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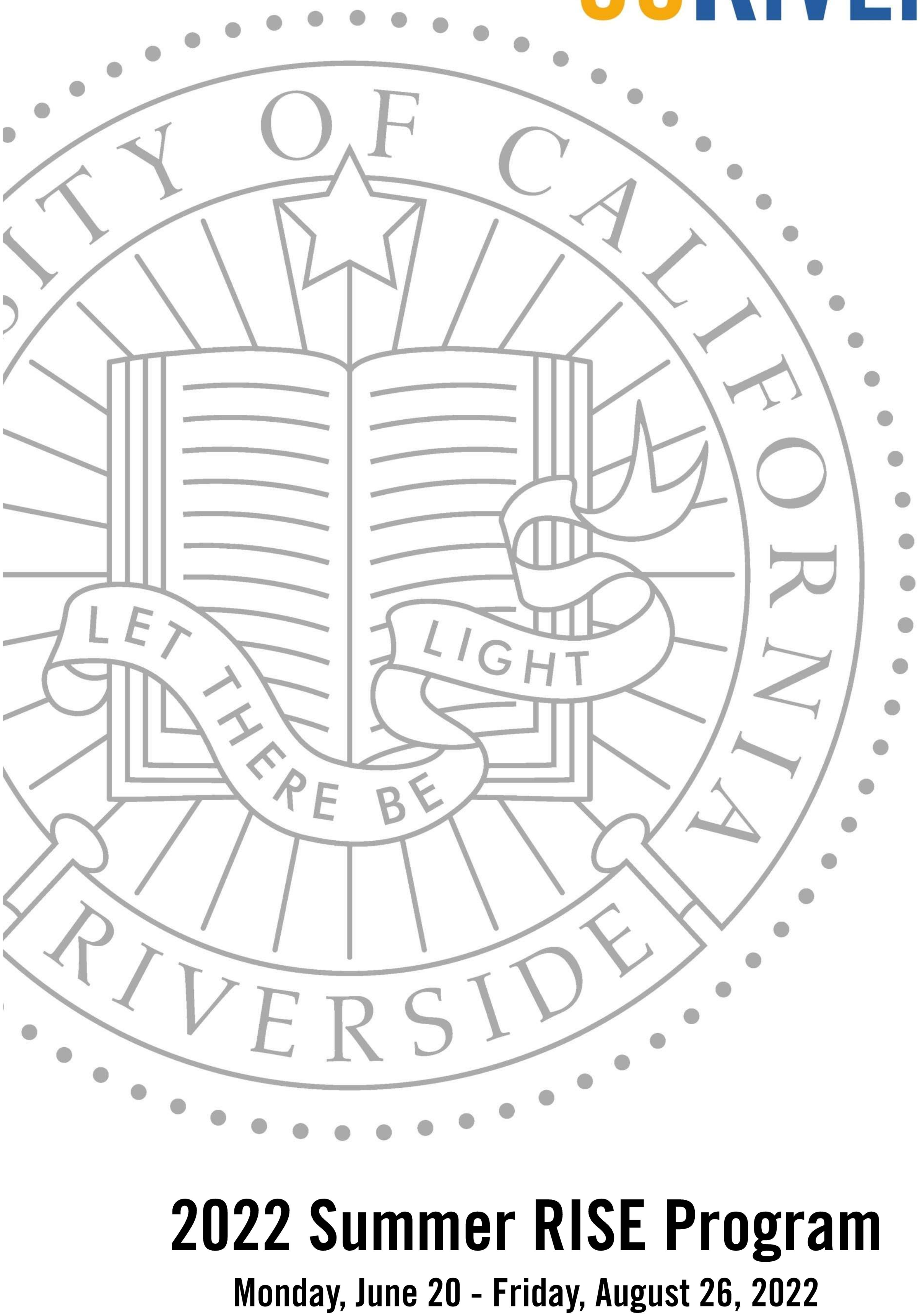

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# 2022 Summer RISE Program

**Monday, June 20 - Friday, August 26, 2022**
**University of California, Riverside**

**Congratulations and Welcome!**

The Research In Science & Engineering [RISE] summer program focuses on student success and retention in the Science, Technology, Engineering, and Mathematics [STEM] fields. This year, students from the College of Natural and Agricultural Sciences are participating in RISE as a member from the Learning Communities CNAS Scholars, Summer Bridge to Research, the Dynamic Genome Scholars, California Alliance for Minority Participation, RCC-B2B Program, or Faculty-sponsored research experience for undergraduates [REUs].

Throughout the summer you were engaged in research, mentored by scientists, and involved in numerous student success activities that you will hopefully find beneficial during your time at and beyond UCR. This symposium represents the culmination of your efforts, but the good news is that more opportunities will present themselves during the coming school year as well.

We congratulate all of the students for their dedication, commitment, and hard work over the past 10 weeks. We also thank all faculty, research scientists, graduate students, undergraduates, and other personnel for helping us make this a successful program. We hope that this has been a rewarding experience for you as you begin your scientific careers and we look forward to watching you succeed for years to come. It has been our pleasure to work with each one of you and we wish you all the best in your future endeavors.

Sincerely,

Connie Nugent

Connie Nugent, Ph.D.
Divisional Dean of Student Academic Affairs

Nhi Tran
Coordinator, RISE

Jim M. Burnette, Ph.D.
Coordinator, Dynamic Genome Scholars

Maura Caceres
Coordinator, CNAS Scholars

# Table of Contents

# RISE Program Overview

Established at UC Riverside in 2010, RISE has been supporting and developing STEM students through summer research opportunities since its inception through summer research programs, symposia, and successfully developing students in the STEM fields. Now in its ***twelfth*** year, it is a ten-week summer research program designed for STEM students from varying educationally and/or economically disadvantaged backgrounds. This year, 79 participants worked under the supervision of a faculty mentor on the mentor's research project. The goal of RISE is to increase the number of outstanding students from diverse backgrounds to become acquainted with one of the most essential traits of a scientific career: Research. Additionally, RISE aims to increase the population of students who pursue the M.S. and Ph.D. degrees by strengthening their academic and professional development. Its primary objectives are to: 1) provide preparation for graduate studies through a research experience in the mentor's laboratory and a variety of workshops; 2) provide a mechanism that fosters faculty/student interrelationships; 3) give the students a first-hand look at graduate opportunities at UCR; 4) assist the students in realizing their potential for graduate studies at UCR and other campuses; and 5) expose the faculty mentors to the possibility of recruiting interns to their departments. RISE was undertaken in coordination with the STEM Pathways Program [STEM], Learning Communities CNAS Scholars, Dynamic Genome program, and the RCC Bridges to the Baccalaureate [B2B] Program.

# Participating Programs

**CNAS Scholars & PERSIST**

The CNAS Scholars program is an extension of the Freshman Scholars Learning Communities [FSLC], one of three allied programs on campus designed to build community amongst first-year students through the collaboration of multiple departments at UC Riverside. It is a program exclusively for first-year CNAS students interested in enhancing their academic performance and UCR experience. The program promotes proven student success by providing workshops and seminars to small groups of students to ensure a successful freshman year in the sciences. Students who successfully complete the FSLC are eligible to apply for a summer research position as a CNAS Scholar through the RISE program.

**STEM Pathways Summer Bridge to Research**

Instituted by the U.S. Department of Education HSI-STEM grant initiatives, the STEM Pathways Program is aimed at supporting underrepresented student populations in the Science, Technology, Engineering, and Mathematics [STEM] fields. A primary focus is to increase the number of students transferring into the STEM fields while improving their success and retention in the university**.** The Summer Bridge to Research program addresses the critical needs of incoming community college transfer students by fostering their transitional success through early research engagement, campus acclimation and completion of a formal transfer transition seminar series.

**Dynamic Genome USDA and HHMI SALSA Summer Scholars**

Rising UCR sophomore students spent ten weeks participating in research as part of the 2022 Summer RISE program. Over half of the students were involved in research exploring the genetic diversity of citrus varieties. A subgroup of students joined faculty and performed research on various topics. All students attended a one-day workshop at Keck Graduate Institute in Claremont, CA to study agribusiness focusing on issues in crop sustainability in California. With guidance from KGI faculty and graduate students, the Summer Scholars identified a threat to economically important crops and proposed a solution along with a recommendation of feasibility based on intellectual property issues, market acceptance, and risk assessment.

**Faculty-Sponsored Research Experiences for Undergraduates (REU**)

Current UCR CNAS undergraduate researchers were sponsored by their respective PIs to participate in Faculty-Mentored research over the summer while engaging as a larger cohort in the STEM community. This year Kurt Anderson PhD, Dawn Nagel PhD, and John Franchak PhD sponsored students through their NSF-Funded grants as a Research Experience for Undergraduates in the RISE Program.

**Bridges to the Baccalaureate**

The Bridges to Baccalaureate Program (B2B) is a partnership between the University of California, Riverside and Riverside City College designed to provide RCC students in underrepresented minority groups with a pathway to research-oriented careers in science, technology, engineering and mathematics at UCR. The B2B program is funded through a grant by the National Institute of General Medical Sciences and the National Institutes of Health.

**California Alliance for Minority Participation (CAMP)**

The California Alliance for Minority Participation [CAMP] is designed for students in the STEM fields pursuing graduate (Master/Doctoral) degrees. CAMP-UCR was established at the University of California, Riverside in 1994 and is funded by the National Science Foundation [NSF] and the University of California Office of the President [UCOP]. CAMP-UCR is a program that works to encourage NSF-declared underrepresented students in the STEM fields to successfully complete undergraduate science degrees and further pursue their studies at the graduate and professional level. CAMP exists at nine of the UC campuses and at various California State Universities, California Community Colleges, independent colleges and universities, and national laboratories that together work to achieve a goal of doubling the numbers of minority students receiving a B.S. or a B.A. degree in the many science disciplines.

# RISE Faculty Mentors

**Biochemistry**
*Dr. Gregor Blaha*

**Bioengineering**
*Dr. Victor Rodgers, Dr. Huinan Liu,*
*Dr. Kevin Freedman*

**Biomedical Sciences**
*Dr. Monica Carson, Dr. Adam Godzik,*
*Dr. Nicholas V. DiPatrizio*
*Dr. Seema Tiwari-Woodruff,*

**Botany and Plant Sciences**
*Dr. Jim Burnette, Dr. Carolyn Rasmussen, Dr. Dawn Nagel, Dr. David Nelson, Dr. Paul Nabity, Dr. Julia Bailey-Serres, Dr. Meng Chen, Dr. Daniel Koenig*

**Chemistry**
*Dr. Yadong Yin, Dr. Michael Pirrung,*
*Dr. Wenwan Zhong,*

**Earth and Planetary Sciences**
*Dr. Andrey Bekker*

**Electrical & Computer Engineering**
*Dr. Samet Oymak, Dr. Salman Asif*

**Entomology**
*Dr. Jessica Purcell, Dr. Kerry Mauck*

**Environmental Sciences**
*Dr. Samantha Ying, Dr. Andrew Gray,*
*Dr. Amir Haghverdi*

**Evolution, Ecology & Organismal Biology**
*Dr. Kurt Anderson, Dr. Kieran Samuk,*
*Dr. Kate Ostevik*

**Mathematics**
*Dr. Javier Gonzalez Anaya*

**Mechanical Engineering**
*Dr. Sundararajan Venkatadriagaram*

**Microbiology & Plant Pathology**
*Dr. Patricia Manosalva,*
*Dr. Alexander Putman*

**Molecular, Cell & Systems Biology**
*Dr. Margarita Curras-Collazo,*
*Dr. Weifeng Gu, Dr. Morris Maduro,*
*Dr. Sachiko Haga-Yamanaka*

**Physics & Astronomy**
*Dr. Roya Zandi, Dr. Michael Mulligan*

**Psychology**
*Dr. Rachel Wu, Dr. John Franchak,*
*Dr. Aaron Seitz, Dr. Khaleel Razak*

**School of Medicine**
*Dr. Ann Cheney*

# Alphabetical Listing

| **Last, First** | ***Page*** |
|---|---|
| Abdulkarim, Sanaa | 9, 34, 54 |
| Agarwal, Shreya | 10, 43 |
| Alba, Jacqueline | 7, 16 |
| Alsuhaibani, Hanadi | 8, 29, 36, 55 |
| Amin, Afraz | 10, 41 |
| Arcelao, Rian | 12, 58 |
| Arevalo, Russel Angelo | 9, 55 |
| Bello, Britany | 8, 25 |
| Benavides, Ramon | 7, 21, 34 |
| Bharadwaj, Nikhil | 9, 33 |
| Campos, Ileen | 7, 17 |
| Chavez, Jair | 10, 43, 54 |
| Choi, Audrey | 7, 20 |
| Chow, Derek | 8, 26, 27, 54 |
| Chow, Matthew | 9, 27, 31, 54 |
| Clement, Bella | 10, 44, 47 |
| Daley, Cameron | 7, 19 |
| De La Torre, Cesar | 10, 47 |
| Domond, Lynn | 12, 56 |
| Duong, Matthew | 10, 40, 46 |
| Elhassanieh, Rafic | 7, 17 |
| Espinoza, Lysdie | 8, 31 |
| Gad El Sayed, Marina | 7, 15 |
| Garcia, Andrew | 8, 24, 55 |
| Gonzalez II, Daniel | 11, 48 |
| Gonzalez, Valerie | 9, 36, 47,55 |
| Grant, David | 8, 26 |
| Guillory, Jordan | 11, 53 |
| Hernandez, Isaiah | 8, 29, 54 |
| Hoang, Tung | 10, 41 |
| Hudnall, Jared | 11, 51 |
| Kang, Angela | 8, 24, 32 |
| Khairi, Sehr | 9, 35 |
| Le, Diane | 9, 27 |
| Lemus, Gustavo | 10, 44 |
| Luna, Crystal | 10, 40 |
| Martin Gonzalez, Juana | 7, 19 |
| Martin, Rosita | 9, 21, 34 |
| Martinez Lopez, Evelyn | 10, 11, 44, 49 |
| Masso, Megan | 9, 32 |
| Mendoza, Ethan | 8, 27, 55 |
| Miguel Carreon, Joshua | 7, 16 |

| **Last, First** | ***Page*** |
|---|---|
| Mikol, Gregory | 7, 15 |
| Miramontes, Gerardo | 8, 28, 55 |
| Montejano Aquino, Christie | 8, 25, 36, 55 |
| Munoz, Alberto | 7, 23 |
| Nguyen, Jennifer | 10, 11, 27, 44, 52 |
| Nguyen, Kenny | 8, 30, 54 |
| Nguyen, Vincent | 9, 37 |
| Nworgu, Ezeonyeoma | 8, 28, 54 |
| Onukaegbe, Uchenna | 9, 36, 55 |
| Patel, Rajeet | 9, 33 |
| Patel, Reena | 10, 12, 44, 58 |
| Portillo, Johan | 11, 52 |
| Quinonez, Reyna | 10, 39, 55 |
| Ramirez, Alondra | 8, 23, 54 |
| Ramirez, Joseph | 8, 30 |
| Reyes, Alberto | 7, 20 |
| Santiago, Michell | 10, 12, 44, 57 |
| Sola, Jacob | 10, 39 |
| Tran, Joylyn | 11, 53 |
| Tran, Son | 9, 35, 54 |
| Vadakkan, Eshal | 11, 49 |
| Velasquez, Jacob | 11, 51 |
| Yadalla, Samhitha | 12, 59 |
| Yoo, Taewon | 9, 27, 36, 55 |
| Zeng, Landley | 11, 56 |

## RISE Symposium Schedule - Wednesday, August 24th, 2022
## (Genomics Auditorium)

| | | |
|---|---|---|
| **8:00 am - 8:45 am** | **Registration & Continental Breakfast** | |
| **8:45 am - 9:00 am** | **Welcome & Opening Remarks** | |
| **9:00 am - 10:00 am** | **Oral Session 1** | |
| | *Speaker* | *Presentation Title* |
| 9:00 am - 9:12 am | Marina Gad El Sayed<br>(Dr. Nicholas DiPatrizio) | Peripheral Endocannabinoids and the Behavioral Expression of Anxiety |
| 9:12 am - 9:24 am | Gregory James Mikol<br>(Dr. Monica Carson) | Differential Gene Expression within Brainstem of A. Alternata Exposed Mice |
| 9:24 am - 9:36 am | Joshua Carreon<br>(Dr. Morris Maduro) | Conserved Role for a Cell Specification Gene in Nematodes |
| 9:36 am - 9:48 am | Jacqueline Alba<br>(Dr. Aaron Seitz) | Understanding the Intricate Relationship Between LC-NE System with Perceptual and Memory Systems in Young Adults |
| 9:48 am – 10:00 am | Ileen Campos & Rafic E<br>(Dr. Jeffrey Bachant & Dr. Connie Nugent) | A Connection Between STN1 and the MCM Complex in Origin Firing |
| **10:00 am - 10:15 am** | **Coffee Break** | |
| **10:15 am - 11:15 am** | **Oral Session 2** | |
| | *Speaker* | *Presentation Title* |
| 10:15 am - 10:27 am | Juana Cecilia Martin Gonzales<br>(Dr. Roya Zandi) | Understanding the Formation of Spherical Viral Capsids Using Statistical Mechanics |
| 10:27 am - 10:39 am | Cameron Daley<br>(Dr. Samantha Ying) | Soil Remediation Through Metal Extractions: Moving the Immovable |
| 10:39 am - 10:51 am | Alberto Reyes<br>(Dr. Andrey Bekker) | Evidence for Oxygen in our Atmosphere within Moroccan Atlas Ranges |
| 10:51 am – 11:03 am | Audrey Choi<br>(Dr. Carolyn Rasmussen) | KATANIN Important for Orderly Cell Division in *Zea Mays* |
| 11:03 am - 11:15 am | Ramon Benavides Jr.<br>(Dr. Dawn Nagel) | Understanding the Plants Circadian Clock Control of Temperature Stress Responses |
| **11:30 am - 12:30 pm** | **Poster Session 1** | |
| | *Speaker* | *Presentation Title* |
| 11:30 am - 12:30 pm | Alberto Munoz<br>(Dr. Monica Carson) | Brainstem Response to Airborne Exposure of Alternaria Alternata Allergens |
| 11:30 am - 12:30 pm | Alondra Ramirez<br>(Dr. Kate Ostevik) | Analyzing the Effect of Transposable Elements on Rice Plant Health and Traits |

| **11:30 am - 12:30 pm** | **Poster Session 1 (continued)** | |
|---|---|---|
| | *Speaker* | *Presentation Title* |
| 11:30 am - 12:30 pm | Andrew Garcia<br>(Dr. James Burnette) | Analyzing Gene Expression and Annotations within Different Strains of Oryza Sativa L. SSP. Japonica |
| 11:30 am - 12:30 pm | Angela Kang<br>(Dr. Kurt Anderson) | The Invasive Community and Largemouth Bass Body Condition |
| 11:30 am - 12:30 pm | Britany Bello<br>(Dr. Seema Tiwari-Woodruff) | Purkinje Cell Pathology in Multiple Sclerosis Human Cerebellum |
| 11:30 am - 12:30 pm | Christie Montejano Aquino<br>(Dr. Sachiko Haga-Yamanaka) | Defensive Behavior Induced by FEL-D-4 in Mice |
| 11:30 am - 12:30 pm | David Grant<br>(Dr. Michael Pirrung) | One Step Carboxylic Acid to Nitrile Conversion |
| 11:30 am - 12:30 pm | Derek Chris Chow<br>(Dr. James Burnette) | The Effect of Inverted Regions on Gene Expression in HEG4 Rice |
| 11:30 am - 12:30 pm | Diane Le<br>(Dr. Khaleel Razak) | Behavioral Effects of Administering CTEP Treatment In A Mouse Model of Fragile X Syndrome |
| 11:30 am – 12:30 pm | Ethan Mendoza<br>(Dr. James Burnette) | Analyzing Differences in Gene Expression in Polymorphic Regions of Chromosomes 10 and 12 in Three Strains of Rice |
| 11:30 am - 12:30 pm | Ezeonyeoma C Nworgu<br>(Dr. Patricia Manosalva) | Phenotypic Variability of Phytophthora Cinnamomi California Avocado Isolates |
| 11:30 am - 12:30 pm | Gerardo Miramontes<br>(Dr. Amir Haghverdi) | Identifying Canopies That Remain Cool During Hot Summer: A Case Study from UCR Surroundings |
| 11:30 am - 12:30 pm | Hanadi Alsuhaibani<br>(Dr. James Burnette) | A Deletion and its Effect on Chr12g34990 in the Genome of Oryza sativa ssp. japonica EG4 Compared to HEG4 and NB |
| 11:30 am - 12:30 pm | Isaiah Hernandez<br>(Dr. James Burnette) | The Effect of Chromosomal Rearrangements on Genetic Expression in Three Rice (Oryza Sativa) Strains |
| 11:30 am - 12:30 pm | Joseph Ramirez<br>(Dr. Gregor Blaha) | Interaction Between the Zinc Binding Domain of RNA Polymerase & the Ribosomal Protein uS3 |
| 11:30 am - 12:30 pm | Kenny Nguyen<br>(Dr. Kate Ostevik) | The Effects of Elevation on Seed Size |
| 11:30 am - 12:30 pm | Lysdie Espinoza<br>(Dr. Huinan Lui) | Antibacterial & Mechanical Properties in Orthopedic Magnesium Based Implants |
| 11:30 am - 12:30 pm | Matthew Chow<br>(Dr. James Burnette) | Investigating HEG4 CHR10 Inversion and EG4 CHR12 Deletion |

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|---|---|---|
| 11:30 am – 12:30 pm | Megan Masso<br>(Dr. Kurt Anderson) | Stomach Content Diversity of Invasive Large Mouth Bass |
| 11:30 am – 12:30 pm | Melvin Hodanu<br>(Dr. Dawn Nagel) | Understanding the Role of BBX Transcription Factors in Abiotic Stress Tolerance in Arabidopsis |
| 11:30 am – 12:30 pm | Nikhil Bharadwaj<br>(Dr. Kurt Anderson) | DO SIZE, PROXIMITY TO LAKES, AND ELEVATION INFLUENCE BIODIVERSITY IN PONDS? |
| **11:30 am - 12:30 pm** | **Poster Session 1 (continued)** | |
| | *Speaker* | *Presentation Title* |
| 11:30 am – 12:30 pm | Rajeet Patel<br>(Dr. Kieran Samuk) | Developing Genetic Resources for the Identification of Thermal Supergenes in Drosophila Pseudoobscura |
| 11:30 am – 12:30 pm | Rosita J. Martin<br>(Dr. Dawn Nagel) | Understanding the Plants Circadian Clock Control of Temperature Stress Responses |
| 11:30 am – 12:30 pm | Russel Angelo Azucena Arevalo<br>(Dr. James Burnette) | The Effect of Deletions in Different Strains of Oryza Sativa |
| 11:30 am – 12:30 pm | Sanaa Abdulkarim<br>(Dr. Monica Carson) | Lung Inflammation from Chronic Exposure to Allergen Induced Sex-Specific Alterations in Gene Expression within the Brainstem |
| 11:30 am – 12:30 pm | Sehr Shahina Khairi<br>(Dr. Monica Carson) | The Impact of Chronic Inhalation Exposure to Alternaria Alternata on the Brain's Immune Status |
| 11:30 am – 12:30 pm | Son Tran<br>(Dr. James Burnette) | Studying the Inversion Caused by Mping in Oryza Sativa SSP. Japonica Varieties |
| 11:30 am – 12:30 pm | Taewon Yoo<br>(Dr. James Burnette) | Market Assessment of Developing Tomatoes Resistant to Bacterial Canker |
| 11:30 am – 12:30 pm | Uchenna Onukaegbe<br>(Dr. James Burnette) | Gene Expression in Nipponbare Oryza Sativa SSP. Japonica |
| 11:30 am – 12:30 pm | Valerie Gonzalez<br>(Dr. Andrew Gray) | Emission Rates and Identifying Tire and Road Wear Exported from San Diego Creek |
| 11:30 am – 12:30 pm | Vincent Nguyen<br>(Dr. Kurt Anderson) | Effects of different pH environments on Microorganism Biodiversity |
| **12:30 pm - 1:30 pm** | **Lunch @ Entomology Courtyard** | |

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|---|---|---|
| **1:30 pm - 2:30 pm** | **Oral Session 3** | |
| | *Speaker* | *Presentation Title* |
| 1:30 pm - 1:42 pm | Reyna Quinonez<br>(Dr. Kieran Samuk) | Optimizing A Phenol-Chloroform Based High Molecular Weight DNA Extraction Protocol for Drosophila Species |

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|---|---|---|
| 1:42 pm - 1:54 pm | Jacob Sola<br>(Dr. Adam Godzik) | Understanding the HVEM Receptor Protein through its Structural Clues |
| 1:54 pm - 2:06 pm | Matthew Duong<br>(Dr. Carolyn Rasmussen) | Defining Dynamic Cell Plate Localization in *Zea Mays* During Mitosis |
| 2:06 pm - 2:18 pm | Crystal Luna<br>(Dr. Maggie Curras-Collazo) | Hypothalamic Oxytocin and Vasopressin Neurons in a Toxicant Autism Mouse Model |
| 2:18 pm - 2:30 pm | Afraz Amin & Tung Hoang<br>(Dr. Weifeng Gu) | CRISPR/Cas9-mediated gene editing in C. elegans PIR-1 |

| **2:30 pm - 2:45 pm** | **Coffee Break** | |
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| **2:45 pm - 3:45 pm** | **Oral Session 4** | |
|---|---|---|
| | *Speaker* | *Presentation Title* |
| 2:45 pm - 2:57 pm | Jair Chavez<br>(Dr. Ann Cheney) | A Practical Way to Combat Diabetes Among Latinos in the Eastern Coachella Valley: The Eat, Move, Live Program |
| 2:57 pm - 3:09 pm | Shreya Agarwal<br>(Dr. Carolyn Rasmussen) | Fluorescent Protein Toolkit For Studying Division Plane Orientation |
| 3:09 pm - 3:21 pm | Gustavo Lemus<br>(Dr. Victor Rodgers) | Experimental Characterization of Inertial Ordering of Flat Plate Non-Neutrally Buoyant Particles in Helical Microchannels |
| 3:21 pm - 3:45 pm | Evelyn Martinez Lopez, Jennifer Nguyen, Michell Santiago, Reena Patel & Bella Clement<br>(Dr. James Burnette) | Amplifying the Fanac2 Gene Found in Strawberries to Increase Drought Resistance |

| **4:00 pm - 5:00 pm** | **Poster Session 2** | |
|---|---|---|
| | *Speaker* | *Presentation Title* |
| 4:00 pm - 5:00 pm | Allison Chan<br>(Dr. Kurt Anderson) | Effects of Increasing Salinity on Freshwater Protists |
| 4:00 pm - 5:00 pm | Alondra Contreras<br>(Dr. Carolyn Rasmussen) | Using Cell Markers to Understand Dynamic Cell Plate Localization in *Zea mays* |
| 4:00 pm - 5:00 pm | Bella Clement<br>(Dr. Kieran Samuk) | Progress Towards Adaptation a High Salt Diet in Experimental Populations in Drosophila Melanogaster |
| 4:00 pm - 5:00 pm | Cesar De La Torre<br>(Dr. Aaron Seitz) | Evaluating Auditory and Perceptual Processing with Ability to Detect Emotions in (ASD) |
| 4:00 pm - 5:00 pm | Daniel Gonzalez II<br>(Dr. Samantha Ying) | Integrating Bokashi Amendments with Microbe-Mediated Sustainable Agriculture |

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|---|---|---|
| 4:00 pm - 5:00 pm | Diane Nguyen (Dr. Daniel Koenig) | The Link between Genetic and Morphological Change in a Long-Term Evolutionary Experiment |
| 4:00 pm - 5:00 pm | Eshal Vadakkan (Dr. Alex Putman) | Virulence of Fusarium Oxysporum F. Sp. Fragariae Obtained from a Fusarium Wilt-Resistant Strawberry Cultivar |
| 4:00 pm - 5:00 pm | Evelyn Martinez Lopez (Dr. Alexander Putman) | A Fusarium Wilt Survey in Lettuce Plants |
| 4:00 pm - 5:00 pm | Gabriel Chavez (Dr. Julia Bailey-Serres) | What is the role of sucrose transporters during submergence in rice (Oryza sativa)? |
| 4:00 pm - 5:00 pm | Jacob Jauregui (Dr. Paul Nabity) | The Effect of Parasites on Plant Defense Hormones at the Genetic Level |

| **4:00 pm - 5:00 pm** | **Poster Session 2 (continued)** | |
|---|---|---|
| | *Speaker* | *Presentation Title* |
| 4:00 pm - 5:00 pm | Jacob Velasquez (Dr. Kevin Freedman) | Biomolecule Sensing using Solid-State Nanopores under Conductive Pulses |
| 4:00 pm - 5:00 pm | Jared Hudnall (Dr. Michael Mulligan) | The Application of Physics to Characterize Artificial Deep Neural Networks |
| 4:00 pm - 5:00 pm | Jennifer Nguyen (Dr. James Burnette) | Differences in Expression of OS10G0145901 in HEG4 vs. EG4 and Nipponbare |
| 4:00 pm - 5:00 pm | Johan Arturo Portillo (Dr. Maggie Curras-Collazo) | Dysregulated Pain Pathways in a Mouse Model of Gulf War Illness |
| 4:00 pm - 5:00 pm | Jordan A. Guillory (Dr. Javier Gonzalez Anaya) | Enumerating the Linearity Regions of Max-Pooling Layers for Convolutional Neural Networks |
| 4:00 pm - 5:00 pm | Joylyn Tran (Dr. Kurt Anderson) | Comparing Chemical and Biological Controls for Algal Blooms |
| 4:00 pm - 5:00 pm | KGI Chili Peppers | Commercial And Biological Effects Of Producing Genetically Modified Root-Knot Nematode Resistant Chili Peppers |
| 4:00 pm - 5:00 pm | KGI Lettuce | Developing Heat Tolerant Lettuce |
| 4:00 pm - 5:00 pm | KGI Rice | Agribusiness with Drought-Resistance Oryza Sativa (Rice) |
| 4:00 pm - 5:00 pm | KGI Tomato | Market Assessment of Developing Tomatoes Resistant to Bacterial Canker |
| 4:00 pm - 5:00 pm | Landley Zeng (Dr. Yadong Yin) | Reversible Plasmonic Tuning by Photo-Manipulation of Thermoresponsive Charged Gold Nanoparticles |
| 4:00 pm - 5:00 pm | Lynn Domond (Dr. John Franchak) | Relation Between Restraint and Infant Sitting Acquisition |
| 4:00 pm - 5:00 pm | Michell Santiago | The Biosynthetic Function of CYP722A |

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|---|---|---|
| | (Dr. David Nelson) | |
| 4:00 pm - 5:00 pm | Mona Tran<br>(Dr. Kerry Mauck) | Investigating the Bindweed Psyllid as a Potential Vector of Candidatus Liberibacter solanacearum in a Previously Undescribed Host Plant |

| **4:00 pm - 5:00 pm** | **Poster Session 2 (continued)** | |
|---|---|---|
| | *Speaker* | *Presentation Title* |
| 4:00 pm - 5:00 pm | Reena Patel<br>(Dr. James Burnette) | The Effect of Gene Expression Based on an Inversion Sequence in Oryza Sativa SSP. Japonica |
| 4:00 pm - 5:00 pm | Rian Arcelao<br>(CNAS Scholars) | Can Formica Francoeuri Ants Share Learned Information with Their Nestmates |
| 4:00 pm - 5:00 pm | Samhitha Yadalla<br>(Dr. Kurt Anderson) | Metabolic Implications of Temperature Fluctuations on Protist Species, Blepharisma |
| 4:00 pm - 5:00 pm | Xitlalli Zavala<br>(Dr. David Nelson) | |
| 4:00 pm - 5:00 pm | Yongyi Wen<br>(Dr. Daniel Koenig) | |

| **5:00 pm - 7:00 pm** | **Dinner & Awards at Entomology Courtyard** |
|---|---|

# ABSTRACTS

# ORAL SESSION 1

## 9:00 – 10:00 am

## Oral Session 1 - 9:00am - 9:12am

### Peripheral Endocannabinoids and the Behavioral Expression of Anxiety

**Marina Gad El Sayed**, Courtney Wood, Nicholas DiPatrizio
Department of Biomedical Sciences, School of Medicine, University of California, Riverside

Cannabis has historically been perceived as an anxiolytic drug. Recent findings have indicated the endocannabinoid system (ECS) as a modulator of anxiety and anxiety-related disorders, like PTSD. The ECS is an endogenous lipid signaling system that is composed of the endocannabinoids, the cannabinoid receptors, and the enzymatic machinery responsible for the production and degradation of endocannabinoids. In rodents, treatment with cannabinoids yields anxiolytic behaviors at low doses and anxiogenic behaviors at high doses. Moreover, genetic removal of the endogenous cannabinoid receptor subtype-1 (CB1R) produces a similarly anxious phenotype. Paradoxically, work from the DiPatrizio lab suggests that mice lacking the CB1R specifically from the intestinal epithelium exhibit a reduction in anxiety-like behaviors on the Elevated Plus Maze test. This study aims to further examine how the conditional removal of CB1R from the small intestinal epithelium will affect the behavioral expression of anxiety in C57BL/6 mice. We will utilize the Cre-Lox method of genetic recombination to remove intestinal CB1R once mice have reached adulthood. We will assess anxiety-like behaviors in adult mice lacking intestinal CB1R and genetically intact littermate controls using the light/dark box test. We hypothesize that mice lacking intestinal CB1R will exhibit an anxiolytic phenotype on the apparatus when compared to controls.

## Oral Session 1 - 9:12am - 9:24am

### Differential Gene Expression within Brainstem of A. Alternata Exposed Mice

**Gregory J. Mikol**, Paula da Silva Frost, Sirajan Kamara, and Monica J. Carson
Carson Laboratory, UCR Department of Biomedical Sciences, University of California, Riverside

Chronic exposure to Alternaria alternata (a common fungal allergen) has been shown to induce a decrease in select innate immune molecules associated with inflammation within the Medulla of mice (Peng, et al. 2018). How will an exposure sufficient to induce an adaptive immune response (>96 hr) affect the expression of genes associated with metabolism within the brainstem of mice? Specially designed exposure chambers allow mice to move freely inside their own cages with access to food and water while inhaling an aerosolized particulate solution of A. alternata, over a 7-day period. Following exposure the brain is extracted and the brainstem is homogenized and treated for extraction of RNA. Analysis using nanoString nCounter® data on ROSALIND bioinformatics software allows for quantification of gene expression through tagging and counting of mRNA molecules. Quantification of gene expression through analysis of mRNA following exposure can provide key insights into the metabolic consequences associated with specific genes. The differential gene expression analysis of comparisons between Alternaria and air exposed mice groups revealed a sex specific difference in the regulation of specific metabolism associated genes. Female mice show a greater number of upregulated genes compared to male mice, and a more robust profile of expression overall. A single gene, SLC16A2, was upregulated in males, but down regulated in females. Solute carrier family 16 member 2 (SLC16A2) is a gene associated with thyroid hormone transmembrane transporter activity and amino acid transmembrane transporter activity (U.S. National Library of Medicine).

## Oral Session 1 - 9:24am - 9:36am

### Conserved Role for a Cell Specification Gene in Nematodes

**Joshua Miguel Carreon**, Esmeralda Rivera, Gina Maduro, Morris Maduro
Department of Molecular, Cell and Systems Biology, University of California, Riverside

In the Maduro Lab we are interested in how genes that are important for development in one species might function in another species. The embryonic development of nematode C. elegans has been studied for many years. We are looking at genes in the closely related species, C. angaria which have similar embryonic development. One of the early embryonic cells, MS, is the precursor of the muscles, pharynx, neurons, and somatic gonads. In C. elegans, the maternally expressed genes mex-1 and pie-1 are important in early embryo development. mex-1 and pie-1 work in different cell lineages, but have the similar functions of preventing the inappropriate differentiation of MS cells. Inappropriate MS fate acquisition would lead to the development of excess muscle. These genes have not been studied in C. angaria. In this project we are using the technique of RNA interference (RNAi) to selectively block the function of these genes; examining the effects on embryonic development. Through this, we hope to gain a better understanding of the evolution of development and the limits of conservation between related, yet distinct species.

## Oral Session 1 - 9:36am - 9:48am

### Understanding the Intricate Relationship Between LC-NE System with Perceptual and Memory Systems in Young Adults

**Jacqueline Alba**, Kimia Yaghoubi, Mohammad Dastgheib, Hadi Kobaissi, and Aaron Seitz
Department of Undergraduate Academic Advising Center, University of California,
Riverside

The locus coeruleus (LC) is known to produce norepinephrine (NE), which projects to areas across the brain that regulate arousal, learning, memory, and orientation responses. However, there is still an insufficient amount of research that undercovers the relationship between LC-NE activity and cognitive function. LC-NE plays an important role in neurodegenerative disorders, and understanding how it works can help us identify potential biomarkers that could indicate them. In this research, we use young healthy adults to complete a series of cognitive tasks while using a handgrip stressor with efforts to stimulate the LC activity while simultaneously having a pupillometry as our indicator for LC activity. We then compute a psychometric function graph that illustrates how each individual is performing across various stimulus levels and performance changes to help differentiate the behavioral performance at different levels of LC activity across perceptual and visual memory tasks'.

## Oral Session 1 - 9:48am – 10:00am

### A Connection Between STN1 and the MCM Complex in Origin Firing

**Rafic Elhassanieh, Ileen Campos**, Alejandro Navarro, Dr. Jeff Bachant, Dr. Constance Nugent
Department of Biological Sciences, University of California Riverside

DNA initiation replication is the process in which DNA is replicated at origins of replication. The main mechanisms that are required to begin this process include DBF4 Dependent Kinase (DDK), a complex of the 2 proteins: DBF4 and CDC7, and MCM2-7 complexes. Additionally, this report is interested in the telomere elongation of the CST complex, which is composed of the proteins CDC13, STN1, and TEN1. This complex recruits telomerase (a complex including RNA and a protein) to elongate telomeres (special DNA sequences which protect the end of linear chromosomes). Previous evidence from this lab has shown that STN1, traditionally understood to only play a role in telomere elongation, plays a secondary role in DNA initiation replication. STN1's overproduction can rescue the maximum viable temperature of DDK mutants. This project hypothesizes that there is a direct physical interaction between STN1 and members of the MCM complex; however, experimentation will begin by probing a direct interaction between STN1 and MCM6. To prove this, the Yeast 2 Hybrid method is being used which utilizes a genetic construct containing three reporter genes: ADE2, His, and lacZ, whose expression is coupled to the proposed interaction between STN1 and MCM6.
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# ORAL SESSION 2

## 10:15 – 11:15 am

## Oral Session 2 - 10:15am - 10:27am

### Understanding the Formation of Spherical Viral Capsids Using Statistical Mechanics

**Juana Cecilia Martin Gonzalez,** Jennifer Castaneda-Gutierrez, Jessica Richardson, and Roya Zandi
Department of Physics and Astrophysics, University of California, Riverside

Viruses are microscopic infectious transmitters made up of a genome (RNA or DNA) encapsulated by a protein shell called the capsid. They replicate using the host cell machinery. Since the capsid plays a vital role in the life cycle of a virus, it is important to explore the physical factors contributing to the kinetics pathway of the capsid formation. To this end, we will employ the law of mass action combined with classical nucleation theory, which depends on the height of the energy barrier between the proteins free in solution and fully formed capsids. Using computer simulations, we can confirm that virus assembly matches experimental results where the viral assembly depends on the concentration of free subunits and fully formed capsids. This insight can help scientists develop treatments and therapies against virus formation.

## Oral Session 2 - 10:27am - 10:39am

### Soil Remediation Through Metal Extractions: Moving the Immovable

**Cameron Daley**, Danielle Stevenson, and Samantha Ying
Department of Environmental Sciences, University of California, Riverside

Contaminated soils are pervasive throughout California which can adversely impact human health for communities living on or in proximity to the soils. Such soils contaminated with high concentrations of lead, hexavalent chromium, arsenic, and polycyclic aromatic hydrocarbons due to anthropogenic pollution must be remediated prior to their use as parks or housing where human exposure is likely. Arbuscular mycorrhizal fungi (AMF) can form relationships with plant hosts that have been shown to enhance plant update of metals from soils as a form of phytoremediation; however, it is currently unknown whether AMF enhance metals uptake in drought tolerant native plants of California. By testing different biological treatments (with and without AMF), we can quantify the effectiveness of metal uptake by AMF associated native plants. We usedX-ray fluorescence and sequential metal extractions to determine the total and mobile concentrations of metals in soils at multiple sites in southern California . Because metal availability is heavily affected through pH, pH of the soils was tested. Preliminary findings show that the metals in the contaminated soils are extractable by the fungi and plants; and of the native plants tested, California buckwheat (Eriogonum fasciculatum) showed the most extraction capability. These initial results show that California buckwheat may be suitable for metal extraction in arid climates such as throughout California.

## Oral Session 2 - 10:39am - 10:51am

### Evidence for Oxygen in our Atmosphere within Moroccan Atlas Ranges

**Alberto Reyes**, Ginny Winters and Andrey Bekker
Department of Earth and Planetary Sciences, University of California, Riverside

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, however. We have seen evidence in the geological record to show that these first signs of 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”. The GOE (Great Oxidation Event), can be tracked in the geochemical record of select rocks from before, during, and after this time period. By observing the ratio of iron and carbon isotopes in carbonates, we are able to see a direct correlation between these isotopes and the oxygen present in the atmosphere. This article in particular observes the exposed neoproterozoic-cambrian rocks from the Anti-Atlas and High Atlas ranges of Morocco. These carbonates undergo a process of micro-drilling to extract a sample that is then used to determine carbon isotope ratios lying within the rock. These Moroccan carbonates, which are approximately 500 million years old, can help aid us in finding smaller fluctuations within the pre existing literature regarding the GOE.

## Oral Session 2 - 10:51am – 11:03am

### Katanin is Important for Orderly Cell Division in ZEA MAYS.

**Audrey Choi,** Stephanie Martinez, Carolyn Rasmussen
Department of Botany and Plant Sciences, University of California, Riverside

KATANIN is a microtubule severing protein that is important for proper microtubule organization and dynamics to promote proper growth and development in eukaryotic organisms. Plant cells have unique mitotic structures during cell division. After interphase, a ring of microtubules, actin filaments, and proteins, called the preprophase band (PPB) forms. The PPB disassembles after prophase to form the mitotic spindle during metaphase. After anaphase, the phragmoplast, an antiparallel microtubule array, forms and expands towards the cell division site, leaving behind a cell plate that will mature into a cell wall. The cell division site is marked by TANGLED1, a microtubule bundling protein. In Zea mays, katanin double mutants have a microtubule severing defect that affects PPB formation and phragmoplast guidance, leading to leaf epidermal cell patterning defects. To determine if the leaf epidermal cell patterning defects seen in katanin double mutants are due to mislocalized TANGLED1, I will use live-cell imaging to investigate the localization of TANGLED1 in katanin double mutants expressing the fluorescent proteins CFP-TUBULIN, to label microtubules, and TANGLED1-YFP, to mark TANGLED1. I hypothesize that TANGLED1 is mislocalized in the katanin double mutant, leading to leaf epidermal cell patterning defects. By investigating the localization of TANGLED1 in katanin double mutants in Zea mays, we can better understand the role and function of KATANIN in division plane orientation. This research helps us learn more about the mechanisms for proper plant growth and development.

## Oral Session 2 – 11:03am - 11:15am

### Understanding the Plants Circadian Clock Control of Temperature Stress Responses

**Ramón Benavides Jr**., Rosita J Martin, Samantha J Cordingley, and Dawn H Nagel
Department of Botany and Plant Sciences, University of California, Riverside

The circadian clock is an internal system that helps living organisms sense time and responds to environmental cues. In plants, circadian rhymes utilize various signals that regulate photosynthesis, flowering, growth, abiotic and biotic responses, and hormone signaling. However, understanding how the circadian clock controls a plant's response to temperature stress remains unknown. In this project, our goal is to determine whether a heat-inducible Arabidopsis transcription factor regulation and contribution to the heat stress response is conserved in crops. The aim of our research is two-fold - to determine whether the rice BBXs are also induced by heat stress and to generate overexpression constructs of the rice BBXs for future functional studies. Using gene expression analysis, we tested whether OsBBX expression is induced in response to a one-hour heat stress (45 o C) treatment in rice seedlings depending on the time of day. In addition, we created constructs where the OsBBX coding sequence was expressed with a 35S promoter and fused to the Green Fluorescent Protein (GFP). These constructs were infiltrated into tobacco leaves to check their cellular localization. Findings from this project will contribute to our continued goal of engineering plants to be more heat stress tolerant and ensure food security for the world's growing population.

# POSTER SESSION 1

## 11:30 am – 12:30 pm

## Poster Session 1 - 11:30am - 12:30am

### Brainstem Response to Airborne Exposure of Alternaria Alternata Allergens

**Alberto Munoz**, Paula Da Silva Frost, Sirijan Karama, Trevor Biddle, Kezyiah Yisrael,
David Cocker, David D Lo, Monica J Carson
Division of Biomedical Sciences, University of California, Riverside

Alternaria alternata is a fungal allergen found throughout the United States. Epidemiologic studies correlate increasing prevalence of asthma symptoms with higher levels of A. alternata antigens in the household. Because the vagal nerve connects the lung to the brainstem, we are testing whether A. alternata allergen exposure sufficient to cause lung inflammation causes changes in the brainstem. Specifically, we test if continuous 7-day airborne exposure to non-infectious A. alternata particulates alters levels of two neuronal presynaptic molecules: synaptophysin, marker for all neurons and vGlut2, a maker for excitatory synapses. By western blot analysis, we find that vGlut2 but not synaptophysin levels are decreased, suggesting a preferential reduction of excitatory synapses. Using immunofluorescence histology, we are testing whether the reduction is localized to specific areas of the neuronal circuit regulating breathing. Therefore, we are exposing brainstem tissue from untreated and A. alternata-exposed mice to fluorescently conjugated antibodies against synaptophysin and vGlut2. We are quantifying the total immunofluorescence and the co-labeling of synaptophysin and vGlut2 in two regions of the brainstem regulating breathing: The pre-BotC which regulates breathing patterns and the Nucleus Ambiguous, which regulates bronchial constriction, a response observed in asthma. These data will show whether the effects of allergic inflammation on breathing may be due in part to effects on brain regions regulating breathing.

## Poster Session 1 - 11:30am - 12:30am

### Analyzing the Effect of Transposable Elements on Rice Plant Health and Traits

**Alondra Ramirez**, Kate Ostevik
Department of Evolution, Ecology, and Organismal Biology, University of California, Riverside

Transposable elements (TEs), also known as “jumping genes,” are recognized as active repetitive DNA sequences that make up a dynamic structure of genomes. Studies have reported that transposable elements not only "jump" but are also found in all organisms including prokaryotes and eukaryotes, most commonly in large quantities. These “jumping genes” have been extensively studied in the plant genome as a critical source of variation that natural selection can act upon. Without transposable elements, plant species may not be able to maintain enough genetic variation to allow them to continuously flourish and continuously adapt to alterations within their environment. On the other hand, it is still possible for the increased mutations that TEs are responsible for to be detrimental to a plant in the short term. Here we analyze the extent to which transposable element activity affects plant health in a variety of rice seeds in five plant lines that includes A119, A123, EG4, HEG4 and Nipponbare. We found that the Nipponbare line containing 1 Ping (50 mPing) was the most successful with a germination rate of 80%. The other lines had a germination rate of 25% for A119 7 Ping (500 mPing), 45% in A123 with 10 Ping (500 mPing), 50% for HEG4 with 7 Ping (500 mPing) and 60% for EG4 with 7 Ping (500 mPing). Thus, indicating that plant lines with least TE activity have shown to have higher germination rates. While suggesting that TEs may have a negative effect on a plant's health in the short term.

## Poster Session 1 - 11:30am - 12:30am

### Analyzing Gene Expression and Annotations within Different Strains of Oryza Sativa L. SSP. Japonica

**Andrew Garcia**, James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, and Susan Wessler
Wessler Campbell Scholars Summer Research Program, Neil A. Campbell Science Learning Laboratory, Department of Botany and Plant Sciences, University of California, Riverside

Strains of rice known as EG4 and HEG4, that stem from a specific cultivar of Oryza sativa L. ssp. japonica, known as Nipponbare (NB), are being analyzed with regards to assessing gene expression and current gene annotations made within a specific area of the genome, particularly on chromosome ten. These three strains of Oryza sativa L. ssp. japonica NB, EG4 and HEG4, exhibit genomic similarity, however, an inversion has appeared in HEG4 because of the transposase coupled with the transposable element mPING. The expression of these genes within each strain will be analyzed using primer design, polymerase chain reaction (PCR & qPCR), DNA/RNA extraction, biological databases, and computational techniques to analyze. For my specific gene, LOC112936594, the flanking gene primers designed successfully produced the desired amplicon size within different samples of gDNA, following this I proceeded to design cDNA primers and they too were successful in producing the desired amplicon within strains tested; HEG4 and NB in particular. After confirming the cDNA primers perform as intended, I conducted a PCR and qPCR utilizing my cDNA primers with cDNA. These primers produced the desired amplicon in S+ cDNA (containing reverse transcriptase) in every strain exhibiting that there may be gene expression within the shoots of each strain relating to this gene. With this result qPCR was the next step and after three attempts, the qPCR primers I designed were not able to produce an amplicon. New primers have been designed but have yet to be tested, this would be the integral to proving expression within the shoots of each strain. The gene being analyzed is still uncharacterized meaning that its function is still unknown and has the possibility of being a pseudogene. Eventually my gene as well as other specified genes within each strain will ultimately be compared in regard to their expression across all strains, as well as the reference strain to determine the effect of the inversion. Through our research we hope to contribute to the existing bioinformatic data regarding Oryza sativa L. ssp. Japonica and transposable elements

## Poster Session 1 - 11:30am - 12:30am

### The Invasive Community and Largemouth Bass Body Condition

**Angela Kang**, William Ota, and Kurt Anderson
Anderson Laboratory, UCR Department of Evolution, Ecology, and Organismal Biology

Largemouth Bass (LMB) are a prevalent invasive species throughout the globe and have been introduced to many urban freshwater systems. In these systems, they are the top invasive predator often sharing habitat with a suite of other invasive species. By assessing how LMB body condition and invasive community diversity co-vary within the Santa Ana River, we assess how invasive species density and composition impact LMB. If the invasive community in each urban gradient continues to grow, then the body conditions of LMB will differ from reach to reach. The greater the distance from the wastewater outflow channel, the higher body condition we see of the LMB population. This can allow us to better understand how this global invasive species responds to other invasive species and their densities. This study consisted of a total of 556 LMB and over 1500 invasive fish that were collected during a wastewater shutdown in 2019 across over three miles of the Santa Ana River. These fish were identified and had various body measurements recorded. For each section of river fish were removed from, we calculated Shannon's and Simpson's diversity of the invasive freshwater community. The LMB body condition (Fulton's K = (weight/ length^3 ) 10^5) was also calculated. Using a scatter plot, we saw that the R-squared value for the Shannon's Diversity Index is 0.272 while the R-squared value for the Simpson's Diversity Index is 0.453. This showed the proportion of variance for the BCI mean. Understanding the diets of LMB aid conservationists in improving the stability of the local river system and can help researchers conduct further experiments on how LMB impacts local freshwater systems.

## Poster Session 1 - 11:30am - 12:30am

### Purkinje Cell Pathology in Multiple Sclerosis Human Cerebellum

**Britany Bello**, Shane Desfor, Seema Tiwari-Woodruff
Division of Biomedical Sciences, School of Medicine at University of California, Riverside

Multiple sclerosis (MS) is an autoimmune, demyelination, neurodegenerative disease of the central nervous system (CNS). Nearly 80% of MS patients lose motor control and exhibit tremors, a consequence of demyelination and inflammation of the cerebellum. Purkinje cells (PCs) are potential targets of MS-induced demyelination, leading to mitochondrial dysfunction and apoptosis. To test the hypothesis that PCs are the target, postmortem MS cerebellar tissue will be evaluated by immunohistochemistry (IHC) and compared to "normal" tissue. First, we will assess the myelination status of the cerebellar tissue by performing IHC with PLP (proteolipid myelin protein) and NF200 (neurofilament axon protein). For analysis,10X image stitching to get an overview of the section and 20X confocal images to get the details will be analyzed. IHC of MS cerebellum shows an increase in demyelination and a decrease in parallel fibers. A significant difference in MS tissue compared to "normal" tissue is observed. Understanding the causes of MS pathology-induced PC demyelination and loss will allow us to find therapeutic treatments to ensure the survival of PCs and other neurons during MS.

## Poster Session 1 - 11:30am - 12:30am

### Defensive Behavior Induced by FEL-D-4 in Mice

**Christie Montejano Aquino**, Mitchell Masterson, Quynh Ann Nguyen, Sachiko Haga-Yamanaka
Department of Molecular, Cell & Systems Biology, University of California, Riverside

Semiochemicals, such as pheromones and predator cues, are released into the environment by animals and can be detected by the same or other species. Predators can be detected this way through the chemical cues that they release. In mice, the accessory olfactory system has been shown to participate in detecting these predator cues. Specifically, the vomeronasal organ (VNO) which is located in the nasal septum has been shown to detect semiochemicals. These cues can activate the VNO sensory neurons and induce an assortment of behaviors ranging from defensive behaviors to mating and aggression. Defensive behaviors can be induced when the VNO recognizes olfactory cues when a mouse comes into contact with a specific predator cue. The predator cue activates the VNO to produce a variety of defensive behaviors like risk assessment or freezing. However, the different types of defensive behaviors induced by predator cues are not well understood. A cat allergen, Fel-d-4, found in cat saliva has been shown to induce risk assessment by activating the VNO in mice. In order to test how this cue induces the behavior output, we made Fel-d-4 (rFeld4) and examined defensive behavior responses upon exposure to different amounts of the recombinant protein. We expect that rFeld4 will induce only risk assessment behavior regardless of its amount, which will indicate that a given type of defensive behavior is triggered by a specific predator cue.

## Poster Session 1 - 11:30am - 12:30am

### One Step Carboxylic Acid to Nitrile Conversion

**David Grant,** Scott Borcher, Nathan Coddington, Michael Pirrung

Department of Chemistry, University of California Riverside

In this ongoing investigation, we explored a 1 step conversion of the carboxylic acid functional group to the nitrile functional group. We explored a method via a silyl amide intermediate. For this purpose, several reactions with various temperatures, atmospheres, solvents and substrates have been carried out into attempts to make the silyl amide intermediate. However, none have worked so far to produce the silyl amide intermediate needed for the full nitrile conversion.

## Poster Session 1 - 11:30am - 12:30am

### The Effect of Inverted Regions on Gene Expression in HEG4 Rice

**Derek Chow**, James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, and Susan Wessler

Dynamic Genome Program, Department of Botany and Plant Sciences, University of California, Riverside

In this study, the effect of inverted regions on HEG4 in comparison to EG4 and Nipponbare (NB) rice, *Oryza sativa ssp. japonica,* on gene expression is being determined. In particular, this study focuses on Os10g0147400, one of the genes in the inverted region of HEG4. This gene is responsible for a protein that acts similar to Auxin, a plant hormone that plays a role in the growth and development of the plant body. DNA samples and primers were prepared and used to conduct a series of PCR-based tests. RNA extracted from rice shoots and roots was copied into cDNA with the use of reverse transcriptase. qPCR has been conducted to quantitatively measure the amount of DNA in our samples. Together, conventional PCR and qPCR will help verify the presence of Os10g0147400 and its expression in HEG4, EG4, and NB, the three different rice varieties in question. This study will help determine if the inverted regions of HEG4 have an effect on gene expression, and if so, what that effect may be.

## Poster Session 1 - 11:30am - 12:30am

### Behavioral Effects of Administering CTEP Treatment In A Mouse Model of Fragile X Syndrome

**Diane Le**, Mawaheb Kassir, Jonathan Lovelace, Anjum Hussain, Khaleel Razak
Department of Psychology, University of California, Riverside

Fragile X Syndrome (FXS) is a genetic neurodevelopmental disorder that causes autism and intellectual disabilities. Affecting 1 in 4,000 males and 1 in 8,000 females, those with FXS exhibit hyperactivity, elevated anxiety, and impaired cognitive and sensory processing. These deficits result from mutations in the X-linked gene Fragile X messenger ribonucleoprotein 1 (Fmr1). Fmr1-knockout (KO) mouse models have shown consistency with observations within humans, displaying seizures, sensory processing deficits, and anxiety. Utilizing Fmr1-KO mice to identify a potential treatment for these symptoms, we administered a drug called 2-chloro-4-((2,5-dimethyl-1-(4-(trifluoromethoxy)phenyl)-1H-imidazol-4-yl)ethynyl)pyridine (CTEP) to KO mice and measured behavioral changes. CTEP inhibits metabotropic glutamate receptor pathways, which are upregulated in FXS. Two types of experiments were run: open field test (OFT) and elevated plus maze (EPM), commonly used to study anxiety and hyperactivity in rodents. Experimental mice with higher anxiety depict decreased exploration and higher activity near the arena’s wall or closed arms. We found that CTEP reduces distance traveled in the OFT across both wild-type (WT) and KO groups, suggesting reduced hyperactivity. There were no statistically significant differences in time spent in the EPM closed arms between WT and KO mice and no effects specific to CTEP, indicating no treatment of anxiety. These results suggest that more effective intervention is needed to target anxiety deficits related to FXS. Using animal models of FXS will continue to help facilitate new treatments to alleviate symptoms in humans.

## Poster Session 1 - 11:30am - 12:30am

### Analyzing Differences in Gene Expression in Polymorphic Regions of Chromosomes 10 and 12 in Three Strains of Rice

**Ethan Mendoza**, James Burnette, Venkateswari Chetty, Derek Chow, Matthew Chow, Alejandro Cortez, Isai Gonalez, Jennifer Nguyen, Susan Wessler, Taewon Yoo
Dynamic Genome Program, Department of Botany and Plant Sciences, University of California, Riverside

This research project is focused on identifying and analyzing differences in gene expression in three strains of Oryza sativa ssp. japonica. These three strains are EG4, HEG4, and Nipponbare (NB) which is our reference strain. The initial aim was to investigate a 120k bp inverted region (this region is not inverted in the template NB strain or EG4 strain), in the Os10g0147400 gene located in this region. After analyzing this gene through computational techniques, primer design, and polymerase chain reactions, it was decided that this gene was likely mis-annotated in the genome browser or is not expressed within the roots or shoots of any of the three strains. The focus was then shifted away from this gene and the inverted region on the 10th chromosome; the new area of interest is a 42k bp deletion in chromosome 12 of HEG4. The new gene (within the deleted region in HEG4) is Os12g34950, and through using similar techniques as previous, differences in gene expression between HEG4, NB, and EG4 may be demonstrated.

## Poster Session 1 - 11:30am - 12:30am

### Phenotypic Variability of Phytophthora Cinnamomi California Avocado Isolates

**Ezeonyeoma Nworgu**, Aidan Shands, and Patricia Manosalva.
Department of Microbiology and Plant Pathology, University of California, Riverside

Phytophthora cinnamomi, the causal agent of avocado phytophthora root rot (PRR), is one of the most destructive oomycete pathogens affecting over 5,000 plant species worldwide. Phytophthora cinnamomi is a highly invasive pathogen that can persist in infected soils as chlamydospores for several years. In California (CA), avocado PRR affects 60-75% of avocado growers causing losses of $40 million dollars annually. An integrated approach using resistant rootstocks in combination with a rotation of fungicides with different modes of action is desirable for managing this disease. In CA, P. cinnamomi populations affecting avocado have been described as clonal, however extensive phenotypic variability have been found in representative isolates regarding fungicide sensitivity, growth rate, and virulence. Here, we characterized the phenotype of four CA P. cinnamomi isolates for growth rate and optimal growth temperature. We found phenotypic variability amongst the four isolates with some isolates showing sensitivity to the change of temperature reflected by their reduced growth rate as temperature increased while other isolates were less sensitive and exhibited consistent growth rate. These results were consistent with previous findings indicating significant phenotypic variability of the isolates despite their clonality. This data can be complemented with population genomic studies to better understand population structure and uncover potential links between the genotype and the phenotype of extremes P. cinnamomi isolates. The phenotypic characterization of the current pathogen populations will inform the selection of new resistant rootstocks harboring resistance to a more diverse pathogen population and the development of appropriate diagnostic tools and chemical control.

## Poster Session 1 - 11:30am - 12:30am

### Identifying Canopies That Remain Cool During Hot Summer: A Case Study From UCR Surroundings

**Gerardo R. Miramontes,** Dr. Connie Nugent, Maura Caceres, Asnish Sapkota and Dr. Amir Haghverdi
Department of Environmental Sciences, University of California, Riverside

Summer days are getting warmer than ever before. Depending on the plant types or the surfaces of different materials, canopy temperatures may differ, and canopies that can remain cool even at the higher ambient air temperature may also help to keep the surroundings cool. Therefore, this study was conducted to evaluate how the canopy temperature of different surfaces around the UCR campus changes at a different time of the day. A handheld infrared thermometer (Fluke 64 Max) was used to measure the canopy temperature, and another handheld sensor (RH390 Precision Psychrometer) was used to record the near-surface air temperature and relative humidity. Data were collected three times a day (8 am, 12 pm, and 3 pm) for seven different days on cloud-free sunny days from 20 different sites, including different vegetation types, concrete surfaces, wooden mulch, and bare soils. Based on the recorded findings, sites with green vegetations, including Peruvian peppertree (PP) and Turfgrass (TG), had the lowest canopy temperature at all times of the day, while sites with Bare Soil, Walking Pavement, and Black Top Road that absorb the most heat throughout the day, displayed the highest canopy temperatures throughout the day. Compared to sites PP and TG which have the lowest mean canopy temperature of approximately 22.8 and 27.1 at 8 AM, at 12 PM it was 32.4 and 35.6, then at 3 PM it was 33.3and 35.8 ℃ throughout the entire day, the canopy temperature at sites for the Bare Soil, Walking Pavement, and Black Top Road had an average of about 30.8, 35.1, and 31.8 ℃ at 8AM, at 12 PM it was 49.8, 55.8, and 49.4 ℃, then at 3 PM it was 54, 55.1, and 54 ℃ which is on average almost 15 ℃ warmer. As a result of the study, the vegetation that were able to keep coolest were those with large and compact vegetation like shrubs, flowering plants, and ivy plants . The sites that had the highest temperatures on average were those were also made of materials that absorb heat the most. These results may help influence what kinds of vegetation are used when landscaping for efficient cooling effects during summer days and warmer climates.

## Poster Session 1 - 11:30am - 12:30am

### A Deletion and its Effect on Chr12g34990 in The Genome of Oryza sativa ssp. japonica EG4 COMPARED TO HEG4 AND NB

**Hanadi Alsuhaibani,** James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, Susan Wessler
Dynamic Genome Program, Rochelle and Allison Campbell Hall, Department of Botany and Plant Sciences, University of California, Riverside

Nipponbare, EG4, and HEG4 are varieties of Oryza sativa ssp. japonica that share many genes. However, there is a gene that is inverted in HEG4 but not EG4 and Nipponbare and another gene which appears to be deleted from EG4 but not HEG4 or Nipponbare.The focus of this investigation will be on the deletion in EG4 and to observe if there is differential gene expression, specifically a gene characterized in the Nipponbare genome on chromosome 12, Os12g34990. PCR, qPCR, Reverse transcription, and cDNA are used to observe if the deletion is present in EG4 and if it results in different gene expression. The ultimate goal is to observe if the gene expression is different between the three varieties at the specific gene and if it is expressed in the roots or shoots, or both. It is expected that the deletion would result in a different gene expression, possibly due to transposable elements.

## Poster Session 1 - 11:30am - 12:30am

### The Effect of Chromosomal Rearrangements on Genetic Expression in Three Rice (Oryza Sativa) Strains

**Isaiah Hernandez**, James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, and Susan Wessler
Dynamic Genome Program, Rochelle and Allison Campbell Hall, Department of Botany and Plant Sciences, University of California, Riverside

The aim of this research project was to identify the difference in gene expression between the three strains of *Oryza sativa*: HEG4, EG4, and Nipponbare. HEG4 has a gene inversion and EG4 has a gene deletion while Nipponbare has neither. This could potentially be the result of a non-autonomous transposable element called mPING, a Transposable element (TE) is a region of genomic DNA that can move and be inserted into other regions in the DNA. In order to compare the difference in gene expression, a region in chromosome 10 that is 120 kilobases and contains 12 genes was studied. PCR, reverse transcriptase, and qPCR were employed to study two out of the 12 genes called LOC4348105 & LOC112936668. The gene of interest in all three rice varieties was targeted using primers to amplify the gene in the rice roots and shoots. The amplification of the gene in the rice roots and shoots through qPCR will determine whether the gene is expressed in the roots or in the shoots or both.

## Poster Session 1 - 11:30am - 12:30am

### Interaction Between The Zinc Binding Domaine Of Rna Polymerase & The Ribosmal Protien Us3

**Joseph Ramirez**, Isaac Rodriguez, Matthew Ruiz and Gregor Blaha
Department of Biochemistry, University of California

In bacteria, transcription and translation are synchronized. To synchronize both processes, the RNA polymerase interacts with the ribosome. Any upsetting of this interaction will reduce the viability of bacterial cells, including bacterial pathogens. One interaction is formed by ribosomal protein uS3 and the β' subunit zinc-binding domain of the polymerase. A high-resolution crystal structure of this interaction will allow us to develop an agent to interfere with this interaction. To accomplish this goal, we designed uS3-zinc binding domain(uS3-ZBD) chimer. We grew transformed Escherichia coli (E.Coli) cells that overexpressed uS3-ZBD. Different conditions of induction were tested to optimize expression and solubility of the protein. Cell lysis was done with different combinations of chemical and physical methods. Our experiments show the uS3-ZBD chimer expression and solubility is optimized with 0.1mM IPTG induction paired with a heat shock in the media during cell growth. Lysis was complete with the chemical combination of EDTA, Triton X and Lysozyme reinforced with a physical method using a cell disruptor. Purification of the chimeric protein was attempted by ammonium sulfate precipitation and Hydrophobic Interaction Chromatography; different types of chromatography need to be tested to maximize the amount of protein we can get purified. When the protein is purified a high-resolution crystal structure can be obtained via X-Ray Crystallography.

## Poster Session 1 - 11:30am - 12:30am

### The Effects of Elevation on Seed Size

**Kenny Nguyen**, Kate Ostevik, Rebeca Hernandez-Gutierrez
Department of Evolution, Ecology, and Organismal Biology, University of California, Riverside

Several studies have shown that elevation has a prominent role in determining the size and number of plant seeds. Many other studies, however, have garnered results in the opposite manner. The varied results are between two correlations, a negative and a positive between elevation and seed size. Seed size fluctuates to fit a plant's environmental needs and challenges. For example, plants in shady environments may produce larger seeds that can grow quickly towards light due to its absence. The lack of crucial nutrients at higher elevations makes plants reside in harsher environments. Here we explore these correlations using Penstemon newberryi, commonly known as Mountain Pride, which is a flowering plant typically found in rocky mountains that thrives at around 9000 ft. This investigation will help us understand if plants, residing at a higher elevation, will invest more nutrients and energy to output a certain number of seeds at a certain size. Our approach is to analyze seeds collected from the Sierra Nevadas along three elevational gradients. A total of 1,505 seed samples, ranging from 9,000 to 12,000 ft were collected for analysis. We utilized two softwares, Fiji and R Studio, to analyze the data. FIJI was applied to count the seeds and measure their average size, using digital images captured by a mobile device. Then R was used to find correlations and produce charts. We found that elevation was positively correlated to total seed investment, indicating that change in elevation displays the indirect relationship of seed size and count. When elevation shifted upwards, seed number increased while seed size decreased. The relationship between elevation and seed number is quite significant. However, a negative correlation was found between elevation and seed size. Our data indicated that the slope was significant. Between the two results found, our data suggest that plants residing at higher elevations will require more energy input into producing more seeds, therefore obtaining a compact seed size to accommodate the lack of environmental nutrition and harsher environments.

## Poster Session 1 - 11:30am - 12:30am

### Antibacterial & Mechanical Properties in Orthopedic Magnesium Based Implants

**Lysdie Espinoza**, Patricia Holt-Torres, and Huinan Liu, PhD
Department of Materials Science and Engineering, University of California, Riverside

While orthopedic implants have bettered the lives of many, there are possible complications that can arise. One of the most severe problems that occur with implantation is infection. Various pathogens can cause infection due to their rapid adhesion to any biomaterial surface and the ability to survive in harsh environments. This study aims to use magnesium-based material to control implant infections because of its biodegradability, antibacterial and mechanical properties. A systematic study was performed on the antibacterial properties of two frequently used magnesium-based materials, pure Mg and ZK60 alloy against a selected biofilm-forming bacterium, *Staphylococcus aureus*. One sample of each material was cultured in 1.0 mL of Luria-Bertani (LB) medium, while other samples had 0.1 mL of the LB dropped onto the material's surface. The findings of this research show no bacteria can be found on the pure Mg and ZK60 samples cultured in the 1 mL LB medium. Bacteria also lose their adhesion properties and can only attach loosely to the surface. An added effect of Mg and ZK60 makes bacteria fission more complicated, leading to a larger cell size and a smaller population overall. The results from this study can be applied to creating new biomedical implants with lower infection rates and less complications for patients.

## Poster Session 1 - 11:30am - 12:30am

### Investigating HEG4 CHR10 Inversion and EG4 CHR12 Deletion

**Matthew Chow,** James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, and Susan Wessler
Dynamic Genome Program, Rochelle and Allison Campbell Hall, Department of Botany and Plant Sciences, University of California, Riverside

Differences in genetic expression in three different strains of rice, Nipponbare, HEG4, and EG4 are investigated in this study. Nipponbare is the standard rice genome used in research and is well characterized. Specifically, HEG4 has an inversion of twelve genes, 120k base pairs long. These twelve genes have not been described yet, so the goal is to characterize and investigate the gene expression differences caused by this. A particular rice gene, Os10g0146200 is the focus of this investigation. It is hypothesized that the inversion in HEG4 will cause the genes to become inactive or code for a different peptide. DNA extraction, mRNA extraction, cDNA synthesis, PCR, gradient PCR, and qPCR were performed in this experiment. The results for qPCR and cDNA PCR with my HEG4 were inconclusive. A deletion in EG4 that HEG4 and NB do not have was also studied. Results showed that the deletion is indeed present on EG4 and not on the other strains of rice. In conclusion, this research is a stepping stone for further research on the HEG4 rice strain inversion and the EG4 rice strain deletion.

## Poster Session 1 - 11:30am - 12:30am

### Stomach Content Diversity of Invasive Large Mouth Bass

**Megan S. Masso,** Angela Kang, William M. Ota, and Kurt E. Anderson, PhD
Anderson Laboratory, UCR Department of Evolution, Ecology, and Organismal Biology

Urban gradients can be seen in the Santa Ana River due to the effects of human development throughout the watershed. These urban alterations affect the habitat and trophic interactions of the invasive largemouth bass with native species. We studied the effects of wastewater and flood control on the largemouth bass diet across multiple reaches of the Santa Ana River. We hypothesized that increased stomach content diversity would correlate with higher body conditions in the invasive predator. We also hypothesize that urban disturbance of a reach would predict Largemouth Bass stomach content diversity. We anticipate that as we move away from wastewater discharges and increase stomach content variety, the largemouth bass body condition will improve. To conduct this study a total of 556 largemouth bass were collected during a wastewater shutdown in 2019 across over three miles of the Santa Ana River. Physical characteristics were taken and stomachs were removed from the largemouth bass and collected for later analysis. Each sample's stomach contents were put into test tubes and the species ingested were classified to order and family if possible. Due to the deterioration caused by digestive processes stomach contents were rarely identified to genus. For each largemouth bass, we calculated body condition ((Fulton's K = (weight/ length^3 ) 10^5) and Shannon's and Simpson's diversity of their stomach contents. We found that the R2 value for Shannon's Diversity Index was 0.115 after using a scatter plot, and the R2 value for Simpson's Diversity Index was 0.494. This two-factor ANOVA reveals that my hypothesis would be disproved due to

## Poster Session 1 - 11:30am - 12:30am

### Understanding the Role of *BBX* Transcription Factors in Abiotic Stress Tolerance in Arabidopsis

**Melvin Hodanu**

The World Health Organization reports food insecurity has been climbing slowly for six years and now affects about 30 percent of the world's population. This is caused by a combination of an increasing number of countries that experience climate extremes and the loss of crop yield per degree warming. Our overarching goal is to understand the mechanisms of abiotic stress response in the model organism, Arabidopsis *thaliana* (Arabidopsis) such that conserved tolerance responses can be engineered in crops for greater yield. Specifically, how plants respond to heat and drought stresses which is not fully understood. The circadian clock is an internal biological system that helps plants coordinate important biological processes with environmental changes through the regulation of gene expression. Previous research in Arabidopsis identified that most members of a transcription factor gene family, *B-box* (*BBX*s), respond to heat stress and for some in a time-of-day dependent context. Identifying the relationship, whether causal or correlational, is one of the goals of our research project. Thus, we are creating bbx mutant lines using *CRISPR/Cas9.* Verified lines will be used to measure physiological parameters such as relative water content, photosynthetic efficiency, and average shoot biomass in response to heat and drought treatments to help identify a functional role for selected BBXs in clock regulation of stress tolerance.

## Poster Session 1 - 11:30am - 12:30am

### Do Size, Proximity To Lakes, And Elevation Influence Biodiversity In Ponds?

**Nikhil Bharadwaj**, Ryan Conway, and Kurt Anderson
Department of Biology, University of California, Riverside

Aquatic insects are crucial to aquatic ecosystems due to their contribution to decomposing material, providing resources for terrestrial ecosystems, and contributing to the ecological flow of energy in aquatic ecosystems. The qualities of habitats likely affect the number of aquatic insects that ponds can support. Colorado alpine ponds have a wide range of sizes, distances to lakes, and stability of habitat in terms of freezing and drying, which makes them a good study system for how these qualities influence biodiversity. Island Biogeography Theory posits that larger and more connected habitats should contain more species than smaller and more isolated ones. Based on this theory, we hypothesized that ponds that were larger and closer to lakes would contain more biodiversity than those that were smaller and further from other lakes. Additionally, we expected that ponds that were at lower elevation would have greater biodiversity than those at high elevation as they should experience less stressful conditions. We collected aquatic insect samples from alpine ponds in Colorado in the Summer 2021 and analyzed them in the following Summer 2022. Samples were sorted to find aquatic macroinvertebrates to undergo further identification. After identification, we used linear regressions to analyze how pond size, distance to lakes, and elevation influences species richness and biodiversity. We did not find significant relationships between distance to lakes or surface area and biodiversity, possibly due to low sample size. A significant negative relationship between elevation and biodiversity was found, supporting our third hypothesis.

## Poster Session 1 - 11:30am - 12:30am

### Developing Genetic Resources for the Identification of Thermal Supergenes in Drosophila Pseudoobscura

**Rajeet Patel**, Dr. Kieran Samuk, Gina Lucas, Evolution, Ecology, and Organismal
Biology, University of California, Riverside

Chromosomal inversions are a class of genetic mutation that occur when a segment of chromosome reverses or becomes “flipped” in orientation. Chromosomal inversions have been investigated due to their connection to evolutionary change, adopting the nickname, “supergenes". In a series of classic studies conducted in the 1940s, Theodosius Dobzhansky observed the frequency of a particular chromosomal inversions found on the third chromosome in populations of Drosophila pseudoobscura (D. pseudoobscura), a species of fruit fly native to southern California. This included populations from the James San Jacinto Mountain Reserve. Dobzhansky found that in warmer months (June-July) these inversions were at their highest frequency and in the colder months (December-February) they were at their lowest frequency. Our research re-examines these classic results and investigates if we could identify genetic markers in D. pseudoobscura to set up further genotyping. The experiment utilized D. pseudoobscura individuals collected from the James San Jacinto Mountain Reserve during June and July (this allowed us to conclude D. pseudoobscura were still present at the site). 124 individuals were genotyped using PCR/gel electrophoresis and analyzed for the supergene. To do this we ran primers Dobzhansky highlighted in his previous work which includes the Treeline (TL), Standard (ST), Chiricahua (CH), and Arrowhead (AR). The primers were successfully amplified on the gels which sets up future research to investigate current inversion frequencies. Amplifying possible inversions is an important step in understanding how climate change affects the frequency of these supergenes in D. pseudoobscura and beyond.

## Poster Session 1 - 11:30am - 12:30am

### Understanding the Plants Circadian Clock Control of Temperature Stress Responses

**Rosita J Martin**, Ramón Benavides Jr., Samantha J Cordingley, and Dawn H Nagel
Department of Botany and Plant Sciences, University of California, Riverside

The circadian clock is an internal system that helps living organisms sense time and responds to environmental cues. In plants, circadian rhymes utilize various signals that regulate photosynthesis, flowering, growth, abiotic and biotic responses, and hormone signaling. However, understanding how the circadian clock controls a plant's response to temperature stress remains unknown. In this project, our goal is to determine whether a heat-inducible Arabidopsis transcription factor regulation and contribution to the heat stress response is conserved in crops. The aim of our research is two-fold - to determine whether the rice BBXs are also induced by heat stress and to generate overexpression constructs of the rice BBXs for future functional studies. Using gene expression analysis, we tested whether OsBBX expression is induced in response to a one-hour heat stress (45 o C) treatment in rice seedlings depending on the time of day. In addition, we created constructs where OsBBX coding sequence was expressed with a 35S promoter and fused to the Green Fluorescent Protein (GFP). These constructs were infiltrated into tobacco leaves to check their cellular localization. Findings from this project will contribute to our continued goal of engineering plants to be more heat stress tolerant and ensure food security for the world's growing population.

## Poster Session 1 - 11:30am - 12:30am

### Lung Inflammation from Chronic Exposure to Allergen Induced Sex-Specific Alterations in Gene Expression within the Brainstem

Sanaa J. Abdulkarim[1,3], Paula Da Silva Frost [2,3], Sirajan Kamara[1,3], Joseph Valdez [2,3], Monica J. Carson [1,2,3]
[1]Division of Biomedical Sciences-School of Medicine, University of California Riverside
[2]Neuroscience Graduate Program, University of California, Riverside
[3]Center for Glial-Neuronal Interactions, University of California, Riverside

Breathing fungal particles induces lung inflammation, generating a systemic inflammatory response that impacts the brain. Our study investigates the chronic exposure to an aerosolized fungal allergen, Alternaria alternata (Alt. alternata), for seven days to consider the impacts on the brain stem of male and female mice. The overall purpose is to understand how the chronic exposure of Alternaria alternata for seven days affects the brainstem of male and female mice. nCounter© Rosalind, software for data analysis of gene expression was used in brainstem samples from males and females, collected after Alternaria exposure. We hypothesized that based on the sex of the mice, both male and female mice react differently to Alternaria. The results indicate that both sexes reacted to aerosolized Alt. alternata, and sex is a variable that influences the response. The gene regulations did not present similar expressions between the male and female mice, yet the main pathways altered were associated with metabolic, immune system responses, and protein synthesis. In males, the genes GPT and CCBL1 are downregulated, and SLC16A2 and CAD are upregulated. In females GABARAP, XDH and PRR5 are the downregulated genes, and H2-K1, MLST8, and LY86 are the upregulated genes. The pathways of glutamine metabolism, amino acid synthesis, and tryptophan/kynurenine metabolism presented a downregulated gene in males. Female mice display antigen presentation, cytokine and chemokine signaling, and endocytosis as upregulated pathways. The findings indicate that some different reactions and expressions take place depending on the sex of the mice.

## Poster Session 1 - 11:30am - 12:30am

### The Impact of Chronic Inhalation Exposure to Alternaria Alternata on the Brain's Immune Status

**Sehr S. Khairi**, Paula da Silva Frost, Sirajan Kamara, and Monica J. Carson
Carson Laboratory, UCR Department of Biomedical Sciences, University of California, Riverside

Allergic disorders, such as anaphylaxis, hay fever, eczema and asthma, now afflict roughly 25% of people in the developed world (The Development of Allergic Inflammation, 2018). In allergic individual's consistent exposure to allergens which compose a portion of the environment causes long term lung inflammation. This inflammatory response of the lungs can impact organ structure and function. Individuals who deal with respiratory conditions can potentially have an increase in symptoms due to inhalation of respiratory allergens. Previous studies have used intranasal solutions and injections to introduce the allergen to the test subject. This study uses a chamber to allow the test subjects to continuously inhale the Alternaria Alternata, a fungal allergen for a set amount of days. Using the Nanostring technology specifically the ROSALIND software gene expression changes were analyzed and interpreted. Despite the lung inflammation from a 5 day exposure of Alternaria Alternata, there is a decrease in specific inherent immune molecules associated with inflammation such as Iba 1 and Toll-like receptor 2 within the brainstem. In this study, a 7 day exposure of alternaria was conducted and the Olfactory bulb region of the brain was collected. The Olfactory bulb is located anterior on the brain above the nasal cavity. This structure receives neural input about odors that are detected by cells in the nasal passage. Exposure to Alternaria leads to sex-based changes in gene expression within the Olfactory Bulb. The metabolic pathways had a sex-based difference in gene expression.

## Poster Session 1 - 11:30am - 12:30am

### Studying the Inversion Caused by Mping in Oryza Sativa SSP. Japonica Varieties

**Son Tran**, James Burnette, Venkateswari Chetty, Alejandro Cortez, Susan Wessler, and Isai Gonzalez
Dynamic Genome Program, Neil A. Campbell Science Learning Laboratory, Department of Botany and Plant Sciences, University of California, Riverside, California 92521

Majority of the world's population uses rice as their primary food staple. It would truly be a shame if a harmful mutation were to happen to the rice varieties. The purpose of this study conducted by Wessler Campbell lab is to investigate the possible detrimental mutations caused by mPing, a nonautonomous miniature inverted repeat transposable element (MITE), on Oryza Sativa ssp. Japonica varieties. More than half of the rice genome is composed of transposable elements and approximately 58 percent of them are MITEs. Among the numerous MITEs two of them happen to exist in HEG4, one of the key rice varieties that we focused on, where it encompasses about 120kbp in chromosome 10. This caused an inversion where the 120kbp region has swapped its orientation and this study is to find any possible detrimental effects of it. This study focuses on a single gene, Os10g0145800, which codes for probable leucine-rich repeat receptor-like protein kinase ( the At5g49770 homolog in Arabidopsis), among the 13 different genes that the 120kbp region covers, and compared inverted HEG4 with Nipponbare and EG4 that does not have an inversion in that area. PCR based experiments (conventional and qPCR) were performed using primers designed to target the gene of interest in order to validate its presence and relative expression patterns in the aforementioned varieties. The presence of Os10g0145800 is verified, however the expression of it is yet to be determined at least in the shoot and root tissue of a premature rice plant. If more time is allowed to continue the project, a real time PCR will be done to determine if the inversion affects the level of gene expression.

## Poster Session 1 - 11:30am - 12:30am

### Market Assessment of Developing Tomatoes Resistant to Bacterial Canker

**Taewon Yoo**, Hanadi Alsuhaibani, Valerie Gonzalez, Christie Montejano, Uchenna Onukaegbe, James Burnette, Steve Casper, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, Ken Gruys, Susan Wessler
Dynamic Genome Program, Department of Botany and Plant Sciences, University of California, Riverside, California, 92521

Bacterial canker is caused by Clavibacter michiganensis ssp. Michiganensis, Cmm for short, a gram positive bacteria that invades the xylem through natural wounds of the plant. Bacterial canker is especially devastating to Solanum lycopersicum because it is known to be heavily contagious and has the ability to survive in soil for long periods of time, especially in greenhouses. This threatens tomato farmers all over the world, especially in cold and humid environments, where greenhouses are necessary. Therefore, we will cross two tomato varieties, E6203, which is susceptible to the bacteria, with Hawaii 7998, which has resistance to the bacteria in order to create a canker-resistant variety for farmers affected (Abebe, Alebel Mekuriaw et al., 2022). If canker resistant tomato seeds are procured, it would greatly reduce labor of weeding, sanitizing, and drying. Not only that, but it would also reduce tomato yield loss from bacterial canker down to a quarter. As there are no significant obstacles in regulation and requires less time and funds compared to gene editing methods, it is a low risk solution which will be viewed favorably when cooperating with seed companies. This method can be implemented to other solanaceous plants, which are susceptible to bacterial canker as well.

## Poster Session 1 - 11:30am - 12:30am

### Gene Expression in Nipponbare Oryza Sativa SSP. Japonica

**Uchenna Onukaegbe**, James Burnette, Venkateswari Chetty, Alejandro Cortez, Susan Wessler, and Isai Gonzalez
Dynamic Genome Program, Neil A. Campbell Science Learning Laboratory, Department of Botany and Plant Sciences, University of California, Riverside, California 92521

Researchers in this lab were assigned one of three strains: Nipponbare, HEG4, and EG4; tasked to analyze and understand the different gene expressions between them. Assigned to Nipponbare, my goal was to see how my gene's expression changed as HEG4 and EG4 diverged from my reference genome. This process involved the constant use and reference of numerous primer designs, DNA and RNA extractions, polymerase chain reactions, gel electrophoresis, and other bioinformatic tools over a 10-week period. Through these different techniques and skills, I could pinpoint my gene's expression in either the shoot or root of these different strains and hypothesize whether it was caused by transposable elements, indels, or using RNA, DNA, or cDNA from the wrong developmental stage of each strain. This was able to be confirmed or denied depending on my ability or inability to reproduce the same results. If I wasn't able to obtain the desired results, I would change one variable at a time in order to have a succinct explanation rather than a plethora of ideas on what worked, what did not, and why.

## Poster Session 1 - 11:30am - 12:30am

### Emission Rates and Identifying Tire and Road Wear Exported from San Diego Creek

**Valerie Gonzalez**, Clare Murphy-Hagan and Andrew Gray
Department of Environmental Sciences, University of California, Riverside

Tire and road wear particles (TRWP) are composed of pieces of tire and road surface produced by the use of vehicles on roadways (Kovochich et al., 2021). These particles are mobilized from road surfaces by wind and runoff and are transported elsewhere in the environment. Although TWRP are emerging as one of the largest sources of microplastic pollution, quantification of TRWP emissions and exports to waterways is understudied. We aim to (1) estimate the emission rate of tire wear particles generated on road surfaces within and (2) identify TRWPs found in sediment. Geospatial data on road usage, road length, and Average Annual Daily Traffic was utilized to estimate the emission rate of TWRP within the Lower San Diego Creek Sub-Basin. Using visual microscopy, approximately 288 suspected TRWPs were extracted from 600 grams (wet weight) of subtidal sediment collected from below the outlet of the watershed. Chemical confirmation of TWRP is not possible by FTIR and Raman spectroscopy, commonly used for other types of microplastics. An alternative method for chemical confirmation of TRWP involves a combination of using a Scanning Electron Microscope (SEM) and Energy Dispersive X-ray Spectroscopy (EDS) to examine particles' morphology and elemental analysis. We are currently developing a standard operating procedure to identify TWRP using SEM and EDS.

## Poster Session 1 - 11:30am - 12:30am

### Effects of different pH environments on Microorganism Biodiversity

**Vincent Nguyen**, Dr. Kurt Anderson, Clara Woodie
Department of Evolution, Ecology, and Organismal Biology

There are many environmental factors that affect the biodiversity of different microorganismal ecosystems. One factor is the pH level, since most species are very sensitive to the pH level or else they will not function optimally. Most microorganisms cannot reside in pH<5. In the human gut, there are numerous microorganisms that reside in this acidic environment. This led me to start this experiment on analyzing microorganism biodiversity at different pH environments.

The aim of this experiment is to observe microbial biodiversity in different pH environments. We found the optimal pH of 5 different microorganisms: Blepharisma, Rotifers, Euglena, Euplotes and Paramecium, and used these ranges to decide what pH levels to further study. We created pH environments from pH 4-11, and created seven replicates of each. We added an equal amount of medium food solution to each treatment bottle to ensure equal growth conditions. We then added X mL of each microorganism based on the amount needed to inoculate 100 individuals in each bottle.

Initially, all species were present in lower pH values. Over time, species richness decreased and present species varied amongst all the pH treatments. There was more species richness in lower pH treatments. The results from this experiment can act as the foundation for larger and more long term projects. Ex: we can create another experiment similar to this one that studies the different pH tolerance of harmful microorganisms that reside in the human gut microbiota and create drugs that eliminate these microorganisms from our bodies.

# ORAL SESSION 3

## 1:30 – 2:30 pm

## Oral Session 3 - 1:30pm - 1:42pm

### Optimizing A Phenol-Chloroform Based High Molecular Weight DNA Extraction Protocol for Drosophila Species

**Reyna Quiñonez** and Kieran Samuk
Department of Evolution, Ecology and Organismal Biology, University of California, Riverside

A way to make sure that long-read sequencing is being used to the best of its capacity is through the use of high molecular weight DNA (HMW DNA). A general protocol for optimizing HMW DNA extraction is still due to make an appearance. The goal is to create a protocol that guarantees a successful HMW DNA extraction with DNA samples of the Drosophila species. While commercialized kits made solely for the use of HMW DNA extraction do exist, they are expensive. For this reason the aim is to optimize a 2 day phenol-chloroform protocol. A total of 24 extractions were made, each one having different variables. The extractions were to be made in groups of 4, each group having different variability. After the first 16 extractions were made, it was discovered that the use of 1-day old samples made it difficult for agarose gel to pick up any DNA when ran. Due to that, the remaining 8 extractions were no longer made with that variable in mind and instead a new variable was introduced. Results indicate that vortexing and the type of pipette tips used in the extraction do matter. Future research can keep this in mind as variables are introduced or removed in order to optimize the protocol.

## Oral Session 3 - 1:42pm - 1:54pm

### Understanding the HVEM Receptor Protein through its Structural Clues

**Jacob Sola**, Dr. Adam Godzik
University of California, Riverside School of Medicine

HVEM is a cell surface receptor protein from the TNF-receptor superfamily that serves a bi-directional, still minimally understood, role in the regulation of the human immune system. It has several ligands including CD160, LIGHT, BTLA, and the IgD glycoprotein that compete for HVEM's surface and differentially regulate a complex network of protein-protein interactions with the ability to positively and negatively regulate the immune system. This gives HVEM the potential to serve as a therapeutic target for a wide range of pathological conditions. Computational methods in this study provide key insight into the structural aspects of HVEM binding to the different ligands. Analysis of the interface interactions of a 3D structural map allows researchers to predict effects of point mutations on specific residues and guide the development of specific therapeutic antibodies, providing another tool in the study of HVEM and its potential role in therapeutics.

## Oral Session 3 - 1:54pm - 2:06pm

### Defining Dynamic Cell Plate Localization in *Zea Mays* During Mitosis

**Matthew Duong**, Vivian Huang, Alondra Contreras, Lindy Allsman, Carolyn G. Rasmussen
Department of Botany and Plant Sciences, University of California, Riverside

Plant cell division is a complex process that is highly different from in mammalian cells. Primarily, plant cells contain cell walls that determine important factors such as rigid cell shape and surface area. Therefore, the creation and placement of these cell walls is critical in cell function. Laying down the cell wall requires precise cooperation from multiple elements. A circular array of microtubules and associated proteins known as the preprophase band (PPB) surrounds the nucleus preprophase, marking the future division plane. To direct cell wall-building materials to this division site, the phragmoplast is used. In this project, I hope to better understand the behavior of multiple elements that relocate to the cell plate. More specifically, I aim to characterize the localization of multiple proteins with suggested involvement in cell plate biogenesis: KNOLLE, Rab1A, Rab2A, and Rab11D. Tracking will be possible through live-cell microscopy (100X) of symmetrically dividing cells in maize (*Zea mays*) containing fluorescent proteins that bind to tubulin as well as the predicted cell plate markers. These images labeling cell plate markers during each phase of mitosis can act as a reference that researchers studying division plane orientation can use in mutant analysis. The N-Phenyl carbamate herbicide chlorpropham (CIPC) splits the phragmoplast via interaction with multipolar spindles. I will additionally be treating samples with CIPC to test whether the viability of the phragmoplast affects localization of cell wall building proteins. Overall, a better understanding of division plane orientation can provide insight into medical conditions such as cancer metastasis.

## Oral Session 3 - 2:06pm - 2:18pm

### Hypothalamic Oxytocin and Vasopressin Neurons in a Toxicant Autism Mouse Model

**Crystal Luna**, Maximilian Denys, Elena Kozlova and Margarita Curras-Collazo
Department of Molecular, Cell and Systems Biology, University of California, Riverside

Polybrominated diphenyl ethers (PBDEs), are a class of flame retardants that can cause endocrine disruption of the thyroid hormone (TH) system, which regulates the prosocial neuropeptides oxytocin (OXT), and vasopressin (AVP). However, it is unclear whether this mechanism underlies the neurobehavioral deficits induced by maternal transfer of PBDEs. Our lab has previously found that maternal exposure to PBDEs can alter social memory in female mice relative to controls and alter gene expression of TH gene markers and OXT and AVP1. Behavioral testing of social novelty preference (SNP) showed that male and female L-DE-71 and TH suppressed with 6-propyl-2-thiouracil (PTU) mice exhibited social memory deficits. However, maternal exposure to levothyroxine (T4) rescued SNP in males and females. In addition, T4 supplementation rescued PBDE-induced reduction of OXT in the paraventricular nucleus of the hypothalamus (PVN). In this study, we further characterized hypothalamic OXT and AVP-ergic cell types to examine the specificity of depletion produced by DE-71, including potential cell death. C57BL/6N dams were exposed to the DE-71 mixture for 10 weeks at 0.1 (L-DE-71), 0.4 (H-DE-71), or 0 mg/kg/d (VEH/CON). Additional groups of dams were treated with PBDEs and T4 (8 µg/100 g BW) or VEH/CON and PTU (50 mg/L), in drinking water2. To differentiate between magnocellular (MCN) and parvocellular cell types in the PVN, the retrograde dye Evans Blue (4%, 0.4 mg/g BW i.p.), which labels only MCN cells, was injected 24 hours before sacrifice. Currently, we are cryosectioning PVN sections and immunolabeling for OXT and AVP and neuronal marker NeuN using dual-label immunofluorescence. Cell-specific quantitative image analysis will be used to quantitate DE-71 exposure and TH treatment effects. This study will provide novel insight into how PBDEs and TH alter the 'social' brain and may contribute to neurodevelopmental disorders, such as autism.

## Oral Session 3 - 2:10pm - 2:20pm

### CRISPR/Cas9-mediated gene editing in C. elegans PIR-1

**Tung Hoang, Afraz Amin**, John Tao, and Weifeng Gu
Department of Molecular, Cell, and Systems Biology, University of California, Riverside

PIR-1 (phosphatase that interacts with RNA–ribonucleoprotein complex 1) is a member of a dual-specificity phosphatase (DSP), which has an RNA polyphosphatase activity, modifying the 5' triphosphate end of RNAs( 5' ppp-RNAs) and converting them to monophosphate RNAs(5'p-RNAs) for degradation with a higher specificity than phosphoprotein. F54C8.4 is the gene that encodes one of three PIR-1 protein homologs in C. elegans. However, the underlying cellular function and target of this F54C8.4 protein have not been discovered. Here, we demonstrate 3 CRISPR/Cas9-based genome editing experiments separately with the F54C8.4 gene in C.elegan to dissect the molecular mechanisms of how F54C8.4 interact with other proteins using Turbo ID tag( Aim 1), how the conditional protein depletion of F54C8.4 affect the C. Elegans using an opt-s3Degron-Flagg tag (Aim 2), and determines the gene expression pattern of F43C8.4 in C.elegan using GFP tag (Aim 3). This paper explains stage 1 of our project, including the CRISPR technique to insert TurboID, opt-s3Degron, and GFP tag into the F54C8.4 gene of C.elegan and the screening of 124 worms from different generations to get the homozygous CRISPR mutant dominant worms, which is essential for the next stage of our project. Overall, this study will help us to understand more about the cellular functions of other members of the PIR-1 family, which will lead to the development of more effective tools to regulate viral and endogenous RNAs and benefit the treatment of human diseases, including cancer and viral infection, thus exerting a significant impact on public health.

# ORAL SESSION 4

## 2:45 – 3:45 pm

## Oral Session 4 - 2:45pm – 2:57pm

### A Practical Way to to Combat Diabetes Among Latinos in the Eastern Coachella Valley: The Eat, Move, Live Program

**Jair Chavez**, Ann Cheney
Department of Social Medicine Population and Public Health, University of California Riverside School of Medicine

A quarter of the population in the Eastern Coachella Valley, in Inland Southern California, is overweight with an average body mass index of 27.5. This primarily Latinx population experiences chronic health conditions related to high body mass index such Obesity and diabetes.

**Study design/methods:** This is a 12-week intervention to prevent diabetes that involves baseline and follow-up data. We measured body mass index, blood glucose, blood draws to assess hemoglobin A1c levels, and participants grip strength. In week 12 of the study, we will collect follow up data. The intervention is Eat, Move, Live a 10-week dietary and life change interventions designed to improve health by reducing diabetes risk. The program puts an emphasis on changing dietary and exercise habits of participants with knowledge to live healthy lifestyles. One major component of the program is to educate people on nutritional information. The exercise portions of the program incorporate cardiovascular and isometric exercises. They are designed to be practical and accessible, meaning home with limited equipment. This study is currently in week six and ongoing. We anticipate participation in the program will lower participants BMI and improve blood glucose levels, both finger prick data and hemoglobin A1c levels. We also anticipate that the health education part of the intervention will have long term improvements on participants' health.

**Conclusion:** This intervention focuses on daily diets and lifestyle changes. The intervention is partial as there is no medication or equipment needed to make these dietary and lifestyle changes.

## Oral Session 4 - 2:57pm - 3:09pm

### Fluorescent Protein Toolkit For Studying Division Plane Orientation

**Shreya Agarwal**, Carolyn Rasmussen
Department of Botany and Plant Sciences, Rasmussen Lab, University of California, Riverside

Proper cell division is crucial in the development of the structure of a plant, and the establishment of a body plan. The Rasmussen lab studies cell division and division plane orientation in plants, using (maize) Zea mays as a model system. Previously transgenic maize expressing different cellular markers fused to fluorescent proteins were created as a tool kit to study cell biology. To genotype for these cell markers, I developed primers using softwares such as A Plasmid Editor, Benchling, OligoAnalysis, and MaizeGDB. Primers were tested using PCR and gel electrophoresis and localization of cell markers were verified with live cell microscopy. As work continues on this project, it is speculated that a reverse primer can be developed to aid in the identification of a specific marker gene involved in division plane orientation. In addition, further testing and troubleshooting will continue in order to develop more forward and reverse primers that can establish the presence of various cellular markers predicted to play a role in division plane orientation. The development of these primers allows us to establish the presence of these markers in transgenic maize in the future. This will aid in understanding which proteins play a role in division plane orientation. Gaining further knowledge on the proteins involved in this process is a step towards helping us understand how division plane orientation works in plants.

## Oral Session 4 - 3:09pm - 3:21pm

### Experimental Characterization of Inertial Ordering of Flat Plate Non-Neutrally Buoyant Particles in Helical Microchannels

**Gustavo Lemus**, Raymond Yeung, and Victor G. J. Rodgers
Department of Bioengineering, University of California, Riverside

Characterizing particle motion in fluid flow is essential to optimizing the throughput and efficiency of microfluidic-based particle sorting devices. Our research group is developing a high-throughput microfluidic solid-phase DNA synthesizer by sorting p-Chips [1], micro transponders on which DNA is constructed. The throughput and sorting efficiency of the DNA synthesizer is mainly dictated by whether the continuously flowing p-Chip particles can be self-ordered, in which each particle is separated by a controlled axial distance. While previous studies have demonstrated inertial ordering of spherical, neutrally buoyant particles, we are expanding the findings by performing experimental studies of aspherical (flat plate), non-neutrally buoyant particles through continuous helical microchannel flows. The conducted particle flow experiments will involve seeding a batch of randomly arranged p-Chips at the top inlet of a 3-D stereolithography printed helical microchannel and delivering a constant flow of fluid (water, acetonitrile) through the channel. We will evaluate the effects of the channel geometry and flow parameters on the average interparticle spacing of the p-Chips. Specifically, we will vary the channel aspect ratio (height/width), helical pitch, diameter, number of revolutions and operate at a range of Reynolds number to evaluate the optimized microchannel design and operating flow for high-throughput particle sorting. We expect that a decrease in the channel aspect ratio will result in a greater average interparticle spacing based on previous studies of flowing spherical, neutrally buoyant beads [3]. Our findings will assist in extending the capabilities of inertial ordering to more applications involving the flow of aspherical particles.

## Oral Session 4 - 3:21pm - 3:45pm

### Amplifying the Fanac2 Gene Found in Strawberries to Increase Drought Resistance

**Bella Clement**[2], **Evelyn Martinez Lopez**[2], **Jennifer Nguyen**[1], **Reena Patel**[1], **Michell Santiago**[2], James Burnette[1], Steve Casper[3], Alejandro Cortez[1], Kenneth Gruys[3], Annalise Gushue[4], Isai Gonzalez[1], Venkateswari Jaganatha Chetty[1], Susan Wessler[1]

1. Dynamic Genome Program, Department of Botany and Plant Sciences, University of California, Riverside, California, 92521.
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3. Keck Graduate Institute of Applied Life Sciences, Claremont, California 91711. 4. Nelson Lab, University of California, Riverside, California, 92521.

Drought is a major environmental stressor that's reducing strawberry crop yields. Understanding a crop's drought response is crucial to the development of varieties that resist drought and increase yield. Our goal is to provide a variety that will survive the uprise in drought. This will be done by overexpressing the FaNAC2 gene to increase drought resistance. If the overexpression is successful, then strawberries will suffer less from water deficit, leading to a better profit margin. To amplify the gene, the cis-elements would be modified via rearrangement, and by increasing the copies of a drought-sensitive cis-element found within the promoter. First, PE:pegRNA complexes would be used for reverse transcription prime editing to generate different cis-element rearrangments. Then, CRISPR SDN-3 would be used to stack drought sensitive cis-elements. Subsequently, the various lines would be genotyped to check if the modifications were successful. Lastly, the progeny would be evaluated to determine which line produces the best responses. Altering the cis-elements has a strong possibility of increasing drought response and producing larger yields with less water. While the rearrangement of cis elements has only been seen in fungi, cis-elements are naturally occuring within the strawberry which gives it a high probability of having the expected results. If FaNAC2 were successfully overexpressed, then farmers could save water and save on water costs. Assuming the product could save 25% water usage, farmers can save an extra $7M in water costs.

# POSTER SESSION II

## 4:00 – 5:00 PM

## Poster Session 2 - 4:00pm - 5:00pm

### Effects of Increasing Salinity on Freshwater Protists

**Allison Chan,** Clara Woodie, Dr. Kurt Anderson
Department of Evolution, Ecology, and Organismal Biology, University of California, Riverside

Climate change and human activity, such as oil mining and gas extraction, cause increasing salinity levels in freshwater. Salinization of freshwater may interfere with the functioning of freshwater ecosystems. The aim of this project is to study the effects of increasing salinity on freshwater protist populations, predator-prey dynamics, and morphology. A previous study conducted by Olson et al indicated that organisms must allocate energy to osmoregulation that could otherwise be spent on growth and reproduction. In order to study this further, we initiated four different treatments of gradually increasing salinity levels: 0.5g NaCl/500mL $H_2O$, 1g NaCl/500mL $H_2O$, 2.5g NaCl/500mL $H_2O$, and 5g NaCl/500mL $H_2O$. Over the course of two weeks, we collected population data for both protist species. Preliminary results suggest that higher high concentrations of saline negatively affect protist populations and morphology – blepharisma in 2.5g NaCl/500mL $H_2O$ were much smaller and did not engage in cannibalism compared to blepharisma in lower salt concentrations. Both protist populations were driven to extinction in 5g NaCl/500mL $H_2O$. Higher salt concentrations also seemed to disproportionately affect predators compared to prey populations. This research emphasizes the negative impact of increasing salinity on freshwater organisms.

## Poster Session 2 - 4:00pm - 5:00pm

### Using Cell Markers to Understand Dynamic Cell Plate Localization in *Zea mays*

**Alondra Contreras**, Matthew Duong, Vivian Huang, Marschal Bellinger, Lindy Allsman, Carolyn Rasmussen
Department of Botany and Plant Sciences, 900 E University Ave. 3126 Genomics, University of California Riverside, CA 92521

The presence of a cell plate is a marker of where the cell wall will form. Plant cells have developed complex structures that determine cell wall formation such as the preprophase band (PPB) and phragmoplast. The PPB is an array of microtubules and microfilaments encircling the nucleus that predicts the future division site, while the phragmoplast promotes transport of cell wall-building materials to the proposed site and builds a cell plate. In my research, I hope to understand the dynamics of cell plate formation by examining the localization of proteins that are involved in endomembrane dynamics or cell plate formation. To determine whether these proteins rely on the integrity of the phragmoplast for cell plate localization, particle tracking and chemical treatments of Chlorpropham and Endosidin 7 will be used to investigate the proteins' cell plate interactions. Particle tracking will require protein visualization using transgenic fusions with fluorescent proteins. Qualitative data will be collected from live cell imaging of plants that contain the transgenic markers using a spinning disk confocal microscope (100X lens). The rate of particle travel over time will be obtained from kymographs generated from particle tracking during mitosis. If these proteins do not show abnormal results with chemical treatment, further investigation will be done to characterize the endomembrane compartments in which these proteins travel on. This research will serve as an informational platform for cell plate dynamics and protein interactions.

## Poster Session 2 - 4:00pm - 5:00pm

### Progress Towards Adaptation a High Salt Diet in Experimental Populations in Drosophila Melanogaster

**Bella Clement**, Dr. Kieran Samuk
Department of Evolution, Ecology and Organismal Biology, University of California,
Riverside CA 92521

Understanding the genetic basis of adaptation is a major goal of evolutionary biology. One approach to doing this is an “evolve and resequence” experiment, in which a population is experimentally adapted to a novel environment and later sequence and compared to the original population. In this study, we explore adaptation to food high in sodium chloride in an experimental population of Drosophila melanogaster. The primary goal of the study was to ascertain the degree of adaptation to a high-salt diet in this experimental population. We performed measurements of adaptation (total adult survival) in both the salt-adapted population and a control non-salt-adapted population. The key result was that salt-adapted flies performed better on food without salt implying that adaptation to the salt environment is not complete. The results of the assays will allow for further exploration of the genetic basis of adaptation to salt. The results of comparing the original population and how they end up are vital to reveal if new mutations and genes evolved during the past experiments conducted.

## Poster Session 2 - 4:00pm - 5:00pm

### Evaluating Auditory and Perceptual Processing with Ability to Detect Emotions in (ASD)

**Cesar De La Torre**, Aaron Seitz, Audrey Carillo, Elkanah lane, Katherine Stravopolous,
UCR Department of Psychology, University of California Riverside.

Autism Spectrum disorder (ASD) is a neurodevelopmental disorder that affects 2% of the US population. The general complications with (ASD) are impaired social communication skills, repetitive and restricted behaviors. The notion that people with (ASD)have distinct visual and auditory processes has been strengthened with many studies. A common outcome is a dysfunctional integration of visual information within the (ASD)population. The present study is assessing the relationship between processing emotional recognition. Study presented is composed of three parts in order to assess how perceptual and auditory differences in (ASD) subjects impact cognitive skills and emotion recognition among children ages 8-12 with ASD. The Assessments are protocolled using accessible mobile games, from UCR Brain Game Center. Some assessments gauge visual processing, while others assess auditory processing. The games include jitter discrimination to evaluate processing abilities. The study also conducts testing to evaluate cognitive abilities of the participants, to account for differences within the spectrum. Finally, subjects will be tested on their abilities to correctly identify emotions using visual and audio cues. We believe that performances on central visual and auditory processing will predict the ability to discriminate facial expression and tone of voice. We hope to add valuable data that helps identify which mechanism of information integration is hindered in people with(ASD). Future directions include visual behavioral therapies that may improve the lives of children with(ASD).

## Poster Session 2 - 4:00pm - 5:00pm

### Integrating Bokashi Amendments with Microbe-Mediated Sustainable Agriculture

**Daniel Gonzalez II**, Benjamin Maki, and Samantha C. Ying
Department of Environmental Sciences, University of California, Riverside

California's burgeoning citrus industry has increased grower interest in more cost-effective strategies for sustainable agriculture production. Agricultural waste materials can be converted into sustainably produced fertilizer alternatives through the bokashi fermentation process; a type of composting where waste material is fermented anaerobically by specialist bacteria. Application of these products can promote plant growth through more inexpensive and sustainable means of production than conventional methods. Billions of pounds of food and agricultural waste are generated annually, some of which can be used to produce bokashi and biochar. Both substances have been shown to act as effective plant growth enhancers, but it is still unknown whether the application of bokashi, biochar, and bokashi+biochar combined can effectively enhance plant growth while increasing soil carbon and nitrogen content. We examined the effect of applying bokashi and biochar amendments, produced using food waste and agricultural byproducts (i.e. almond shells), on citrus plant growth and soil carbon/nitrogen content. Water extractable organic carbon and nitrogen (WEOC/N), total organic carbon (TOC), and total nitrogen (TN) were tracked in test soils over a 6-month experiment. Our results thus far demonstrate that all treatments show a decrease in WEOC and a substantial increase in WEON within the experimental soil over the first month of the experiment. However, biochar application does help to retain higher levels of WEOC in comparison to soils without biochar. Analysis of changes in TOC and TN content in test soils indicates that soils that are both amended with biochar and treated weekly with bokashi show improved C:N ratios and increases in TN over time, potentially indicating that these treatments in combination may create favorable conditions for microbial growth and nitrogen retention.

## Poster Session 2 - 4:00pm - 5:00pm

### The Link between Genetic and Morphological Change in a Long Term Evolutionary Experiment

**Diane Nguyen,** Keely Brown, Erik J Amézquita, Michelle Y Quigley, Tim Ophelders, Jacob B Landis, Elizabeth Munch, Daniel H Chitwood, and Daniel Koenig
Department of Botany and Plant Sciences, University of California, Riverside, California

Adaptation in multicellular organisms is often ascribed to shifts in developmental patterning. But, the process of developmental evolution is rarely observed in real time. Here, we characterize developmental variation in seed shape across half a century of evolution in a long-term experiment with barley, the composite cross II (CCII). We comprehensively characterized 37,948 seeds for variation in shape using computerized tomography (CT) scans of 875 individual spikes collected from generations $F_0$, $F_{18}$, and $F_{58}$ in the CCII. Uniform manifold approximation and projection (UMAP) was then used to extract 12 dimension-reduced morphological traits. Evolution of seed phenotypes by itself can predict the results of whole genome sequencing of the population, suggesting that selection has driven changes in morphology over time. We pinpoint the genomic basis of adaptive shifts in seed morphology in the population using genome wide association studies (GWAS). Our work directly links selection on developmental evolutionary change to molecular variation over the course of half a century of evolution.

## Poster Session 2 - 4:00pm - 5:00pm

### Virulence of *FUSARIUM OXYSPORUM* F. SP. *FRAGARIAE* Obtained from a Fusarium WILT-Resistant Strawberry Cultivar

**Eshal Vadakkan,** Evelyn Martinez-Lopez, Valentina Valencia Bernal, Hannah Ayala, Dr. Alexander Putman
Department of Microbiology and Plant Pathology, University of California, Riverside

Usage of resistant cultivars is one of the only effective and sustainable solutions to preventing Fusarium wilt, caused by the soil-living fungus *Fusarium oxysporum* f. sp. *fragariae* (FOF). In 2021 in Santa Maria, a severe outbreak of Fusarium wilt was found in one field planted with a strawberry cultivar that should have resistance, raising the possibility that a new pathogenic race of FOF that has overcome plants' resistance may be present in California. The purpose of this study was to determine the pathogenic race of samples of FOF. The pathogen was isolated into pure culture from infected plants and grown for identification. Roots of either strawberry cultivar Monterey, which is susceptible to FOF race 1, or Fronteras, which is resistant to race 1, were dipped in a concentrated suspension of FOF spores. Including a water control, the isolates tested were 628 and 629, isolated from the Santa Maria case, 724, a positive control for FOF race 1, and 717, *F. oxysporum* f. sp. *lactucae* which acted as a negative control. To assess disease development, plants will be rated on a categorical scale of one to five with one being healthy and five being dead. Future work could include population genetics to determine the relationship of the isolates in question with endemic populations in California.

## Poster Session 2 - 4:00pm - 5:00pm

### A Fusarium Wilt Survey in Lettuce Plants

**Evelyn Martinez Lopez**, Valentina Valencia Bernal, Hannah Ayala, and Alexander Putman
Department of Microbiology and Plant Pathology, University of California, Riverside

Arizona and California produce about 98% of the lettuce yield for the United States. Fusarium wilt is a disease caused when the soilborne pathogen Fusarium oxysporum, or, f. sp. lactucae (FOL) penetrates roots and colonizes the plant's xylem tissue. Fusarium wilt is a significant problem in lettuce production that has caused losses mostly in the warmer temperature areas of AZ and CA. Recently, it has started affecting lettuce crops in cooler temperature areas of CA. To determine if the spread of the disease is caused by a new population of FOL, a pathogenicity test and morphology characterization were conducted to compare potential new populations with established populations. Lettuce plants with Fusarium wilt symptoms were processed using aseptic techniques to isolate FOL into pure culture. To determine the pathogenicity of FOL, the isolates are used to inoculate lettuce plants to observe symptoms. Water control lettuce plants were observed with the inoculated plants on a predetermined scale to rate after two weeks to conclude whether F. oxysporum was the cause of wilting symptoms. By determining the pathogenicity of Fusarium sp., growers have a chance to make changes in order to produce a healthy yield of lettuce.

## Poster Session 2 - 4:00pm - 5:00pm

### What Is The Role Of Sucrose Transporters During Submergence In Rice (Oryza Sativa)?

**Gabriel Chavez,** Matthew Prior, Julia Bailey-Serres
Department of Botany and Plant Sciences, University of California, Riverside

Climate change has increased the chances of severe weather events around the world, especially droughts and floods. These occurrences severely impact our global food supply by destroying crops and placing millions at risk of starvation. To address this issue, we seek to better understand the submergence resilience of rice so that this knowledge can be used to improve other crops' resilience to extreme weather events. A key player in this investigation are the SWEET membrane-bound transporters which move sugars from photosynthetic source tissues to sink tissues (shoot base and roots) for storage and metabolism. Submergence experiments followed by qualitative and quantitative reporting of starch in the shoot and shoot base of rice will be employed to investigate the role these transporters play during a flood.

## Poster Session 2 - 4:00pm - 5:00pm

### The Effect of Parasites on Plant Defense Hormones at the Genetic Level

**Jacob Jauregui,** Brandi Lofton, Adeel Zafar, Paul Nabity
Underrepresented Students Pursuing Agriculture-Related Careers, Department of Botany and Plant Sciences, University of California, Riverside

Parasites are known to manipulate hosts using secretory molecules named effectors. Effectors may contain conserved motifs named ankyrin repeats, which are found in genes that are responsible for cell-cell signaling, cell cycle regulation, and inflammatory responses. Daktulosphaira Vitifoliae (grape phylloxera) have effectors with ankyrin repeats, which may have a correlation with D.vitifoliae manipulating hosts through manipulation of defense genes. This experiment was conducted in 2 parts, the first was performing transient mutations with nonhost Nicotiana Benthamiana, containing phylloxera ankyrin effector genes 3005712 and 3008264 and then synthesizing cDNA to measure gene expression of defense genes. The second was planting Vitis, infesting the plant with phylloxera, synthesizing cDNA, and measuring gene expression of defense genes. This design showed the response each plant had to the overexpressed effectors and the relationship between Jasmonic Acid(JA), Salicylic Acid(SA), and Ethylene(ET). The data suggests expression in Jasmonic Acid and Ethylene genes were lowered while Salicylic Acid promoting genes were induced in Nicotiana Benthamiana. The data in Vitis suggested that Jasmonic Acid and Ethylene had a mutualistic relationship. Due to time constraints Salicylic Acid related genes were not measured. To continue this study we will measure the expression of Salicylic Acid related genes in Vitis and infest it with the same overexpressed effectors. Since D.vitifoliae are deterred by JA-dependent defenses, the effectors manipulate the plant defense pathway by repressing JA and favors the induction of SA dependent defenses, suggesting the host defense is manipulated by the effectors to benefit the parasite.

## Poster Session 2 - 4:00pm - 5:00pm

### Biomolecule Sensing using Solid-State Nanopores under Conductive Pulses

**Jacob A. Velasquez**, Kevin Freedman
Department of Bioengineering, University of California, Riverside

Biomolecules are the fundamental building blocks of life, therefore a clear understanding of how they interact within their environment is paramount to understanding the individual structure and dynamics of the molecule. Nanostructure/pore technology is an emerging field that encompasses a more in depth understanding of biomolecules by operating optical and or electrical sensors while utilizing various techniques to manipulate molecules using electrical forces. Utilizing transport, chemical, physical, electronic, and membrane phenomena in nanopores governs the overall translocation of biomolecules. A nonscale solid-state nanotube aperture with denaturing solution submerged in an analyte containing glucagon and leucine enkephalin at various concentrations as a parameter was used to determine peptide length using applied voltages over time. The characterizations were then analyzed using MATLab software by comparing dwell time differences and current amplitude changes.

## Poster Session 2 - 4:00pm - 5:00pm

### The Application of Physics to Characterize Artificial Deep Neural Networks

**Jared Hudnall** and Michael Mulligan, PhD
Department of Physics and Astronomy, University of California Riverside

Physics as a field of study has long sought to describe complicated physical processes with simple mathematical equations that serve to characterize and predict their emergent behavior. Modeling such systems by analyzing each of its contributory components individually in addition to the dynamic nonlinear relationships between those components has proven, in some cases, to be impossible due to the arbitrarily high number of parameters a system might have. Artificial deep neural networks, a form of artificial intelligence modeled after the central nervous system in animals, are one such system, where each component can be taken to be a neuron in the network, each connected to a set of other neurons in the system. Each connection can be taken as a set of parameters, transforming the network inputs and the signals of the neurons before it, creating exceedingly complicated system dynamics. The output of a deep neural network may be determined by upwards of millions of parameters, depending on the network architecture, creating a challenging system to model. We aggregate scientific literature by physicists and computer scientists to explore the attribution of mathematical tools developed in physics, statistics, and pure mathematics toward a tractable theoretical analysis of deep neural networks, a cross-disciplinary endeavor that exploits the power of these tools to characterize complicated systems. Characterizing the behavior of deep neural networks has applications in all facets of human society in which these systems are used, including aerospace engineering, business analytics, autonomous vehicles, healthcare, weather forecasting, cybersecurity, and more.

## Poster Session 2 - 4:00pm - 5:00pm

### Differences in Expression of OS10G0145901 in HEG4 vs. EG4 and Nipponbare

**Jennifer Nguyen,** James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, and Susan Wessler
Dynamic Genome Program, Rochelle and Allison Campbell Hall, Department of Botany and Plant Sciences,
University of California, Riverside, California 9252

*Oryza sativa* was first domesticated in China as *ssp. japonica*, and since then it has been cultivated into various strains. The three strains being investigated are Nipponbare, Gimbozu EG4, and Gimbozu HEG4. Compared to NB and EG4, HEG4's genome has a sequence of ~125k nucleotides which has been inverted due to the presence of numerous mPing nonautonomous transposable elements. As such, this study will investigate a gene from this sequence in particular to discover the different ways the gene Os10g0145901 is expressed between these three strains of *japonica*, and explore the influence the inversion has on gene expression. By using primer BLAST, reverse transcription, polymerase chain reaction, and gel electrophoresis, the presence of the gene was verified and its expression levels were tested. In addition, whether or not the gene was differentially expressed between the shoot and root was tested. Expression differences between the three strains couldn't be verified. However, it does seem the gene is only expressed in root cells. The genes involved in the experiment will eventually be sequenced for accuracy, which should improve future analyses of this region. Understanding the differences in gene expression between these different cultivars of a crop can reveal how transposable elements and inversions can affect gene expression.

## Poster Session 2 - 4:00pm - 5:00pm

### Dysregulated Pain Pathways in a Mouse Model of Gulf War Illness

**Johan Portillo**, Elena Kozlova, Clara Berdasco, and Margarita Curras-Collazo
Department of Molecular, Cell and Systems Biology, University of California, Riverside

Gulf War (GW) Illness is recognized as a chronic disorder characterized by various symptoms including fatigue, chronic pain, and cognitive problems, that still affect one- third of US veterans that served in the Persian GW. Being an illness whose pathophysiology is yet to be established, we aim to correlate altered brain function with neuroinflammation in a GW mouse model. Adult male mice were divided in two groups: Sham/S, exposed to saline and stress; and GW/S, exposed to GW agents 5d/wk for 28 days: PB (8.7 mg/kg/d), PER (1.3 mg/kg/d) in 70% ETOH, 33% DEET in 70% EtOH (75 μl/30 g bw) and 5 min/d stress (n=8-16; 4 months of age). After 150 days of exposure to GW agents, a hot plate test (HPT) was conducted at two different temperatures (46C ±0.5 and 53C ±0.5), and latency to withdrawal was measured as a pain response. After HPT, mice were perfused in 4% PFA. The brain was cut in a cryostat, and immunofluorescence using anti-GAFP (1:750) was performed to identify astrocytes. Images were obtained using epi-fluorescence microscopy from cortical amygdaloid nuclei (PLCo), a region related to pain pathways. The number of GFAP positive cells were counted using Fiji software. HPT showed different results between the two temperatures. While there was no significant difference at 53C, there was at 46C (16.14 ±1.74 Sham/S, 24.19 ±3.2 GW/S, t test). The number of astrocytes in the PLCo showed no significant differences between the two groups. In conclusion, there is an altered pain mechanism, made evident by the HPT, in the mice exposed to GW agent. However, the hypothesis that neuroinflammation is related to this alteration, is not supported by lack of astrogliosis.

## Poster Session 2 - 4:00pm - 5:00pm

### Enumerating the Linearity Regions of Max-Pooling Layers for Convolutional Neural Networks

**Jordan Guillory**, Javier González Anaya, Patricio Gallardo Candela
Department of Mathematics, University of California ,Riverside

Convolutional neural networks (CNN's) are central tools in the application of machine learning to audio, image, and text processing. CNN's have been successful in a wide range of applications because of their ability to identify characteristic features of complex sets of data with a relatively low computational cost. Max-pooling layers (MPL's) are key components of CNN's that reduce the number of parameters used by the network while making it more robust to small changes in the input data. From a mathematical point of view, MPL's are piecewise linear functions. Counting the number of linearity regions for piecewise linear functions arising in the theory of neural networks has been an active area of research in the past few years. We use a technique recently introduced that relates the number of linear regions of an MPL to the problem of counting vertices, in particular geometric objects, referred to as Minkowski sums of simplices. As a result, we give an exact count for the case of 3-dimensional inputs.

## Poster Session 2 - 4:00pm - 5:00pm

### Comparing Chemical and Biological Controls for Algal Blooms

**Joylyn Tran**, Clara Woodie, Dr. Kurt Anderson
Department of Biology, University of California Riverside

Due to human activities such as high input agriculture, there is an increased risk of nutrient runoff which often causes algal blooms. Algal blooms pose ecological problems like consuming the oxygen in the water when the algae decays and releasing toxins. Out of many solutions, there is no consensus on which solution is best and if biocontrols are comparable in effectiveness to chemical control. Using chemicals might have unintended consequences like directly or indirectly disrupting biochemical processes. So, it may be better for the environment to use predators to naturally remove it. We compared the potency of bleach as the chemical solution and Tetrahymena and Euplotes as the biological solution to determine the effectiveness of biological controls vs chemical controls in decreasing algae count. We prepared 5 different treatments of 5 replicates each: just algae, algae treated with bleach, algae treated with Tetrahymena , algae treated with Euplotes, and algae treated with Tetrahymena and Euplotes. We compared the density of algae across the treatments and the control in order to see if there is a significant difference. Preliminary results show that each treatment had less alage density compared to the control. However, no factor significantly outperformed the others. Even though these results show that biological factors do not outperform chemical factors, it still shows that biological factors can be as effective at combating algal blooms. Therefore, we have a method which could be a healthier alternative when compared to a chemical control which may disrupt the health of the local ecosystem.

## Poster Session 2 - 4:00pm - 5:00pm

### Developing Heat Tolerant Lettuce

**Isaiah Hernandez**[1], **Derek Chow**[1], **Kenny Nguyen**[1], **Jair Chavez**[1], **Ezeonyeoma Nworgu**[1]
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Increasing temperatures due to climate change has decreased lettuce production in California. The resulting lettuce shortage has skyrocketed consumer prices up 67% in just 2021. California is the United States' leader of lettuce production, as it is responsible for approximately 70% of the nation's lettuce. We aim to build a solution to increase the heat tolerance of lettuce which will subside the lettuce storage and consumer rates. Research studies on lettuce related to heat tolerance have found a family protein called LsHsp70. One gene in particular called LsHsp70-2711 increases the heat resistance in lettuce when exposed to high temperatures. Studies show that overexpressing the LsHsp70-2711 gene reached a maximum gene expression level at 42 C. On the other hand, reducing the expression of this gene accelerated the elongation of the lettuce stems. With that said, we hope to use CRISPR-dCas9 to upregulate the LsHsp70-2711 gene. If done successfully, this solution can effectively increase the lifespan of lettuce and potentially increase lettuce production by 20%.

## Poster Session 2 - 4:00pm - 5:00pm

### Agribusiness with Drought-Resistance Oryza sativa (rice)

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*Oryza sativa,* also commonly known as rice, is a leading world-staple crop that can be found in almost every diet and culture in the world. Rice is an important agricultural crop grown in California, being the second largest producer of rice in the US and bringing in millions of dollars in revenue to the California economy. However, drought and global warming have affected the harvesting and processing of rice due to the extensive water consumption used in the process. The gene we are interested in, GMTDN1, also known as Gylma.17G047300, is found in soybean with the properties and functions of resisting abiotic conditions such as drought. This gene was used to make genetically modified wheat by other researchers, resulting in drought-resistant wheat that consumed less water and had a 15% yield increase. As rice and wheat are in the same family of species, specifically the Poaceae family, we believe that genetically engineering our rice with the Glyma.17G047300 will produce the same beneficial results as wheat. We thoroughly investigated the technical, scientific, and market aspects regarding our transgenic rice with the Glyma.17G046300 gene. We eventually came to the conclusion that while it is an interesting idea that should be given fair consideration, the reality of the experiment is that strict GMO laws in California are too big an obstacle to overcome.

## Poster Session 2 - 4:00pm - 5:00pm

### Market Assessment Of Developing Tomatoes Resistant To Bacterial Canker

**Hanadi Alsuhaibani, Valerie Gonzalez, Christie Montejano, Uchenna Onukaegbe,Taewon Yoo,**
James Burnette, Steve Casper, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez, Ken Gruys, Susan Wessler
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Bacterial canker is caused by Clavibacter michiganensis ssp. Michiganensis, Cmm for short, a gram positive bacteria that invades the xylem through natural wounds of the plant. Bacterial canker is especially devastating to Solanum lycopersicum because it is known to be heavily contagious and has the ability to survive in soil for long periods of time, especially in greenhouses. This threatens tomato farmers all over the world, especially in cold and humid environments, where greenhouses are necessary. Therefore, we will cross two tomato varieties, E6203, which is susceptible to the bacteria, with Hawaii 7998, which has resistance to the bacteria in order to create a canker-resistant variety for farmers affected (Abebe, Alebel Mekuriaw et al., 2022). If canker resistant tomato seeds are procured, it would greatly reduce labor of weeding, sanitizing, and drying. Not only that, but it would also reduce tomato yield loss from bacterial canker down to a quarter. As there are no significant obstacles in regulation and requires less time and funds compared to gene editing methods, it is a low risk solution which will be viewed favorably when cooperating with seed companies. This method can be implemented to other solanaceous plants, which are susceptible to bacterial canker as well.

## Poster Session 2 - 4:00pm - 5:00pm

### Commercial and Biological Effects of Producing Genetically Modified Root-Knot Nematode Resistant Chili Peppers

**Andrew Garcia, Russel Arevalo, Ethan Mendoza, Gerardo Miramontes, Reyna Quinonez**, James Burnette, Alejandro Cortez, Venkateswari Chetty, Susan Wessler, Ken Gruys, Steven Casper
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The Keck Graduate Institute Agribusiness Project consists of formulating viable botanical solutions for modern day environmental problems that plague crops around the world, especially within the United States; the crop our group focuses on is chili peppers. Our goal is to provide a better theoretical alternative to the current solutions in place in an attempt to significantly deter pests, specifically nematodes, that ravage chili pepper populations across the U.S. Through research of existing literature, we identified a nematode resistance gene (R gene) known as the Mi gene present in wild type tomatoes. This gene has been successfully implemented in different tomato cultivars throughout the U.S. and has been proved to confer resistance with only a portion of the transferred gene. With tomatoes being a close relative of chili peppers as a part of Solanaceae family, we expect the transformation of chili peppers to succeed and commercialize chili pepper seeds containing the Mi gene and potentially develop a line of genetically modified chili peppers.

## Poster Session 2 - 4:00pm - 5:00pm

### Reversible Plasmonic Tuning by Photo-Manipulation of Thermoresponsive Charged Gold Nanoparticles

**Landley Zeng**, Zepeng Cai, Licheng Cao, Yadong Yin
Department of Chemistry, University of California, Riverside

Metal nanostructures display distinctive optical characteristics due to localized surface plasmon resonance, allowing them to be used in a range of applications, such as chemical sensing, optoelectronics, and photothermal treatment. Herein we demonstrate the reversible assembly of thermoresponsive charged colloidal gold nanoparticles (AuNPs) at a size of around 15 nm by capping them with strong phosphine ligand molecules (BSPP, bis(p-sulfonatophenyl) phenylphosphine dihydrate dipotassium salt). The combination of the photothermal conversion property of the plasmonic nanoparticles and their thermoresponsive reversible assembly enables exploiting light-controlled color-switching. Our result shows that BSPP-coated AuNPs modified soft materials have a restricted spectrum of color changes spanning from blue to red when they assemble at low temperatures and disassemble after heating. The color contrast could potentially offer a new dimension of practical applications for 2D and 3D printing and writing.

## Poster Session 2 - 4:00pm - 5:00pm

### Relation Between Restraint And Infant Sitting Acquisition

**Lynn Domond,** Dr. John Franchak, Perception, Action, and Development Lab, University of California Riverside

Does caregivers' use of prolonged restraint in seating devices affect infants' acquisition of independent sitting? As an infant begins to sit independently—without needing help from their caregiver or furniture—they have the freedom to use their hands to explore objects and can more easily look at faces (Adolph & Soska, 2014). The purpose of this study is to test whether infants who are more often restrained by furniture such as baby walkers, car seats, etc., learn to sit at a later age compared with infants who spend less time restrained. Using an ecological momentary assessment survey, the experiences of 23 infants were collected while they were 5 months old to examine if there was a relationship between their daily restraint and age of sitting acquisition. Caregivers reported whether the infant was being restrained within each day they received the EMA survey. We compared the restraint times between infants who were sitting by the time they were 6 months with those who had not begun to sit by then. Preliminary analyses showed that the infants who began sitting by 6 months spent 58.2% of their time restrained, while those who were not yet sitting were restrained 70% of the time, which was not a statistically significant difference, $t(20) = -1.37$, $p = 0.19$. Regardless, the pattern of means was consistent with our predictions, suggesting that with further research and a larger sample size, we may find evidence that infants who are restrained for longer learn to sit later.

## Poster Session 2 - 4:00pm - 5:00pm

### The Biosynthetic Function of CYP722A

**Michell T. Santiago**, Annalise M. Gushue, David C. Nelson
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Strigolactones (SLs) are multifunctional plant hormones that regulate leaf growth, nutrient starvation, and shoot branching. SLs are signaling molecules that promote root colonization by the beneficial symbiont, arbuscular mycorrhizal fungi, and stimulate the germination of root parasitic weeds that kill the host plant. Overall, a clear understanding of SLs is needed to improve their use and reduce damage by root parasitic weeds. SLs have been categorized into two major classes, canonical and non-canonical. In the Cytochrome P450 722 family (CYP722), CYP722C synthesizes canonical SLs, but CYP722A and CYP722B are functionally uncharacterized. In Arabidopsis thaliana, canonical SL was not detected but a homologous CYP722A gene was discovered. We will use AtCYP722A to begin understanding the function of this clade. I hypothesize that if CYP722A synthesizes SL, CYP722A functions will be dependent on the SL receptor, D14 in A. thaliana. We will determine this by evaluating if CYP722A overexpression still suppresses hypocotyl elongation in the d14 background. Previously, Agrobacterium-mediated transformation was used to generate CYP722A overexpression lines in Arabidopsis with a fluorescent seed coat reporter. The homozygous lines were crossed with SL-signaling mutants. Then I collected and screened for fluorescent F2 progeny seeds. After transplanting, I evaluated SL-related hypocotyl, cotyledon, and shoot-branching phenotypes to prioritize F2 plants for PCR genotyping. Lastly, we began genotyping these F2 progeny for homozygosity of the SL-signaling mutant alleles. Preliminary results suggest that CYP722A is an SL biosynthetic gene. We will continue genotyping the F2 crosses and complete the epistasis test so we can evaluate our hypothesis.

## Poster Session 2 - 4:00pm - 5:00pm

### Investigating the Bindweed Psyllid (B. Maculipennis) as a Potential Vector of Candidatus Liberibacter solanacearum in a Previously Undescribed Host Plant (S. Umbelliferum)

**Mona Tran,** Jaimie Kenney and Kerry E. Mauck
Department of Entomology, University of California, Riverside

*Candidatus* Liberibacter solanacearum (CLso) is a psyllid-transmitted, unculturable bacterial plant pathogen in the taxon *‘Candidatus’(Ca.)* Liberibacter, which is known to threaten crop production and pose food insecurity. Currently, there are 8 described haplotypes of this plant pathogen worldwide: G, F, A, U, E, D, C, and B. Previously, *Bactericera (B.) cockerelli*, the potato psyllid, was CLso’s only known vector in the U.S. *Bactericera (B.) maculipennis*, the bindweed psyllid, is a recently described vector of CLso. While *B. maculipennis* has been observed to feed on plants in the Solanaceae family, a sister family to their host ‘bindweed family’ Convolvulaceae, little research has been done on if they can successfully reproduce and develop on Solanaceous plants. With all this in mind, after finding and collecting *B. maculipennis* on *Solanum (S.) umbelliferum* (Solanaceae) in the field, we screened them for CLso and reared them on various Solanaceous plants to study potential viable reproductive host plants. Our results suggest this population of *B. maculipennis* collected carries a currently unpublished novel strain of CLso and has an unexpected reproductive host plant.

## Poster Session 2 - 4:00pm - 5:00pm

### The Effect of Gene Expression Based on an Inversion Sequence in Oryza Sativa SSP. Japonica

**Reena Patel**, James Burnette, Venkateswari Chetty, Alejandro Cortez, Isai Gonzalez,
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of Botany and Plant Sciences, University of California, Riverside, California 92521

We looked at three different strains of Oryza sativa ssp.japonica (Rice), Nipponbare, HEG4, and EG4. To compare the difference in gene expression, I analyzed part of chromosome 10 of HEG4 that is 120 kilobases and contains 12 genes. This study focuses mainly on Os10g0145200, one of the genes in the inverted region of HEG4. The goal of this lab is to look at the different rice strains to see the different genetic expression between the three strains. I was tasked with analyzing the Nibbonbare gene expression. Meaning, I was to learn if this gene is present in Nipponbare. We are testing to see that all three strains have the gene of interest. It is also known that the gene of interest is inverted in HEG4, and not in nipponbare and EG4. PCR, reverse transcription, cDNA, and qPCR were used to see if the gene of interest is expressed in all three strains. If the gene of interest is expressed in the strain, whether the gene of interest is expressed in the roots or shoots or both can be evaluated. As of now, it has been revealed that Nipponbare has an expression in the roots.

## Poster Session 2 - 4:00pm - 5:00pm

### Can Formica Francoeuri Ants Share Learned Information with Their Nestmates

**Rian Arcelao** and Abigail Pelliteri
Department of Entomology, University of California

The ability for a species to communicate where possible food resources are which can enhance forgin efficiency and increase food intake for an ant colony. We devised an experiment in which we will test 50 Formica francoeuri ant workers from one colony to determine if they have the ability to transfer information of food rewards associated with specific odors to other workers in their colony. 25% of the sample will be trained to associate one scent with a sugar reward and another scent will be used as a control with water. The trained ants will be pooled with the rest of the untrained sample for 24 hours.Then, the entire ant sample will be individually given a choice test of the two scents. The testing phase consists of each odor being placed in one arm of a Y-Tube, and individual workers being scored based on which odor they approach first. Using this data, we will perform statistical analyses to determine if the percentage of ants choosing each scent is significantly different from the null expectation of 50%. These trained ants will as well be distinguished from naive ants. We will then investigate the connection between brain size and associative learning ability, measuring head width as a proxy for brain size. We predict that information transfer will occur during the 24-hour period and that the ants that appear to learn to associate the odor with the sugar reward will tend to have larger brain sizes than those who do not show learning ability. Naive ants will have this same association as they gain the information from the trained population.

## Poster Session 2 - 4:00pm - 5:00pm

### Metabolic Implications of Temperature Fluctuations on Protist Species, Blepharisma

**Samhitha Yadalla**, Dr. Kurt Anderson, Ph.D Candidate Clara Woodie, Department of Evolution, Ecology, and Organismal Biology, University of California, Riverside, CA 92521

Temperature plays an important role in the density and distribution of species. In this project, the aim is to study the impact of temperature on Blepharisma, a model unicellular protist, in terms of density and overall morphology. Our previous observations suggest that changes in temperature can accelerate or inhibit the metabolism of a species. We initiated 3 treatments at various temperatures to examine this further: a control treatment (70°F), a heat treatment (84.2°F), and a cool treatment (66°F). 50 mL of low medium and 100 individuals of Blepharisma were placed in each of the 8 bottles per treatment. The heat and cool treatments were placed in an incubator to maintain proper temperatures, while the control treatment was placed at room temperature. In each of the bottles, population growth rate, density, and morphological changes of the protist species were recorded daily over the course of 1 week. Preliminary results suggest that higher temperatures accelerate the metabolism of Blepharisma— they grow in density faster than the control treatments. The high temperature, however, is not as sustainable and has more negative morphological impacts over time exhibited by; smaller size, slower movement, more cysts, and less pigmented protists. This research contributes to the larger understanding of the effects of temperature changes for protists in their environments— whether that be a host organism or a natural water source. Interpreting such data can lead to improvements in medical pharmacology and can contribute to conservation management in the face of global climate warming.

## Poster Session 2 - 4:00pm - 5:00pm

XITALI ZAVALA

## Poster Session 2 - 4:00pm - 5:00pm

YONGYI WEN

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