa, Wen Zhang, Dr. Haofei Zhang
Department of Chemistry, University of California, Riverside

Organic peroxides (POs) are molecules found everywhere on Earth which play a significant role as intermediates for reactions in the atmosphere, controlling much of life including the climate and human health. In particular, these molecules make up a majority of secondary organic aerosol (SOA) particles, which are formed from the oxidation of volatile organic compounds (VOCs) in the atmosphere. Although their formation has been extensively studied and observed in the gaseous phase, there nevertheless remains substantial gaps in understanding their formation during multiphase oxidation. This creates cause for concern, as these compounds contain free radicals, unpaired electrons that pose significant harm to human health in the form of disruption of cellular membranes, leading to damage in DNA. Consequently, the focus of this research was on understanding the formation of POs through heterogeneous oxidation of ten organic aerosol surrogates. These compounds provide an excellent model system for a majority of common reactive atmospheric compounds, as they contain a variety of functional groups responsible for much of the oxidative reactions discussed previously. Equipment which simulated atmospheric conditions included a flow tube reactor containing UV light and ozone to drive the oxidative reactions, and an atomizer to aerosolize each compound. Thermal dissociation-chemical ionization mass spectrometry was also key in detecting the organic products formed from each surrogate. Results of these experiments demonstrated multiphase oxidation throughout each of the surrogates studied, contributing heavily to the field of OA chemistry via a greater understanding of the formation of organic hydroperoxides in the particle phase.

EMULSION SELF-ASSEMBLY OF ZnS:Mn2+ QUANTUM DOTS TOWARDS MECHANOLUMINESCENT NANOPARTICLES FOR OPTOGENETICS APPLICATIONS

Dae Kim, Zhongxiang Wang, and Dr. Yadong Yin
Department of Chemistry, University of California, Riverside

Mechanoluminescence (ML) is light emission resulting from any mechanical action on a solid and can have many applications in modern society including stress sensing, dynamic display and optogenetics. Among them, optogenetics adopts ultrasound and ML nanoparticles to generate photons to noninvasively control biological processes within targeted cells. The dimension of mechanoluminescent nanoparticles needs to be below 200 nm to ensure smooth circulation through blood vessels without congestion. However, current mechanoluminescent particles usually demonstrate large particle sizes (>10 μm), which is not applicable to optogenetics. Herein, we creatively employed an emulsion self-assembly approach to assemble ZnS:Mn2+ nanocrystals of 9 nm in diameter into spherical nanoclusters below 200 nm. To avoid particle sintering during the following high-temperature calcination, silica is coated around the nanospheres. We find that the calcined samples remained the particle size below 200 nm and more interestingly, they produced bright mechanoluminescence of yellow light upon mechanical pressure stimulations. This work represents the first successful attempt in using an emulsion self-assembly method to fabricate mechanoluminescent nanoparticles with ideal size, and it provides promising feasibility in applying these nanoparticles in optogenetics.

PATHOGENIC EFFECTS ON CERATINA GUT MICROBIOMES WITHIN SOUTHERN CALIFORNIA WASTEWATER REGIONS

Ragasnigdha Maddula, Lyna Ngor, Dr. Quinn McFrederick
Department of Entomology, University of California, Riverside

Bees play a vital role in ecosystem health, providing essential pollination services that bolster biodiversity, agriculture, and economies. Their pollination fosters plant fertilization, bolstering natural ecosystems by enhancing plant growth and ecological balance. Most bees are native wild species and their absence can disrupt insect-plant interactions causing ecosystem imbalances. Thus, safeguarding these pollinators is pivotal for ecological harmony. Honey bees develop gut microbiomes from hives, while wild bees acquire theirs from their surroundings. Honey bee colonies are prone to pathogen outbreaks due to their population density while solitary wild bee nests reduce the likelihood of widespread pathogen spread. Thus, studying wild bees becomes crucial as a backup plan in the event of honey bee colony threats, like the previous Colony Collapse Disorder. As research on pollinator gut microbiomes grows, the relationship between wild bee microbiomes and their habitat environments remains largely unstudied. This project aims to explore how the gut microbiomes of wild Ceratina bees are impacted by their surroundings, investigating the influence of pathogens and wastewater residues on their gut health. Ceratina bees, also referred to as small carpenter bees, are solitary Apidae members globally. They create single nests in decaying wood cavities, stocking each cell with pollen and sealing them with waterproof secretions for protection. Because wild bees acquire their gut microbiome from their environment, I hypothesize that wild bee gut microbiomes will mirror their environment, and considering this, I predict that bees from polluted environments would harbor pathogens like Crithidia, Serratia, and Burkholderia Spp.. Using PCR, our lab compares DNA segments of pathogenic bacteria, leveraging their unique patterns for identification and detection. Essentially, these experiments shed light on leveraging environmental changes to improve conditions for bee populations.

STRUCTURE-FUNCTION PROPERTIES OF A NEMATODE DEVELOPMENTAL PROTEIN

Shruti Nemlekar, Gina Maduro, Dr. Morris Maduro
Department of Molecular, Cell, and Systems Biology, University of California, Riverside

In the Maduro Lab we are interested in studying the genes that direct different cells in an embryo to become specified in the model organism, the nematode C. elegans. In our project, we are studying two different forms of protein made by a gene called elt-3. The longer protein, isoform B, can specify cells to make gut, while the shorter isoform A lacks this ability. The difference between the two isoforms is the presence of an additional 91 amino acids at the amino end of ELT-3B. We are testing versions of the elt-3 protein where we remove progressively more of ELT-3B and see if these are still capable of specifying gut. This project involves creating artificial genes in plasmids that are then introduced into the animals by microinjection. We then determine whether that version of ELT-3 still specifies gut. So far, we have been able to remove up to 33 amino acids from ELT-3B without affecting function. Our goal is to identify what part of ELT-3B is essential to make gut, which will tell us how proteins like ELT-3 might have evolved different specification properties.

HARNESSING σ-DQI VIA THE SYNTHESIS OF MOLECULAR SILICON SWITCHES

Grace Wang, Lan Pham, and Timothy A. Su
Department of Chemistry, Su Lab, University of California, Riverside

Single-molecule junctions represent the ultimate limit of miniaturization for electronic devices, where individual molecules are tethered between electrodes and used as the active switching components of electronic circuitry. This presentation describes an unprecedented approach to create new single-molecule switches by harnessing a conformation-dependent quantum transport property that is unique to polysilanes called destructive σ-quantum interference (σ-DQI) that typically occurs for cisoid-oriented polysilane wires. We explore the use of chemical and mechanical triggers to switch between the insulating σ-DQI cisoid state and a conducting state where the polysilane backbone is in a transoid orientation to access high ON/OFF switching. This approach highlights the potential impact of harnessing σ-DQI in creating new forms and concepts of molecular electronic switches.

THE RELATIONSHIP BETWEEN THE INFERTILITY OF VARROA DESTRUCTOR MITE AND THE TEMPERATURE.

Steve Zhang, Genesis Chong and Boris Baer
Department of Entomology, University of California, Riverside

Over the past 12 months, the US has lost almost half of its honey bees. This is a serious concern because more than 80 crops of agricultural interest depend on their pollination services. A key contributor to colony collapses is the ectoparasitic mite Varroa destructor. A few treatments have been developed and have become increasingly less effective as the mites have developed resistance. given that the mites started to become resistant. Consequently, we need to develop novel management tools as a matter of urgency. Recent research revealed that Varroa mites are sensitive to elevated temperatures.our experiments study the performance of these parasites under different temperatures. Bee larvae are bred from multiple hives and are exposed to mites in a simulated hive environment. Mites and larvae are exposed to a daily heat shock of 36 degrees Celsius for two hours over a time period of six days. An initial experiment confirmed that the bee larvae are more resistant to heat stress than mites. Noteworthy challenges were encountered during preliminary trials, including premature mortality of bee larvae and mites. Strategies were implemented, involving modifications in container composition, humidity levels, larval nutritional provisioning, and ventilation dynamics, culminating in partial resolution of these challenges. These results could be essential to the selection of future breeding stock with increased mite tolerance., especially since honey bees are known to change the temperatures inside their hives and increase them as a form of social fever in response to disease infections.

ORAL SESSION 2

IDENTIFYING NON-OBVIOUS GENES IN YARROWIA LIPOLYTICA INVOLVED IN ACETATE TOLERANCE

Yuna Aguilar, Nicholas R. Robertson, Varun Trivedi, Adithya Ramesh, Chase Lenert-Mondou, Anthony Arteaga, Marcus Harland-Dunaway, Robert Jinkerson, Ian Wheeldon
Department of Chemical Engineering, University of California Riverside

Yarrowia lipolytica, a yeast known for its versatility, has become a focal point in biotechnology because of its unique traits of high lipid production, substantial Acetyl-CoA pool, and its ability to utilize diverse carbon sources, including Acetate. Here, we harnessed Y. lipolytica's full potential by employing CRISPR-Cas9 to enhance its ability to utilize Acetate as an alternative carbon source, while ultimately improving its Acetate tolerance. Our approach revolves around combining a previously studied library with machine learning to create an optimized library that consists of 24,000 unique gRNAs. Through the identification of these genes are we able to develop a new version of Yarrowia lipolytica that grows significantly faster than wild-type, while exhibiting improved acetate tolerance

FLUORESCENCE STUDY OF MAGNESIUM OXIDE AND MAGNESIUM HYDROXIDE NANOPARTICLES WITH GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA

Amanda Arrieta, Patricia Holt-Torres, Dr. Huinan Hannah Liu
Department of Bioengineering, University of California, Riverside

Previous studies found that magnesium oxide nanoparticles (nMgO) had antibacterial effects against two Gram-negative and three Gram-positive bacteria, and magnesium hydroxide nanoparticles (nMg(OH)2) were antibacterial against Staphylococcus epidermidis. Currently, the specific mechanisms are unknown, but several have been suggested in previous studies. Understanding these mechanisms may lead to their potential in a clinical setting, for example, with surgical implants to aid in postoperative infection mitigation. To identify these antibacterial activities, fluorescence dyes have been integrated into studies involving bacteria exposed to nMgO or nMg(OH)2 to identify suspected mechanisms. These may include Gram-negative bacteria membrane permeability, Gram-negative and Gram-positive plasma membrane depolarization, reactive oxygen species detection, and the effects of reactive oxygen species. Observing fluorescent dye reactivity will reveal if nanoparticle activities include one or more or these mechanisms in bacterial cells. Results of this study are expected by the end of August 2023. Overall, this study will give further insight into the nature of nMgO and nMg(OH)2 effects on bacteria and will aid in downstream research involving nMgO and nMg(OH)2.

EVALUATION OF SURVIVORSHIP OF HOMALODISCA VITRIPENNIS IN ARTIFICIAL DIET SYSTEMS

Cynthia De Leon[1], Inaiara de Souza Pacheco[1], Timothy Roose[1], Eric Cheang[1], Luis Velez[1], Dr. Linda L. Walling[2], Dr. Richard A. Redak[1], Dr. Peter W. Atkinson[1]

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Glassy-winged sharpshooters (GWSS), Homalodisca vitripennis, are an invasive species brought to Southern California from the Southeastern United States. They are pests that serve as vectors for the bacterium Xylella fastidiosa to several plants. In grapes, X. fastidiosa causes Pierce's disease (PD) which has demonstrated significance both agriculturally and economically in Southern California. The goal of this experiment is to validate an artificial diet system which can sustain the GWSS for at least 24 hours. To develop this system, factors such as light direction, type of diet, temperature, humidity, space, and diet orientation needed to be considered. 20 adult insects were starved for 5 hours prior to the experiment and subsequently confined in plastic cages containing a sachet composed of an artificial diet homogeneously distributed between two parafilm layers. The encaged insects were kept in a dark box with an opening for the artificial light under a 14:10h (light: dark) photoperiod for 24 hours. Several trials were performed testing different diet orientations, light orientations, temperatures, and humidity. To confirm the feeding capabilities of the insects, the size and amount of salivary sheaths present on the parafilm layers were analyzed. High mortality rate was observed with few salivary sheaths on all experiments. Based on these results, it was possible to infer that the insects probed and attempted to feed, however the diet was not sustainable enough to keep them alive for the full 24 hours. More tests are being performed to readjust the diet system to properly sustain GWSS in vitro for a longer duration of time and thus enable X. fastidiosa transmission experiments. With the knowledge acquired on those experiments, it will be possible to create new strategies to block X. fastidiosa transmission by GWSS and contribute to solving the problem of diseases such as PD without the need of pesticides.

THE GROWING CHANGES OF THE El NIÑO SOUTHERN OSCILLATION

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Every two to seven years, a great shift in sea surface temperatures naturally occurs across the Pacific Ocean, which not only has drastic effects on ecosystems above the ocean, but those within it. This naturally occurring phenomenon is known as El Niño Southern Oscillation (ENSO), and its effects are caused by a reduction in wind currents that run across the Pacific Ocean. However, with the rise in greenhouse gases (GHGs) and aerosols in the Earth's atmosphere and subsequently a warming climate, the typical magnitude and patterns of ENSO have changed. By utilizing the Energy Exascale Earth System Model (E3SM) from 1850-2014, our study analyzes how GHGs and aerosols impact ENSO. We specifically used E3SM historical-GHG and historical simulations, the former of which is driven only by human induced GHG changes while the latter is driven by all factors caused by humans. Through the comparisons of the two simulations, we discovered that GHGs were responsible for hindering the ENSO variability, owing to the strengthened annual cycle of sea surface temperature in the eastern equatorial Pacific. This hindered ENSO variability corresponds to a lower Bjerknes stability index, which is primarily due to decreased positive feedback. Moreover, we found that GHGs were mainly responsible for creating the Central Pacific variant of ENSO, which is a more recently observed trend. Ultimately, this study diagnoses the relationship of climate data taken over a span of nearly two centuries, in order to help bridge the gap between the known and the unknown of this fascinating phenomenon.

DEGRADING AN ANCIENT ENZYME

Kawon Pyo, Yuan Liu, and Dr. Jernej Murn
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IMPACT OF VARYING BIOCHAR ON DNA REMOVAL FROM SOLUTION

Sierra Rupp, Mike Schmidt

DNA removal from solution has many applications in treating recycled wastewater for agricultural purposes. The presence of antibiotic resistant genes in untreated wastewater poses a public health risk, which stresses the importance of finding efficient ways to treat it. The DNA can be removed by means of Biochar adsorption. Biochar is produced when organic feedstocks undergo the process of pyrolysis at high temperatures. This study in particular was conducted in order to investigate the influence of varying biochar feedstock in DNA removal. Previous studies have proven biochar's ability to remove DNA from solution, however none so far have delved into the influence of biochar feedstock on this removal. Four different biochars were produced at 500 C. The feedstocks used to produce the biochar were manure, mustard (an invasive plant species), macadamia nut shell, and orange peels. The biochars were characterized for specific surface area, cation exchange capacity, ash/volatile content, elemental analysis, and FTIR. A series of adsorption experiments were then run with a fixed amount of biochar and differing concentrations of DNA (0 –200 mg/L). Mechanisms of DNA adsorption onto each biochar were inferred from the results of characterization and adsorption experiments. Each biochar's ability to adsorb the DNA was determined by looking at the amount of DNA remaining in solution after the adsorption process. Using the Freundlich isotherm, it was determined that mustard has the highest adsorption affinity, followed by manure, orange peel, and macadamia nut shell. When the ionic conditions were changed, mustard still had the highest absorbance affinity. Understanding which biochar performed the best and why is crucial for future wastewater treatment practices and determining the most efficient way to remove the harmful antibiotic resistant genes present.

STUDYING THE EFFECTS OF TREATED WASTEWATER IN RADISH BULK SOIL

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Antibiotic resistance is a growing phenomenon that threatens global health largely due to the misuse and overuse of antibiotics. Agriculture is of particular concern because soils are constantly exposed to low-level additions of antibiotics through treated wastewater and manure which can encourage the emergence of antibiotic-resistant bacteria and genes. As the emerging antibiotic resistance due to the application of treated wastewater can encourage the transfer of this resistance from soil to vegetables posing a risk to human health, the organization raised the question of the viability of using that water for agricultural purposes. If an anti-biotic-resistant bacteria were to invade the produce, it would eventually end up in the consumer's body. This study investigates the transport of Antibiotic-resistant bacteria (ARB) through a soil-to-plant system by estimating the number of antibiotic-resistant bacteria and the abundance of antibiotic-resistant genes in bulk soil. For this study, bulk soil samples under 4 different treatments were collected and three bacteria (Escherichia coli, Pseudomonas, and Salmonella) were isolated under different selective conditions. These conditions included: no antibiotic addition, the addition of acetyl sulfanilamide, cefalexin, trimethoprim/sulfamethoxazole, and streptomycin. MIC tests were also performed to determine each isolate's level of resistance to antibiotics. Colonies with high levels of resistance will be selected and sent out for whole-genome sequencing. The results of this study indicate that there are more antibiotic-resistant bacteria with higher levels of resistance within the bulk soil treated with reusable water with unspiked manure over 6 weeks.

POSTER SESSION 1

NEW HOPE AGAINST THREAT OF SUPERBUGS

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In recent medicine, the ever increasing antibiotic resistance of bacterial pathogens has raised significant concerns. Genetic mutations and natural selection act upon DNA to confer antibiotic resistance, making antibiotics less efficient and lead to the development of increasingly untreatable bacterial infections. One way to stem the tide of antibiotic-resistant bacteria is to identify new targets for antibiotics. One such target is the coupling of transcription and translation. Transcription and translation occur in the same cellular compartment in bacteria. As a result a messenger RNA can be translated while being transcribed. In my research I will provide structural evidence of Transcription-Translation Coupling in bacteria. This will help better understand the unique biological mechanisms of bacteria that can be exploited in the development of new antibiotics. The key players of transcription and translation are the RNA polymerase (RNAP) and the ribosome, respectively. Some domains in bacterial RNAP have been found to have regulatory functions in transcription. One such domain is the zinc-binding domain (ZBD). The ZBD plays multiple roles in the binding of DNA and RNA and of transcription regulators for transcription initiation, elongation, and termination. However, the mechanism/ binding interaction of ZBD and uS3 is not clear. In my research, I will try to visualize the interaction between ZBD and uS3 at the molecular level using X-ray crystallography. I will provide an overview of current developments regarding ZBD's regulatory functions in bacterial transcription. Though I have yet to get crystals, I purified different ZBD-uS3 fusion using a His-SUMO tag using Nickel chromatography.

BIAS CORRECTING SIMULATED STREAMFLOW BY UTILIZING MACHINE LEARNING

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Climate change and water management in the Colorado River Basin have severely declined streamflow in recent decades. Streamflow observations at Lees Ferry AZ, located at the Upper Colorado River Basin, have been utilized for bias correcting time-series of simulated streamflow under historic and climate change scenarios from thirty-one global circulation models. These models represent Representative Concentration Pathways (RCPs) of 2.6, 4.5, 6.0, and 8.5 . Beginning from the lowest to largest, the numerical values of the RCPs correlate to the predicted concentrations of greenhouse gas emissions in the year 2100. An Exploratory Data Analysis was first performed to compare simulated streamflow at different time periods with observations. Time-series regression models represent a significant declining trend in simulated flow and intra-annual plots display strong seasonality when compared to that of observed streamflow. RMSE was in range of 550 m3/s, solidifying the significant bias between simulated and historical streamflow. Results indicate the magnitude of bias ranges from 250m3/s to 1500m3/s in summer months. Deviations display a majority of data points concentrated around zero suggesting the projected values were within the range of the observed value. A Random Forest model was constructed based on the observed flow as a target variable and a simulated flow as a predictor variable. Random Forest machine learning produced models with a ~25% correlation while regression models displayed as low as 17% correlation. Further investigation is required in order to determine if introducing predictor variables such as temperature and precipitation will improve accuracy of the bias correction model.

THE EFFECTS OF FIRE EVENTS ON NATIVE BUMBLE BEE HEALTH IN THE SIERRAS

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Department of Entomology

Although fire events can be devastating to landscapes and affected populations of the firepath, smaller, naturally-occurring, or controlled burning has been shown to induce pyrodiversity. The main goal of our research is to assess the effects of fire on native, wild bumble bee health. Health, in this context, relates to the size parameters of collected Bombus vosnesenskii individuals. Bumblebees play a vital role as pollinators in the wild but are also necessary for agricultural purposes. Our research seeks to understand how native bumblebees have been affected by recent fire events and whether or not bumblebees benefit from these historically-recurring events. In this preliminary research period, used to establish a protocol for this pilot project, eight predetermined sites were chosen to collect samples on the Sierras. Four sites were directly impacted by the KNP Complex Fire in 2021, while the other four locations did not. To determine fire impact on bumble bee species, we used health metrics focusing on the most common species within the study area, B. vosnesenskii. Eighty specimens of B. vosnesenskii workers were collected at sites during three-hour sampling periods or until 10 individuals were captured, whichever occurred first. The specimens were chilled on ice to calm and allow easier handling for measurements of wings, head size, and weight. Additionally, floral surveys were taken to assess food supply, pollen loads were collected when available for molecular assessment, and observational counts of floral presence were recorded for further research. The presence of non-native Apis mellifera in direct competition with B. vosnesenskii in all sites was also recorded. The early data analysis shows that the average wing cell size, average body mass, and average head size are all larger in specimens from burn sites vs. sites that did not experience fire events recently. This data suggests that fire events can have a positive effect on bumble bee health metrics.

WEED DETECTION IN AN ONION FIELD THROUGH DRONE IMAGING FIELD

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Weeds compete with crops for valuable resources making their removal essential, which can be expensive, labor intensive, and require pesticides. Efficiency improvements are needed in the use of resources for weed control. We imaged an onion field with a drone-mounted sensor to test our hypothesis that reflectance of multiple wavelength bands from plant tissue can distinguish onions and weeds growing among them. Spectral analysis of the images produced a normalized difference vegetation index (NDVI) map from the individual bands. Preliminary results indicate our model is 95% accurate. Multispectral analysis could be useful for creating weed maps in agricultural fields for precision removal.

OPTIMIZATION OF SALICYLIC ACID-BASED POLY(ANHYDRIDE-ESTER) HOMOPOLYMER SYNTHESIS

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The salicylic acid-based poly(anhydride-ester) (SAPAE) homopolymer is a unique polymer that is biodegradable, biocompatible, and bioactive. It possesses the ability to hydrolytically degrade, triggering the controlled release of salicylic acid over an extended period of time. This polymer is the focus of many cutting-edge studies which explore its applications to solve challenges ranging from bone regeneration to localized drug-delivery and beyond. In this study, we synthesized the SAPAE homopolymer and surveyed its ability to form microspheres. This compound was created in a three-step procedure where, first, a salicylic-adipic (SAA) diacid was synthesized, then formed into a monomer, and finally polymerized into the SAPAE homopolymer. After each step in the procedure, the resulting compound underwent various characterization methods confirming the structures and purity of each compound. The success of each step was determined by the reproducibility of desired results. The SAA diacid was successfully synthesized three times with consistent reproducibility and purity. The SAPAE homopolymer synthesis resulted in low molecular weights with varying values. This may be due to the SAA diacid not fully acetylating during the monomer synthesis procedure, as the monomer characterization revealed traces of SAA diacid still present at the end of the monomer synthesis step. Because of this inadequacy in molecular weight, the SAPAE homopolymer synthesis must first be troubleshooted and optimized before it can be applied to the formation of microspheres. Future work includes applying the SAPAE formulations to plants to study effects of the polymer on plant growth and defense.

MOLECULAR DYNAMICS INSIGHTS INTO BUBBLE NUCLEATION IN LIQUID ARGON

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Neutrino detection remains an evolving frontier, with the intricacies of bubble formation in liquid argon playing a central role. This study employs the LAMMPS Molecular Dynamics Simulator, a tool traditionally applied in condensed matter research, to shed light on this phenomenon. Capitalizing on the Leonard-Jones chemical potential, recognized for its adeptness with argon, we investigate nucleation probabilities after specific energy depositions in liquid argon. Our focus remains distinctly on argon due to its alignment with the Leonard-Jones model.

CHARACTERIZATION OF THERMOREGULATED BBX GENES IN RICE

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The circadian clock is an internal mechanism in plants, responsible for coordinating developmental and physiological processes throughout the day. This internal mechanism is modulated by a series of transcriptional-translational feedback loops, which oscillate expression of core-clock genes and allow plants to synchronize with environmental cues. B-Box (BBX) proteins are a family of transcription-factors, which are light-regulated, and contribute towards growth, developmental processes, and abiotic stress response. Previous studies in Arabidopsis thaliana, implicate a link towards BBXs and the heat stress response, as well as interactions with the core-clock mechanisms. However, the role of BBXs in the heat stress response in rice is not fully understood. To address this, my aim is to understand the role of OsBBX29 towards heat tolerance in rice. My project's goal is to over-express OsBBX29 in rice and perform growth and physiological assays, in the context of heat stress. Over-expression constructs were generated through amplifying our gene of interest through the use of PCR from cDNA, and gateway cloning, inserting our gene into a plasmid with an over-expression promoter and fluorescent tag. To determine the subcellular localization and whether the construct encoded a functional protein, I infiltrated tobacco leaves, and visualized OsBBX29 with confocal microscopy under ambient and heat stress conditions. Preliminary results suggest that OsBBX29 is localized primarily in the cytoplasm, with minor signaling in the nucleus. Future work will involve the creation of transgenic rice lines, and will further aim towards increasing heat stress tolerance in crop plants.

DYNAMIC RESPONSE OF NDVI TO SOIL MOISTURE VARIATIONS UNDER DIFFERENT CLIMATE AND CROP TYPES IN CALIFORNIA

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Gaining a deeper understanding of the dynamic patterns in soil moisture across space and time is essential for advancing precision agriculture techniques and enhancing the effectiveness of irrigation schedules. The in-situ soil moisture observations are nonetheless still very scarce and have rarely been measured on a regular basis and lack over large spatial scales due to financial limitations and require important efforts to be put in place. The great advances in remote sensing applications in recent decades provide alternative strategies for obtaining spatial fields of soil moisture. Therefore, this study investigates the covariation of soil moisture with the normalized difference of vegetation index (NDVI) from Sentinel- 2 satellite data, while also exploring the influence of climate and crop type. In-situ soil moisture was collected in California in 2022 from a total of 1110 sites, which represent 6 types of vegetation types (almonds, cherries, pistachios, walnuts, grapes(table), grapes(raisins)) and two types of climate regimes: mediterranean climate and semi-arid climate. The cross-correlation analysis was used to estimate the time-lag for NDVI to respond to the change of soil moisture. Moreover,this research investigates whether there is any difference of time-lag in terms of vegetation type and climate regime. The outcomes of this analysis not only provide insights into correlations between NDVI and soil moisture, but also reveal the impacts of climate and vegetation at various temporal scales. The findings of this research could be used to improve the link between hydrological processes and biogeochemical processes in land surface models, which will provide useful benchmarks for modeling studies using coupled vegetation climate models.

UNDERSTANDING THE ROLE OF RICE BBX TRANSCRIPTION FACTORS IN HEAT STRESS RESPONSES

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The circadian clock is a 24-hour timekeeping mechanism in most living organisms that regulates interactions with the environment. In plants, the circadian clock controls responses to the environment, including heat stress, in part by modulating the expression of genes involved in heat tolerance. Artificially overexpressing these clock-controlled genes, some of which are transcription factors, may clarify their role in heat tolerance. B-Box transcription factors (BBXs) in plants play a role in many plant processes including regulating plant growth and development, seedling photomorphogenesis, anthocyanins biosynthesis, flowering, and hormonal pathways, and stress responses. Overexpression of BBXs in rice combined with heat related physiology and growth assays may provide a better understanding of their role in heat responses. To overexpress BBXs in rice, we fused the coding region of the transcription factor to the ubiquitin promoter to increase the expression and a green fluorescent protein (GFP) to monitor the localization. To test proper generation of the fusion protein and to visualize the subcellular localization of the BBXs, we infiltrated tobacco leaves and monitored them using confocal microscopy. Preliminary data indicates that my construct (OsBBX 16) has a cytoplasmic subcellular localization in tobacco leaves. Future work will be to create transgenic rice lines to determine whether these BBXs play a role in heat tolerance in rice.

DECIPHERING THE MECHANISMS OF PLK POLAR LOCALIZATION

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In plants, developmental cues are integrated with environmental signals to coordinate appropriate cellular and whole plant responses. Plasma membrane proteins sense endogenous and environmental signals to initiate these responses. POLARLY LOCALIZED KINASEs (PLKs) are transmembrane receptor proteins targeted to the lateral domains of root cells. PLK1 and PXC2, closely related proteins, accumulate at the inner and outer lateral domain of the plasma membrane in endodermal and cortex cells, respectively. Our results indicate that PLK1 lateral polarization has unique attributes and is not regulated by the same mechanisms as other polarized transmembrane proteins. PLK1 is part of a subclade of proteins, including the MEE62 subgroup, that are polarly localized. To better understand how their polar localization is achieved, we are examining the role of the kinase domain in localization. To achieve this, we mutated specific amino acids to assess their influence over localization in the protein and deleted the kinase domain. We introduced mutations into the kinase domains of four genes encoding PLKs. The consequences of these mutations on the MEE62 subgroup proteins are ongoing and require analysis over multiple generations to discover the localization of these genes. The impact of kinase domain mutations and deletion in PXC2 are being examined in the root by confocal microscopy. We predict that the kinase domains help inform the polar localization and/or stability of the PLKs. Studying protein localization allows us to better understand the function of these proteins in plant growth and survival.

INCREASING CO2 INTAKE AND ALUMINUM RESISTANCE IN PLANTS

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Using the plant Arabidopsis thaliana, the lab aims to identify substantial increases in carbon outputs relevant to carbon capture and resistance to aluminum toxicity. The lab can determine if the plants have been successfully modified by measuring how resistant (length of its roots) it is to aluminum-soaked gels. The modification can be applied to all plants. Currently, one specific gene site has been identified that can be modified. We hope to use our technology to decrease our carbon output in the atmosphere, which can reduce the impact of global warming. In addition, due to the resistance to aluminum toxicity, we hope that our modified plants can in areas with aluminum abundance, predominantly in South America and Africa, thus increasing the production of our food supply.

ADULT FUNCTIONAL COMPOSITION STRONGLY DETERMINES SEEDLING FUNCTIONAL COMPOSITION RATHER THAN ENVIRONMENTAL CONDITIONS

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Forests are important for biodiversity and provide many resources for society, yet are threatened by drought, pests, and changing fire regimes. Critical to managing for healthy forests, is understanding what drives variation in seedling communities – the small trees that will grow to be the next generation of forests. Importantly, it is unclear the degree to which biotic factors (adult trees) and abiotic factors (soils and topography) influence the biodiversity of seedling communities. Within the 4-ha San Jacinto Forest Dynamics Plot (SJFDP) in Southern California USA, we explored how the relative importance of multiple assembly processes influence seedling functional diversity by measuring 6 functional traits on seedlings (individuals under 1 m in height). To assess variation in functional diversity, we examined how the functional composition (Community weighted means; CWM) and functional diversity of seedlings was influenced by 12 topo-edaphic environmental variables (soils and topography) and the functional composition of the adult community (woody stems larger than 1 cm diameter). We found that for all traits seedling functional diversity was more strongly influenced by adults, than by the local soil environment, though the strength of this relationship varied among traits. Overall, these results suggest that biotic interactions such as competition and facilitation may play a stronger role in determining the functional diversity of seedling communities than local topo-edaphic conditions. Moreover, these findings suggest that forest management efforts that remove adult trees may inadvertently impact seedling communities.

SURFACE WATER AND GROUNDWATER CHEMISTRY VARIABILITY IN THE SOUTHERN SIERRA NEVADA

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Mountains are an important source of water for arid and semi-arid environments. Since they are at higher elevation, mountains experience higher precipitation and colder temperatures which means more snow is available for streamflow and groundwater recharge. However, there is uncertainty how mountain system processes contribute to groundwater recharge. We aim to investigate the temporal and spatial variation of surface water and groundwater chemistry in the Kaweah River watershed to better understand the processes that control water chemistry. This was done by analyzing monthly river and well samples for the 2022-2023 period. A pH titrator was utilized to determine the alkalinity and pH of samples. Inductively coupled plasma spectrometry (ICP) was used to examine the major ion concentrations. Our results show that rivers located in the upper regions of the watershed have lower concentrations of ions. This is likely due to snowmelt compared to rivers located in lower regions. Our next steps would be to implement a mixing model to quantify proportions of groundwater discharge to stream along elevation gradient and continue collecting and analyzing more samples to further examine the temporal changes in the stream chemistry.

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MICE SELECTIVELY BRED FOR WHEEL RUNNING DECREASES OBSESSIVE COMPULSIVE BEHAVIORS

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Obsessive-compulsive disorder (OCD) is commonly indicated by the repetition of meaningless behaviors. In humans, individuals with OCD exhibit such actions as frequent washing of hands or counting. Over time, a variety of animal models have been created for evaluating obsessive compulsive behaviors as a means to understand and test treatments, one of which is the rodent marble burying test. In rodents, burying is a repetitive behavior utilized against aversive stimuli, and previous studies have often linked the amount of stimuli buried as a method to quantify obsessive compulsive behaviors. In this study, we used marbles to provoke the burying behavior. We utilized 64 mice from four replicate lines that have been selectively bred for high voluntary wheel-running activity (HR mice) for 105 generations and 64 mice from the four non-selected control (C) lines to examine differences in obsessive compulsive behaviors between control mice and high activity mice. The experiment was conducted by placing 15 marbles into a standard living cage with one mouse, leaving them alone for 30 minutes, then scoring the number of marbles buried. Our results indicate that selective breeding for high voluntary exercise has resulted in statistically fewer marbles buried compared to the control mice, indicating that the HR mice have less obsessive compulsive behavior than non-selected controls.

THE SYNTHESIS OF A NEW RARE-EARTH-FREE TERNARY BORIDE Hf2MOs5B2 (M=Fe,Mn,Co)

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Developing a new innovative rare-earth-free (REF) permanent magnetic materials (PMM) as alternatives to the highly efficient yet scarce rare-earth-based PMMs presents a significant ongoing challenge within the realm of scientific research. The REF PMM, Hf2MIr5B2 (M = Fe, Mn) was discovered utilizing Density Functional Theory (DFT), which predicted pronounced interchain M-M spin-exchange coupling alongside substantial magnetocrystalline anisotropy energies (MAE) within the novel compounds. This confluence of attributes signifies a promising foundation for inherent properties of PMM.The present study outlines a high pure strategic synthesis strategy for Hf2MOs5B2 (M = Fe, Mn, Co) based on the premise of osmium's substantial spin-orbit coupling. Employing DFT, the compound Hf2MnOs5B2 exhibits a conspicuously favorable ferromagnetic energy of 11.8 meV, indicating a potentially alluring magnetic behavior. While the synthesis and X-ray characterization of these three novel materials were successful, a more nuanced experimental investigation into their intrinsic magnetic nature is still pending.

RELATIONSHIP BETWEEN PARENT MOVEMENT AND INFANT POSITION IN DAILY LIFE

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Sedentary behavior is a growing health concern worldwide. For caregivers, their level of activity might be related to their infants' activities, with studies revealing locomotor synchrony (coordinated joint movements) in laboratory settings (Hoch et al 2021). However, little is known regarding how infant posture relates to caregiver behavior in natural home environments. Similar research often involves laboratory-conducted studies that foster unnatural conditions for the caregiver and infant. Thus, this in-home study aims to examine the relationship between parent movement and infant posture in daily life. Based on previous lab-conducted experiments involving free-play, we might expect significant relations between parent movements and infant positions . However, since home environments involve various daily activities that entail more than free-play, we may see smaller relations between parent movements and infant positions. Inertial sensors allow us to capture the infant's posture (sitting/sitting restrained, prone, upright, or supine) and parents' movements (sedentary or mobile). This study observed 29 participants with infants between 4-14 months old. Preliminary analyses revealed no statistically significant correlations between any of the infants' positions and parents' sedentary time ($ps > 0.1$, $rs < 0.2$). These results suggest no relationship between parent movement and infant posture. The proportion of sedentary behavior among the caregivers in our study (M = 79.2%) was found to be greater than a related investigation (Healy 2011) of adults' sedentary time (M = 60.9%). This finding suggests that caregivers exhibit a larger proportion of sedentary behavior compared to average free-living adults, indicating a possible health disparity between the two demographics.

INFANT-ROBOT INTERACTION PROXEMICS

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Previous research has explored the proximity between adults or children with other humans or robots, but there is limited research involving proximity levels in infant-robot interaction. The objective of this research is to investigate infant-robot distances that promote higher engagement, resulting in improved mobility. It revolves around quantifying the exact distance at which an infant performs a specific action as a response to a robot's action. Video recordings of the first and last of eight sessions from five typical development infants and one Down syndrome infant were analyzed to assess changes in behavior and development. Infants' actions are annotated across sessions of spontaneous mobility within a robot-enriched environment, facilitated by both a humanoid and a wheeled robot. The Euclidean distance between the infant's body and each robot was quantified across distinct action categories directed at both robots. The categories include actions such as reaching, establishing contact, and transitional mobility. We calculate proximity-action probabilities and establish interaction zones based on the degree of interaction. By defining precise proximities for specific actions, these findings have the potential to guide focused motor interventions and aid personalized treatment.

PROPERTY ANALYSIS OF BLACK SOLDIER FLY FRASS AND THE ADULT'S AFFINITY FOR INDOLE

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The utilization of black soldier fly (BSF, Hermetia illucens) larvae for agricultural purposes has been gaining traction due to their ability to transform food waste and upcycle it into protein, oil, and several other useful byproducts. The main byproduct by volume is frass, which is insect manure with high levels of chitin (a substance that helps plants defend against pests and pathogens) from shed larval exoskeletons.The application of frass produced by BSF has not been explored extensively. Hence, to better understand its untapped potential, 4 experiments were conducted. First, frass' efficacy in protecting gold crown melons against ZYMV (Zucchini Yellow Moasic virus) was tested. The second experiment examined frass' effectiveness as a standalone biofertilizer for gold crown melons in comparison to other fertilizers. Third, the growth of melons was evaluated when treated with frass in complementation with various levels of NPK (Nitrogen, Phosphorus, and Potassium- all vital nutrients for plants). Finally, while substantial scientific literature focuses on the larvae, there is a lack of studies dedicated to understanding the adults' behavior. Filling in this gap could lead to optimized rearing practices that would maximize BSF oviposition (egg-laying) rates. The fourth experiment is about studying adult responses to indole, an odorant that can be found in plants and decaying organic material. Data collected from these 4 studies could assist researchers worldwide in obtaining a more holistic understanding of the capabilities of the BSF- both its frass and adult behaviors.

WIND VS. GRAVITY: HOW SEED DISPERSAL MODES AFFECT THE LEVEL OF GENE FLOW AMONG ALPINE PLANTS

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Seed dispersal plays a pivotal role in the movement of plant seeds to different habitats. Various dispersal methods lead to different directions and distances of seed travel, influencing the amount of gene flow and thus the extent to which the populations are connected. *Artemisia scopulorum* is dispersed by wind and is, therefore, expected to display higher genetic variation and less genetic structure among its populations than *Geum rossi*, a gravity-dispersed flowering plant. We used *Stacks* to identify single nucleotide polymorphisms (SNPs) in the DNA extracted and sequenced from our plant samples, and then employed the *STRUCTURE* software to assign each specimen to the best-fit population based on the observed patterns of variation. To better visualize our data, we conducted a principal component analysis (PCA) in R using the *SNPRelate* package, reducing the dimensions of the datasets while preserving its covariance. We expect that the PCA will demonstrate less differentiation among populations of *A. scopulorum* due to more gene flow compared to *G. rossi*. The results aim to improve our understanding of how distinct seed dispersal modes impact connections among alpine plant populations and provide valuable insights for future studies concerning the survival and conservation of these species in response to climate change.

ABSTRACT

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One of the main obstacles in molecular biosensing, such as detecting nucleic acids, is the challenge posed by the low concentration of the target molecules. Often, this requires employing techniques like amplification of the target or amplification of the signal. In this study, we introduce an innovative device, consisting of micro-beads arranged in a stacked fashion within a nano-sieve structure, designed for on-chip concentration of fluorescence nanoparticles. To create this nano-sieve device, we employ standard photolithography and wet etching techniques on glass. The micro-beads are confined within the device's channel using a flexible PDMS cap, acting as a filter to prevent the passage of nano-sized features. Fluorescent nanoparticles are then introduced into the nano-sieve, where they accumulate at the front-end of the micro-bead matrix, while the buffer fluid flows through the channel. Our previously gathered data demonstrates that within just one minute of experimentation, observable red fluorescence is emitted by the nanoparticles. Prolonged experiments yield even stronger fluorescence signals, as a greater number of nanoparticles are gathered within the channel. To showcase the applicability of this innovative system for molecular biosensing, we utilize the CRISPR-Cas13a complex for identifying specific target RNA. In the presence of the target RNA, the Biotin-FAM labeled single-stranded RNA (ssRNA) reporters undergo denaturation, thereby preventing the binding of streptavidin-coated fluorescent nanoparticles and anti-FAM coated magnetic beads. Conversely, when no target RNA is present in the assay, the ssRNA probes remain intact, facilitating the linking of fluorescent nanoparticles with the anti-FAM coated magnetic beads. Consequently, in the presence of target RNA, fluorescent nanoparticles are present within the assay and can be captured and concentrated within the nano-sieve. This on-chip concentration technique is of paramount importance for detecting low-intensity nanoparticles and target RNA. Each individual nano-sieve possesses dimensions of 4 mm × 8 mm, thereby enabling the patterning of numerous nano-sieves on a single chip. This multiplexing capability allows for the simultaneous processing of multiple samples.

MECHANISMS OF TRANSMISSION DISTORTION IN *FORMICA CINEREA*

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Supergenes are linked clusters of genes which may consist of coadapted alleles. These are responsible for the coloration in butterflies, male mating type in Ruffs, and social form in ants. Previous research shows that *Formica* ants have a supergene on chromosome 3 which underlies colony queen number. In *Formica cinerea*, the haplotypes P1 and P2 underlie multi-queen, or polygyne, colonies; and MA and MD underlie single queen, or monogyne, colonies. In this species there is also a chromosome 9 supergene linked with the supergene on chromosome 3. These co-transmitted supergenes may contain selfish genetic elements which can alter the Mendelian transmission via mechanisms such as maternal effect killing or meiotic drive. Previous research shows *Formica selysi* has the maternal effect killing mechanism, wherein a heterozygous polygyne queen's eggs will die if they do not express the antidote to a maternally inherited toxin. In contrast, meiotic drive refers to the overrepresentation of one haplotype in eggs laid by heterozygous queens. To look for selfish genetic elements, we extracted the DNA from *Formica cinerea* queens, eggs, and larvae, amplified targeted DNA fragments, and used allele specific enzymatic digests to assess genotype. Digested DNA fragments were visualized through gel electrophoresis. So far, we've observed that *Formica cinerea* ants have a P2 haplotype which is significantly more prevalent among samples than the P1 haplotype, which suggests a possible role of meiotic drive. Our goal is to further understand supergene evolution and how supergenes are inherited across generations.

PBDE-INDUCED GENE DYSREGULATION OF SOCIAL NEUROPEPTIDES OF MALE MICE OFFSPRING

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Autism Spectrum Disorders (ASD), marked by social communication deficits, have surged in prevalence with potential links to environmental factors. Our lab's research suggests that maternal exposure to polybrominated diphenyl ethers (PBDEs) can impact female offspring's social memory and oxytocin (OXT), vasopressin (AVP), and pituitary adenylate cyclase-activating peptide (PACAP) expression but whether PBDEs cause similar disruption in male offspring is unknown. We tested the hypothesis that a penta-PBDE mixture, DE-71, reduces *Oxt*, *Avp* and/or *Adcyap1* and/or their receptors (*Avp1ar, Oxtr*, *Adcyap1r1*) in the SON region of the social neural network (SNN) in males. Mouse dams were subjected to either 1) low DE-71 (0.1 mg/kg/d, **L-DE-71**), 2) high DE-71 (0.4 mg/kg/d, **H-DE-71**) dose, or vehicle oil (**VEH/CON**), for 10 weeks. Adult male offspring were sacrificed and the brains were cryosectioned and micropunched for SNN regions. After RNA isolation, RT-qPCR was used to analyze expression of these genes relative to the VEH/CON group. The results of RNA isolation in SON showed little contamination of protein/DNA (260/280 ratio: 1.85±0.19) and organic contaminants (260/230 ratio: 1.08±0.35) and a yield of 65.81±25.65 ng/uL. We found an apparent reduced expression of *Avp1ar* and *Oxtr* in the SON and a significant increased *Adcyap1r1* in H-DE-71 (One-way ANOVA, Tukey's *post-hoc*, $p<.05$, n=11-14/group). PBDEs may affect social behavior and neurodevelopment via neuropeptide expression and may be a risk factor for ASD in males as well as females.

IDENTIFICATION OF *BOTRYOSPHAERIACEAE* SPECIES CAUSING AVOCADO BRANCH CANKER DISEASE IN SOUTHERN CALIFORNIA

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Avocado (*Persea americana* Mill.) is a significant crop to California's economy, planted in Southern and Central California. Avocado is susceptible to multiple diseases including avocado branch canker (ABC) disease, caused by several fungal species and genera in the family *Botryosphaeriaceae* as well as species of the *Colletotrichum* genus. ABC is a stress related disease developing into a prevalent issue throughout avocado orchards, causing substantial economic losses. ABC causes depressed cankers on trunk and branches. The infection can advance to the vascular system of a tree blocking the water and nutrition flow, weakening it, and leading to branch and twig dieback. In this work we collected around 400 isolates from diseased avocado samples from orchards in Riverside, San Diego, and Ventura counties for fungal isolation and identification using morphological and molecular methods. After cutting samples into small pieces, we disinfected them with 5% bleach for 2 min, 75% ethanol for 1 min and rinsed twice with sterile distilled water. Plated onto growth media and stored at 25 °C in the dark, colonies were purified using agar plug method. For molecular identification, DNA was extracted from mycelia of 7-day-old cultures of 60 isolates using a DNA extraction kit. The partial nucleotide sequences were amplified from the internal transcribed spacer (ITS-1F/ITS-4R), elongation factor (EF1-688F/EF1-986R), and ß-tubulin (BT2-A-F/BT2-B-R). PCR products will be sequenced and analyzed using phylogenetic analyses to identify the fungal species. Identifying and characterizing causal agents of this disease will assist in developing the appropriate control measures to reduce yield loss.

USING GAMMA-RAY SPECTROMETRY TO STUDY PLANT SOIL RELATIONSHIPS IN LETTUCE FIELDS

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The Salinas Valley in California is a major vegetable production area. However, agriculture in this region has a sizable footprint on surface and ground water quality due to sub-optimal nutrient application. Within-field precision nutrient management is recognized to reduce the environmental footprint of agriculture in other US regions. Unfortunately, it is not a common practice in the Salinas Valley for a variety of reasons, such as: the lack of on-farm rigorous tests and feasibility analyses. To address this issue, this research aims to investigate the within-field relationship between soil texture and lettuce growth curves. This investigation served as a preliminary viability assessment of soil-based precision nutrient management in the Salinas Valley. In our research, we surveyed 10 lettuce fields in the Salinas Valley in July 2022 with a Gamma Ray Spectrometer. We used Gamma Ray Total Counts maps as an indicator for particle size fraction spatial variability in the topsoil (0-40cm). Furthermore, we used PlanetScope NDVI (Normalized Difference Vegetation Index) time series to characterize the crop growth at the sites between January 2022-December 2022. Preliminary correlation analyses suggest that crop NDVI correlates with Gamma Ray Total Counts at most fields. The results suggest that soil spatial variability played an important role in determining lettuce growth in 2022. Soil-based management zones may, therefore, be an effective means for improving agricultural management in the Salinas Valley. Future work will investigate how Gamma Ray soil maps may help optimize fertilizer usage and minimize the risk of nutrient leaching, groundwater contamination, and runoff.

BIOCHAR-BASED WATER POLISHING SYSTEMS: A MEANS OF PREVENTING ANTIBIOTIC RESISTANCE DEVELOPMENT IN TREATED MUNICIPAL WASTEWATER

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Traditional wastewater treatments are relatively ineffective in removing antibiotic residues. Utilization of treated municipal wastewater (TMW) in crop production may be harmful as exposure to antibiotics and horizontally transferred antibiotic resistance genes (ARGs) can provoke antibiotic resistance development in environmental bacteria. Antibiotic resistance is a cause for concern as it limits medical treatment options to millions annually. Adsorption of antibiotics using biochar is regarded as an effective, sustainable, safe, and cost-friendly option to reduce antibiotic contaminants in TMW. Mechanizing this process, we created two types of pinewood biochar-based water polishing systems in a lab-scale setting. (i.e, filters with either a mixture of sand/biochar or a single biochar layer in between two sand layers) Since these systems are customizable in their constitution, pinewood biochar was selected based on its high adsorptive properties found in our batch biochar studies. To understand their efficacy, TMW spiked with antibiotics was pumped through these systems, and their effluent was sampled daily. TMW with varying concentrations of antibiotics was also applied to earthworm-soil systems to assess antibiotic accumulation and ARG development under varying polishing system efficiencies. Based on the concentration of antibiotics and the prevalence of antibiotic resistance genes present in the polished water and earthworm-soil systems, we can understand how effective these systems are in mitigating the dissemination of antibiotics and ARGs. In the future, the most effective biochar-based water polishing system will be scaled-up for field studies which could offer one strategy for mitigating antibiotic resistance development in agricultural settings.

BIOMASS ACCUMULATION AND MINERAL NUTRITIONAL VALUE OF SPINACH AND RADISH IRRIGATED WITH TREATED MUNICIPAL WASTEWATER.

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The state of California generates approximately four billion gallons of treated municipal wastewater (TMW) daily. The TMW can be used to irrigate landscapes, nurseries, food, and non-food crops. TMW has not been sufficiently studied for the irrigation of vegetable crops. In this work, we tested local TMW for the irrigation of spinach (*Spinacia oleracea* L., cv. Seaside) and radish (*Raphanus sativus* L., cv Sora) plants cultivated in large outdoor pots filled with a 2:1 basal mixture of sand and loamy sand soil. Irrigation waters were either tap water (TW) or TMW, both adjusted to provide an equivalent of a half-strength Hoagland nutrient solution. Thus, the treatments were T0 – tap water control, T1-TMW, T2 – tap water + 2% cow manure, T3 – TMW + 2% cow manure. Spinach and radish were seeded in a greenhouse, transplanted three weeks later to outdoor pots, and cultivated from May 9 to June 7, 2023. Radish tubers and leaves and spinach leaves were oven dried, finely ground, evaluated for dry biomass accumulation, and analyzed for macronutrients (N, P, K, Ca, Mg, and S), micronutrients (Mo, Cu, Mn, Fe, Cl, and Zn), and Na. Treatments were compared by analysis of variance (ANOVA) with Tukey's test at 5% significance. There was no significant effect between TW or TMW for nutrient accumulation or biomass for both spinach and radish. Manure significantly increased leaf K and P and decreased Ca and Mg in spinach. However, decreased Ca and Mg had no detrimental effect on spinach leaf biomass. For crops irrigated with TW or TMW, manure led to a significant decrease in leaf Na in both crops. Manure led to a significant increase in spinach leaf biomass. Our results support the use of TMW and cow manure in the production of irrigated vegetable crops.

TENSOR-BASED ANOMALY DETECTION IN CROP SATELLITE DATA OVER TIME

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Machine learning, a rapidly advancing sector in computer science, involves collecting vast amounts of data, intelligently identifying hidden patterns, and categorizing data using algorithms. Our effort will imprint machine learning methods to detect anomalies within California-based crop fields over time via satellite data. These anomalies can produce data indicating a pest infestation, disease, or other issues affecting a crop's growth. Tensors are multidimensional arrays that allow a facile implementation of multitudinous data. Considering this, we can also decompose tensors under the process of tensor decomposition. Tensor decomposition allows us to derive hidden patterns or "anomalies" from a tensor. Furthermore, we will determine the benefits and flaws of each tensor method. Tools and techniques from other experiments will be implemented throughout this project. CalCrop21, a dataset covering California's central valley at a 10m image resolution, crucial for eliminating unnecessary noise in big data analysis. Using Tensorly, a quick and efficient Python library for tensor methods, enables direct tensor decomposition, tensor learning, and tensor algebra operations. We can output a Normalized difference vegetation index Value (NDVI), allowing to distinguish how "green" a crop is. Apparent insight into the NDVI value predominantly linked to a spatiotemporal pattern can be achieved through a visualization method derived from a latitude and longitude graph. We'll evaluate these graphs by how well the tensors can find anomalies in the satellite dataset and how they compare to other tensor methods. This concludes the experiment's goal of using visualization and tensor techniques on satellite data to identify and manage anomalies, thereby conserving resources in agriculture.

INVESTIGATING THE BIOCHEMICAL ACITIVITY OF PIR-2

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In eukaryotic cells precursor mRNA is transcribed with a 5’ triphosphate group and capped with a guanine nucleotide in the nucleus, and then it is exported to the cytoplasm for translation. Viruses also generate RNA with a 5’ triphosphate group at certain stage of their life cycle, usually in the cytoplasm. Eukaryotic cells divide multiple mechanisms to detect viral triphosphorylated RNA in the cytoplasm based on RNA structure and modifications including the 5’ end triphosphate group since cellular RNA and viral RNA have different 5’ end groups. The polyphosphate PIR-1 family is highly conserved in the animal kingdom and its members may modify either protein or RNA or both. We previously demonstrated that represented member PIR-1 is capable of removing a pyrophosphate from triphosphorylated RNA both in vitro and in vivo; PIR-1 is also involved in silencing viruses in C. elegans likely by modifying/removing triphosphorylated RNA. Here we are investigating the in vitro function of PIR-2, of PIR-1 paralog. Like PIR-1, PIR-2 is also an essential protein, suggesting PIR-1 and PIR-2 aren’t overlapping functions. Since PIR-2 is similar to PIR-1, we are suspecting it may also modify triphosphate RNA rather than phosphorylate the protein. In this project we generated recombinant wild type and catalytic-dead proteins and assayed its activity on triphosphorylated RNA and phosphorylated protein in vitro. We will also investigate its role in vivo.

CHEMICAL CAMO: CUTICULAR HYDROCARBONS HELP CALIFORNIA ANTS KNOW FRIEND FROM FOE

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The Argentine ant, *Linepithema humile*, is an invasive ant species from South America known to displace native ant species in their introduced territories. The Argentine ants' aggressiveness may play a key role in their invasion success, but cues that elicit aggression are not fully understood. This project tested the role of cuticular hydrocarbons (CHC) in interspecific and intercolonial identification and its relationship to aggressiveness. We examined this by adding CHCs from a native ant (*Forelius pruinosus*) and two different supercolonies of *L. humile* to focal individuals of *L. humile* or *F. pruinosus*. We conducted behavioral assays to assess aggression toward and by focal ants when confronted by 3 *L. humile* individuals. We found that aggression was highest in our interspecific treatment where 1 *F. pruinosus* interacted with 3 *L. humile*. We also found aggression was at its lowest when our focal ant was 1 *L. humile* treated with *L. humile* odor. Adding another species' cuticular hydrocarbons to our focal ants revealed that our focal ants had varied reactions to both nestmates and non-nestmates. This study contributes to our understanding of how chemical signaling mediates ant-ant interactions.

TESTING A METHOD FOR STUDYING INTERACTIONS BETWEEN mRNA-BOUND PROTEINS

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RNA-binding proteins (RBPs) regulate mRNA, often by binding to the 3' untranslated region (3'UTR). Multiple RBPs can bind mRNA simultaneously and may interact. The RBP Pumilio (PUM) and the protein Argonaute coupled with microRNA (miRNA) typically destabilize mRNA and lead to its decay. Although the locations of PUM and AGO binding sites in 3'UTRs are known, their effects on each other and on mRNA activity are under investigation. In many cases where the binding sites are close together, it has been observed that interaction occurs between PUM and AGO. This project aims to investigate the extent to which PUM and AGO interact using a library of reporter plasmids. A library of 3'UTR fragments with fluorescent reporters GFP and mCherry was used. Gene sets included a wild type and versions with mutant binding sites if applicable: mutated miRNA binding site (mm), mutated PUM binding site (mP), and mutated miRNA and PUM binding sites (mPm). The goal of this portion of the project is to create test reporter plasmids in a low-throughput format. Test fragment sets were extracted from this library via PCR. Fragments were inserted into vectors to form constructs, which were then grown in *E. coli* and verified for the correct insert. Constructs for several test fragment sets are undergoing development. In future steps, the constructs will be transfected into dox-inducible PUM and DICER cells which will be analyzed via fluorescent reporter assays for the activity and potential interactions of the PUM and AGO sites in the mRNA fragments.

IMPACT OF ANTIBIOTICS ON AGRICULTURAL SOIL MICROBIOME

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Antimicrobial resistance (AMR) in the food production industry poses alarming health risks. The use of treated municipal water (TMW) for agricultural irrigation offers a sustainable solution to the already exhausted water resources. TMW and soil amendments such as animal manure are used in the irrigation of crops. They contain traces of residual antibiotics which allow for the presence of AMR on the soil microbiomes to develop. The objective of this study was to elucidate the effects of residual antibiotics entering via irrigation through the liquid phase (TMW) and solid phase (animal manure) on the soil microbiome. Spinach and radish plants were cultivated with tap water (control), TMW (with antibiotics), and manure (with different antibiotic concentrations). After six weeks of growing, the impact of antibiotics on soil microbiomes were determined by 16S rRNA amplicon sequencing and qPCR. The result of this study will provide a better understanding on how the soil/plant continuum reacts with the residual antibiotics in the irrigated TMW and animal manure.

SPREAD OF ANTIBIOTICS THROUGH TREATED WASTEWATER-SOIL-PLANT CONTINUUM

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Treated municipal wastewater (TMW) is potentially useful for agricultural crop irrigation, helping to reduce the demand on potable water sources. However, conventional wastewater treatment plants might not effectively remove emerging contaminants of concern, such as antibiotics. Therefore, using TMW for agriculture may pose a risk for the agricultural soil, crops, and ultimately human health due to the development of antimicrobial resistance in agricultural systems. As such, it is necessary to provide farmers with proven, cost-effective approaches to reduce the transfer of antibiotics from soils into the food chain. In this study, we used locally collected TMW spiked with the common antibiotics sulfamethoxazole and trimethoprim (10 and 100 ppb) to irrigate spinach plants grown under controlled conditions. As a mitigation strategy, we also amended the soils with biochars (derived from biosolids and pine wood), which it was hypothesized would strongly adsorb the antibiotics in the soil matrix and prevent their uptake by the spinach. Soils and plant materials were collected after the experiment and solvent-extracted to assess the fate and transport of the antibiotic in the soil/plant continuum. The preliminary results indicated that biochar amendment reduced the spinach uptake of both antibiotics relative to the control (no biochar treatment). The pine wood biochar was particularly effective, likely due to its very high surface area which increases antibiotic adsorption potential. The results suggest that biochar amendment of soil may offer an effective, low-cost approach for preventing the dissemination of antibiotics, and hence antibiotic resistance, in agricultural food chains.

GENETIC DISSECTION OF MEcPP-MEDIATED BIOFILM SUPPRESSION

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Biofilm provides a safe environment to nurture growth of bacteria and isolate them from adverse stresses such as antibiotics, which causes various problems in the human health and within the industry. Preliminary research in the Dehesh lab has shown that accumulation of the intermediate metabolite, called methylerythritol cyclodiphosphate (MEcPP), within the methyl-D-erythritol phosphate pathway greatly reduces biofilm formation. To further understand the molecular mechanism of the MEcPP-mediated biofilm suppression, the Dehesh lab has identified 250 transposon insertion mutants with recovered biofilm formation despite high levels of MEcPP. To investigate the mechanism of MEcPP-mediated biofilm suppression and identify the causative mutation, we use arbitrarily primed PCR combined with the Nanopore sequencing technique to identify the transposon insertion sites in these mutants. Our experiment is currently ongoing, therefore data collection is pending. Through the sequencing data, we will have an overview of the molecular components involving the MEcPP-mediated biofilm suppression. The outcome of this research will advance our understanding of biofilm formation, which can help fight against the biofilms-resulted problems in human health and the industry.

EXAMINATION FOR ANY EFFECTS ON GENE EXPRESSION DUE TO A CHROMOSOMAL INVERSION

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On chromosome 10 of some *Oryza sativa* strains, there is an inversion that includes 15 individual genes. This inversion is known to be a result of insertions of the transposable element miniature *Ping* (*mPing*), but the effect of the inversion on these genes has been largely unresearched. To look into these effects, several strains of rice were used: A123, Nipponbare, HEG4, and EG4. The focus was placed largely on the latter two, HEG4 and EG4, as these strains are nearly identical on chromosome 10, with a key difference: EG4 has no inversion, while HEG4 has the *mPing*-induced inversion. Four loci inside this inversion were identified for testing: *Os10g05570, Os10g05660, Os10g05680*, and *Os10g05690*. Before testing began, RNA and gDNA were extracted from each strain, and primers for PCR and qPCR were designed for each gene. Reverse transcription was done on the RNA to yield cDNA for use in PCR. Initially, testing was done using PCR on the extracted gDNA from each strain to ensure the primers correctly worked on the target gene, and following this, the same primers were used on cDNA to identify whether the genes were being expressed. There is not much known about these genes' functions, but further testing is required including qPCR and research into these genes to see how this inversion impacts the rice plant's growth and development.

INVERTED GENOME AND THEIR EFFECT ON *ORYZA SATIVA* GENE

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Oryza sativa, commonly referred to as rice, plays a vital and diverse role as a global nutritional staple, which constantly undergoes research for ongoing enhancements. In this experiment, we focused on the characterization of varying transposon insertions in the genomes of different rice strains, namely *A123*, *EG4*, *Nipponbare*, and *HEG4*. Transposable elements play a vital function in generating new genes and preserving existing ones by facilitating the movement and recombination of chromosomal fragments. We analyzed these different strains to determine the presence of particular genes on Chromosome 10 following the lineage's interplay of inversions and insertions by the transposon. Through DNA extraction and primer design, we were able to isolate the different genes in the 4 strains of rice. Primers for genes *Os10g05580*, *Os10g05590*, *Os10g05620*, and *Os10g05630* were designed utilizing BLAST and Benchling. Through PCR and gel verification, we were able to confirm that genes *Os10g05580*, *Os10g05620*, and *Os10g05630* were present in all 4 strains. This suggests to us consistent gene presence in the inverse genes in *HEG4*. However, with *Os10g05590* it only appeared in *Nipponbare*, proposing to us that this gene's presence in the genome was altered, thus resulting in its absence. We hope our research holds potential implications for understanding genetic diversity and evolution within the rice population and underscoring the necessity of deciphering intricate genomic mechanisms for any future rice related studies.

MPING INSERTION IMPACTS ON GENE PRESENCE IN ORYZA SATIVA STRAINS

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Oryza sativa, commonly known as rice, is the most globally consumed crop. As the world population continues to grow, the issue of producing enough food necessitates the exploration of novel agricultural genetic variations, allowing for the growth of sustainable and economically viable crops. Research on the genetic mechanisms of rice, particularly transposable elements, have served as a point of interest attributable to the advantages in controlling gene expression, regulation, mobilization, and recombination. Our experiment was performed to determine if mPing insertions in the inverted *HEG4* strain against the *EG4*, *A123*, and *Nipponbare* strains resulted in genomic diversification. Genomic DNA extractions were tested for gene loci *Os10g05600, Os10g05550, Os10g05610,* and *Os10g05540* on chromosome 10. Preliminary results show that the *Os10g05550* locus was present on all of the strains, while the *Os10g05600* and *Os10g05610* gene loci were present only in the *Nipponbare* strain, and *Os10g05540* was only found in *A123*. Further research may explore the development of genetically modified *O. sativa* through the use of transposable elements.

ANALYZING SALT STRESS RESPONSES IN MAIZE KATANIN MUTANTS

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Investigating plant salt stress responses is vital due to rising soil salinity within agricultural settings. Microtubules–tubulin polymers facilitating cell division, elongation, and intracellular movement–reorganize to promote plant resilience to environmental stimuli such as salt and temperature stresses. Katanin, a microtubule-severing protein, influences microtubule dynamics and has previously been proven as important for salt stress responses in the model plant Arabidopsis thaliana (Yang et al. 2019). This project examines whether katanin mutants in the model monocot crop plant Zea mays (maize) have differing salt stress responses from wild type. To study the impact of salt on maize root growth, we conducted initial salt experiments where we grew 150 seedlings segregating for katanin mutants in five different salt concentrations. Preliminary germination results suggested that heterozygous mutants had higher salt tolerance than the homozygous mutants and wild type, but all treatments displayed considerable variability. Root growth data analysis revealed that heterozygous plants generally had more stable root growth rates than wild type and homozygous plants. The heterozygous and homozygous mutants were shown to have higher salt tolerance via longer root length over the span of 10 days than wild type. Further experiments with larger sample sizes in two concentrations will be done to confirm our findings and test the differences in wild-type and heterozygous plant salt responses compared to homozygous mutants. The discoveries made from this study can contribute to salinity-specific agricultural improvements as well as the better understanding of the role that cytoskeleton modifications play in stress responses.

CHARACTERIZATION OF ACT DOMAIN REPEAT GENES IN ARABIDOPSIS THALIANA

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Karrikins are smoke derived compounds that promote germination in plants. Understanding how plants perceive karrikins (KARs) and how karrikins regulate plant growth will benefit both farmers and consumers. Karrikins mimic an endogenous compound in plants known as KAI2 Ligand (KL). However, this molecule has not been discovered. In Arabidopsis Thaliana, KARs/KL, are perceived by the receptor KARRIKIN INSENSITIVE2 (KAI2) which then interacts with MORE AXILLARY GROWTH2 (MAX2) in order to degrade SUPPRESSOR OF MAX2 1 (SMAX1). We found that ACT DOMAIN REPEAT PROTEINS (ACRs) enhance KL and KAR metabolism in plants. ACRs have 4 ACT domains which bind small molecules. Thus, ACR proteins may be able to bind molecules such as amino acids. I tested responses to glutamine and arginine in ACR5 overexpression lines. Homologous ACR proteins in Oryza sativa bind glutamine and they bind arginine in humans. To test this hypothesis, I completed a series of root and hypocotyl assays comparing wild type to knockout of kai2, kuf1, and overexpression of 35S:ACR5, with different concentrations of arginine and glutamine. The results show that there are significant effects in both hypocotyl length and root length with the presence of arginine and glutamine. Overexpressing ACR5 reduces root length but enhances glutamine responses. Glutamine caused wild type hypocotyls to significantly increase, however, it caused 35S:ACR5 hypocotyls to significantly decrease. The root lengths of ACR5 are consistently smaller than wild type under normal conditions and both genotypes have shorter roots when treated with arginine. The data shows that responses to arginine in ACR5 overexpression are repressed. Moreover, 35S:ACR5 seedlings are less sensitive to arginine. These results suggest ACR5 regulates amino acid and karrikin responses.

UNDERSTANDING THE INVOLVEMENT OF RLK-RELATED TO IRK4 (RRI4) IN ROOT DEVELOPMENT

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Within living systems, the activation and repression of cell division is vital to multicellular eukaryotic organism function and development. Specifically in plants, cell division orientation is critical for proper growth and development. Understanding the mechanisms involved in the orientation of plant cell divisions will lead to a better understanding of how tissues are patterned and cell fates are established. In the Arabidopsis root, the precise organization of cells and tissues allows for differences in normal development of the root to be easily observed. The examination of two related receptor-like kinases (RLKs), IRK and PXC2, shows that a double mutant exhibits excess endodermal longitudinal anticlinal cell divisions, thus resulting in a wider root. To have a deeper understanding of how these proteins repress cell divisions, I am working to understand the function of RLK-related to IRK4 (RRI4). IRK and RRI4 are in the same protein subgroup and we predict they may have similar functions in the root. To test this, I will examine transcriptional and translation reporters to determine where and when RRI4 is expressed and if it is polarized. I will also examine mutant combinations to determine if these proteins have redundant functions in the repression of cell division. My work will help us further understand the involvement of RRI4 in the relationship between lateral cell polarity and repression of cell division in plants.

MICROBIOME IN 16S BARLEY SEEDS

Nicole Ormeno

When thinking about beneficial things for plants, people would never associate bacteria and plants together. Past studies have shown that certain bacteria can enhance plants in a variety of ways. In this current study, we will identify different types of bacteria and archaea in barley seeds. We will use a normal seed that was grown on a field, a seed that was grown in a greenhouse, a seed that was bleached, and a bleached seed embryo. We will extract the DNA from each sample to see if a band appears. This will help us see if the bands are strong enough to withstand PCR. From there, we will perform PCR to amplify the DNA. If the PCR is successful, we will purify the DNA to create our DNA supernatant. Next, we will send our DNA to get sequenced. Lastly, we will use the sequence to identify the different types of bacteria in the 16S gene. We are currently continuing with this project and have no results. Our goal after this project is to see if there are any beneficial bacteria in the barley seeds or within the environment and if the bacteria are inheritable. If there are beneficial bacteria in the plant, we plan to do the same procedure with fungi, in hopes to get successful results to further our project.

ORAL SESSION 3

INTERPLAY OF VARIOUS TRANSCRIPTION-RELATED PROTEINS ON CELL IDENTITY

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Proteins play a vital role in comprising our physical characteristics as well as maintaining bodily processes and other functions. They are constructed from the nucleic acid known as messenger RNA (mRNA), which in turn is constructed from DNA, the genetic information in each of our cells. This mRNA-from-DNA relationship is known as transcription. Cellular regulation of transcription, controlling the when and where of mRNA production, plays a critical role in differentiation, a dynamic process in which a cell with generic features develops specialized functions, such as immune cell functions. However, the exact relationship between transcription regulation and cellular differentiation is unknown. Histone chaperones are a diverse class of proteins that help regulate all DNA-mediated processes and are a good subject for study into this relationship. By targeting the DNA replication-associated histone chaperone CAF-1 and the transcription-associated SPT6, we used loss-of-function assays to investigate the relationship of these molecular processes in maintaining the identity of granulocyte-macrophage progenitor cells (GMPs). GMPs are niched in the bone marrow and have the potential to differentiate into white blood cells, such as neutrophils. We report that depletion of histone chaperones SPT6 and CAF-1 alters the progenitor identity by allowing different transcription-related factors, such as the AP-1 transcription factor family, to drive alternative gene programs. To validate these findings, we are establishing a CRISPRi system in GMPs to transcriptionally silence these genes, which will allow us to confirm the functional importance of our transcription factor candidates. These findings could improve understanding of blood diseases like leukemia.

TARGETING TLR4 AND MMP-9 TO LIMIT NEUROPATHOLOGY AFTER BRAIN INJURY

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Traumatic brain injury (TBI) often leads to epilepsy through multiple mechanisms which are not well understood. TBI causes inflammatory responses including increased Toll-like receptor 4 (TLR4) signaling, and blocking TLR4 after TBI reduces risk for epilepsy. We examined whether TLR4 signaling could act through increasing Matrix metalloproteinase-9 (MMP-9), an enzyme critical for synaptic remodeling, to alter cell loss and circuit changes after TBI. Juvenile rats (PD25-28) were subject to fluid percussion injury (FPI) which leads to reproducible hippocampal dentate neuronal loss and increased risk for epilepsy. Both FPI and sham-injured animals were injected intraperitoneally with either DMSO (vehicle), TLR4 antagonist (CLI-095), or MMP-9 blocker (SB-3CT) immediately after injury. Rats were perfused 6 weeks later and slices underwent Nissl staining to quantify cell numbers in the dentate and immunostaining for the zinc transporter ZnT3 to reveal recurrent sprouting of mossy fibers into the Inner Molecular Layer (IML). FPI in juvenile mice did not lead to mossy fiber sprouting. FPI rats that received DMSO treatment showed fewer hilar Nissl stained neurons compared to sham injured rats. However, the number of Nissl stained neurons was not different between sham and FPI mice following either CLI-095 or SB-3CT treatment. These data indicate that TLR4 and MMP-9 antagonists can reduce neuronal loss after TBI. Future studies should examine the link between TLR4 and MMP-9 and determine whether age at TBI influences development of mossy fiber sprouting.

NOREPINEPHRINE INHIBITION AND NEURAL RESPONSES TO PUPS IN MALE CALIFORNIA MICE

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The neural mechanisms underlying paternal care in biparental mammals are not well understood. The California mouse (Peromyscus californicus) is a monogamous rodent in which fathers provide extensive care to their offspring. While virtually all fathers are attracted to pups, virgin male California mice vary widely in their behavior toward experimentally presented unrelated pups, ranging from attacking to avoiding to huddling and grooming pups. A previous study in our lab found that pharmacologically inhibiting synthesis of the neurotransmitter norepinephrine (NE) reduces the propensity of virgin California mice to interact with pups. However, we do not yet know if inhibiting NE synthesis influences neural activation in response to pup stimuli. Therefore, the current study examined the effects of inhibiting NE synthesis on pup-induced c-Fos immunoreactivity, a cellular marker of neural activity, in the bed nucleus of the stria terminalis (BNST), a brain region associated with parental care and anxiety. The selective and potent dopamine β-hydroxylase inhibitor nepicastat was administered to inhibit NE synthesis. Virgin males were injected with nepicastat (75 mg/kg, i.p.) or vehicle 2 hours prior to exposure to either an unrelated pup or novel object for 60 minutes. Following the 60-minute stimulus exposure, mice were sacrificed and their brains collected for c-Fos-immunohistochemistry. Our results suggest that nepicastat treatment did not alter c-Fos expression in the BNST following pup exposure. Overall, results from these experiments may provide an understanding of the role of NE in the regulation of paternal responsiveness in a biparental species.

AGENT-BASED MODELING OF NEUTROPHILS IN WOUND HEALING

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Wound healing in the human body involves an orchestration of various cellular responses. As the first responders to a skin wound, neutrophils swarm to the wounded region to fight bacteria. They migrate toward the wound region in an amoeboid mode. Neutrophils are short-lived, and early stages of neutrophils' chemotaxis consist of at least three steps: 1) neutrophils close to the wound respond and migrate to the wound, 2) first responder neutrophils die, leaving cell fragments and releasing signals in the region, calling for more neutrophils, and 3) intercellular responses through diffusive signals are triggered, further amplifying the swarming. To investigate the individual behaviors in neutrophil swarming, we develop an on-lattice, agent-based model on neutrophil swarming. Using the agent-based model, we investigate the effect of neutrophils' short lives on their chemotaxis behaviors and identify the key factors that guarantee the success of neutrophil swarming dynamics.

ROLE OF ESTROGEN IN SOYBEAN OIL INDUCED WEIGHT GAIN

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Reduced estrogen levels in older women are correlated with increased weight gain, with its key role in regulating weight gain and metabolism being at the forefront of this. Studies have shown that a decrease in this key hormone plays a major role in the accumulation of visceral fat, overall body mass increase, and obesity. Older female mice, particularly those that have reached menopause, are more susceptible to weight gain due to their decreased estrogen levels. Soybean oil (SO) is the most widely consumed edible oil in the US with its consumption increasing exponentially over the last several decades. This increase in consumption correlates with the prevalent obesity epidemic. Previous studies in our lab have demonstrated that a high SO diet can lead to obesity and diabetes in male mice, regardless of age. However, younger female mice tended to not gain weight on a high SO diet. This study aims to investigate whether SO causes obesity in older female mice and whether estrogen plays a role in this weight gain. The experimental setup includes three groups of age-matched female mice being fed one of the following three diets: i) an SO based high fat diet, ii) a custom low-fat diet, iii) standard rodent diet. Body weights of the mice were measured weekly and glucose and ketone body measurements were taken at regular intervals to track development of obesity and diabetes. The results show that the SO diet causes obesity and diabetes in the older female mice, suggesting that lack of estrogen is key in inhibiting weight gain in females.

QUANTITATIVELY MEASURING THE EFFECTS OF GENETIC MOSAICISM

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The objective of this project is to develop a stem cell-based model system in which to quantitatively measure the effects of genetic mosaicism resulting from LINE-1 on human CNS and brain-like neural network development, function, and learning. LINE-1 is an example of a retrotransposon, a genetic parasite that exists within the genomes of all advanced life and which is capable of "copy-paste" replication through a process called retrotransposition. When LINE-1 is misregulated, accumulated mutations due to retrotransposition can result in "genetic mosaicism," which is a condition where each cell in the developing brain is genetically unique. Misregulation of LINE-1 retrotransposition or its repair processes is linked to various diseases, like Ataxia Telangiectasia (AT), Autism Spectrum Disorder (ASD), schizophrenia, and bipolar disorder. So far, we have focused on inducing LINE-1 retrotransposition in human induced pluripotent stem cells (hiPSCs). The human genome already contains ~100 active LINE-1 elements, but they are expressed from their weak, native promoters whose activity is repressed by their host cells. We want to instead express a synthetic LINE-1 element coupled to a fluorescent reporter from a stronger promoter, so that we can upregulate LINE-1 activity and track retrotransposition by fluorescence microscopy. First, we grew hiPSC colonies, monitoring their progress every day. Upon maturity, we transfected the cells with either our fluorescently tagged LINE-1 construct ("LRE3-EGFP") construct or a mutated, nonfunctional control ("JM111-LRE3-EGFP"). Upon transcription and retrotransposition, the EGFP gene will be expressed, which can be detected through fluorescence, thus allowing us to detect retrotransposition. After transfection, we grew the cells once again, looking for fluorescence, which would indicate if retrotransposition was happening or not. In our most recent batch, we observed fluorescence in the LRE3-EGF batch of cells, but not the JM111-LRE3-EGFP batch. This is promising, as it indicates induced retrotransposition.

KNOCKOUT OF *LsARF3* IN *LACTUCA SATIVA* TO INCREASE BOLTING RESISTANCE

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Lactuca sativa, also known as lettuce, is a staple crop for many cultures around the world. Despite an increasing need for greater crop yields, global warming has caused decreases in agricultural productivity. Lettuce is a hardy plant with an optimal growing temperature range between 60°F to 75°F. Temperatures above this threshold induce bolting, which renders the crop non-consumable. Major lettuce-growing states such as California and Arizona are impacted the most and have to accommodate the rising temperatures through early harvest and relocation. We propose a solution to the bolting problem with a knockout of the *LsARF3* gene, an auxin response factor, which has been shown through preliminary research to reduce bolting rates when underexpressed. We will use CRISPR-Cas9 mediated mutagenesis to knockout the gene, with emphasis on creating a non-GMO product. By performing a knockout on *LsARF3*, we aim to enhance lettuce yield and quality through longer maturity timeframes. We hypothesize that this technology can also serve as a long-term investment for agriculture in light of climate change.

POSTER SESSION 2

NEUROMESODERMAL PROGENITORS AND THEIR CONTRIBUTION TOWARDS NEURAL CREST CELLS

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Neural Crest Cells (NCCs) are a multipotent population of cells, unique to vertebrates, capable of differentiating into a wide assortment of derivatives, including craniofacial bone and cartilage, as well as peripheral nervous system neurons and glia. Traditionally, NCC are thought to originate from the ectoderm. However, recent reports have linked their origin with Neuromesodermal Progenitors (NMPs). As the name indicates, this progenitor population generates either neural or mesodermal derivatives, and it is thought that they can also contribute to NCC. NMPs are characterized by the coexpression of Neural and Mesodermal genes (Sox2 and Bra, respectively), while NCC expresses Pax7. To reassess the contribution of NMPs to NCCs, I first tested the specificity of antibodies against these markers to examine their expression in chick explants. These explants are obtained from the posterior open neural plate of HH8-10 chick embryos, set on collagen gels, and either analyzed at time “0” or after 16 hours of culture via immunofluorescence. A total of five trials were conducted inspecting the NMP region and the anterior/posterior neural folds of the open neural plate. Pax7 and Bra cells were readily visible in Trial 5 and Sox2 in Trial 4. While these observations suggest an abundance of Pax7 positive cells located around the posterior and anterior neural folds, more experiments are needed to rigorously assess the contribution of NMPs to NCC.

THE F3’5’H GENE ON ANTHOCYANIN PIGMENT IN *PENSTEMON* ALONG AN ELEVATIONAL GRADIENT

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In this study, we examine a gene expected to be responsible for floral color change from blue to pink between two species of *Penstemon* found along an elevational gradient, *Penstemon davidsonii* and *Penstemon newberryi*. In particular, our focus is on the Flavonoid 3’5’-hydroxylase (F3’5’H) gene, a principal component of the anthocyanin pigment pathway. A thorough analysis of the F3’5’H gene within these species of *Penstemon* will help to determine the repeatability of evolutionary changes in this gene across species of flowering plants. We do this by using PCR to amplify the F3’5’H DNA sequence which is then visualized by running gel electrophoresis. The resulting gel contains information that allows us to distinguish between DNA fragments of varying lengths, therefore making intact copies of the F3’5’H gene discernable from those that are inactive because of deletions. After imaging the gels, genotyping the individuals, and compiling the resulting data, we can draw conclusions about the function and role of F3’5’H. We expect short DNA fragments to correlate to pink flowering individuals, long fragments to correlate to blue flowering individuals, and heterozygotes to have a hybrid mix of colors. Because the two species, pink *Penstemon newberryi* and blue *Penstemon davidsonii*, are found at different elevations, we expect to see a correlation between genotype and elevation. From this, we can conclude that the color shift caused by the loss of function of the F3’5’H gene may be a reflection of parallel evolution and the *Penstemon*’s repeated adaptation to environmental constraints.

NUEROSCIENCE UNDERLYING APHANTASIA ABSENCE OF IMAGERY

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In everyday settings, humans are crowded by visual information that may or may not be relevant to their current task. When navigating important information, it is beneficial to mentally visualize items (e.g., house keys) to complete a visual task (e.g., locking the door when leaving the house). An underlooked population is those who are unable to 'see' in their minds, a condition called aphantasia. Are these individuals at a disadvantage compared to their visual counterparts? Do these disadvantages hinder everyday learning, such as in schools or workplaces? My research investigates the cognitive profiles of imagery (or lack thereof) and how the brain functions differently when imagery is poor or impossible. Through a series of EEG and eye-tracker experiments, we use complementary techniques to measure behaviors and biological responses. While running experimental sessions and analyzing large coding datasets, one main concern was the subjectivity of accurately assessing one's own imagery. Our results show an exciting new objective method to measure visual imagery and the first physiological evidence of aphantasia. Interestingly, aphantasic individuals report fewer and qualitatively impoverished dreams compared to controls. Establishing a comparatively moderate expected effect size of $d = 0.5$, with 80% power and a highly conservative alpha of 0.0002 (Statistical Analyses in Methods), we estimated that at least 170 participants would be required in each comparison group. These questionnaires assessed self-reported multi-sensory imagery, episodic memory and future prospection, spatial abilities, mind-wandering and dreaming propensity, and response to stressful life events. The aim of the present study was to investigate the subjective impact of visual imagery absence on cognition.

A CONDUCTIVE 3D BIOPRINTED PLATFORM FOR NEURAL TISSUE REGENERATION

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The advanced adaptability of 3D bioprinting has ushered in innovative strategies in regenerative medicine. The potential of highly personalized 3D bioprinting stands to transform both neuroregenerative medicine and the treatment of debilitating conditions. These conditions include traumatic brain injury and neurodegenerative diseases such as Alzheimer's and Parkinson's. Given the limited regenerative potential of the mammalian central nervous system, 3D bioprinting of cell-laden constructs in vitro or at the defect site has the potential to promote the regeneration of damaged neural tissue. Achieving optimal outcomes in neuroregeneration through 3D bioprinting hinges on designing a bioink that provides a tissue-like microenvironment for the survival and maturation of neuronal cells. In this study, we developed a bioink comprised of gelatin methacrylate (GelMA) and bio-ionic liquid (BIL), termed "BioGel". This composition leverages BIL's conductivity, providing physiological cues for neuronal cell maturation and functionality. Human induced pluripotent stem cell-derived neural stem cells (i-HNSCs) were incorporated into the 3D bioprinted constructs. Evaluation of cytocompatibility through cell viability tests showed good survival and significant proliferation of i-HNSCs embedded in the scaffold matrix. These findings underscore the tremendous potential of the BioGel platform in advancing therapeutic strategies for neuroregenerative diseases.

CLIMATOLOGICAL AND AGRICULTURAL INFLUENCE ON CALIFORNIA GROUNDWATER TRENDS

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Agriculture in California depends heavily on groundwater extraction, which could in turn impact groundwater levels. This study investigates the possible correlation between well water depletion and proximity to farmland. We are concentrating primarily on the differences between agricultural and non-agricultural sites and how they may be amplified due to precipitation and other factors. Groundwater level observations for a 2010-2018 period were extracted from the USGS groundwater level monitoring network in California. The 2014 California Crop Cover Map was used to determine well location in relation to farmlands and other major land uses in the state. We included data from 361 wells corresponding to 780,000 measurements for the analysis. We performed exploratory data analysis in Python to understand trends and variability in groundwater level observations using linear univariate regression and boxplots, respectively. Preliminary findings suggest that groundwater levels in both agricultural and non-agricultural areas are declining for the analysis period. When analyzing the trend at each site, in higher precipitation percentiles, the slope for farmland is much higher than for non-agricultural land, indicating faster depletion rate. These early findings show that proximity to farmland correlates to well water depletion, which suggests a causal relationship. Further research, possibly using a larger data set and different data science techniques, is needed to solidify any results.

AN ASSAY FOR LOCAL ADAPTATION IN DROSOPHILA MELANOGASTER

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When two populations colonize distinct environments, different environmental pressures select for traits well suited to their respective environments in a process called “local adaptation.” It is generally understood that as a population evolves traits that make it better suited to a certain environment, those same changes inadvertently cause the population to be less suited to others. This phenomenon is called an adaptive trade-off. For example, a population that, over time, adapted to a high-salt diet may no longer be fit for a low-salt diet, and vice versa. However, it remains unclear how often local adaptation results in an adaptive trade-off. Here, we show that differences in food’s salt content among populations can lead to local adaptation as well as the adaptive trade-off phenomenon. We found that in controlled reciprocal transplant assays, populations of salt adapted and non-salt adapted populations of *Drosophila melanogaster* both displayed a “home site advantage.” This is in line with the generally accepted relationship between local adaptation and adaptive trade-off. Our results demonstrate how local adaptation has the potential to bring about the trade-off phenomena. We anticipate that our assays will add to the existing body of knowledge with regard to local adaptation and adaptive trade-offs. Additionally, *Drosophila melanogaster* is a common model species in the field of population genetics, and a quantitative assay with regard to local adaptation and adaptive trade-off using this species will be relevant in the field.

DROSOPHILA MELANOGASTER ENDOGENOUS PLA2 PROVIDES TOLERATION AGAINST INFECTION

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In insects such as *Drosophila melanogaster, Phospholipase* A2 (PLA2) are effector proteins that play an important role in immunity and other physiological functions. PLA2's cleave cellular, non-cellular, and exogenous phospholipids to create eicosanoid precursor arachidonic acid. It can also cleave saturated, monounsaturated, and polyunsaturated fatty acids. *D. melanogaster* is an important model for immunity and has led to numerous translatable immunological discoveries for humans. By having large volumes of offspring and a short maturation period, *D. melanogaster* is an efficient and reliable model to test immunological properties. CG1583 encodes for an endogenous PLA2 in *D. melanogaster* and is the focus of study in this paper. CG1583 was expressed recombinantly and purified by nickel purification. Activity and ligand binding preferences of the protein were tested by mass spectrometry. To test any immunomodulatory effects, 180 flies were coinjected with varying doses of *Streptococcus pneumoniae* and 40ng CG1583. After injection, 8 flies per replicate from both the control and tested group were plated to count colony forming units (CFU). This was done both directly following injections as well as 24 hours after. Data shows that CG1583 provides a tolerating effect against various doses of *S. pneumoniae*. This was determined by analyzing the CFU bacteria growth at the 0-hour and 24-hour marks as well as the percent survival. Although bacteria growth is not inhibited by CG1583, survival data shows a clear increase in survival against the bacterial challenge.

EVALUATION OF THE PHENOTYPE AND FITNESS COST ON *WHITE* AND *CINNABAR* MUTANTS

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Eye color genes are used to validate molecular tools such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats and CRISPR-associated proteins) by providing a visible phenotype of the mutations. The purpose of this study was to identify phenotypes and fitness costs associated with mutated eye color genes in comparison to the wild type in two important agricultural insect pests *Bemisia tabaci* and *Homalodisca vitripennis*. A literature review was conducted on the phenotypes of white mutants of *Drosophila melanogaster*, which is the model organism for insects and has extended studies about its eye color genes. The DNA, amino acid, and phenotype differences of *white* mutants between *D. melanogaster* and *B. tabaci* can inform current and future gene editing experiments. Additionally, the embryo and nymphal development of two mutant lines of *H. vitripennis* were evaluated in comparison to the control wild type. Those lines were generated by CRISPR-mediated mutation of the *cinnabar* and *white* genes. Six to eleven egg masses from each line were collected and the embryo and nymphal development were recorded daily on a leaf-disc system. The number of days between each stage of development, as well as the percentage of eggs and nymphs that developed, was then analyzed. It was found that *white* mutants took an average of 7.38 days to hatch, while having a hatching rate of 12.43%. In contrast, c*innabar* mutants took an average of 7.23 days to hatch, while having a hatching rate of 61.84%. Wild type eggs had an average hatching time of 7.05 days and had a hatching rate of 56.70%. Since *white* eggs had a significantly lower hatching rate than that of wild type, the results may indicate that *white* mutants have reduced fitness, while *cinnabar* mutants do not.

IN VITRO STEM CELL MODELS TO PREDICT ADVERSE EFFECTS OF CHEMICALS ON BONE DEVELOPMENT

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About 3% of all birth defects have been linked to the prenatal exposure of pregnant women to environmental toxicants, which is roughly 3,600 babies per year. Many of these babies are born with heart or brain defects. Musculoskeletal defects, including malformations in facial and other bones, represent many of these birth defects. Since many chemicals in our environment are untested for their safety, the embryonic stem cell test (EST) was introduced in the early 90s to predict toxicity *in vitro* without the use of animals. The EST uses embryonic stem cells from the mouse (mESCs) to mimic bone development in the embryo. During a 20-day period of *in vitro* differentiation, mESCs are exposed to a toxicant at different concentrations. Cytotoxicity and matrix calcium production is then tested with an MTT assay and a calcium assay, respectively. For example, differentiating mESCs were exposed to ethylparaben, a paraben naturally found in fruits and insects which acts as an antimicrobial agent in skincare products. It was found that the dose where cell viability remained unchanged, but produced a decrease in calcification was at an ID50 Calcium value of 208.5 µg/mL, which potentially indicates inhibition of osteogenic differentiation at subtoxic concentrations. From a safety perspective, this suggests that pregnant women can unknowingly be exposed to environmental toxicants, including in their skincare, which can adversely affect their babies. This research will allow efficient screening of these toxic chemicals and observe their effects on osteogenic differentiation, as the expected impact is to better understand how toxicants affect embryonic bone development.

ROBUST POSE PREDICTION FOR OCCLUDED BODY PARTS: APPLICATION IN GAIT ANALYSIS FOR A MOUSE PARKINSON'S DISEASE MODEL

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Machine learning is an increasingly useful tool in neurodegenerative disease research for its ability to provide deeper insights into disease pathogenesis, diagnostic tool development, and behavior analysis when determining the effectiveness of proposed models and therapeutics. In particular, using computer vision tools for markerless bodypart tracking enables researchers to perform unbiased, extensive analysis on massive datasets of animal behavior footage. However, the leading pose estimation toolkits, such as DeepLabCut (A. Mathis, et al. 2018), which perform with remarkable accuracy on visible keypoints, fail to accurately track keypoints which are invisible due to background- and self- occlusions. Here we present a new adaptation of the DeepLabCut pose network, which incorporates a mean teacher structure and adaptive occlusion to produce a model which is robust to keypoint occlusion (D. Kim, et al. 2022). For model evaluation we follow the PCK metric used by D. Kim et al., which measures the Percentage of Correct Keypoint predictions. The model performance on occluded joint prediction notes a 19% increase in PCK@0.01 (within 1% of the image width: 5.5 pixels) when compared to the original DeepLabCut model. Furthermore, when performing pose analysis on a novel video (3.6K frames) using our model, we note a 32% increase in the proportion of keypoint confidence scores above the threshold of 0.6 (range: 0.0 to 1.0), allowing for cleaner and more cohesive pose data. We therefore propose that our adaptations equip the DeepLabCut model to produce improved pose predictions for both occluded keypoints and novel video data.

IMPACT OF A KETOGENIC DIET ON THE EXPRESSION OF HEPATIC HNFα ISOFORMS

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Ketogenic diets (KD) and other dietary interventions like intermittent fasting diets/regimes have become widespread in America among other health trends focused on weight loss. Physiologically, the mechanism of action of KD centers around the liver's ability to maintain glucose and lipid homeostasis via glycogen breakdown, gluconeogenesis, and ketogenesis. When one follows a ketogenic diet or fasts for long enough, there is a "metabolic switch" that occurs allowing one to utilize ketone bodies for energy instead of glucose, the body's primary energy source. This switch lies between gluconeogenesis, which occurs after blood glucose and glycogen stores have been depleted, and ketogenesis. Hepatocyte Nuclear Factor 4α (HNFα) is one of the main transcription factors involved in this metabolic switch of using fat as the energy source, instead of glucose. HNFα has two promoters, P1 and P2, which regulate the expression of different HNFα isoforms. Different HNFα isoforms drive different metabolic processes. P1 promotes the expression of theHNFα1 isoform, which drives gluconeogenesis, while P2 promotes the expression of the HNFα7 isoform which drives ketogenesis. Changes in the relative expression of these isoforms can have an impact on the metabolic pathways in the body. We and others have shown previously that high fat diets can impact the balance between the isoforms in various tissues, including the intestines and liver. The goal of this project is to determine the effect of a KD on the expression of P1- and P2-HNFα protein in the livers of mice that had been fed a ketogenic diet.

ANALYZING SALT STRESS RESPONSE IN MAIZE KATANIN MUTANTS

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Salt stress is a large and increasingly growing problem in agriculture. The widespread use of irrigation leads to increased levels of salinity and can be detrimental to plant growth and development. In fact, according to the USDA's article on Salt Problems in Irrigated Soils, "[I]t is possible for an acre of irrigated land to receive as much as 25 tons of salt in 1 season." In salt, microtubules in the cell depolymerize and form a new array. An enzyme, KATANIN, works by severing microtubules at crossover sites to maintain regulatory cortical microtubule organization. This is important to consider because microtubule dynamics are essential for many processes, such as cell division, elongation, and stress response in plants. A study was published examining the response of the *katanin* mutant in *Arabidopsis* under salt stress, and showed that KATANIN may play a role in that pathway, but whether maize responds similarly is yet unknown. We are conducting an experiment to determine if *katanin* mutants have a greater resistance towards salt stress in maize by comparing relative root growth rates of homozygous or heterozygous mutants for one katanin allele, versus wild-type plants when grown under various salt concentrations (0, 25, 50, 75, and 100 mM NaCl). Although preliminary results suggest that heterozygous katanin mutants have a higher salt tolerance, due to the sample size, further research is needed in order to draw a firm conclusion. This research could potentially be applied to promote a higher crop yield from plants undergoing salt stress.

Identification and Functional Characterizations of U2AF1-R-loop Interactions in MDS/AML Diseases

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U2AF1 (U2 small nuclear RNA auxiliary factor 1) is an essential splicing factor involved in the recognition of 3' splice sites (3'SS) of precursor messenger RNAs (pre-mRNAs) in most eukaryotes. Recent clinical studies showed that mutations in *U2AF1*, especially at codons 34 (S34F and S34Y) and 157 (Q157P and Q157R), are strongly associated with myelodysplastic syndromes (MDS), acute myeloid leukemia (AML) and lung cancer. Ectopically expressed U2AF1 mutants (i.e., U2AF1S34F and U2AF1Q157P) in human cells led to a global elevation of R-loops and Pol II pausing at transcriptional start sites (TSSs). These findings suggested a functional role of U2AF1 in transcriptional regulation at gene promoters. **However, the underlying mechanism(s) remain(s) unclear, and very little is known about U2AF1's functions at promoter regions.** Given that R-loops are enriched in promoter regions of highly transcribed genes and play important roles in gene regulations, **we hypothesize that U2AF1 may participate in gene regulation through interacting with promoter R-loops, where mutations in U2AF1 may alter U2AF1-R-loop interactions.** Moreover, the augmented R-loops induced by U2AF1 mutations may influence the stability of the U2AF1-R-loop complex, thereby contributing to the development of relevant diseases. Hence, a systematic investigation about how U2AF1 and disease-associated U2AF1 mutants interact with R-loops will provide molecular insights into how mutations in U2AF1 contribute to disease development.

In this study, we will examine the interaction between R-loop and wild-type U2AF1 as well as two disease-associated mutants (i.e., U2AF1S34F or U2AF1Q157P) *in vitro*. To this end, we constructed His-EGFP-U2AF1WT plasmid by amplifying the *U2AF1* gene from a cDNA library and ligating it into pET28a-EGFP plasmid. Subsequently, we employed a site-directed mutagenesis technique for introducing S34F and Q157P site mutations into His-EGFP-U2AF1WT plasmid to obtain His-EGFP-U2AF1S34F and His-EGFP-U2AF1Q157P plasmids, respectively. The sequences of these three plasmids were confirmed by Sanger sequencing. The resulting plasmids will be transformed into DE3 *E. coli* for protein expression, and subsequently subjected to His-tagged protein purification by HisTrap column. After obtaining recombinant His-EGFP-U2AF1WT, His-EGFP-U2AF1S34F and His-EGFP-U2AF1Q157P proteins, we will measure their binding affinities toward R-loops or other DNA/RNA probes using electrophoretic mobility assay (EMSA) experiments.

In the future, we will also investigate how mutations in U2AF1 affect U2AF1-R-loop interactions in HEK293T cells, and assess the functional consequences caused by U2AF1 mutations and elevated R-loops in HEK293T cells and MDS-relevant MDS-L cells. We expect that U2AF1-R-loop interactions will modulate the biological functions of U2AF1 in cells, and this regulation can be altered by U2AF1 mutations.

TESTING *STAPHYLOCOCCUS EPIDERMIDIS* RESISTANCE DEVELOPMENT TO MAGNESIUM OXIDE NANOPARTICLES

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Multidrug-resistant bacteria (MDR) are a major threat to prosthetics, medical devices, and implants. A common MDR bacteria is *Staphylococcus epidermidis,* which thrives on the surface of the skin and mucous membranes. *S. epidermidis* are Gram-positive bacteria and usually harmless, but their introduction into an open wound can lead to pathogenesis. Because of increasing bacterial resistance to antibiotics, nanoparticles have been investigated as promising alternative antibacterial treatments. Here, we are examining the effects of magnesium oxide (nMgO) exposure to *Staphylococcus epidermidis*. For this initial *in vitro* experiment, we determined the highest concentration of nMgO survived by *S. epidermidis* exposure for 24 hours. This concentration coincided with the previously identified nMgO minimum bactericidal concentration (MBC) in lag phase *S. epidermidis.* Future research will use the lowest concentration of 0.7 mg/ml nMgO against *S. epidermidis* as an initial starting point for resistance development experiments and expect to reach a concentration where *S. epidermidis* no longer grows when exposed to nMgO. Applications of nMgO may reduce implant-associated infection by incorporating nMgO into medical devices such as implants and provide alternative treatments for multidrug resistant (MDR) bacteria like *S. epidermidis*.

CHARACTERIZING LIGUELESS DOUBLE MUTANTS IN MAIZE

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Maize leaves are composed of two major zones, the sheath and the blade. The sheath provides support for the plant and the blade is responsible for the majority of photosynthesis. At the blade-sheath junction there are two specialized structures, the auricle and ligule. Auricles are wedge shaped structures formed towards the margins of the leaf that act as a hinge to regulate blade angle and the ligule is a fringe of epidermal cells that closes the gap between successive leaves. These structures arise from the preligule band (PLB) which is made early in development at the junction between blade and sheath zones. Previous work using atomic force microscopy revealed distinct spatiotemporal patterns of cell wall rigidity during ligule formation.

In order to better understand the relationship between these mechanical patterns and ligule development, we are comparing the patterns observed in wild type to those observed in *liguleless1-R*; *liguleless2-R* double mutants, which lack a ligule and auricle. I am processing data from atomic force micrographs of the double mutants to identify patterns in cell wall rigidity in the sheath and blade regions. At the moment, the data is still being processed therefore there are no outstanding results.

MATERNAL PBDES AFFECT OFFSPRING SOCIAL BRAIN CIRCUIT ACTIVATION

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Polybrominated diphenyl ethers (PBDEs) are household flame retardants. PBDEs have been banned because they are associated with neurobehavioral deficits, however, they are still detected in humans and the environment. We have shown that maternal transfer of an industrial mixture of PBDEs, DE-71, causes autistic-like social deficits and deregulated social neuropeptide/receptor gene expression in female offspring. We hypothesized that prenatal DE-71 exposure would decrease social stimuli signaling in the social neural network (SNN). C57BL/6N mouse mothers (GD0-PND21) received cornflake treats with low dose DE-71 (0.1 mg/kg/d, L-DE-71), high dose DE-71 (0.4 mg/kg/d, H-DE-71) or vehicle control (VEH/CON). Exposed mice were sacrificed at PND30 and transcardially perfused 90 min after a 3 min social exposure. Brains were cryosectioned and immunoprobed for c-Fos, a marker of neuronal activity. The number of c-Fos positive cells (normalized to ROI) was greater in the basolateral amygdala of socially exposed groups as compared to sham, VEH/CON (4.3 fold, Student's t-test, $p<0.05$, n=3-4 mice/group) and L-DE-71 (4.3 fold, Student's t-test, $p<0.05$, n=3) but not H-DE-71 (ns, n=2-3). Group comparisons using one-way ANOVA followed by Tukey's *post-hoc*, indicated that c-Fos count in socially exposed VEH/CON groups was greater than L-DE-71 (5.5 fold, $p<0.05$) and H-DE-71 (14.6 fold, $p<0.05$). These results suggest that social deficits produced by developmental exposure to PBDEs may be caused by altering social cue signaling in the SNN.

FORENSIC FLY DIVERSITY IN RIVERSIDE HEAT

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Assessing decomposition rate is an important aspect of forensic science, allowing investigators to determine timelines and methodologies relevant to the scene. Previous studies on UCR campus have studied decomposition rates using pig carcasses during all seasons except summer, leaving a gap in our understanding in this field. Due to the higher temperature, lower humidity, and lack of precipitation in the summer, the rate of decomposition is anticipated to be faster with insects that thrive in hotter months and are more likely to be present. This experiment studies the diversity of forensic flies in Riverside during July through August using two different models.The first model is a beef liver trap with four locations around UCR campus, and the second model is a pig corpse in the agricultural operations area close to the campus. Using the flies collected from all sites, we are determining the diversity of flies attracted to these traps in the summer. We will also be collecting other insect diversity because any insects attracted to or feeding on the liver or pig are forensically relevant. While the study is ongoing, one blow fly species (*Lucilia sericata)*, known to be one of the first flies to arrive at a corpse, has been the most commonly collected from the liver samples. There is a likelihood that after the end of August there may be reared flies that have emerged that could not be added to the data, but currently the pig attracts more diversity of flies than the liver.

LEARNING TO FLY DRONES FOR MULTISPECTRAL IMAGE ANALYSIS IN AGRICULTURE

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Agriculture has been fundamental to the rise of civilization but is difficult to optimize and is site specific. Localized variation in soils, climate, and pests strongly influence productivity. Technological innovations from the moldboard plow to digital agriculture have allowed humanity to efficiently develop. One of the more nascent applications is flying drones over crop fields to capture multispectral images. This type of application allows rapid detection of anomalies, such as pests and weeds, and facilitates timely interventions that maintain productivity. Missions begin with setting up flight plans within a GCS (ground control station) that's programmed into the drone to collect georeferenced data. The camera strapped to the drone captures a string of precisely interspaced images based on the flight plan. They are then processed to create maps to facilitate detection of relevant properties such as the weed species present and their population densities. Software's such ArcGIS and You Only Look Once (YOLO) are used to accomplish this. Preliminary steps for acquiring these images are underway. Our goal is to push the research in drone-agriculture applications forward to optimize crop health and growth.

IMPROVING COMPUTATION TO UNDERSTAND MOLECULAR CRYSTAL STRUCTURE

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Improving understanding of crystal structure can help advance pharmaceutical drug development and material design. Combining x-ray diffraction, ab initio computational methods, and NMR Spectroscopy is the best practice for determining molecular crystal structure. The most commonly used ab initio methods for crystal structure optimization use planewave density functional theory (DFT). However, a correction must be introduced to accurately capture dispersion interactions in molecular crystals. Adding a correction to periodic DFT methods based on a fermi-type damping function can have a considerable impact on improving the accuracy of the optimized crystal structures. The present work explores the optimization of the damping parameter in the D2* dispersion correction using predicted NMR observables as a metric for gauging the accuracy of the optimized crystal structure. Specifically, NMR observables such as the electric field gradient tensor and chemical shift anisotropy tensor are strongly influenced by electronic structure. Alternative dispersion correction methods were tested with extensive benchmark sets containing 17-O, 14-N, 15-N, and 35-Cl nuclei. Using high-accuracy NMR calculations, we find that setting the damping parameter to 3.5 in the D2 correction produces structures whose predicted NMR observables more closely match experiment. In addition, the preliminary evidence suggests that the D3 dispersion correction, commonly used in molecular crystal structure optimization, underestimates hydrogen bond length compared to the optimized D2* correction. Insights gleaned from these benchmark studies can be applied on a wider scale to nonperiodic sites of proteins and pharmaceuticals.

DETECTION OF CARBONYLS IN ELECTRONIC CIGARETTE EMISSIONS UNDER SECONDHAND VAPING

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Electronic-cigarettes have been referred to as a “safer” alternative to regular cigarettes, and they come in a variety of flavors. Different types of flavors have been tested to analyze the structural change the e-liquid exhibits. The structure of electronic cigarette particles evolves through its phase change from liquid to gaseous state. How e-cigarette emissions interact in passive vaping conditions, or secondhand smoke, is not fully understood. To analyze secondhand vaping emissions, e-cigarette aerosols were injected into a 2-m3 sealed chamber under varying conditions in the presence of (1) zero air, (2) room air, and (3) ozone. Aerosol samples were collected, extracted, and analyzed using a gas chromatography mass spectrometer (GC/MS). *O*-(2,3,4,5,6-Pentafluorobenzyl)hydroxylamine (PFBHA) derivatization was performed to cap the carbonyl functional group, and solid phase microextraction (SPME) was used to extract PFBHA-carbonyl oxime products prior to GC/MS analysis. Enhanced carbonyl formation is expected for vaping aerosols samples exposed to indoor oxidants, such as ozone, which may result in greater health risks for bystanders. Secondhand vaping emissions can roam around indoors for long periods of time. Those exposed to such conditions, inhale these aerosol particles that can result in harm. Carbonyls are very reactive and can alter the body, and to quantify such, a future project would be cell exposure to assess their potential health risks.

HOME-BUILT ATOMIC FORCE MICROSCOPE

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The characterization of materials at the nanoscale level requires high spatial resolution techniques beyond optical microscopy. Our research focuses on developing a home-built atomic force microscopy (AFM) which uses a micromechanical cantilever to scan and measure the topography of material surfaces. Two key components are involved, an optical detection scheme to sense the small deflection of the cantilever, and a mechanical stage that can position the sample with nanometer precision. In this work, we assembled the hardware components, tuned the laser alignment, characterized the photodetector response, tested approaching on a sample surface. We are in the process of implementing the feedback control with a digital signal processing unit. We will develop operation modes for both contact and tapping AFM. The AFM will be used to characterize various atomically thin materials and image novel structures such as moire patterns that can be constructed by stacking multiple layers of 2D materials. The AFM also is helpful in imaging cells and molecules helping us better visualize complex biological structures at very high resolution.

EXPRESSION OF GENES ASSOCIATED WITH MATRIX REMODELING PATHWAY IS AFFECTED BY TREM2 IN A SEX AND AGE DEPENDENT MANNER

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Persistent systemic inflammation has been shown to contribute to the development of neurodegenerative disorders, such as Alzheimer's Disease (AD) as well as increase sensitization to future inflammatory activators. Alzheimer's Disease is the most common cause of dementia and is characterized by the formation of extracellular beta-amyloid plaques and neurofibrillary tangles within neurons. Symptoms of the disease and susceptibility gradually worsen with age. Other factors such as sex also play a role in susceptibility to AD and other neurodegenerative disorders, as females are two times as likely to develop AD. Mutations in Triggering Receptor Expressed on Myeloid Cells 2 (TREM2) have been shown to cause an increased risk for development of AD, and total deficiency in humans leads to severe early onset dementia and eventual early mortality. Transcriptomic analysis of male and female mice within three age groups that were challenged with intraperitoneal injections of lipopolysaccharide (IP-LPS) suggests that TREM2 plays a role in the differential expression of matrix remodeling genes at different life stages. Matrix metalloproteinases (MMPs) are proteins that digest the extracellular matrix (ECM) and allow for increased infiltration of immune cells into tissue and have been shown to play an important role as inflammatory components that contribute to the pathogenesis of AD. Matrix Metalloproteinase 12 (MMP12), a gene that codes for a metalloelastase, is associated with matrix remodeling and was found to be differentially expressed in an age and sex dependent manner after exposure to IP-LPS. The differential expression of genes associated with matrix remodeling within the context of age, sex, and phenotype following systemic inflammation suggests a connection between TREM2, the extracellular matrix, and the pathogenesis of AD.

TARGETED DESUMOYLATION OF PIRNA PATHWAY PROTEINS

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SUMO (Small Ubiquitin-Like Modifier) is a post-translational modifier protein best known for mediating protein-protein interactions and protein localization in a myriad of cellular pathways. Among these, SUMOylation was recently identified as a widespread modification of multiple proteins involved in the piRNA pathway - an essential pathway for transposon repression in the germline and fertility - although its mechanistic role in this process is still unclear. To better elucidate the roles of SUMOylation in the piRNA pathway, it is important to selectively disrupt the SUMOylation of specific protein targets. SUMO gets covalently attached to lysine side chains in target proteins. However, SUMOylation sites can be redundant which prohibits traditional loss-of-function studies as mutating multiple lysines can result in unintended consequences on protein function beyond that from the targeted modification. To overcome these challenges, we propose a novel strategy for specific SUMOylation depletion through the artificial recruitment of SUMO protease activity to protein targets. Specifically, we have developed and aim to prove the efficacy of a recombinant fusion protein containing the catalytic domain of the conserved SUMO protease Ulp1 fused to GFP nanobody. This fusion protein aims to selectively de-SUMOylate GFP-tagged target proteins. This system promises to enable loss-of-function studies of protein SUMOylation in various biological contexts including but not limited to the piRNA pathway, thereby illuminating fundamental molecular mechanisms that underlie essential cellular processes.

THE CRITICAL ROLE OF HUMAN SMALL UBIQUITIN-LIKE MODIFIER FOR INFLUENZA VIRUSES

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Due to the deadly nature of the flu and the unreliable efficacy of available vaccines, we tried to understand how the flu viruses take advantage of human genes for their infections with the hope of developing new treatment methods. We aim to understand the interactions of viral infection on human proteins, particularly the SUMOylation cascade, using the qFRET method from viral as well as host proteins expressed in engineered bacterial cells. Using electroporation, we introduced modified DNA into the *Escherichia coli* cells to determine whether the genetically engineered bacteria produced human or viral proteins. We also added fluorescent protein genes to these proteins to allow us to observe, track, monitor, and later study how these proteins interact. We hope this research will help further our understanding of how viruses interact with the host in order to discover better medicine for treating viral infections. As a result, this research could lead to faster and novel approaches to treating influenza and other viruses in the future.

IMAGE FILTERING FOR ACCURATE MICROCHIP TRACKING IN MICROFLUIDIC CHANNELS

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The integration of microchips in microfluidic channels is useful for applications in biotechnology such as multiplexed bioassays and combinatorial synthesis. To realize these applications, a fundamental understanding of how microchips flow in rectangular microchannels is necessary to optimize their throughput. With computer vision, we can perform noise filtering to pre-process image frames and track microchips in microchannels. Because noise reduction is essential for the accurate analysis of microchip motion, we present an approach that preserves important image details and removes artifacts. In this study, we propose a noise filtering methodology to optimize the filtering operation and a set of filtering parameters for highly accurate microchip tracking. Using a top-mounted high-speed camera capturing videos of microchips in microfluidic channels, we leverage image processing and the computer vision analysis of recorded videos to detect and track microchip transponders. By using the known channel width of our system, we can calibrate our images and calculate the expected microchip area and perimeter. Wiener and Laplacian filtering successfully removed image artifacts. Changing neighborhood size parameter [5,5] showed a difference of 0.21 pixel. Data shows there is a difference of ~3 pixels between evaluated perimeter and expected perimeter, indicating an error of ~0.16-mm or a maximum of 24% error relative to channel width. This suggests further development of the methodology used in calibrating our image is necessary. Because the limiting factor of microchip sorter throughput is sorting speed, accurately assessing these microchips will advance the viable applications of synthetic biology, combinatorial DNA libraries, and DNA digital data storage.

UNDERSTANDING THE EVOLUTION OF REPRODUCTIVE INCOMPATIBILITIES IN *DROSOPHILA MELANOGASTER*

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Intrinsic incompatibility is the manifestation of lower fitness in hybrid organisms when compared to their parental species, independent of environmental effects. Intrinsic barriers play a key role in speciation. An example of intrinsic incompatibilities at work is how they can aid in the development of genetic divergence between populations and species (Coughlan and Matute 2020). A major unresolved question is the rate at which intrinsic incompatibilities arise – do they take many thousands of years to evolve, or can we observe them on shorter timescales? To approach this question, we created F1 hybrids from salt and non-salt adapted *Drosophila melanogaster* lines that have been undergoing independent evolution for approximately 500 generations. A total of 14 trials were conducted where the hybrids were created through the use of five salt-adapted D. *melanogaste*r females and five non-salt adapted *D. melanogaster* males per trial. The flies were to reproduce for a timeframe of a week. We then quantified survival by counting emerges per day per trial. These results were then compared to crosses from pure types to test for the presence of intrinsic incompatibilities. We anticipate that identifying these intrinsic incompatibilities will be a starting point toward identifying genes involved in infertility in both flies and humans.

ROLE OF ESTROGEN IN SOYBEAN OIL INDUCED WEIGHT GAIN

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Reduced estrogen levels in older women are correlated with increased weight gain, with its key role in regulating weight gain and metabolism being at the forefront of this. Studies have shown that a decrease in this key hormone plays a major role in the accumulation of visceral fat, overall body mass increase, and obesity. Older female mice, particularly those that have reached menopause, are more susceptible to weight gain due to their decreased estrogen levels. Soybean oil (SO) is the most widely consumed edible oil in the US with its consumption increasing exponentially over the last several decades. This increase in consumption correlates with the prevalent obesity epidemic. Previous studies in our lab have demonstrated that a high SO diet can lead to obesity and diabetes in male mice, regardless of age. However, younger female mice tended to not gain weight on a high SO diet. This study aims to investigate whether SO causes obesity in older female mice and whether estrogen plays a role in this weight gain. The experimental setup includes three groups of age-matched female mice being fed one of the following three diets: i) an SO based high fat diet, ii) a custom low-fat diet, iii) standard rodent diet. Body weights of the mice were measured weekly and glucose and ketone body measurements were taken at regular intervals to track development of obesity and diabetes. The results show that the SO diet causes obesity and diabetes in the older female mice, suggesting that lack of estrogen is key in inhibiting weight gain in females.

LANTHIONINE KETIMINE ETHYL ESTER EFFICACY IN PROMOTING REMYELINATION

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Despite extensive research into therapeutic agents for promoting myelination and mitigating axonal damage, successful treatments remain limited. Lanthionine Ketimine Ethyl Ester (LKE) has emerged as a promising candidate, exhibiting significant potential in promoting remyelination and upregulating Myelin Basic Protein (MBP) and ProteoLipid Protein (PLP) levels. Remarkably, LKE has also demonstrated the ability to facilitate the formation of thicker myelin sheaths (Dupree et al.). While the underlying mechanisms behind LKE's beneficial effects are not yet fully understood, its potential for remyelination positions it as a valuable therapeutic agent. In this study, we sought to evaluate the efficacy of different LKE concentrations and assess potential toxicity using a combination of the Cuprizone mouse model and normal mouse models. Coronal brain sections were subjected to in-depth analysis, employing various cocktail stains (MBP + NF200, Iba1 + GFAP, CC1 + olig2, Nav1.6 + Caspr) to investigate LKE's effects within the Corpus Callosum. Six mouse groups, each comprising five female mice, were included in the analysis: Normal, 6 Wk DM (Cuprizone model for six weeks), 6 Wk DM + LKE (10 ppm), 6 Wk DM + LKE (30 ppm), 6 Wk DM + LKE (100 ppm), and 6 Wk DM + LKE (250 ppm). LKE administration was delivered in trace amounts via the mouse's chow in the experimental groups. The MBP + NF200 Stain was carefully examined, with specific attention to the S1 Region of the Corpus Callosum in coronal sections. Ultimately LKE could serve as a stepping stone for not only the future of therapeutics, but understanding intricate mechanisms behind Multiple Sclerosis.

EVIDENCE FOR ATMOSPHERIC O2 WITHIN MOROCCAN ATLAS RANGES CARBONATES

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In the Earth’s atmosphere today, Oxygen makes up 21% of the air we breathe. This percentage of oxygen was not always found in the Earth's atmosphere since in the past, atmospheric oxygen levels would range as low as 1%-10%, we have seen evidence in the geological record to show that these increased signs of atmospheric oxygen in our atmosphere could have come from a time between 2.4 to 2.1 billion years ago, through a process titled the “Great Oxidation Event” (GOE). The GOE can be tracked geochemically, through a selection of rocks from before, during, and after this period, to demonstrate significant atmospheric changes. By observing the ratio of d18O , carbon and nitrogen isotopes in carbonates, we are able to see a correlation between isotopic fractionation and atmospheric O2. This study in particular observes the exposed 500 Mya Neoproterozoic-Cambrian carbonates from the Anti-Atlas and High Atlas ranges of Morocco, Africa. Here, over 50 samples are processed via a diamond-coated micro-drill to extract sample powder that is then used to determine d18O and d13C ratios within the rock. Results thus far have shown us nitrogen (d15N) levels consistent with this time interval. Learning more about the complex relationships between multiple isotopic systems can help us better understand their correlation to atmospheric conditions and can better inform us of geochemical changes throughout Earth’s evolution.

MODELING REACTION KINETICS WITH ORDINARY DIFFERENTIAL EQUATIONS

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I solved action kinetics problems involving elementary chemical reactions by applying ordinary differential equations. I used MATLAB to generate simulations for non-linear problems. Nonlinear equations can be very tricky to solve - especially when modeling a physical or a chemical process. I used a program in MATLAB called ODE45 Solver to compute the solutions for the non-stiff ODE. Interestingly I was able to find a pattern that related the weight from which each constant rate carried relative to its set of reactions with respect to the given concentration of each species involved in the chemical reaction during a time span of the duration of the reaction. Furthermore, I applied the Law of Mass Action to model a complex biochemical reaction using the Michaelis-Menten kinetics approach. I controlled the vector quantities of each direction of the anticipated reaction mechanism which mimicked the Michaelis-Menten model for a reversible process. I was able to show that the reaction profile for an enzyme kinetic reaction carries dependency on the magnitude of the quantity of each direction from which each reaction took place. Thus, the velocties of the constant rate reactions of the forward and reverse process manners when comparing their kinetic energies. I was able to detect that the most cost-effective method to produce products was by setting up k1»k2 and k3»k4 but the key was to approximate a rate reaction that would k1=k3. My future project is to learn more complicated models to enable me to learn how to compute brain mechanisms related to language.

CHARACTERIZATION OF HTLV TAX-INDUCED DNA DAMAGE

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The human T-lymphotropic virus type 1 is the first cancer-causing retrovirus to be discovered, affecting up to 10 million people and causing adult T-cell leukemia/lymphoma. HTLV encodes a protein known as Tax that is involved in transactivation of viral transcription, induction of DNA damage, and cell cycle arrest. It is not well understood, however, how Tax induces these phenotypes, nor whether it does so in vivo. We are interested in studying the mechanisms underlying Tax-induced DNA damage and cell cycle arrest to better understand the role of Tax in the viral life cycle. Moreover, we will be studying these phenotypes among three Tax orthologs representing different HTLV subtypes to better understand whether conserved domains can be linked to conserved HTLV phenotypes, and what regions/functions may be important for causing leukemia/lymphoma. Here, I first overexpress different Tax orthologs in U2OS cells and assay their expression via Western Blot. I will next assay whether the different Tax orthologs are able to cause DNA damage by performing immunofluorescence assays to detect the DNA damage markers ɣH2AX and 53BP1, both different markers of double-strand breaks. We will also determine whether the Tax orthologs can cause G2/M cell cycle arrest in a cell culture model. Our findings will allow us to better understand if the different Tax orthologs are able to induce DNA damage and cause G2/M arrest, what domains are responsible for these phenotypes, and if they correlate with certain disease outcomes.

IDENTIFYING MISFOLDED PROTEINS USING VARIOUS J DOMAIN PROTEINS

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Protein misfolding occurs for a multitude of reasons; specifically, a focus of the Genereux lab is quantifying protein misfolding in response to environmental stressors. Protein misfolding causes a number of negative side effects including diseases such as Parkinsons and Huntington's disease, cell death along with several other side effects. In the Genereux lab, we use DNAJB8, a protein within the J domain “family” of proteins, to bind and separate misfolded proteins from other biological complexes for analysis. Cells are transfected with this chaperone protein, drug treated, and lysed. DNAJB8 binds to misfolded proteins, and together they are purified and stringently washed so that the misfolded proteins can be quantified. However, that one chaperone protein may not be adequate to identify all types of misfolded proteins. Using other J domain chaperone proteins may perfect the assay by pulling down proteins DNAJB8 is not capable of latching onto or a greater amount of protein. The proteins being directly compared to DNAJB8 include DNAJB1, DNAJB2a, DNAJB4 and DNAJB6b. Thus, I have performed 2 duplicates of experiments with the assay listed above, excluding the use of drug treatments, to be able to identify if the use of other chaperone J domain proteins improves the current assay.

FEAR DISCRIMINATION

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Humans continually rely on their past encounters and memories to help them make decisions depending on what kind of situation they are in. Because of this, it’s an interesting feat to dive deeper into how one is able to learn to differentiate between safety and danger. Clinically, this problem is significant because a number of patients report mental issues relevant to anxiety and impairment in safety learning is the hallmark of post-traumatic stress disorder (PTSD). To better understand the brain network mechanisms, Korzus laboratory developed a behavioral task for mice to learn safety using fear discrimination task consisting of three major phases: habituation, classical Pavlovian fear conditioning (FC) followed by differential fear conditioning (DFC), where animals learn how to distinguish between contextual conditioned stimulus (CS+), which is always paired with aversive US (mild electric shock) and similar but not the same safe stimulus (CS-), which is never reinforced. After initial fear generalization during early DFC, animals learn distinction between CS+ and CS- showing high fear to CS+ and low fear to CS-. My project involves testing a variety of contextual attributes to establish an effective contextual fear discrimination learning paradigm. In future, we will utilize this improved behavioral paradigm to further understand neural circuit mechanisms underlying fear discrimination learning using optogenetics in combination with Calcium recording from hundreds of neurons from medial prefrontal cortex. These studies should point out the critical neuronal processes engaged during fear modulation and enhance our understanding of brain mechanisms guiding safety learning.

IDENTIFYING MISFOLDED PROTEINS USING VARIOUS J DOMAIN PROTEINS

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Protein misfolding occurs for a multitude of reasons; specifically, a focus of the Genereux lab is quantifying protein misfolding in response to environmental stressors. Protein misfolding causes a number of negative side effects including diseases such as Parkinsons and Huntington's disease, cell death along with several other side effects. In the Genereux lab, we use DNAJB8, a protein within the J domain “family” of proteins, to bind and separate misfolded proteins from other biological complexes for analysis. Cells are transfected with this chaperone protein, drug treated, and lysed. DNAJB8 binds to misfolded proteins, and together they are purified and stringently washed so that the misfolded proteins can be quantified. However, that one chaperone protein may not be adequate to identify all types of misfolded proteins. Using other J domain chaperone proteins may perfect the assay by pulling down proteins DNAJB8 is not capable of latching onto or a greater amount of protein. The proteins being directly compared to DNAJB8 include DNAJB1, DNAJB2a, DNAJB4 and DNAJB6b. Thus, I have performed 2 duplicates of experiments with the assay listed above, excluding the use of drug treatments, to be able to identify if the use of other chaperone J domain proteins improves the current assay.

FEAR DISCRIMINATION

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Humans continually rely on their past encounters and memories to help them make decisions depending on what kind of situation they are in. Because of this, it’s an interesting feat to dive deeper into how one is able to learn to differentiate between safety and danger. Clinically, this problem is significant because a number of patients report mental issues relevant to anxiety and impairment in safety learning is the hallmark of post-traumatic stress disorder (PTSD). To better understand the brain network mechanisms, Korzus laboratory developed a behavioral task for mice to learn safety using fear discrimination task consisting of three major phases: habituation, classical Pavlovian fear conditioning (FC) followed by differential fear conditioning (DFC), where animals learn how to distinguish between contextual conditioned stimulus (CS+), which is always paired with aversive US (mild electric shock) and similar but not the same safe stimulus (CS-), which is never reinforced. After initial fear generalization during early DFC, animals learn distinction between CS+ and CS- showing high fear to CS+ and low fear to CS-. My project involves testing a variety of contextual attributes to establish an effective contextual fear discrimination learning paradigm. In future, we will utilize this improved behavioral paradigm to further understand neural circuit mechanisms underlying fear discrimination learning using optogenetics in combination with Calcium recording from hundreds of neurons from medial prefrontal cortex. These studies should point out the critical neuronal processes engaged during fear modulation and enhance our understanding of brain mechanisms guiding safety learning.

EFFECT OF PERCEPTUAL LEARNING ON VISUAL PERFORMANCE AFTER CENTRAL VISION LOSS

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Macular degeneration (MD) is one of the leading causes of blindness and is estimated to affect 288 million people by 2040. Those affected by MD must rely on their visual periphery to perform a multitude of tasks such as reading and recognizing faces. Perceptual learning (PL) is a method used to help people with MD train their visual periphery. PL was examined in three domains of vision: early visual processing, mid-level visual processing, and attention and eye movements. To achieve a further understanding of PL and how the brain is affected by MD, training tasks were made that exercise these three domains. These tasks are accompanied by eye tracking which allows for a simulated scotoma to be placed on the screen in the center of a person's line of sight. This scotoma prohibits the use of central vision putting participants with healthy eyes into conditions similar to people with MD. This paper focuses on one of the tasks utilizing the scotoma, contour integration. The contour integration task involves distinguishing a shape from a background which is associated with mid-level visual processing. Contour integration utilizes adaptive procedures that can obtain a participant's thresholds of visual performance during the task. A small number of participants were run through the modified task and thresholds of accuracy, response time, and difficulty were identifiable. With an accurate understanding of participants' visual abilities, it is possible to analyze the effectiveness of the training procedures and produce a standardized method for helping people with MD.

EXAMINATION OF GRAM-NEGATIVE *ESCHERICHIA COLI* RESISTANCE DEVELOPMENT TO MAGNESIUM OXIDE

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Some Gram-negative bacteria, for example, *Escherichia coli*, are known to be antibiotic-resistant and are frequently linked to healthcare-associated infections (HAIs). Therefore, targeted research has been ongoing to identify new biomaterials to minimize emerging antibiotic-resistant strains and HAIs. Previous research shows that magnesium oxide nanoparticles (nMgO) have antibacterial effects. However, the development of bacterial resistance to nMgO has not been explored. Here, we show that *E. coli* may acquire resistance after repeated exposure to increasing nMgO concentrations. Using consistent methods, *E. coli* previously exposed to 10.0 mg/mL of nMgO survived to 20.0 mg/mL nMgO. Our preliminary results demonstrate that *E. coli* displays increasing resistance to higher concentrations of these nanoparticles. This study of bacterial resistance can provide information to ensure the effective use of nMgO for antibacterial activities in the future. Further studies are needed to determine the specific mechanisms of *E. coli* resistance to nMgO.

WESTERN BLOTS DIFFERENTIATE ECTOPIC AND ENDOGENOUS MYC

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MYC is an oncoprotein that plays a pivotal role in cell proliferation, however, occasionally MYC is overexpressed and if this overexpression is left unregulated it has been found that this is highly correlated with an uncontrollable growth and division of cells. Despite this there are still a lot of details that are unknown about MYC. In order to further enhance our understanding of MYC we decided to introduce MYC in mammary epithelial cells known as MCF10A. However, it was still unclear if the cells took in the MYC we introduced. As a result of this uncertainty a western blot was performed in order to determine if ectopic MYC was overexpressed in these cells. It was found that each type of cell had an overexpressed level of ectopic MYC.

MOLECULAR DYNAMICS, 5F9R, AND CRISP-CAS9 USING VMD

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The modern achievements of technology have made it possible for humans to see events that would have been impossible, never to be seen. Molecular Dynamics is one of many achievements of technology. Molecular Dynamics is a computational technique that is used to understand the atomic level changes of a protein or molecular system. Molecular Dynamics, although being primary on a computer, uses important methodologies. One of these methods being the equations of motion from Isaac Newton. By utilizing the molecular visualization software of modern computers like VMD (Visual Molecular Dynamics) I was able to observe the protein 5F9R along with all of its fluctuations and interactions. While observing the protein I also put my head into observing CRISP-Cas9, a gene editing tool. The VMD software isn't just limited to showing us all the features of the 5F9R protein, it can show us every protein that is modeled with all of its discovered features in the Protein Data Base (PDB). I learned that 5F9R protein had a single-guided RNA along with its double DNA with the DNA being primed for cleavage. CRISP-Cas9 is a gene editing tool with three core components, two RNA's and one compartment for protein. The largest implication with my finding is that there is still more to find using Molecular Dynamics. The simulations created using molecular dynamics only grow more accurate and complex with time. Proteins I observe can have a clearer look upon observation thanks to better biophysical processes. In conclusion, Molecular Dynamics simulations provide the ability to view proteins such as 5F9R in a clean and high-quality way. This scientific achievement could pave the way for better breakthroughs with biomedical technology.

MAGNETIC QUENCHING OF TRIPLET POSITRONIUM TO CONFIRM BOSE EINSTEIN CONDENSATION

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Positronium (Ps) Bose Einstein Condensate (BEC) naturally annihilates into gamma rays photons (high energy packets). This may allow for the fusion of Deuterium, a way to generate energy that doesn't produce greenhouse gasses or long lasting radioactive waste. The main experiment will attempt to form Ps BEC, therefore it is necessary to prove that Ps BEC is formed. Singlets Ps naturally annihilate into two gamma rays, which makes it possible to measure the energy of Ps through the angular distribution of their two-gamma annihilation. The proof of Ps BEC formation is a large number (~106) of Ps condensing at the ground (lowest energy) state. However, BEC is formed through triplets Ps , which decay into three instead of two photons. Consequently, it is necessary to create a magnetic field pulse that will convert triplet into singlet Ps. A suitable pulsed field may be produced by sending a 200 Amperes pulse lasting for 10 ns through a fine wire located about 0.1 mm from the BEC. Multiple variables were tested to improve the current production, including the resistance at the emitter end of the transistors, the length of the circuit wirings, different types of transistors, and isolating the transistors' circuits from each other. An intense brief pulse of 150 amperes lasting for 8 nanoseconds was produced from two ZTX 417 avalanche transistors with isolated emitters and collectors.

FORMALDEHYDE YIELD IN OZONOLYSIS OF ETHENE AND PROPYLENE

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Ozonolysis is one of the major oxidation pathways of unsaturated VOCs (volatile organic compounds) in the troposphere, which leads to the production of carbonyls and carbonyl oxides. Ethene and propene are among the most abundant unsaturated VOCs in the troposphere. Ozonolysis of these alkenes can produce formaldehyde and other carbonyl compounds. Formaldehyde yield from ozonolysis of ethene has been reported with a wide range from 66% to 110%, due to the complexity of the ozonolysis reaction network. Recent theoretical studies found that ozonolysis of ethene can also generate ketohydroperoxide (KHP), besides the formaldehyde and formaldehyde oxide pathway. This new mechanism was proven by direct measurement in recent experimental works. In the case of propene ozonolysis, formaldehyde, acetaldehyde and potentially some KHP can be produced. Yet, the branching ratio between carbonyls and KHP is still an open question. Thus, measuring formaldehyde yield is important for understanding the mechanism of ozonolysis of alkenes. In this work, near-UV cavity ringdown spectroscopy was used in combination with a flow reactor. Concentrations of ozone with and without alkenes were monitored using its broad UV spectra absorption features, giving the amount of consumed ozone. Concentration of formaldehyde produced in ozonolysis was also measured using its sharp absorption features in the same wavelength region. The yields of formaldehyde were then calculated from the ratios between formaldehyde concentrations over the consumed amount of ozone.

TRANSFER OF THE *Ve1* GENE IN *CAPSICUM ANNUUM* TO ERADICATE VERTICILLIUM DAHLIAE

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Verticillium wilt is a common soil-borne pathogen that kills 20-50% of the crop in an infected field and perseveres over long spans of time; chilis are a part of that crop group. There is no current treatment for this fungus, however recent studies have shown the *Ve1* gene, found in tomatoes is an immune receptor that responds to and recognizes the *Ave1* effector protein transmitted from *Verticillium dahliae*. The gene can be inserted into the genome of other plants. The *Ve1* gene codes for leucine rich repeats - receptor - like proteins (LLR-RLP) that work as transmembrane signals following hormone and defense signal pathways to create the defense genes responsible for resistance. The gene is replicated using lab designed primers and using agrobacterium mediated gene transfer, the *Ve1* gene will be inserted into the chili pepper genome. Further experiments will be done for the testing of the quality and resistance of the gene within the chili pepper, and analysis will be done on the limited market size to expand our market.

CREATING RENEWABLE ENERGY FROM *VITIS VINIFERA* WASTE BY PROMOTER SWITCHING OF *S. CEREVISIAE*

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Economic problems surrounding the use of fossil fuels have drawn attention to reusable energies through the utilization of crop waste. A crop with substantial economic concerns, but vast forms of reusability is Wine Grapes, scientifically known as *Vitis vinifera.* Each year over six trillion gallons of wine are consumed worldwide, resulting in over 12 million tons of waste from wine production. This waste consists of acids that, if left untreated, pollute streams, soil, and groundwater. The current means to eradicate Grape waste is by sending it to city-owned composters and landfills, raising questions about the economic and environmental safety that happens after it is processed. Our research explores an alternative to the current waste control measurements by utilizing sugar extraction and anaerobic digestion of pomace to yield two forms of renewable energy: ethanol and biogas. By extracting the sugars at an accelerated rate through the conversion of the conditional promoter in *Saccharomyces cerevisiae* to a constitutive promoter through the use of restriction enzymes and DNA Ligase on the *TEF-1* promoter site of the *SUC2* gene, the minimized sugar content would increase anaerobic digestion rates. Biogas would be produced from anaerobic digestion and the extracted sugars would be fermented into ethanol. Our paper researches the functional, regulatory, and economic risks, along with revenue possibilities, depicted by this solution. The success of this technology would help reduce the negative economic impact that grape pomace presents while possessing huge potential to augment the production and creation methods of renewable energy.

GENETICALLY MODIFYING *BOTRYTIS CINEREA* RESISTANCE IN STRAWBERRIES

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The average strawberry farmer currently spends $700 on fungicides per acre annually to protect their crops from being destroyed by pathogens. With fungicide bans being enforced, many crops are increasingly susceptible to infection by gray mold, or *Botrytis cinerea*, especially as climate change enhances both global warming and infection rates. We propose to eliminate the need for fungicides by inserting a Cauliflower Mosaic Virus (CaMV) 35S promoter alongside our target genes FabZIP46, WRKY11, and WRKY75 into the strawberry. These genes are associated with the production of immune defense molecules, such as jasmonic acid, salicylic acid, and pathogenesis-related proteins, which naturally decrease in production as the strawberry matures. The CaMV promoter will express the genes past the ripening of the strawberry, therefore enhancing the crop's ability to defend itself against *Botrytis cinerea*. This modification will be done through agrobacterium mediated transformation into the callus from a strawberry plant, and the callus will be regrown into a viable modified plant. Ideally, this genetically modified strawberry would be a cost-effective transgenic approach that results in higher crop survival rates and more fruitful yields.

ORAL SESSION 4

INVESTIGATING THE ROLE OF SLEEP DISTURBANCE IN EXECUTIVE FUNCTION DEFICITS FOUND IN 22q11.2 COPY NUMBER VARIANT CARRIERS

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Copy number variations (CNVs) in the 22q11.2 locus are among the most common genomic rearrangements in the human genome and greatly increase the risk of neurodevelopmental disorders. 22q11.2 CNV carriers have been found to exhibit deficits in both executive function (EF) and sleep, however, the role of sleep disturbances in these EF deficits is unclear. To address this gap, the relationship between sleep and EF was examined in individuals with a 22q11.2 Deletion (22qDel; n=56; Mage=18.9 + 9.9, 48% male) and 22q11.2 Duplication (22qDup; n=29; Mage=17.5 + 11.9, 55% male). Participants completed a lab-based measure of EF (Penn Computerized Neurocognitive Battery) and a real-world EF measure (Behavior Rating Inventory of Executive Function). Sleep disturbance was measured by the Structured Interview of Psychosis-risk Syndromes (SIPS). Linear mixed effects models testing a group-by-score interaction and covarying for age and sex tested these relationships. Worse sleep was associated with both worse real-world EF (b=0.33, p=0.02) and EF accuracy (b=-0.26, p=0.04) in 22qDup, but not 22qDel carriers. Worse real-world EF was associated with worse EF speed performance only in 22qDup carriers (b=-0.38, p=0.01). These results suggest that increased sleep disturbance is associated with real-world and lab-based deficits in EF in 22Dup carriers. Further, EF speed performance may be indicative of real-world executive functioning difficulties in 22qDup, but not 22qDel carriers.

COOPERATIVE POINT AND AXIAL CHIRALITY FOR MORE SELECTIVE BRØNSTED ACID ORGANOCATALYSIS

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Brønsted acid organocatalysts (BAOCs) (Figure 1) are highly modular catalysts capable of activating a wide range of substrates to different C-C and C-X bond-forming reactions. In most cases, BAOCs are constructed from a chiral backbone. However, the Toste and Sigman groups recently reported a novel BAOC scaffold where the chiral backbone was intentionally replaced with a stereocenter distal to the active site. If this distal stereocenter alone rendered their BAOC catalytically competent, then we believe uniting a stereocenter and a chiral backbone on one scaffold can create even more selective catalysts. We plan to access the stereocenter on BAOCs by replacing the achiral sulfonamide center of N-triflylphosphoramide (NTPs) with a series of chiral sulfonamide isosteres. We herein present our ongoing synthetic efforts to demonstrate the feasibility of this design. Once we access the proposed scaffold, we will determine if the installed stereocenters significantly improve asymmetric induction by comparing the performance of the stereoenriched BAOCs scaffolds against their achiral NTP analogs in a diagnostic Nazarov cyclization. We expect that the data gained from these experiments will equip researchers with a new avenue to design selective BAOC scaffolds.

IDENTIFYING LC3 BINDERS FOR THE DEVELOPMENT OF A NOVEL AUTOPHAGOSOME TARGETING AND LYSOSOMAL DEGRADATION ASSAY

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Autophagy is an essential mechanism for homeostatic maintenance through clearance and recycling of unneeded or damaged intracellular components via a lysosome-dependent degradation program. Disruption of the autophagic process can result in a harmful protein imbalance as seen in neurodegenerative diseases such as Parkinson, Alzheimer, and Huntington disease that are caused by abnormal accumulation of aggregate-prone proteins. There remains a need for the development of degrader type drugs to enable selective degradation of disease-associated proteins since current targeted protein degradation technologies such as LYTAC and PROTAC are limited to extracellular proteins and small proteins associated with the ubiquitin proteosome pathway, respectively. Our goal is to develop a novel degradation technology to target a wider range of proteins to the autophagy pathway via delivery to main effector protein LC3. We aim to synthesize a chimeric molecule composed of a small LC3 binder linked to an adaptable target binding domain that will shuttle degradation targets to the autophagosome bound LC3. Linking these distinct domains will generalize the catalog of proteins available for recruitment to the autophagosome for degradation. This summer we developed a high throughput autophagosome degradation assay to identify the small LC3 binder for the chimeric shuttling molecule using an inducible LC3 binding Luciferase reporter.

CAFFEINE ADMINISTRATION PREVENTS CPAP-INDUCED RESPIRATORY DEPRESSION IN A PRETERM MOUSE MODEL

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About 1 in 10 infants are born prematurely in the United States. Most preterm infants exhibit respiratory complications such as apnea and require life-saving modes of respiratory support. Continuous positive airway pressure (CPAP) is one respiratory support modality which elevates lung volume and improves blood oxygenation. However, lung inflation activates pulmonary stretch receptors and mechanosensitive ion channels, which initiates the vagally-mediated inspiratory inhibiting Hering-Breüer reflex (ie. apnea). Further, most preterm infants also receive caffeine, a respiratory stimulant that decreases apnea. Using a mouse model of neonatal CPAP, we investigated whether: 1) the prolonged (days) lung inflation by CPAP depresses respiratory drive [decreased respiratory frequency (fR) and/or tidal volume (VT)]; and 2) whether it can be prevented by caffeine administration. Newborn mice received CPAP (6cmH2O, 3 h/day) for the first postnatal week together with daily subcutaneous (5mg/kg) injections of caffeine. Whole-body plethysmography was performed 2 weeks later (3 weeks) to measure fR and VT. Compared to control mice, CPAP decreased fR (but not VT), which was prevented by daily caffeine. The decreased fR was associated with increased airway expression of the piezo family of mechanosensitive ion channels. We speculate that the decreased drive to breathe by CPAP may result from inputs from airway stretch/mechanosensors, and caffeine may be protective. In summary, positive pressure support may have long-term side-effects contributing to decreased respiratory drive and apnea in preterm infants, while caffeine has therapeutic benefits.

IMPROVING THE COVALENT KINASE INHIBITOR DEVELOPMENT PIPELINE WITH CHEMICAL PROTEOMICS

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Covalent kinase inhibitors (CKIs) are a unique class of therapeutics with several advantages over traditional reversible inhibitors. However, designing and developing selective CKIs remains a challenge in the field. In vitro kinase reactivity panels are often used to test for a CKI's selectivity, but these methods fail to capture the global proteome reactivity of such inhibitors against non-kinase proteins. Advances in chemical probe-based proteomic methods have allowed for the complete protein target identification of CKI's in cells, yet often produce biased results due to the cell-line of choice. To overcome these issues, the Zaro Lab is developing a screening platform that seeks to identify protein targets of CKIs across a diverse set of cell lines. Importantly, we will optimize our coverage of the human kinome in live cells through the development of a cell line panel which maximizes the number of kinases containing targetable cysteines in a minimal number of cell lines. This approach will allow us to survey kinase specific cysteine reactivity in a native proteome, while considering non-kinase off targets (i.e., proteins harboring highly reactive cysteines). Our preliminary data suggests differences in protein expression, abundance, and interactions across different cell types are all characteristics that drastically impact the apparent selectivity of CKIs. We now plan to build off this data to qualitatively and quantitatively identify the protein targets of such CKIs using mass spectrometry. Our work will establish a more holistic approach to the characterization of CKI's which we hope will streamline the development of truly selective CKI's.

EXPLORING SEX DIFFERENCES OF OXYCODONE INTAKE AND ΔFOSB LEVELS IN RODENTS

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Addiction to the semi-synthetic opioid, oxycodone, has grown over the years since originally prescribed for pain relief, and deviation from the intended use of this drug leads to long-term changes in neurological function. Overexpression of transcription factor, ΔFosB, upon chronic drug use is a known mechanism that supports long-term neurobiological changes underlying addiction. However, more research is required to understand the role of ΔFosB and sex differences in oral oxycodone consumption. The objective of this study was to investigate the expression of ΔFosB in the nucleus accumbens (NAc) of the brain in response to voluntary oral oxycodone consumption in rats and compare the findings between sexes. Long-Evans rats (n=2 males, n=2 females) were subjected to a two-bottle choice (TBC) paradigm of water and oxycodone (0.1 mg oxycodone/1 mL water) for a period of 24 hours per day for 14 days. Brain NAc sections were taken from the oxycodone-exposed rats, and ΔFosB expression was assessed via immunohistochemistry. An unpaired t-test between sexes determined that females ingested significantly higher doses of oxycodone ($p<0.0001$) compared to males. A strong positive correlation ($r=0.9827$, $p=0.0173$) showed that higher doses of oxycodone consumption were associated with an increase in NAc ΔFosB expression. This study ultimately supports the conclusion that a TBC paradigm can result in molecular neuroadaptation via accumulation of ΔFosB in the NAc of oxycodone-addicted rats, and female rats are more likely to partake in oxycodone consumption.

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