2nd Annual

CSU Summer Symposium at UCLA

August 14, 2017
1:00 - 3:30 p.m.
Geffen Hall Learning Studio

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CSU SUMMER SYMPOSIUM AT UCLA

Abstract Book

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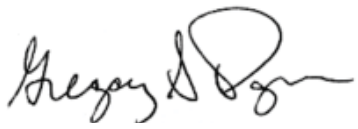
Welcome to the second annual CSU Summer Symposium and Graduate Program Fair at UCLA!

We are happy to have you join us for an afternoon featuring research presentations by students from neighboring CSU campuses, and information sessions on graduate training opportunities in STEM at UCLA. The aim of the Symposium and Fair is to promote scientific exchange and provide information on graduate educational opportunities as a way to strengthen interactions between CSU capstone research programs and UCLA graduate programs.

UCLA offers a wide variety of exceptional graduate programs in STEM. The college, with Divisions of Life and Physical Sciences, is located on a single campus with the School of Medicine and hospital. This proximity provides a wealth of research training opportunities and promotes a collaborative and collegial culture of discovery and innovation that crosses traditional academic boundaries and spans disciplines, departments and schools. Our UCLA STEM community is built on core values of openness, inclusion, and respect that foster creativity and excellence by embracing a diversity of backgrounds, experience, ideas, and approaches.

We welcome CSU participants and extend thanks to our UCLA graduate program representatives.



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Associate Dean of Bioscience Graduate Education, David Geffen School of Medicine
Associate Dean of Graduate Education, College of Life Sciences

CSU SUMMER SYMPOSIUM AT UCLA

Schedule of the Day

1:00 – 1:30 Welcome

1:30 – 2:30 Tabling with concurrent rotating 20-minute information sessions

1:30 – 1:50	Information Session 1
1:50 – 2:10	Information Session 2
2:10 – 2:30	Information Session 3

2:30 – 3:30 Tabling continued with concurrent CSU Poster Session

Poster session will highlight CSU students planning to apply to UCLA who are participating in broadening participation capstone research programs such as MARC, IMSD, MBRS Rise, HMMI and others.

Light refreshments will be served.

1 The Influence of Political Correctness and Social Dominance Orientation on Sentencing for Cases Involving Police Brutality

ERICK R. AGUINALDO, Miguel Lazaro, Courtney Morrison, Priscilla Sanchez, Russ K.E. Espinoza

CSU Fullerton, MARC

Among the police officers accused of brutality that stand trial, few are found guilty. This juror bias in favor of police may be partially explained by Social Dominance Orientation (SDO; Sidanius & Pratto, 2001), which implies that an individual prefers social hierarchy and dominance over lower status groups. Political correctness (PC), a person's level of not wanting to offend others, may also contribute to police favoritism in criminal trials. The current study examined if jurors' level of SDO and PC influence decisions for officers accused of killing an unarmed victim who is European-American, African-American, or Hispanic. It was hypothesized that persons high in SDO and low in PC would be more favorable to White officers accused of killing an unarmed minority. A 2 (juror SDO: low or high) X 2 (juror PC: low or high) X 3 (victim race: African-American, Hispanic, or European-American) between-participants design was conducted. Two-hundred and ninety-one mock jurors read a criminal court case where an unarmed victim was killed by the arresting police officer. Jurors were asked to render a verdict, recommend a sentence, and answer culpability and demographic questions. As hypothesized, a MANOVA revealed a significant three-way interaction between juror SDO and level of PC, and victim race. Mock jurors high in SDO and low in PC were less punitive toward the White officer accused of murdering an African-American victim. These jurors found the officer less culpable on blame, and were more confident in a correct decision compared with all other conditions.

2 Assessing Cysteine Residue Thiol Status of t-DARPP, A Protein Involved in Chemoresistance

JESUS A. ALDANA-MENDOZA, Philip Farias , Jamil Momand

CSU Los Angeles, NIH MBRS RISE

The gene PPP1R1B expresses t-Darpp, a protein that activates protein kinase A and the AKT pathway in breast cancer cells. t-Darpp, when overexpressed in breast cancer cells, also confers resistance to trastuzumab, a therapeutic that binds to the Her2 receptor. Although t-Darpp expression is relatively high in gastric, breast and colon cancers, its structure is unknown. Human t-Darpp has two cysteine residues that can be exploited to explore t-Darpp structure, Cys36 and Cys119. Methoxypolyethylene glycol-maleimide (Mal-PEG) was used to determine whether recombinant t-Darpp cysteine thiols are on the surface of the protein and to find out if they are reversibly oxidized. This study shows that the two cysteine thiols are either buried or oxidized. Further work will be conducted to distinguish between these two possibilities.

3 Design and Synthesis of c2tm, a de novo Cyclic Homodimer Trans Membrane Protein

JONATHAN ALDANA-MENDOZA, William Degrado

CSU Los Angeles, MARC

Transmembrane (TM) proteins play critical roles in cell surface markers, receptors, and can serve as ion channels. These proteins make up about 30% of the entire proteome, yet only .1% of known structures in the Protein Data Bank (PDB). Despite the gaps in structure analysis of TM proteins, we hypothesized that a de novo design and synthesis of a tm protein cold be carried out with accurate prediction of its secondary structure. We report the synthesis of c2tm a cyclic anti-parallel homo-dimer alpha-helical protein. With it's secondary structure aligning well with our prediction. We carried out our design by relying on structural motifs of alpha-helical proteins; to set parameters for searching naturally occurring alpha-helices in the PDB. Then using these naturally occurring proteins to analyze any sequence preference given the alpha-helical structure. We carried out the synthesis of this peptide using solid phase Fmoc synthesis, and performed reverse phase HPLC to purify the product. Structure analysis was performed on the product through circular dichroism, infrared/vibrational, and NMR spectroscopy. The synthesis and accurate prediction of this alpha-helical tm protein, demonstrates our capacity to predict structure and function of from amino acid sequence. This knowledge will help better understand tm protein interactions and allow us to incorporate this knowledge into the design of other tm proteins.

4 Integrating the Early Behavioral and Physiological Development of the Respiratory Capacity in Young Humpback Whales

KRISHA ALGOSO, Rachel Cartwright, Cori Newton

CSU Channel Islands, NSF LSAMP

As humpback whales age, they develop the adaptive capacity to hold their breath for extensive periods of time. Key adaptations that are important for muscle maturation to extend dives in hypoxic conditions include resistance to pH changes, increasing myoglobin levels to store oxygen, and development of specific fiber type compositions. Typically, marine mammal calves require postnatal development of these muscle adaptations; however, limited information is available regarding the level of muscle maturity of humpback calves and how it relates to their dive capacity. Therefore, humpback calf myoglobin levels, muscle buffering capacity, and muscle fiber type compositions were determined. To analyze myoglobin concentrations, myoglobin was extracted from swim muscles, run under an assay, and measured by applying Reynafarje's method. Buffering capacity was determined by homogenizing muscle tissue samples and titrated with drops of NaOH to shift the pH one unit. In addition, composition of type I and II muscle fibers was determined by immunohistochemical staining. Collected results overall have shown that young humpbacks have lower myoglobin levels leading to short-term oxygen storage, lower buffering capacity, and an increase in fast twitch muscle fibers in comparison to older humpback whales. The findings of this study support that immature muscle biochemistry correlates with observed calf dive durations, indicating that the energetic behavior of juvenile calves is developed to increase survival. Understanding the relationship between muscle biochemistry and dive capacity plays a significant role in understanding how humpback whale calves adapt to improve their foraging abilities, avoid predation, and strengthen their modes of survival.

5 Characterizing the Relationship Between Vacuolar pH and Vacuole Morphology

JEAN LUKE CAMPOS, ROBERTO CARLOS SEGURA, and Mark Chan

San Francisco State, MARC

Vacuole and lysosome functions—including ion storage and protein degradation—play large roles in human diseases such as lysosomal storage disorders and Alzheimer's. In order for these functions to occur properly, vacuolar pH must lie within a specific range. Due to the breadth of the vacuole's function, pH regulation has direct implications in cellular age. Despite this, the relationship between vacuolar pH and the size and shape of the vacuole has remained understudied. The proton pump for vacuoles, the V-ATPase, is a protein complex that spans the vacuole membrane. An increase in the vacuole's membrane surface will increase the number of proton pumps present on the vacuole, and should therefore lower the pH. To test our hypothesis about the relationship between vacuole morphology and vacuolar pH, we use confocal microcopy to collect single cell data comparing the surface area and volume of yeast vacuoles to their pH. The dye, BCECF will be used to measure pH within yeast vacuoles. At the same time, the lipophilic dye, FM-4-64 will be used to stain the vacuole membrane. Then, using computational image analysis, we will reconstruct three-dimensional models of vacuoles to measure their volume and surface area. If our hypothesis is accurate, we predict that there would be an inverse relationship between vacuolar pH and the surface area of the vacuole.

6 Rhythmic Generator Neuron Layer In Central Pattern Generator Network

AMADEO C. CANDIDO, Ismael Perez, Deborah Won

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Spinal plasticity has been shown to enable the possibility of restoring capabilities to walk in spinal cord injured patients. Research is advancing the development of therapies, such as peripheral nerve, or neuromuscular, electrical stimulation, which could encourage plasticity-dependent rehabilitation. To promote systematic design of such therapies, we are developing a computational model of a central pattern generator (CPG) network which exhibits long-term plasticity based on a physiologically feasible mechanism. We are using this model to understand whether and how neuromuscular electrical stimulation could potentially restore normal CPG behavior through synaptic plasticity of spinal motorneurons. We present results of reciprocal inhibition in the rhythmic generator level of the CGP network where each neuron is a conductance based model. We also demonstrate the nullclines produced by the rhythmic generator layer to show existence of a limit cycle due to the system being similar to the Van der Pol oscillator, implying that reciprocal inhibition is intrinsic to the system. This is a first step to analyze the effects of post synaptic calcium concentration on the time constant associated to the Ia afferent-motoneuron synaptic weight, which can lead to restoration of rhythmic behavior from our neural network persists and provides a platform for exploring rehabilitative therapies for spinal cord injury.

7 Gene Expression Analysis of Brain RNA from Mucolipidosis IV Knockout Mouse Model

JONATHAN A. CHACON, Amber M. Cornelious, Silvia Orozco, Sam Behseta, Archana McEligot, and Math Cuajungco

CSU Fullerton, BD3-REAP

Mucolipidosis IV (MLIV) is an autosomal recessive disorder that is characterized with neuronal and retinal degeneration. MLIV is caused by loss of function mutations in the human Mucolipin-1 gene, which encodes Transient Receptor Potential Mucolipin-1 (TRPML1) protein. Our laboratory has previously reported abnormal intracellular zinc concentration in MLIV patient fibroblasts, human TRPML1-knockdown cells, and Trpml1-knockout (KO) mouse brain tissues. These observations indicate that the loss of zinc homeostasis plays an underlying role in MLIV pathology. To further examine the mechanisms behind zinc dyshomeostasis in MLIV, we analyzed the brain transcriptome of three Trpml1 KO and three wild-type control mice using RNA-Seq. Data analyses of the biological replicates revealed marked reduction in the transcripts of zinc transporter SLC30A3 (ZnT3), and transmembrane (Tmem)-163 genes, whose protein products both localize within brain synaptic vesicles. Similar reductions were also observed for Metallothionein (MT)-1 and MT2 isoforms, whose protein products serve as reservoirs to prevent intracellular zinc overload. These data imply that the intra-lysosomal zinc elevation observed in MLIV could be potentially due to failure of constitutive zinc transport and buffering in MLIV brain cells. Overall, our findings suggest that the loss of TRPML1 function perturbs the expression of specific genes necessary for intracellular zinc homeostasis. In future studies, we aim to investigate whether the abnormal transcript levels of ZnT3, Tmem163, Mt1, and Mt2 aptly reflect their protein levels in animal and cell culture models of MLIV.

8 Differential Action of Purifying Selection Explains the Evolution of the Major Chaperone Sub-Network in Humans

CHRISTINA CHAVEZ, Kyle Hess, Jacqueline Ellis and Nikolas Nikolaidis

CSU Fullerton, MARC

Elucidating how genetic variation contributes to human evolution, adaptation, and disease predisposition is an overarching goal in modern human genetics. Molecular chaperones as key orchestrators of cellular homeostasis and adaptation are critical for cell health and disease in humans. However, the impact of the evolutionary process on their function and diversification remains largely unknown. In this study, we explored the micro-evolution process of an important component of the human chaperone network, composed by Hsp70s, Hsp40s, and BAGs, by analyzing single nucleotide polymorphisms (SNPs). The results can be summarized as follows: (a) in 90% of the genes the number of non-synonymous SNPs (nsSNPs) is higher than the number of synonymous SNPs (sSNPs). (b) Sixty percent of the genes had a significantly higher SNP density than the surrounding genes. (c) Eighty percent of the genes had significantly higher SNP density within their exonic regions as compared to both intronic and un-translated regions. (d) The majority of genes contained more sSNPs than nsSNPs within known functional regions (domains), while the number of sSNPs is similar between domains and non-domain protein regions. (e) On average only 15% of the genes contained a nsSNP on an amino acid position of known function. (f) Calculations of synonymous and non-synonymous distances revealed the action of strong purifying selection, the intensity of which varied dramatically both between and within the gene families. Collectively, these results suggest that strong purifying selection due to functional constraints shaped the evolution of the major chaperone sub-network in humans.

9 Algal Bioreactor Design and Development

GABRIEL CORTEZ and Erich Fleming

CSU San Marcos, NSF LSAMP

Particular algae strains create lipids that can be exploited to manufacture renewable biofuel. Lipid producing algae strains need nutrients and light to grow, similar to ethanol producing crops. Algae's advantage over these crops is that it has greater energy density. Current algae lipid cultivation is expensive to conduct, and therefore prohibiting production of algae biofuels. Our research is focused on creating a cost-effective bioreactor system to grow lipid producing algae efficiently at prolonged cycles. The bioreactor is an acrylic cylinder chamber that froths algae cells in suspension using a cross design airlift mechanism. Our bioreactor was tested under various air flow rates and light intensities to determine the optimal growth conditions for algae species Chlorella Vulgaris.

10 Defining the expression domains of Arabidopsis thaliana glutaredoxin genes

OSCAR DAVALOS, Miguel A. Rosas, Francisco Fernandez, Ahmad Ehrary, and Matthew A. Escobar

CSU San Marcos, NSF LSAMP

Glutaredoxins are small redox enzymes that use glutathione as a substrate to reduce disulfide bonds in target proteins. Plants have far larger numbers of glutaredoxins than other organisms, largely due to a unique clade of class III glutaredoxins that is exclusively found in higher plants. Previously, we functionally analyzed a cluster of five class III glutaredoxin genes arranged in a tandem array on Arabidopsis thaliana chromosome 4, demonstrating that these genes act as negative regulators of primary root growth. The purpose of this study was to characterize the specific cell- and tissue-level gene expression domains of three of these glutaredoxin genes: AtGRXS5, AtGRXS6, and AtGRXS8. The promoter regions of each of these glutaredoxins were cloned upstream of the reporter gene GUS (beta glucuronidase) in a plant expression vector, which was used for plant transformation. Colorimetric GUS assays were then performed on the transgenic Arabidopsis plants expressing AtGRXS5pro::GUS, AtGRXS6pro::GUS, and AtGRXS8pro::GUS gene fusions. All three genes showed similar expression domains, with GUS activity localized exclusively in root and shoot vascular tissue, throughout plant development. Expression of AtGRXS6 and AtGRXS8 was also significantly upregulated by nitrate, with GUS activity >6-fold higher in plants grown in media containing nitrate compared to nitrate-deficient media. Histological studies are currently underway to further define the cell-level localization of glutaredoxin gene expression within the vascular tissue. Collectively, our findings suggest that glutaredoxins may play an important role in nutrient signaling in plants, tying root system development to the availability of nitrogen in the soil.

11 Toward (Z)-Selective Alkene Isomerization Catalysts and Potential Anti-Cancer Agents

ESTEBAN DELGADO III, Erik Paulson, and Douglas B. Grotjahn

San Diego State, IMSD

The Grotjahn lab has developed ruthenium-based catalysts that are highly selective in the production of (E) alkenes from terminal alkenes. The cyclopentadienyl (Cp)-catalyst produces a mixture of internal (E) isomers, while pentamethylcyclopentadienyl (Cp*)-catalyst selectively produces (E)-2 alkenes in up to ca. 95% yield. Currently, there are several alkene isomerization catalysts that convert terminal alkenes to internal (E) alkenes relatively selectively, but fewer that select for (Z) alkenes. As a result, an unmet need is to have a catalyst that makes (Z) alkenes which tolerate polar functional groups, including alcohol and acid OH groups. We hypothesize that the high (E)-selectivity originates from the bifunctionality of the phosphine ligand, which incorporates a pendant base moiety to transfer protons. To reverse the selectivity, we are synthesizing modified Cp ligands that incorporate bulkier R groups and a pendant base on the Cp ring. These ligands will be attached to ruthenium and iridium to make new alkene isomerization catalysts and potential anti-cancer agents, respectively. We believe the new ruthenium catalyst can shift the selectivity of isomerization to produce mostly Z-alkenes. In addition, the iridium-based anti-cancer agents could expand the existing set of Cp-iridium complexes that significantly reduce cancer's ability to become resistant to small-molecule therapy. Overall, the synthesis and characterization of our functionalized cyclopentadienyl ligands, their respective ruthenium and iridium complexes, as well as their efficacy toward selective alkene isomerization and cancer therapy, will be presented.

12 Virtual spatial trivalent graphs and braids

ABIGAYLE L. DIRAK, Rita Post, Erica Sawyer, and Carmen Caprau

Fresno State, NSF LSAMP

A virtual spatial trivalent graph diagram (virtual STG diagram) is a trivalent graph immersed in a plane, which contains finitely many transverse double points, each of which has information of over/under or virtual crossings. We regard virtual STG diagrams as combinatorial objects up to an equivalence relation induced by certain combinatorial moves for virtual STG diagrams. Then a virtual spatial trivalent graph is the equivalence class of a virtual STG diagram. Moreover, we say that two virtual STG diagrams are equivalent if they belong to the same equivalence class.

A virtual trivalent braid is a braid similar to the notion of a classical braid, but may contain trivalent vertices and virtual crossings, in addition to classical crossings. The closure of a virtual trivalent braid with n endpoints on top and n endpoints in the bottom is a virtual STG diagram. Therefore, we can study virtual trivalent braids to gain information about virtual spatial trivalent graphs.

In this presentation we describe our method for converting any virtual STG diagram into an equivalent diagram in braid form. We also provide conditions for having two virtual trivalent braids whose closures yield equivalent virtual STG diagrams. In other words, we provide Alexander- and Markov-type theorems for virtual spatial trivalent graphs and virtual trivalent braids.

13 The importance of the Los Angeles urban forest for sustaining migratory bird populations

SEVAN ESAIAN and Dr. Eric M. Wood

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

The Los Angeles metropolitan area (LA) is home to one of the most diverse urban forests on the planet with estimates suggesting nearly 600 native and non-native tree species are distributed throughout the region. The large diversity of native and non-native trees in the urban environment is likely responsible for attracting a diverse assemblage of wintering migratory birds, which are predominantly native species that spend upwards of seven months of the annual cycle (October – April) in the region foraging on the surface of trees for food items including insects and fruits. While it remains clear that LA is a hotspot for urban biodiversity, it is unknown exactly which factors influence interactions among birds and trees throughout LA. This is important to understand to help improve management of the LA urban forest for sustaining a major component of southern California biodiversity, the wintering bird community. During the winter of 2015 and 2016, we found strong support that native trees were highly preferred as foraging substrates by wintering migratory birds while non-native trees were avoided. We are building on our initial work and have the following objectives within our study: (1) determine patterns of bird foraging success on varying tree species, (2) uncover disparities in the diversity of birds and trees along a socioeconomic gradient, and (3) investigate drivers, whether they are socioeconomic or 'natural', which may influence patterns of bird and tree diversity throughout the city.

14 Titration of Modified Histone H3 for the Detection of Salt Bridges by NMR Spectroscopy

ZOILA M.ESTRADA-TOBAR, Daniel Fuentes, Cecilia I. Zurita-Lopez

CSULA, NSF LSAMP Bridge to the Doctorate

Histone N-terminal tails are subject to covalent post-translational modifications that affect fundamental cellular regulatory mechanisms. Specifically, methylation of arginine-8 and phosphorylation of serine-10 within histone H3 have been shown to influence gene expression. The mechanism behind the two PTMs is ambiguous; it is unclear whether methylation and phosphorylation coexist or whether one PTM inhibits or enhances the other. Moreover, an intramolecular salt bridge between arginine-8 and phosphorylated serine-10 was computationally modeled, suggesting that methylation of arginine-8 could break the salt bridge interaction, thus prevent phosphorylation. Since hyper-phosphorylation of serine-10 has been correlated to certain cancers, we set out to physically characterize the formation of this salt bridge between arginine-8 and phosphoserine-10 by nuclear magnetic resonance (NMR) spectroscopy. We hypothesized that phosphorylation of serine-10 forms a salt bridge with neighboring arginine-8. Thus, its phosphorylation will prevent neighboring methylation of arginine. 31P NMR was used for salt bridge detection because the natural isotopic abundance of phosphorus (100 %) is high enough to observe without the need for isotopic labeling. To calculate the relative free energy of the salt bridge, we carried out a 31P NMR titration using four modified peptides that correspond to histone H3. Preliminary data confirm the formation of a salt-bridge. Further studies will include Heteronuclear Single Quantum Correlation (HSQC) NMR titrations to verify the electrostatic interaction in recombinant histone H3(1-33) tail. The detection of a salt-bridge will lead to mechanistic insights and expose the contributions of pH in the modification of histone H3 tails.

15 Examining the role of PKX in induced motor neurons from human ALS patients

FRANCISCO FERNANDEZ, Liu Meng-Lu, Zhang Chun-Li

CSU San Marcos, STEM-CELL SURF

Amyotrophic lateral sclerosis (ALS) is an adult-onset neurological disease characterized by selective loss of motor neurons. Direct reprograming technology that converts human fibroblasts to human induced motor neurons (hiMNs) is arising as a tool to model ALS disease. The purpose of this study is to determine the role of PKX, a little-known gene identified through pharmacological studies, in motor neuron survival during ALS pathogenesis. We applied the CRISPR-Cas9 system to knockdown endogenous PKX expression. A sgRNA scaffold expressing a PKX protospacer element was sub-cloned into the lentiviral vector LentiCRISPRv2. Efficiency of CRISPR-sgPKX was determined by Western blot analysis of PKX protein in HEK293T cells. It was found to be moderately downregulated after 72 hours. A third-generation lentivirus was then used to deliver CRISPR-sgPKX scaffold during ALS patients' fibroblast to motor neuron reprograming. After 14 days post-viral infection (dpi), hiMNs survival was examined by staining of neuron-specific marker TuJ1. It was found that neuronal survival was significantly increased when compared to control at 14 dpi (t-test, $p<0.001$). This preliminary data indicates an important role of PKX in controlling survival of ALS motor neurons. Nonetheless, further work is needed for more efficient knockdown of PKX expression in cells. This may include optimization of sgRNAs for PKX or using a shRNA-dependent approach.

16 Mechanisms of WNT1 Gradient Formation in the Chick Spinal Cord

Frederick Santana, SAMUEL GOODFELLOW, Edward Elizarraras, Lisa Galli, and Laura W. Burrus

San Francisco State, CSUPERB

Dysregulation of the Wnt signaling pathway is implicated in embryonic defects, neurodegenerative diseases and cancers. Using the chick model for vertebrate development, we focus on understanding the mechanisms underlying Wnt gradient formation. WNT1 is known to form a dorsal-ventral gradient in the spinal cord (SC) of developing vertebrate embryos. Previous studies have identified that Porcupine and Wntless(WLS) play critical roles in regulating Wnt secretion and gradient formation. Despite these advances, little is known about how Wnts are transported to target cells. Though believed that Wnts were primarily transported via diffusion, recent studies in Drosophila and zebrafish have shown that Wnts can be transported via actin-based signaling filopodia. We hypothesized that filopodia are involved in the transport of WNT1 in the developing SC. To test this hypothesis, we first generated biologically active WNT1-GFP and WLS-mCherry fusion proteins. The constructs were then transfected into the SC and live images were collected using confocal microscopy. In the absence of WLS-mCherry, WNT1-GFP was primarily localized to the ER and Golgi and no filopodia-like projections were visualized. Upon co-expression of WLS-mCherry with WNT1-GFP, much of the WNT1-GFP was redistributed to the cell surface. Strikingly, we observed large numbers of filopodia-like projections containing both WNT1-GFP and WLS-mCherry. Thus, our results show that co-expression of WLS with WNT1 1) induced the formation of new filopodia-like projections and 2) promoted the localization of WNT1 to these structures. To further understand the molecular mechanisms underlying the localization and transport of WNT1 in filopodia, we are currently investigating the importance of palmitoylation for WNT1 transport and characterizing the molecular profile of these filopodia-like projections.

17 Characterization of microbial communities in the Mojave Desert biological soil crust and their association with Syntrichia caninervis in hyper- and hypolithic habitats

JAMEKA S. JEFFERSON and Kirsten M. Fisher

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

The Mojave Desert is home to a variety of organisms including microbes, lichens, and mosses. Together, these organisms form a community known as the biological soil crust (BSC). Microbes and mosses are major components in the BSC as well as in microhabitats underneath semi-translucent quartz rocks in the Mojave Desert. Characterization of BSC composition has been focused on individual organisms (mosses or microbes), which limits understanding how BSC organisms co-exist in various microenvironments. Our goal is to use environmental sequencing of 16S rRNA to characterize microbial communities in four BSC microhabitats. Characterizing BSC microbial community composition in the presence and absence of mosses will provide insight into the process of BSC formation. This project is novel in its investigation of microbial community composition in both hyperlithic (exposed surface) and hypolithic (beneath semi-translucent quartz) desert microenvironments. The presence of moss in the BSC could potentially influence microbial composition and increase its diversity by providing additional heterogeneous habitat, altered moisture regimes, and a supplemental source of carbohydrates. The composition of microbial communities may also vary in hyper- and hypolithic microhabitats. With this work, we aim to better characterize how the presence of BSC plants (moss) modulates microbial community composition and diversity, which could potentially inform decisions for conservation of BSC structure and function.

18 3-O-Aminoalkyl-3′,4′,5′-Trimethoxyflavonols: Synthesis and Cell-Based Evaluation as Anti-Prostate Cancer Agents

MAIZIE LEE, Xiang Li, Guanglin Chen, and Qiao-Hong Chen

Fresno State, NSF LSAMP

Twelve 3-O-aminoalkyl-3′,4′,5′-trimethoxyflavonols have been designed and synthesized for the evaluation of their anti-proliferative activity. The syntheses were completed through aldol condensation followed by Algar-Flynn-Oyamada (AFO) reaction, O-alkylation, and N-alkylation. Their structures were characterized by interpreting the 1H and 13C NMR spectra. Their antiproliferative activity towards three human prostate cancer cell lines was assessed by WST-1 proliferation assay. Our results indicate that eight out of twelve 3-O-aminoalkyl-3′,4′,5′-trimethoxyflavonols are significantly more potent than the parent 3′,4′,5′-trimethoxyflavonol in inhibiting the cell proliferation in three human prostate cancer cell models. 3-O-Aminoalkyl-3′,4′,5′-trimethoxyflavonols are generally more potent towards PC-3 and LNCaP cell lines than DU145 cell line. The introduction of a dipentylaminopropyl group to 3-OH not only increase the antiproliferative potency but also the ability in activating PC-3 cell apoptosis. Our findings imply that suitable modification on 3-OH of trimethoxyflavonol can further enhance it's in vitro anti-proliferative potency and PC-3 cell apoptosis induction.

19 Lipid Peroxidation in the Leaves of ltp4 and ft/ltp4 in Arabidopsis thaliana

KAYLA K. LOVE and Robert L. Vellanoweth

CSU Los Angeles, NIH MBRS RISE

Our goal is to determine if there is a change in Lipoxygenase (LOX) activity at the floral transition in ltp4 and ft/ltp4 in regenerating Arabidopsis thaliana. Studies show in Arabidopsis during long days, the flowering hormone Flowering Locus T (ft), which is present in leaves, translocates to the shoot apical meristem and induces flowering. Also, the activities of catalase and ascorbate peroxidase (APx), which remove H2O2 produced during cellular metabolism, decline. Our previous research demonstrates, that during this decline in scavenger activity there is an increase in 13-lipoxygenase (13-LOX) activity which catalyzes chloroplast lipid peroxidation. We also found that that LTP3/4 and FT/LTP3/4 are upregulated during the floral transition. Knockdowns of these genes results in their redevelopment with basal rosettes formed from the axillary meristems, an increased lifespan of 2+ years and ft/ltp4 flower 7 months late. This occurs after the first round of reproduction and apparent death. We hypothesize, that the mutational loss of LTP3/4 and FT during the floral transition, prevents the rapid movement of a LOX derived oxylipin flowering hormone to the shoot apical meristem. However, LOX activity has not been confirmed in the mutant plants. Thus, I will measure lipid peroxidation in ltp4 and ft/ltp4 during this transition utilizing the FOX assay and LOX activity will be monitored though changes in absorbance readings during lipid peroxidation. This study will be helpful in developing techniques to improve on this oxylipin pathway and increasing crop yield efficacy.

20 Do Water-Borne Cues Mediate Density Dependent Reproductive Effects in the Sea Slug Genus Alderia?

LISA M. LUGO and Patrick J. Krug

CSU Los Angeles, NIH MBRS RISE

Recent mating history, mating group size, and water-borne chemical signals can influence allocation between female versus male roles in hermaphrodites. Prior studies showed that more frequent mating and crowding decreased egg production by the hermaphroditic sea slugs Alderia willowi and A. modesta whereas egg masses stimulated oviposition; however, these effects could be due to dissolved pheromonal cues or physical contact. Theory predicts reallocation from egg production to male functions in larger mating groups, but hypodermic insemination could also decrease egg production as a cost of mating at higher densities. Egg masses could stimulate oviposition either by acting as a physical substrate for egg attachment, or by releasing peptide pheromones as observed in other sea slug groups. To distinguish whether changes in egg production were due to chemical cues or physical access to mates/egg masses, paired slugs were exposed to chemical signals of slugs, egg masses, or both together. Water-borne cues from adults inhibited egg production in the absence of more frequent mating, suggesting cues indicating larger group size cause reallocation away from female functions as predicted by theory. Dissolved cues from other egg masses stimulated egg production, consistent with pheromonal induction. Concurrent exposure to cues from both slugs and egg masses changed egg output in a non-additive but inconsistent manner across trials. My research supports theoretical predictions of sexual selection on hermaphrodites, and provides insight into how chemical signaling mediates population ecology, and how reproductive interference between Alderia spp. may contribute to setting their respective range limits in northern California.

21 Determination of the Dissociation Constant of the EF-TU-GTP-Aminoacylated TRNA Complex

COLLIN M. MARSHALL, Javier Cabello-Villegas, and Nils G. Walter

CSU Fullerton, NIH MARC

Investigating the kinetics that describe the binding of aminoacylated tRNA to EF-Tu-GTP provides additional information about the mechanism of translation, which in turn, may assist with the development of antibiotics. It is hypothesized that the dissociation constant (KD) corresponding to the EF-Tu-GTP-uncharged tRNA ternary complex is greater than the KD corresponding to the EF-Tu-GTP-Glycine tRNA ternary complex. To address this question, a ribonuclease protection assay was carried out using fluorescently labelled uncharged and glycine coupled tRNA at uridine 46 (U46). The purpose was to measure the amount of tRNA degradation that occurred in each reaction mixture that contained different concentrations of EF-Tu-GTP. An aliquot from each reaction mixture was transferred to a Dot Blot apparatus, and the intensity of the signal was visualized using a Typhoon Phosphoimager. It is predicted that the KD corresponding to the binding between EF-Tu-GTP and uncharged tRNA is considerably greater in comparison to the KD associated with the binding between EF-Tu-GTP and aminoacylated tRNA. These results would verify the previously identified role of EF-Tu-GTP in chaperoning aminoacylated tRNA to the aminoacyl site (A site) of the ribosome facilitating protein synthesis. Future studies may seek to resolve the crystal structure of the ternary complex in order to locate the regions of EF-Tu-GTP that are responsible for binding to the aminoacylated tRNA in order to better understand this biochemical activity.

22 Integrative species delimitation supports 13 taxa in the Elysia tomentosa complex (Heterobranchia: Sacoglossa), including seven cryptic species in the Indo-Pacific

MELANIE MEDINA and Patrick J. Krug

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Sacoglossan sea slugs in the 'Elysia tomentosa' complex are large-bodied consumers of the highly invasive and ecologically devastating "killer algae", Caulerpa taxifolia and C. racemosa, but are taxonomically challenging. Only two names have been proposed for Pacific complex members (E. tomentosa, E. expansa) but diverse morphotypes and prior molecular surveys suggested several cryptic species. The Caribbean species E. subornata was proposed as biocontrol, but its feeding behavior was not effective for controlling C. taxifolia. As a better understanding of the identity and biology of all complex members may facilitate biocontrol efforts, we sought to resolve long-standing uncertainty about the number of species in this group. Molecular species delimitation of 183 specimens, using the mitochondrial barcoding COI gene and the nuclear histone 3 gene, supported seven candidate species in the tropical Indo-Pacific (at least five undescribed), as well as six in the Caribbean (two newly described, one undescribed). Ecological data moreover indicate some species prefer different Caulerpa spp., with significance for control of introduced algae. However, variation in penial armature in the E. tomentosa complex suggests sexual selection contributed to the divergence of sympatric sister species, consistent with work on other sacoglossan groups where host use is conservative. Comparative analyses on reproductive structure variation will be conducted to test our hypothesis that genital morphology has a direct role in reproductive isolation in this complex.

This research is covered by NSF grant OCE-1130072, and funding for the Cal State LA LSAMP-BD Cohort XIII program provided by the NSF grant HRD-1602210.

23 Characterization of the Interloop Disulfide Bond in High Affinity Binding of Camel VHH to Listeria monocytogenes

MATTHEW N. MENDOZA, Moeko Toride, Teresa Brooks, and Cory L. Brooks

Fresno State, NSF LSAMP

Listeria monocytogenes is a food-borne bacterial pathogen that provokes the fatal disease, listeriosis. Nearly 1,600 people contract listeriosis annually, with over 260 fatalities. L. monocytogenes expresses a virulence factor, Internalin B (InlB), that facilitates internalization into host cells. InlB exhibits a leucine-rich repeat (LRR) region that interacts with host cell receptors and is thus a site for therapeutic intervention. Camels, llamas, and alpacas possess unique heavy chain antibodies. Cloning the antigen-binding domain produces the smallest known antigen-binding fragment: the VHH, single-domain antibody, or nanobody. The camel VHH R303 binds InlB-LRR with high affinity and neutralizes L. monocytogenes. R303 possesses three complementarity-determining regions (CDRs) that function in antigen binding. The CDR3 of R303 is characteristically longer than the other CDRs and a non-canonical interloop disulfide bond between CDR1 and CDR3 may function to stabilize the binding interaction with InlB. To examine the role of this disulfide bond in InlB binding, the interloop disulfide bond was removed from R303 via site-directed mutagenesis. Indirect ELISA demonstrated that the binding affinities of wild-type and cys-mutant R303 are nearly identical. Fluorescence microscopy demonstrated that cys-mutant R303 neutralizes L. monocytogenes. Circular dichroism spectroscopy determined that the melting temperatures of cys-mutant R303 and wild-type R303 are dissimilar. X-ray crystallography will be performed to analyze the structural intricacies of the interaction of cys-mutant R303 and InlB. This study provides evidence that the interloop disulfide bond is not critical to high-affinity binding of R303 for InlB, however, the interloop disulfide bond is significant to the thermal stability of R303.

24 Synthesis and Physical Analysis of an Interdigitated Capsule

OSCAR M. MUNOZ, Jacqueline Saldana, and Linda M. Tunstad

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Non-covalent interactions between molecules are a key feature of supramolecular studies. Host-guest chemistry is a category of supramolecular chemistry, which focuses on the design of pre-organized chemical systems for binding. Host-guest binding is reversible and shows promise for the development of molecular separation technology and toxic remediation. The synthesis and study of an interdigitated quinoxaline capsule, or container molecule, is the focus of this project. Resorcin[4] arene comprises both ends of the container, each is enhanced with quinoxaline moieties, and the capsule is completed with a connecting tetraazaanthracene linker. This bridged two-cavitand construct is expected to be able to enclose a variety of guests via non-covalent interactions. The quinoxaline units of the capsule can undergo a topological shift (kite to vase and vice-versa) by adjusting environment conditions (temperature, solvent and pH), which should allow the capsule to open and close to capture and release guest species. The capsule's conformational preferences will be determined via variable temperature and variable pH 1H-NMR. Through 1H-NMR experiments, the kite/vase switch will be investigated to provide information on the capsule's behavior in specific solvents. The behavior will then be exploited in the study of complexation with potential guests.

The funding for the Cal State LA LSAMP-BD Cohort XIII program is provided by the
National Science Foundation under Grant # HRD-1602210.

25 Characterization of Transmembrane (TMEM)-163 Protein Membrane Topology

KATIA NIÑO, Kyelo Torres, Tiffany Rivas, Math P. Cuajungco

CSU Fullerton, NIH MARC

We previously identified the TMEM163 protein in search of interaction partners for the Transient Receptor Potential Mucolipin-1 ion channel. TMEM163 was predicted to have six transmembrane (TM) domains with amino (N)- and carboxyl (C)-termini facing the cytoplasmic side of the plasma membrane. Although the function of TMEM163 remains to be fully elucidated, a previous report showed that it binds zinc, nickel, and copper. Investigations in our laboratory revealed that TMEM163 could be a zinc transporter; however, our bioinformatics analysis showed that the predicted membrane topology of TMEM163 could either have N- and C-termini facing intracellularly or extracellularly. We hypothesize that the termini of TMEM163 are located extracellularly based on our preliminary observation that it transports zinc into the cells. We performed site directed mutagenesis (SDM) to insert hemagglutinin (HA) peptide tags between each transmembrane domain, and either at the N- or C-terminus end of the protein. We then transfected human embryonic kidney (HEK)-293 cells with each corresponding TMEM163 clone containing an inter-TM HA tag and a control vector. Using immuno-cytochemistry (ICC), two parallel trials of transfected cells were either permeabilized or non-permeabilized. The images were then analyzed using fluorescence microscopy. Overall, our preliminary data suggest that TMEM163 confers extracellular N- and C-termini, which contradicts the published predicted protein topology in the literature. Additional investigations in our laboratory to validate the observed membrane topology of TMEM163 will use different peptide tags. Knowledge from this study could open new research avenues on the structure and function of TMEM163 in zinc transport.

26 Surface Display of Antigens on the Surface of Gram-Negative Bacteria

BENJAMIN E. NITTAYO, N. Danielle Ebelt, Sachin S. Jadhav, Charmaine F. Soco, Edwin R. Manuel

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Within the last twenty years, research on bacterial anti-cancer therapies has grown rapidly. Anti-cancer therapies using bacteria have shown greater efficacy in delivering chemotherapeutic molecules to tumors than traditional methods of drug delivery. Bacteria are well suited to deliver chemotherapeutics to tumors because of their innate abilities to home in, enter, and colonize solid tumors. Bacteria are also logistically convenient because they can be detected externally to track their localization in tumors and can be induced at specific times or locations to produce drugs.

Although gram-negative enteric bacteria like Salmonella have a natural ability to penetrate tumor cells, some tumors are more challenging for bacteria to enter than others. Hyaluronan (HA), a glycosaminoglycan abundant in the extracellular matrix of organs, is the main driver of both the stromal desmoplasia and vessel constriction common in PDA tumors and HA-rich tumors which are often resistant to chemotherapeutics. To address this issue, my laboratory plans to engineer Salmonella with an inducible PEGylated human recombinant hyaluonidase (PEGPH20) on its outer membrane using the AIDA-I autotransport system. With PEGPH20 on the surface of the Salmonella, the bacteria should be able to break down HA and deliver the chemotherapeutics to the tumor.

Before engineering Salmonella with PEGPH20, we have engineered E. coli, another gram-negative enteric bacteria, to express green fluorescent protein (GFP) on its outer surface using the AIDA-I autotransport system when induced by isopropyl B-D-1-thiogalactopyranoside (IPTG) as proof of concept. GFP expression on the outer surface of E. coli was confirmed by immunofluorescence microscopy.

27 Identification of antibacterial inhibitors and their cellular targets using HTS and TIPA II

ROGELIO NUNEZ FLORES, Shakila Rahman, Howard Xu

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

With the rapid emergence and spread of bacterial resistance to existing antibiotics, the need of rapidly discovering and developing novel antibiotics is of upmost importance. Amongst the high throughput screening methods for identifying compounds that possess promise in bactericidal and inhibitory properties, it is vital for development of future antibiotics to understand the mechanisms by which these compounds exert their activities. A bottleneck in antibiotic discovery and development is the difficulty and time-consuming task of determining the mechanism of action (MOA) of antibacterial compounds. In this research endeavor, we work towards identifying bacterial inhibitors through high throughput screening of a 40,000-compound library. Upon obtaining hit compounds demonstrating antibacterial effects, these compounds of interest will then be tested in a disk-diffusion based platform of target identification (Target Identification Platform for Antibacterial version 2; TIPA II) leveraging a collection of clones in a mutant host strain of Escherichia coli (E. coli), AS19. The collection of these clones consists of individual overexpressed essential genes. This mutant strain has a more permeable membrane which would render the bacteria more sensitive to compounds with moderate to low potency and allow us to identify compounds that one would pass over due to poor initial results. This secondary screening through TIPA II will assist in determining the mechanism of action (MOA) in which the compounds target bacterial vital functions. The significance of these findings will facilitate the discovery and development of novel antibiotics with new MOAs.

28 Redox status affects virulence potential in Pseudomonas aeruginosa

Tyler Birges, Amorette Guzman, JUSTIN OKONKWO, Jason Thomas, Bethany Hazen, Mamta Rawat, Tricia Van Laar

Fresno State, NSF LSAMP

Low molecular weight (LMW) thiols are involved in protection against oxidative stress through the detoxification of reactive oxygen species (ROS). One of the most important LMW thiols is glutathione (GSH), which is able to reduce ROS, becoming oxidized to glutathione disulfide (GSSG) in the process. GSSG can be recycled to GSH through the activity of glutathione reductase, a critically important step for the regeneration of GSH and thus protection against ROS. Pseudomonas aeruginosa is a Gram-negative bacterium normally found in soil and water that can cause opportunistic infections, particularly in the lungs of cystic fibrosis (CF) patients. To further study the role of GSH in P. aeruginosa, we obtained mutants in numerous genes responsible for GSH biosynthesis and recycling. We found that the gshA mutant does not produce any GSH and has a slight growth delay when compared to wild type. The gshA mutant is also defective for biofilm formation, supporting the idea that the redox state of P. aeruginosa is important for biofilm formation. We noted that the GSH mutant has reduced levels of swimming and swarming motility and pyocyacin production when compared to wild type. Finally, the gshA mutant has increased sensitivity to antibiotics and oxidative stressors. Taken together, these data suggest that an imbalance in the redox state of P. aeruginosa may decrease its virulence.

29 Engineering Sequence Specific RNA Endonucleases Using a Pentatricopeptide Repeat Platform

MARIO J. PIZARRO-ROJAS, Michael L. Hayes

CSU Los Angeles

Pentatricopeptide repeat (PPR) proteins are a family of RNA-binding proteins prevalent in plants. They have emerged as potential tools for study and editing RNA due to their versatility and flexibility. Recently there has been a boom in the generation of tools for DNA genome editing. Yet, this is not the case for RNA editing tools. Current RNA based tools, such as RNA interference, have demonstrated to be difficult in practice and have limited applications. Protein-based technologies for RNA editing rise as a new contender. PPR proteins recognize their RNA cognates in a nucleotide sequence specific manner using a reprogrammable combinatorial amino acid code. This makes them great candidates as a toolbox to engineer RNA-binding proteins with a customized specificity. In this study, we aim to explore the ability to engineer site-specific RNA endonucleases using PPRs as the RNA recognition domain and RNAseI as the catalytic domain. Success of engineering PPR endonucleases can provide a new toolbox for gene knockdown assays when RNA interference technology cannot be used. Furthermore, they may provide a new antiviral defense tool against RNA viruses.

30 Homology Modeling and Simulations of Human P-glycoprotein

EXEQUIEL PUNZALAN, Yong Ba

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P-glycoprotein is a promiscuous ATP-binding transporter that binds and exports a wide array of drugs. It is believed that its overexpression in tumor cells is one of the main causes of multidrug resistance in these cells. Several crystal structures of proteins related to human P-glycoprotein have been solved in recent years. Since there is a lack of crystal structure for human P-glycoprotein, these homologous proteins are used as templates to build three-dimensional structure models. The present work aims to incorporate docking and dynamics simulations to explore the binding mode of anticancer drugs such as chlorambucil-tempol in the generated homology models. Overall, these simulations can help elucidate the binding and efflux mechanisms of P-gp on anticancer drugs.

31 The Kazhdan constant associated to a Cayley graph

MARCOS A. REYES, Mike Krebs

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Kazhdan constants relative to groups who yield isomorphic Cayley graphs are computed. The Kazhdan constant is dependent on the nontrivial irreducible representations of the respective group and the generating set. In particular, we focus on the group of integers under addition modulo n, with generating set {1, n−1} and the dihedral group, D2n with generating set {s, rs} where r denotes a rotation of 2ϖ/n and s is any reflection in the dihedral group. The groups we are considering, with these two generating sets, are known to give a special Cayley graph, namely a cycle graph with n vertices. The question we are investigating is as follows: if two Cayley graphs are isomorphic, does this imply that their corresponding Kazhdan constants are equal?

32 Understanding the Role of Post-translational Modifications on the Splicing Activity of Two Related RNA Binding Proteins

JANICE REYNAGA, Niroshika Keppetipola

CSU Fullerton, NIH MARC

The process of alternative splicing is regulated in part by RNA Binding Proteins. The Polypyrimidine Tract Binding Protein (PTBP) is an RNA binding protein that has many functions including alternative splicing regulation and mRNA localization. The PTBP gene family has 3 paralogs; PTBP1, PTBP2 and PTBP3. The paralogs have high primary structure identity and similar domain organization yet have tissue specific expression patterns and different splicing effects on certain target exons. In our study, we focus on related proteins PTBP1 and PTBP2. PTBP1 is expressed near ubiquitously, however is absent in neurons and muscle cells. PTBP2 is expressed in neurons. The two proteins have 74% primary structure identity however exert different splicing outcomes on certain regulated exons. Recent studies indicate that multiple determinants over the regions of the two proteins dictate their differential splicing activity. Mass spectrometry studies highlight that the two proteins are post-translationally modified with phosphate, acetyl and ubiquitin groups. The hypothesis underlying our studies is that post-translational modifications dictate the differential splicing activity of the two proteins. To test this, we overexpressed PTBP1 and PTBP2 in mammalian cells and probed for protein phosphorylation via Phos-Tag gel electrophoresis and for ubiquitylation using modification specific antibodies. Our results indicate that the N-terminal region is phosphorylated differently in the two proteins. We plan to probe PTBP1-PTBP2 hybrid proteins to identify domain specific modifications that may dictate the splicing activity of the two proteins.

33 Motion and Gesture Compliance Control for High Performance of a Wheeled Humanoid Robot

SALVADOR ROJAS, He Shen

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Humanoid robots have the potential to help or even take the place of humans working in extreme or undesirable environments, such as space explorations. Wheeled humanoids are robots that combine the mobility of mobile platforms, and the dexterity of an articulated body and two robotic arms. To perform like a human being, these robots normally are designed with a high center of mass, which makes it challenging to maintain stability while achieving high performance on complex and unpredictable terrain. Inspired from how humans react to balancing themselves, a compliance control method is studied to help the wheeled humanoid robot developed at the Robotics Laboratory at Cal State LA to achieve high dynamic performance while scouting over uneven terrain. The upper body of the robot is modeled as a manipulator with two degrees of freedom. Then, the dynamic model of the whole robot system is presented. Furthermore, a nonlinear compliance control of both wheel motions and gesture movements is derived to ensure the stability of the humanoid robot while tracking desired reference trajectories. Finally, the performance of the proposed compliance control system is demonstrated on various uneven terrain conditions in a simulated environment.

34 Fractionation of Zea mays Chloroplast Extracts Competent for RNA Editing Activity to Determine Sufficient Complex Members

RAFAEL SANDOVAL, Michael L. Hayes

CSU Los Angeles, NIH MBRS RISE

About 28 C-to-U editing events are found in chloroplasts and hundreds can be found in mitochondria RNA transcripts in the crop plant, Zea mays. PPR proteins have been observed to play a role in specifying C targets for this RNA editing activity. However, PPR proteins are not the only members involved in RNA editing in Zea mays—recently, it has been discovered that OZ1 (Organelle Zinc finger 1), Rip2/Rip9, Rip1, and ORRM (Organelle RRM), are also involved in RNA editing. However, it is not known how these proteins interact with each other mechanistically. Also, it is unknown whether all required members have been identified. This experiment will investigate the members of the RNA editosome critical for RNA editing activity in Zea mays.

35 Monosynaptic Tracing of Neuronal-Glial Connections

ALEXANDRA D. SAXBERG, Laura A. Cocas

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Neuroinflammatory disorders such as Multiple Schlerosis (MS), are associated with damaged myelin, the sheath that aids in transmission of action potentials. Important mechanisms regarding the myelination are unknown, specifically, the communication between oligodendrocyte precursor cells (OPCs). Recently, work has revealed that oligodendrocyte precursor cells (OPCs) receive temporary synapses from neurons prior to myelination. The function of the synapses that form on the OPCs is unknown. OPCs ultimately differentiate into oligodendrocytes that make myelin that ensheath neurons and speed up conduction. This finding suggests that neuronal-glial communication is vital for myelination. An advantageous way to monitor their neuronal-glial connections would be to use monosynaptic viral circuit tracing. By making OPCs exclusive to retroviral infection, we will be able to show connection between OPCs and neurons. To do this, we will examine the number, location, and types of neuronal inputs onto OPCs during early postnatal development. Using this tracing method, we could show an increase in connectivity during myelination. Recent research has demonstrated that increase in activity could increase myelination. Using electroporation, we will increase sodium and potassium pumps to increase and decrease activity of neurons. Tissue analysis will be done using western blot analysis of myelin basic protein (MBP), which is an essential component to myelin. We postulate that neuronal-glial connections and activity are vital for both myelination of neurons in development and remyelination after injury. Understanding of the temporary synapses OPCs receive from neurons could contribute to the mechanism of myelination and contribute toward combatting disorders like MS.

36 Clarifying the Boundaries Between Sea Slug Species: Resolving the Elysia ornata Species Complex

ARIEL SHERMAN and Patrick J. Krug

CSU Los Angeles, NSF LSAMP

Historically, identification and differentiation of shell-less gastropods have been difficult because these animals lack obvious countable (meristic) or continuous morphological traits; thus, similar-looking but evolutionarily distinct species have often been grouped under one name. The Elysia ornata complex is a group of morphologically similar, colorful species of sea slugs that contain kahalalides, anti-cancer compounds currently being tested in clinical trials. Despite the potential importance of Elysia species to drug discovery work, much of their taxonomic status is unclear. The two Pacific names E. marginata and E. grandifolia have been applied inconsistently due to vague original descriptions, and the nominal species E. ornata was reported from multiple ocean basins. To resolve the number and identity of species in this complex, one mitochondrial and one nuclear gene were sequenced from 58 specimens sampled from three Caribbean locations and eight sites spanning the Indo-Pacific. Molecular phylogenetic and species-delimitation methods supported nine distinct species: E. ornata (Caribbean), the morphologically distinct E. rufescens (Pacific), and seven cryptic Pacific species. All candidate species are being morphologically characterized by quantitative analysis of dorsal vessel networks, radular traits, and penial characters; trait data will be used in integrative species delimitation analyses to test species hypotheses based on genetic data. Taxonomic research on the Elysia ornata complex should guide future drug discovery work by determining which species contain known kahalalides, versus which species have not been chemically characterized and may therefore contain new, medically useful compounds.

37 Investigating the role Mad linker phosphorylations play in Drosophila wing development

HUGO A. URRUTIA, Abigail Aleman, and Edward Eivers

CSU Los Angeles, NSF LSAMP Bridge to the Doctorate

Signaling is an essential cellular event required for normal growth and development. One of the major signaling families in animals is the transforming growth factor-B (TGF-B) super-family. This large group can be further subdivided into the Decapentaplegic (Dpp)/BMP and the TGF-B/activin/Nodal sub-families. The Eivers' lab is currently investigating how a phospho-serine code in the central/linker domain of the transcription factor Mad modulates bone morphogenetic protein (BMP) signaling during Drosophila development. Previous work by Aleman et al. (2014) identified that cyclin dependent kinase 8 and Shaggy phosphorylate serines 212, 208 and 204 in the linker domain of Mad. These linker phosphorylations have been shown to play an essential role in controlling the range of BMP signaling in embryonic tissues and demonstrated these phosphorylations result in signal termination via Mad degradation (Aleman et al. 2014). More recently Urrutia et al. (2016) identified Dullard as a Mad phosphatase, which dephosphorylates the Mad linker and C-terminal domains, which we hypothesize is a mechanism to recycle Mad proteins for additional rounds of signaling. These discoveries have increased our understanding how the BMP pathway is regulated during development. The purpose of this research project is to investigate if Mad linker phosphorylation plays a role in wing development.

38 Morphological and Genetic Diversity of the Parasitoid Wasp (Dinocampus coccinellae) in the United States

YUMARY M VASQUEZ, HANNAH M VANSANT, Arun Sethuraman

CSU San Marcos, NSF LSAMP

Dinocampus coccinellae is a parasitic wasp that affects more than 40 species of predatory lady beetles worldwide. Predatory lady beetles are utilized as a form of organic biocontrol in United States agriculture, generating profits upwards of $395 billion annually (USDA 2012 Agriculture Census). In this study, 41 parasitoid wasps and 6 species of predatory lady beetle hosts were collected in Kentucky, Illinois, New York and Kansas. Morphological analyses were performed using microscopic imaging and weighing to identify a size correlation between parasite and host. Genetic information was collected using the NucleoSpin XS (Macherey-Nagel) protocol, and whole genome sequencing of D. coccinellae was used to determine signatures of adaptive evolution involved in host-switching and host-specificity. Preliminary results have shown significance (P value < 0.05) between the wasp mass and the predatory lady beetle mass. These results have shown a need to provide further analysis for these parasitoid wasps beyond morphological differences. With a host survival rate of less than 25% following attachment of the parasite D. coccinellae, the effect of these organisms has implications on both the ecosystem as well as the agriculture economy throughout the country.

39 Rain Gardens – Remediating Storm Water Run-off: A Case Study Along Ballona Creek in Culver City

JAY VARGAS, Andre Ellis

CSU Los Angeles, NSF LSAMP

The Ballona Watershed is located on the west side of Los Angeles county, California. The watershed is approximately 130 square miles and empties into the Pacific Ocean via the Ballona Creek; a 9-mile channelized waterway. The watershed is highly urbanized with 49% of its area covered in roads, rooftops, and other impervious surfaces. As a result, storm water runoff transports metals, pollutants, toxicity, and waste into the creek. The Santa Monica Bay Restoration Foundation (The Bay Foundation), and other stakeholders, have put in place a Best Practice Management Plan (BMP), which includes installing a rain garden (Fig 3), along a commercial zone on the eastern bank of the Ballona Creek. The objective of the rain garden is to capture, treat, and infiltrate storm runoff from surrounding streets and existing development. The goal of this study is to examine the removal efficiency of the rain garden by calculating the difference of metal concentrations, such as copper (Cu), lead (Pb), and zinc (Zn), between the influent water and the water captured by the rain garden, and to determine the mechanism by which the heavy metals are being transported. This study will help better understand the removal properties of the rain garden, and its impact to the water quality of the Ballona Creek, so that the Santa Monica Bay Restoration Foundation, and other local agencies, can more effectively implement future environmental remediation projects.

40 Pesticide Evaluation in Neural Stem Cells

JOSE VERA, Jason Bush

Fresno State, McNair

Worldwide, 5.6 billion tons of pesticides are produced annually (Alavanja et al. 2014). Pesticides have been linked to neurodegenerative diseases such as Parkinson's (PD) and Alzheimer's (AD) (Richardson et al. 2014). AD affects 44 million people worldwide and these numbers are expected to triple in the next forty years (Alzheimer's Association et al. 2016). Parkinson's disease affects ten million individuals worldwide. By 2030, these numbers are expected to increase by an astounding 80 percent (PD Foundation, 2016). The estimated health-care costs associated with these diseases in estimated to be in the billions. Major breakthroughs in slowing the pathology of PD and AD remain elusive through there is much research being conducted in these fields (Crow et al. 2016).

The Central Valley is considered the agricultural heartland of California for its billion-dollar economy. Our preliminary data obtained in collaboration with Sanford Burnham Prebys Medical Discovery Institute (SBP) showed cerebral cortical explant cultures experienced cytotoxic effects when exposed to high concentrations of the pesticides paraquat and maneb in vitro. We propose to evaluate the impact of an antioxidant supplement designed to reduce the level of free radicals in neural stem cells before pesticide treatment. We hypothesize that the antioxidant will reduce the cytotoxic effects induced by these pesticides on the neural stem cells. If the hypothesis is supported, then consumption of the antioxidant supplement may help reduce the pesticide exposure risk to susceptible populations.

41 Creation of Protein-Coding Constructs for the Development of a Reverse Genetics System for Rose rosette virus

ALLYSON WEIR, Lissette Garcia, and Melanie Sacco

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Rose rosette virus (RRV) is a negative-sense RNA virus with seven known RNA segments and eight open reading frames. Thus far, assigned gene functions are only putative based on homology, so our goal is to reconstitute infectious RRV from cloned DNA copies of the genome for reverse genetics studies. Our approach is based on the Bunyavirus system, the most similar mammalian virus to RRV with an already established reverse genetics system. This system uses three types of constructs: a specific RNA polymerase, viral genomic RNA-coding constructs, and their respective protein-coding constructs. In order to produce a working virus, RNA segments are being cloned in the form of cDNA under control of a T7 RNA polymerase promoter for transcription of genomic RNAs without modifications to ensure that viral genomic RNAs are replicated and not recognized by host ribosomes. The T7 RNA polymerase promotor has been successfully cloned and is being tested for expression in planta using the binary expression vector pBIN61. Viral protein-coding constructs are being created for expression using the same vector. Four constructs are currently being tested for expression, and four constructs are still being cloned. We will study the function of each gene through transient expression of individual proteins in Nicotiana benthamiana and manipulation later in the reverse genetics system. Understanding the function of each gene will allow further study on how the virus causes the hallmark symptoms of Rose rosette disease.

Presenter Program Interest

Biochemistry, Biophysics & Structural Biology

2 Jesus Aldana-Mendoza
3 Jonathan Aldana-Mendoza
4 Krisha Algoso
7 Jonathan Chacon
11 Esteban Delgado
14 Zoila (Zoe) Estrada-Tobar
18 Maizie Lee
19 Kayla Love
21 Collin Marshall
23 Matthew Mendoza
24 Oscar Munoz
27 Rogelio Nunez Flores
29 Mario Pizarro Rojas
32 Janice Reynaga
34 Rafael Sandoval
35 Alexandra Saxberg
37 Hugo Urrutia

Bioinformatics

2 Jesus Aldana-Mendoza
3 Jonathan Aldana-Mendoza
8 Christina Chavez
15 Francisco Fernandez
28 Justin Okonkwo
38 Yumary Vasquez

Presenter Program Interest

Cell & Developmental Biology

3 Jonathan Aldana-Mendoza
4 Krisha Algoso
5 Jean Luke Campos
5 Roberto Carlos Segura
9 Gabriel Cortez
10 Oscar Davalos
11 Esteban Delgado
16 Samuel Goodfellow
25 Katia Nino
26 Benjamin Nittayo
28 Justin Okonkwo
29 Mario Pizarro Rojas
32 Janice Reynaga
34 Rafael Sandoval
37 Hugo Urrutia
40 Jose Vera

Gene Regulation

5 Jean Luke Campos
5 Roberto Carlos Segura
10 Oscar Davalos
16 Samuel Goodfellow
23 Matthew Mendoza
25 Katia Nino
29 Mario Pizarro Rojas
34 Rafael Sandoval
36 Ariel Sherman
37 Hugo Urrutia
41 Allyson Weir

Presenter Program Interest

Genetics & Genomics

5 Jean Luke Campos
5 Roberto Carlos Segura
7 Jonathan Chacon
8 Christina Chavez
9 Gabriel Cortez
10 Oscar Davalos
17 Jameka Jefferson
23 Matthew Mendoza
25 Katia Nino
28 Justin Okonkwo
29 Mario Pizarro Rojas
36 Ariel Sherman
38 Yumary Vasquez
41 Allyson Weir

Immunity, Microbes & Molecular Pathogenesis

4 Krisha Algoso
5 Roberto Carlos Segura
9 Gabriel Cortez
15 Francisco Fernandez
17 Jameka Jefferson
23 Matthew Mendoza
25 Katia Nino
26 Benjamin Nittayo
27 Rogelio Nunez Flores
28 Justin Okonkwo
29 Mario Pizarro Rojas
32 Janice Reynaga

Presenter Program Interest

Molecular, Cellular & Integrative Physiology

5 Roberto Carlos Segura
9 Gabriel Cortez
10 Oscar Davalos
15 Francisco Fernandez
23 Matthew Mendoza
26 Benjamin Nittayo
29 Mario Pizarro Rojas
32 Janice Reynaga
34 Rafael Sandoval
37 Hugo Urrutia

Molecular Pharmacology

2 Jesus Aldana-Mendoza
14 Zoila (Zoe) Estrada-Tobar
16 Samuel Goodfellow
18 Maizie Lee
23 Matthew Mendoza
24 Oscar Munoz
29 Mario Pizarro Rojas
38 Hannah Vansant

Neuroscience

5 Jean Luke Campos
6 Amadeo Candido
7 Jonathan Chacon
35 Alexandra Saxberg
40 Jose Vera

Presenter Program Interest

Physics & Biology in Medicine

7 Jonathan Chacon
9 Gabriel Cortez
11 Esteban Delgado
24 Oscar Munoz
27 Rogelio Nunez Flores
28 Justin Okonkwo
29 Mario Pizarro Rojas
36 Ariel Sherman
38 Hannah Vansant

Chemistry

11 Esteban Delgado
14 Zoila (Zoe) Estrada-Tobar
18 Maizie Lee
19 Kayla Love
23 Matthew Mendoza
24 Oscar Munoz
29 Mario Pizarro Rojas
30 Exequiel Punzalan

Ecology & Evolutionary Biology

13 Sevan Esaian
17 Jameka Jefferson
20 Lisa Lugo
22 Melanie Medina
36 Ariel Sherman

Engineering

6 Amadeo Candido
27 Rogelio Nunez Flores
33 Salvador Rojas
39 Ricardo Vargas

Presenter Program Interest

Mathematics

6 Amadeo Candido
12 Abigayle Dirdak
31 Marcos Reyes

Psychology

1 Erick Aguinaldo

Physics & Astronomy

6 Amadeo Candido

Presenter Institution

California State University, Channel Islands

4 Krisha Algoso
9 Gabriel Cortez

California State University, Fullerton

1 Erick Aguinaldo
7 Jonathan Chacon
8 Christina Chavez
21 Collin Marshall
25 Katia Nino
32 Janice Reynaga
41 Allyson Wei

California State University, Los Angeles

2 Jesus Aldana-Mendoza
3 Jonathan Aldana-Mendoza
6 Amadeo Candido
13 Sevan Esaian
14 Zoila (Zoe) Estrada-Tobar
17 Jameka Jefferson
19 Kayla Love
20 Lisa Lugo
22 Melanie Medina
24 Oscar Munoz
26 Benjamin Nittayo
27 Rogelio Nunez Flores
29 Mario Pizarro Rojas
30 Exequiel Punzalan
31 Marcos Reyes
33 Salvador Rojas
34 Rafael Sandoval
35 Alexandra Saxberg
36 Ariel Sherman
37 Hugo Urrutia
39 Ricardo Vargas

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10 Oscar Davalos
15 Francisco Fernandez
38 Yumary Vasquez
38 Hannah Vansant

Fresno State

12 Abigayle Dirdak
18 Maizie Lee
23 Matthew Mendoza
28 Justin Okonkwo
40 Jose Vera

San Diego State University

11 Esteban Delgado

San Francisco State University

5 Jean Luke Campos
5 Roberto Carlos Segura
16 Samuel Goodfellow