

# 7<sup>th</sup> Annual UC Davis Postdoctoral Research Symposium

UC Davis  
Conference  
Center

March 18, 2022  
Davis, CA

## Abstract Book



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# Postdoctoral Research Symposium 2022 (PRS 2022) Organizing Committee



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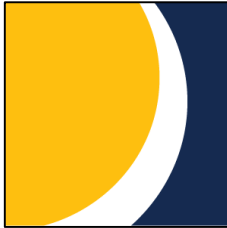
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# Program

- 8:00 – 8:50 am      Registration, Breakfast, and Posters set up      Triangle Room and Lobby
- 9:00 – 9:20 am      Opening Remarks by PSA and Associate Deans      Ballroom A
- 9:25 – 10:25 am      Parallel Oral Session 1      Conference Rooms A and B, Ballroom A

## **Session 1A, Conference Room A: Entomology and Nematology**

Chair: Marwa Zafarullah

- 9:25 am    **Buddhi Achhami**, Entomology and Nematology: *Measurement of insecticide spray coverage using water sensitive cards for aerial and ground applications in cotton*
- 9:45 am    **Lisa Chamberland**, Entomology and Nematology: *Global biogeography and evolution of net-casting spiders*
- 10:05 am   **Benjamin W Lee**, Entomology and Nematology: *A proactive approach to prepare for the invasion of Tuta absoluta into California*

## **Session 1B, Conference Room B: Computational Science and Engineering**

Chair: Debapriya Chakraborty

- 9:25 am    **Esteban Montenegro-Montenegro**, Department of Neurology, *Fit Indices in Bayesian Structural Equation Modeling: Testing measurement invariance*
- 9:45 am    **Sandeep Kumar Singh**, Electrical and Computer Engineering: *Quantum Wrapper Networking*
- 10:05 am   **Mohammad Ismail Hossain**, Electrical and Computer Engineering: *High Temperature Photonic Materials for Thermophotovoltaic Applications*

## **Session 1C, Ballroom A: Molecular Biology**

Chair: Dorothy You

- 9:25 am    **Diem Thu Nguyen**, Department of Medicine and Epidemiology: *B-Glucan Immunostimulation Against Columnaris and Streptococcosis in a White Sturgeon (Acipenser transmontanus) Model*
- 9:45 am    **Kyuyoung Lee**, Department of Medicine and Epidemiology: *Genome-informed characterization of equine influenza virus H3N8 spread at US and global scale and molecular evolution in hemagglutinin gene*
- 10:05 am   **Xiangyu Fan**, Department of Molecular and Cellular Biology: *Control of Motor Landing and Processivity by the CAP-Gly Domain in the KIF13B Tail*

- 10:30 – 10:45 am    Coffee Break      Ballrooms B + C

# Program

10:50 – 11:50 am Parallel Oral Session 2 Conference Rooms A and B, Ballroom A

## Session 2A, Conference Room A: *Plant Science*

Chair: Nathalie Aoun

10:50 am **Caspar Donnison**, PES: *Using Bioenergy with Carbon Capture and Storage (BECCS) to mitigate climate change and co-benefits from California's forests*

11:10 am **Mukund Rao**, Plant Science: *Asynchronous phenologies of photosynthetic carbon assimilation and tree-growth in temperate oaks scaled from cells to satellites*

11:30 am **Ramona Abbattista**, Plant Science: *Oxylipin-mediated stress response in CR10 walnut genotype susceptible to *Phytophthora pini**

## Session 2B, Conference Room B: *Animal Science*

Chair: Dorothy You

10:50 am **Pauline Zablocki-Thomas**, CNPRC: *Neural correlates and effect of jealousy on cognitive flexibility in the female titi monkey (*Plecturocebus cupreus*) - Preliminary results*

11:10 am **Hugo F. Monteiro**, Department of Population Health and Reproduction: *Integration of rumen and lower gut longitudinal microbiomes improves prediction for feed efficiency and production traits in dairy cows*

11:30 am **Kaisen Lin**, Air Quality Research Center: *The Spatial Distribution of Particles from Little Cigar Smoke Deposited in Rat Lungs*

## Session 2C, Ballroom A: *Pharmacology*

Chair: Vanessa Dartora

10:50 am **Miguel Martín-Aragón Baudel**, Pharmacology: *Enhanced pS1928 underlies increased CaV1.2 clustering and coupled gating compromising arterial reactivity in hyperglycemia and diabetes*

11:10 am **Jessica Caldwell**, Pharmacology: *Heterogenous cyclic AMP signaling in the intact heart is sex dependent*

11:30 am **Chidera Alim**, Pharmacology: *Nitrosylation of cardiac CaMKII at Cys290 mediates mechanical-afterload induced increase in Ca transients*

12:00 – 12:30 pm Plenary Speech 1: Dr Prasant Mohapatra

Ballroom A

12:35 – 1:20 pm Lunch

Lobby and Patio

# Program

1:30 – 2:20 pm Parallel Oral Session 3

Conference Rooms A and B, Ballroom A

## Session 3A, Conference Room A: *Ecology and Conservation Biology*

Chair: Nathalie Aoun

1:30 pm **Subhashni Raj**, Human Ecology: *Connected and Extracted: Two sides of the same coin? Understanding how centrality in the global wheat supply chain affects global hunger using a network approach*

1:45 pm **Leticia Cavole**, Wildlife, Fish and Conservation Biology: *Reconstructing Longfin Smelt Life History Using Otolith Geochemical Analysis*

2:00 pm **Austin Spence**, Wildlife, Fish, and Conservation Biology: *Late-summer temperature anomalies drive population change at avian range margins*

## Session 3B, Conference Room B: *Animal Science and Internal Medicine*

Chair: Lifeng Jiang

1:30 pm **Yuanjun Shen**, Internal Medicine: *Vps34 Up-regulation Promotes Smooth Muscle Cell Proliferation and Survival in Pulmonary Arterial Hypertension*

1:45 pm **Sarah Carp**, California National Primate Research Center: *Monkey visual attention does not fall into the uncanny valley*

2:00 pm **Dorothy You**, Division of Pulmonary, Critical Care, and Sleep Medicine: *Early-life Exposure to Wildfire Smoke Results in Dysregulated Pulmonary Immune Responses in Rhesus Macaques*

## Session 3C, Ballroom A: *Clinical Medicine*

Chair: Everlyne Ogugu

1:30 pm **Orly Tonkykh**, Betty Irene Moore School of Nursing: *Family involvement during older adults' acute hospitalization: Families', patients', and nurses' perceptions*

1:45 pm **Sherveen Riazati**, PMR: *Inter-joint coordination pattern and variability reveal distinct gait instability in stroke survivors*

2:25 – 3:25 pm Poster Session

Ballrooms B + C

3:30 – 3:40 pm Coffee Break

Ballrooms B + C

3:45 – 4:15 pm Plenary Speech 2: Dr Pamela Ronald, Panel Discussion

Ballroom A

# Program

4:25 – 5:25 pm Rapid Talks Session

Conference Rooms A and B

## **Session 4A, Conference Room A: Agriculture**

Chair: Noreen Karim

- 4:25 pm **Jiyoon Yi**, Biological & Agricultural Engineering: *AI-enabled biosensing for rapid identification of pathogens in food and agricultural water*
- 4:35 pm **Todd Harwell**, Center for Community and Citizen Science: *Examining the Role of Community and Citizen Science in California's Marine Protected Areas*
- 4:45 pm **Malathy Palayam**, Department of Plant Biology: *Structural insights into photoactivation of plant Cryptochrome-2*
- 4:55 pm **Maisa M M Lima**, Viticulture and Enology: *Characterization of the organic acids profile on Pinot noir wines from fifteen different vineyards*
- 5:05 pm **Juliano Toniato**, VEN: *Effects of ash aging to the chemical quality of wine*

## **Session 4B, Conference Room B: Biomedical Science**

Chair: Yuanjun Shen

- 4:25 pm **Kwangwook Kim**, Animal Science: *Trace amounts of antibiotic is detrimental to the health of weaned pigs*
- 4:35 pm **Lifeng Jiang**, Department of Internal Medicine: *Akt-dependent glycolysis-driven lipogenesis supports proliferation and survival of human pulmonary arterial smooth muscle cells in pulmonary hypertension*
- 4:45 pm **Vanessa Dartora**, Biomedical Engineering: *Chitosan Hydrogels Containing MK2 inhibitor peptide-Loaded Nanoparticles to Facilitate Percutaneous Absorption and Dampen Local Inflammation for Atopic Dermatitis Treatment*
- 4:55 pm **David Young**, Physical Medicine and Rehabilitation: *Real-Time Kinetic Biofeedback Facilitates Locomotor Learning to Increase Ankle Power During Gait*
- 5:05 pm **Shenq-Shyang Huang**, ETOX: *DDT and DDE attenuate beige differentiation and thermogenic function in adipocytes*

5:30 – 7:00 pm Award Ceremony and Dinner

Ballrooms A + B + C



# Plenary Speaker 1 - Dr. Prasant Mohapatra



**Dr. Prasant Mohapatra** is a distinguished professor in the Department of Computer Science and is also serving as a vice chancellor for research in the University of California, Davis. He has held several important positions in UC Davis including Dean and Vice Provost of Graduate Studies, Associate Chancellor, Interim Vice Provost, Chief information officer as well as Department Chair of Computer Science over a period of about 15 years. Before UC Davis he has sparkled in various other private and public organizations and corporations including Iowa State University, Michigan State University, Intel Corporation and Panasonic Technologies, to mention a few. He has earned popularity in the domains of wireless and mobile networks, cybersecurity and internet protocols publishing more than 350 papers from projects funded by reputable organizations such as National Science Foundation, US Department of Defense, US Army Research Labs, Panasonic Technologies, Intel Corporation, Hewlett Packard among others. We are very proud to have him speak with us at the PRS 2022 and are cordially grateful for his time.

## Plenary Speaker 2 – Dr. Pamela Ronald



**Dr. Pamela Ronald** is a distinguished professor in the Department of Plant Pathology whose research interests lie in infectious disease biology and environmental stress tolerance. Her research work not only revealed new mechanisms of infection detection and response by plants and animals but also helped develop high yielding rice varieties grown by more than six million farmers across India and Bangladesh. She is named one of the world's most influential scientific minds by Thomson Reuters, one of the world's 100 most influential people in biotechnology by Scientific American, a World Agricultural Prize Laureate by the Global Confederation of Higher Education Associations for Agricultural and Life Sciences and one of the Grist's 50 innovators. Besides, she has received numerous awards and titles including National Geographic Innovator, the Louis Malassis International Scientific Prize, and USDA National Research Institute Discovery Award. We are grateful for her commitment to join us at the PRS 2022 and give us an opportunity to inspire even more.

# Oral Abstracts

## Oral Session 1

9:25 – 10:25 am

### Session 1A, Conference Room A: *Entomology and Nematology*

#### **Measurement of insecticide spray coverage using water sensitive cards for aerial and ground applications in cotton**

Buddhi Achhami and Ian Grettenberger

*Department of Entomology and Nematology*

Insecticide efficacy relies on adequate coverage on the target plants. Application parameters (e.g., spray volume) and application methods (e.g. airplane or tractor) affect coverage. In cotton fields, insecticide applications can be made using airplane or tractor-mounted sprayers. Determining coverage that is achieved, including at different locations in the plant canopy is critical to assess how effective we expect a given application to be. To examine the variation of spray coverage in aerial and ground applications, we deployed water-sensitive cards on the fifth and ninth nodes of cotton plants in the cotton fields receiving insecticide applications. The spray volumes were 5 or 10 gallons per acre for aerial and 20 gallons per acre for ground application. We recovered the cards after the application, scanned the cards, and conducted image analysis to calculate percent area coverage. The average coverage (% of area) was 23.9% on the fifth and 14.6% on the ninth node for ground application, while coverage for aerial application was 3.5% and 0.9% on the fifth and ninth node. The ground application covered more canopy than aerial applications, but to measure insecticide efficacy at these levels of coverages need to assess the target insect population, which is our next step.

#### **Global biogeography and evolution of net-casting spiders**

Lisa Chamberland

*Department of Entomology and Nematology*

Net-casting spiders (Deinopidae) comprise a charismatic family with an enigmatic evolutionary history. There are 67 described species of deinopids, placed among three genera, *Deinopis*, *Menneus*, and *Asianopis*, that are distributed globally throughout the tropics and subtropics. All deinopids share a characteristic net-casting hunting strategy; however, morphologically, these spiders are quite diverse. Notably, *Deinopis* and *Asianopis* are often identified by their giant light-capturing posterior median eyes (PME), whereas *Menneus* has non-enlarged PMEs. Recent molecular phylogenetic studies targeting species-level relationships within *Deinopis* and *Asianopis*, revealed intriguing relationships, including that *Deinopis* is paraphyletic with respect to *Menneus*. The focus of this study was to reconstruct a genus-level phylogeny of Deinopidae with the aim of investigating the group's global biogeography, resolve the placement of *Menneus*, and investigate PME size evolution. We employed a character-rich ultra-conserved element (UCE) dataset (1018 loci; 40 taxa) and a taxon-rich cytochrome-oxidase I (COI) dataset (1279 base pairs; 270 taxa) to infer the evolutionary history of deinopids. Late Cretaceous/early Paleogene divergence and ancestral range estimation indicated that dispersal has played an important role in generating the disjunct distributions across genera and species. Phylogenetic results support the monophyly of *Menneus* and single reduction of PME size in deinopids. We also found evidence for a Western Hemisphere *Deinopis* clade, and we proposed the NEW SYNONYM of the Eastern Hemisphere *Deinopis* and *Asianopis*.

# Oral Abstracts

## **A proactive approach to prepare for the invasion of *Tuta absoluta* into California**

Benjamin Lee, Kris Godfrey and Ian Grettenberger

*Department of Entomology and Nematology*

The South American tomato leafminer, *Tuta absoluta*, is a devastating pest of tomatoes globally and poses a significant threat to tomato production in the United States. Broad-spectrum insecticides and indigenous natural enemies have had some success in controlling *T. absoluta* in invaded regions, however insecticide resistance is widespread and variation in natural enemy communities across regions makes reliance on biological control difficult. To improve the U.S. tomato industry's response to *T. absoluta* invasion into the US, our studies will i) determine the efficacy of organic and conventional insecticides against appropriate life stages of *T. absoluta* and ii) identify indigenous parasitoids that may attack *T. absoluta* and the potential role of parasitoid control in California. We have developed an assay to evaluate insecticides registered for lepidopteran pests in tomatoes on colonies of *T. absoluta* within the Contained Research Facility at UC Davis. Using a closely related endemic moth, *Keiferia lycopersicella*, we infested sentinel tomato plants to survey parasitoid communities in the Sacramento and San Joaquin Valleys and have identified several candidates for biological control of *T. absoluta*. Further testing of insecticide and biological control efficacy will help to enable a rapid response to invasion by *T. absoluta* into the US.

## **Session 1B, Conference Room B: Computational Science and Engineering**

### **Fit Indices in Bayesian Structural Equation Modeling: Testing measurement invariance**

Esteban Montenegro-Montenegro<sup>1</sup>, Mauricio Garnier-Villarreal<sup>2</sup> and Todd Little<sup>3</sup>

<sup>1</sup>*Department of Neurology Alzheimer's Disease Center*, <sup>2</sup>*Sociology Department Vrije Universiteit Amsterdam*,  
<sup>3</sup>*College of Education, Texas Tech University*

The study aimed to evaluate goodness-of-fit indices in the context of Bayesian Structural Equation Modeling (BSEM) and invariance testing in multigroup models. Garnier-Villarreal and Jorgensen (2020) adapted several approximate fit indices usually applied in the frequentist approach. They provided evidence that supports the use of traditional SEM frequentist fit measures in Bayesian models; simultaneously, their results gave ground to the question of how to implement these Bayesian fit measures to test the assumption of invariance from a Bayesian perspective. We focused our simulation on testing the Bayesian formulation of indices such as the Comparative Fit Index (CFI), Tucker Lewis Index (TLI), Normed Fit Index (NFI), McDonalds Centrality Index (Mc), and Gamma Hat ( $\Gamma$ ) index. This study showed preliminary findings that support the implementation of the Bayesian CFI, and Bayesian  $\Gamma$  in invariance testing. This work is part of a broader effort to provide more evidence of appropriate fit measures in BSEM and find procedures to rule out the presence of measurement bias in multigroup Bayesian latent models

# Oral Abstracts

## Quantum Wrapper Networking

Sandeep Kumar Singh, Mehmet Berkay On, Roberto Proietti and S. J. Ben Yoo

*Department of Electrical and Computer Engineering*

Classical Internet employs buffering, switching, and routing functionality to send information over thousands of kilometers of under-sea fiber-optical cables, while exposing the data to attackers. Quantum networks provide an alternative paradigm where data can be encoded into photonic degrees of freedom, e. g., polarization, and transmitted as entangled (correlated) photons. This secures quantum bits (qubits) from attackers due to its properties, such as qubits cannot be amplified, duplicated or measured without altering them. However, the future quantum networks need to imitate the functionality of classical Internet, which is challenging. We are developing a quantum wrapper (QW) protocol, which wraps a quantum payload, i.e., actual information, into a header carrying routing information, as shown in Figure 1. The header and payload are transmitted separately in time or frequency without affecting the data. This will ensure that our QW protocol can incorporate today's networking protocols and coexist with classical network. In this symposium, we will present our initial findings in terms of quantum bit error rate of successively transmitted entangled photons from a source to a receiver, and the performance of quantum communication channel under perturbation.

## High Temperature Photonic Materials for Thermophotovoltaic Applications

Mohammad Ismail Hossain<sup>1</sup>, Margaret A. Duncan<sup>2</sup>, Mariama R.S. Dias<sup>3</sup>, Tao Gong<sup>1</sup>, Stuart Ness<sup>2</sup>, Fox Thorpe<sup>2</sup>, Scott J. McCormack<sup>2</sup>, Marina S. Leite<sup>2</sup> and Jeremy N. Munday<sup>1</sup>

<sup>1</sup>*Department of Electrical and Computer Engineering*, <sup>2</sup>*Department of Materials Science and Engineering*,

<sup>3</sup>*Department of Physics, University of Richmond*

Thermophotovoltaics (TPVs) have attracted great attention in the research community owing to their potential for high conversion efficiency while translating radiated energy from a high-temperature source into electricity. In a TPV system, the thermal emitter plays a critical role in determining the overall system's performance. So far, several emitter concepts have been proposed; nevertheless, their successful practical realization at high temperatures is challenging. The current study focuses on designing and experimentally testing optical emissive structures at high temperatures (>1000 °C) with customized spectra. The influence of temperature on the optics of photonic materials for the emitter structures is investigated using a high-temperature stage (which can go up to 1500 °C), integrating sphere (VIS to NIR range), Fourier transformed infrared spectroscopy (VIS to MIR range), and VIS to NIR spectroscopic measurements. Electromagnetic simulations and analytical calculations further validate the experimental results. Our investigations result in a set of potential materials that can be used to build a potential thermal emitter for the thermophotovoltaic applications. We believe that the proposed thermal emitter design has a high potential to outperform currently available TPV devices and reach efficiencies above 40% at modest temperatures.

# Oral Abstracts

## Session 1C, Ballroom A: *Molecular Biology*

### **$\beta$ -Glucan immunostimulation against columnaris and streptococcosis in a white sturgeon (*Acipenser transmontanus*) model**

Diem Thu Nguyen<sup>1,2</sup>, David Marancik<sup>2</sup> and Esteban Soto<sup>1</sup>

<sup>1</sup>*Department of Medicine and Epidemiology,* <sup>2</sup>*Department of Pathobiology, St. George's University School of Veterinary Medicine, True Blue, Grenada*

*Flavobacterium columnare* and *Streptococcus iniae* represent the two most important bacterial pathogens of cultured sturgeon. However, at present there are no commercially available vaccines to prevent against infections and treatment options are limited. In this study, the effects of dietary  $\beta$ -glucan supplementation on disease were examined by exposing 0.3%  $\beta$ -glucan-fed fish to the pathogens in laboratory-controlled challenges. Morbidity and mortality were monitored for 15 (*F. columnare*) or 30 (*S. iniae*) days post-challenge (dpc). Additionally, transcript levels for pro-inflammatory cytokines, regulatory cytokines and acute phase proteins (APP) in the spleen and gills were investigated at different time points post-challenge. No evidence of protection was observed in fish fed  $\beta$ -glucans and challenged with the bacteria. Moreover, significantly greater mortalities were observed in fish immunostimulated and challenged with *F. columnare* ( $p < 0.05$ ), likely associated with acute inflammatory response as haptoglobin and serotransferrin transcripts in the gills were significantly higher in fish fed  $\beta$ -glucans and challenged with *F. columnare* at 1 dpc. Transcript levels for all tested cytokines and APP in the spleen were similar amongst treatment groups. The results from this study suggest that  $\beta$ -glucan supplementation at the concentration and rate investigated provides no-benefit to white sturgeon against *F. columnare* or *S. iniae*.

### **Genome-informed characterization of equine influenza virus H3N8 spread at US and global scale and molecular evolution in hemagglutinin gene**

Kyuyoung Lee<sup>1</sup>, Nicola Pusterla<sup>2</sup>, Samantha M. Barnum<sup>2</sup>, Dong-hun Lee<sup>3</sup> and Beatriz Martinez-Lopez<sup>1</sup>

<sup>1</sup>*Center for Animal Disease Modeling and Surveillance (CADMS) Department of Medicine and Epidemiology,* <sup>2</sup>*Department of Medicine and Epidemiology,* <sup>3</sup>*Department of Pathobiology and Veterinary Science, the University of Connecticut*

Equine influenza virus (EIV) is a highly infectious pathogen and a global burden in the equine health. Since the late 1970s, EIV H3N8 subtype has globally spread, and its evolution results in continual emergence of novel variants. This study evaluated the pattern of EIV spread at the United States (US) and global scale and molecular evolution in hemagglutinin (HA) gene. Our study used 297 HA genome of EIV H3N8 strains globally collected from 1963 to 2019 to estimate phylogeography at US and global scale. Amino acid substitution and selection pressure in the HA gene were measured to evaluate the molecular evolution. Phylogeography of global EIV H3N8 showed that one globally dominant lineage mostly emerged from North American and spread to other countries. US EIV strains generally spread from Southern and Midwestern regions to other two US regions. Our study observed significant antigenic drift and the HA gene substituted about three nucleotides per year. Current EIV strains accumulated 11 amino acid substitutions compared to the FC1 vaccine strain. Our findings will inform equine veterinary practitioners and policy makers in equine health to implement risk-based preventive and control measures such as cost-effective border quarantine protocol and vaccine strain update.

# Oral Abstracts

## **Control of Motor Landing and Processivity by the CAP-Gly Domain in the KIF13B Tail**

Xiangyu Fan and Richard J. McKenney

*Department of Molecular and Cellular Biology*

Flavobacterium Microtubules are a major component of the eukaryotic cytoskeleton that play crucial roles in diverse cellular process. Posttranslational modifications (PTMs) of tubulin dimers regulates the dynamics and organization of microtubules, as well as the interactions between microtubules and microtubule-associated proteins (MAPs). One unique PTM on microtubules is the cyclical removal and addition of the C-terminal tyrosine of  $\alpha$ -tubulin. CAP-Gly (cytoskeleton-associated protein glycine-rich) domain containing proteins specifically recognize tyrosinated microtubules, a property exploited to regulate and spatially localize diverse microtubule effectors. KIF13B is a member of kinesin-3 family, which contains a conserved C-terminal CAP-Gly domain. How the CAP-Gly domain affects KIF13B's motility along microtubules is unknown. Here, we investigated the interaction between KIF13B's CAP-Gly domain and the tyrosinated C-terminal tail domain of  $\alpha$ -tubulin. We found that KIF13B's CAP-Gly domain strongly influences the initial motor-microtubule interaction, as well as the processive motility of KIF13B along microtubules. The effect of the CAP-Gly domain on kinesin-MT binding is specific to the nucleotide state of the motor domain, suggesting an interplay between the N-terminal motor domain and C-terminal CAP-Gly domain underlies the KIF13B-microtubule interaction. These results reveal that specialized tail domains may play active roles in the initiation and continuation of kinesin motor movement.

**Oral Session 2**

10:50 – 11:50 am

**Session 2A, Conference Room A: *Plant Science***

## **Using Bioenergy with Carbon Capture and Storage (BECCS) to mitigate climate change and co-benefits from California's forests**

Caspar Donnison<sup>1</sup>, Robert Holland<sup>2</sup>, Malcolm North<sup>1</sup>, Lindsay-Marie Armstrong<sup>2</sup>, Felix Eigenbrod<sup>2</sup> and Gail Taylor<sup>1,2</sup>

<sup>1</sup>*Department of Plant Sciences,* <sup>2</sup>*University of Southampton, UK*

California's vast forest ecosystems are becoming net sources of carbon emissions owing to drought-related mortality and wildfire seasons, driven by climate change and exacerbated by a history of poor forest management. However, these forest resources could be managed by utilising millions of tonnes of biomass from thinning operations and removing dead standing trees to deliver negative emissions through Bioenergy with Carbon Capture and Storage (BECCS). Our analysis explores some of the constraints and opportunities to deploying BECCS in California, using forest biomass to fuel BECCS power stations. A 'hotspot' analysis identifies potentially optimal locations in the forested Sierra Nevada where biomass extraction can deliver environmental and social co-benefits including wildfire mitigation, recreation, air quality, and increased water availability. Our results indicate a limited and potentially important role that BECCS could serve in Californian climate policy. Pricing these valuable co-benefits in a payment for ecosystem service policy would support their delivery through BECCS. Given the limited awareness of BECCS technology, and evidence of lukewarm public support as well as social legitimacy issues concerning the technology, this emphasis on delivery of co-benefits could be a crucial means of achieving social legitimacy for BECCS in California, and inform BECCS policy globally.

# Oral Abstracts

## **Asynchronous phenologies of photosynthetic carbon assimilation and tree-growth in temperate oaks scaled from cells to satellites**

Mukund Palat-Rao<sup>1,2,3</sup>, Arturo Pacheco-Solana<sup>3</sup>, Johanna Jensen<sup>4</sup>, Bar Oryan<sup>3</sup>, Milagros Rodríguez Catón<sup>1,3</sup>, Troy Nixon<sup>3</sup>, Caroline Leland<sup>3</sup>, Laia Andreu-Hayles<sup>3</sup>, Troy Magney<sup>1</sup>, William J. D'Andrea<sup>3</sup>, Natalie Boelman<sup>3</sup>, Róisín Commene<sup>3</sup>, Dorothy Peteet<sup>3</sup>, Pierre Gentine<sup>5</sup>, Nicole Davi<sup>3,6</sup> and Kevin L. Griffin<sup>3,4</sup>

<sup>1</sup>Department of Plant Sciences, <sup>2</sup>University Corporation of Atmospheric Research, <sup>3</sup>Lamont Doherty Earth Observatory, Columbia University, <sup>4</sup>Ecology, Evolution, and Environmental Biology, Columbia University, <sup>5</sup>Department of Earth and Environmental Engineering, Columbia University, <sup>6</sup>Department of Environmental Science, William Paterson University

Photosynthesis and tree-growth are interconnected processes that are independently modulated by environmental variables. The lack of co-located high spatiotemporal resolution measurements of photosynthesis and growth has limited our understanding of their relationship with each other and their environment. Here, we study photosynthesis and tree-growth at near-instantaneous timescales using in-situ remote-sensing, point dendrometers, wood anatomy, and Pulse Amplitude Modulated chlorophyll fluorescence. Tree and leaf-level measurements are being made on eight oak (*Quercus* spp.) trees in a temperate forest in southern New York. Specifically, we will determine the periods of initiation and cessation of tree-growth, the periods of canopy development and senescence, and the attainment and loss of the full photosynthetic capacity. Preliminary data for 2021 suggests that oaks commenced radial growth in the first week of April approximately one-month prior to canopy development that was not completed until the first week of May. Further, the development of foliar photosynthetic capacity lags leaf expansion by nearly two weeks. This two-week lag between the completion of leaf expansion and subsequent development of photosynthetic capacity is not captured by remote sensing metrics. These results have the potential to help refine our understanding of photosynthesis and tree-growth with implications for terrestrial carbon cycling.

## **Oxylipin-mediated stress response in CR10 walnut genotype susceptible to *Phytophthora pini***

Ramona Abbattista<sup>1</sup>, Paulo A. Zaini<sup>1</sup>, Steven H. Lee<sup>1</sup>, Charles A. Leslie<sup>1</sup>, Sriema L. Walawage<sup>1</sup>, Cai-Zhong Jiang<sup>1,3</sup>, Gregory T. Browne<sup>2,3</sup>, Takao Kasuga<sup>2,3</sup> and Abhaya M. Dandekar<sup>1</sup>

<sup>1</sup>Department of Plant Sciences, <sup>2</sup>Department of Plant Pathology, <sup>3</sup>Crops Pathology and Genetics Research Unit, USDA-ARS

Oxylipins are oxygenated polyunsaturated fatty acids which regulate defense and stress responses both in animals and plants. During oomycete infection eicosanoid-type elicitors are released into the apoplast, triggering oxidative burst, plant phospholipases and oxidative enzymes, which lead to oxylipin cascade inside the plant cell. Accumulation of oxylipin hydroxy fatty acids (HFAs) in plant is a biomarker of oomycete infection but, HFAs' role, is still uncertain. Indeed, while cytotoxic  $\alpha$ -HFAs and linoleate diols (LDs) regulate human immune response driving the inflammation, their role is unknown in plant. Investigating oomycete-induced oxylipins may lead to novel treatments for walnut diseases caused by *Phytophthora*. Metabolomic and transcriptomic analyses of walnut genotypes susceptible, CR10, and resistant, RX1, to *P. pini* were performed in our group. Lipids exhibited the strongest contrast between CR10 and RX1 metabolic baseline. HFAs as 2-hydroxyoleate ( $\alpha$ -HFA), 9 and 13-HODE, 9,10-DiHOME (LDs), and 9,10,11-TriHOME were significantly higher in *P. pini*-infected CR10 standing up as disease biomarkers with their related genes,  $\alpha$ -dioxygenase, 9 and 13-lipoxygenase, P450s and epoxide hydrolases. Our findings unraveled oxylipin-mediated stress responses in walnuts, which may lead to new diagnostic and genetic tools for disease management alternatives to conventional pesticides.



# Oral Abstracts

## Session 2B, Conference Room B: *Animal Science*

### **Neural correlates and effect of jealousy on cognitive flexibility in the female titi monkey (*Plecturocebus cupreus*) – Preliminary results**

Pauline B. Zablocki-Thomas<sup>1</sup>, Logan E. Savidge<sup>1,2</sup>, Lynea Witczak<sup>1,2</sup> and Karen L. Bales<sup>1,2</sup>

<sup>1</sup>California National Primate Research Center, <sup>2</sup>Department of Psychology

Jealousy is a social emotion that elicits behavioral reactions from an individual toward a threat to a valuable relationship. Monogamous species exhibit jealousy-type behaviors as an adaptive response to preserve the relationship. Jealousy is also a complex emotion composed of several basic negative emotions: fear of loss, anxiety, suspiciousness and anger. Negative emotions like anxiety may impair cognitive processes such as cognitive flexibility, an ability important for coping with new situations. However, little is known about how complex social emotions influence cognitive flexibility. To understand the interaction between jealousy and cognitive flexibility, presented a jealousy provoking scenario to female titi monkeys, followed by a reversal learning test and a PET scan. Behaviorally, females reacted with more locomotion in the jealousy condition but it did not significantly affect performance during the reversal task. This study could bring new insights on neural, behavioral and physiological correlates in the context of jealousy and cognitive flexibility, and enable a comparison of jealousy between males and females in this primate species.

### **Integration of rumen and lower gut longitudinal microbiomes improves prediction for feed efficiency and production traits in dairy cows**

H. F. Monteiro,<sup>1</sup> Z. Zhou,<sup>2</sup> M. S. Gomes,<sup>3</sup> P. M. G. Peixoto,<sup>4</sup> E. C. R. Bonsaglia,<sup>1</sup> I. F. Canisso,<sup>3</sup> B. C. Weimer<sup>1</sup> and F. S. Lima<sup>1</sup>

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Fermentation of dietary nutrients in the gastrointestinal tract of ruminants is a key mechanism utilized to meet daily energy requirements. Especially in high-producing dairy cows, the gastrointestinal microbiome plays a major role in the breakdown of indigestible plant polysaccharides and supply most amino acids, fatty acids, and gluconeogenic precursors for milk synthesis. Although the rumen microbiome received great emphasis over the years due to its pivotal contribution to gastrointestinal tract fermentation, the lower gut microbiome contributions to production efficiency in dairy cows remain poorly characterized. We investigated the relationship of these two fermentation sites with key production efficiency traits in high-producing Holstein dairy cows throughout lactation. We found that both microbiomes were stable throughout lactation, yet nutritional factors play a significant role in shaping gastrointestinal microbiome diversity. The rumen microbiome, for instance, had a composition highly dependent on feed intake levels. In contrast, the lower gut microbiome was more associated with an enhanced ability of the animal to extract more out of dietary nutrients. Therefore, the lower gut microbiome might be an important contributor to optimizing predictions of production traits. These findings are key elements to support more efficient and sustainable livestock production.

# Oral Abstracts

## The Spatial Distribution of Particles from Little Cigar Smoke Deposited in Rat Lungs

Kaisen Lin<sup>1</sup>, Chris Wallis<sup>1</sup>, Emily Wong<sup>2</sup>, Patti Edwards<sup>3</sup>, Laura Van Winkle<sup>2,3</sup>, Bahman Asgharian<sup>4</sup>, and Anthony Wexler<sup>1,5,6,7</sup>

<sup>1</sup>Air Quality Research Center, <sup>2</sup>Department of Anatomy, Physiology & Cell Biology, <sup>3</sup>Center for the Health and Environment, <sup>4</sup>Applied Research Associates Inc, Albuquerque, <sup>5</sup>Department of Mechanical and Aerospace Engineering, <sup>6</sup>Department of Civil and Environmental Engineering, <sup>7</sup>Department of Land, Air and Water Resources

Quantifying the dose of tobacco smoke and its deposition location in the respiratory system is important in understanding its toxicity, addiction, and health effects. There have not been many studies that investigated the pulmonary spatial distribution of inhaled particles from tobacco smoke, especially with little cigar products. Given the increasing popularity of little cigars, especially in young populations, there is an urgent need to conduct research and collect data on this topic. Our study explored the local deposition of particles from combusted Swisher Sweets regular and menthol-flavored little cigars in rat lungs. We exposed 12-week old male and female Sprague-Dawley rats to smoke particles at a mass concentration of 100 mg/m<sup>3</sup>. The levels of trace metals, which serve as indicators of smoke particles, were quantified with inductively coupled plasma mass spectrometry. The results showed that more particles were deposited in the left and caudal lobes than in other lung regions, indicating a heterogeneous deposition pattern for smoke particles. We also observed that the particle clearance process was slow, suggesting that particles can retain for a long time in the lungs and are likely to cause more adverse health effects.

## Session 2C, Ballroom A: Pharmacology

### Enhanced pS1928 underlies increased Ca<sub>v</sub>1.2 clustering and coupled gating compromising arterial reactivity in hyperglycemia and diabetes

Miguel Martín-Aragón Baudel, Victor A. Flores-Tamez, Junyoung Hong, Gopyreddy R. Reddy, Abby E Burns, Johannes W. Hell, Madeline Nieves-Cintrón and Manuel F. Navedo

*Department of Pharmacology*

L-type Ca<sup>2+</sup> channel Ca<sub>v</sub>1.2 plays key roles in muscle contraction and gene expression. These channels have been shown to gate in unison (e.g. coupled gating) amplifying Ca<sup>2+</sup> influx and regulating cell function. In arterial myocytes, Ca<sub>v</sub>1.2 coupling is increased during diabetic hyperglycemia, yet the mechanisms for induction of this gating modality are poorly understood. Here, we hypothesized that phosphorylation of Ca<sub>v</sub>1.2 at S1928 is critical for induction of Ca<sub>v</sub>1.2 coupling and clustering, amplification of Ca<sup>2+</sup> influx and arterial myocyte contraction in response to high glucose (HG) and diabetes. Using a multiscale approach, we found an increase in Ca<sub>v</sub>1.2-mediated activity, coupling frequency and clustering in humans with diabetes. Similar results were observed upon HG in mouse arterial myocytes, but not cells from a mouse in which S1928 was mutated to alanine to prevent its phosphorylation (S1928A). These observations translated into enhanced myocyte contractility and *in vivo* modifications in arterial diameter and blood flow upon HG exposure which were absent in S1928A mice. Comparable Ca<sub>v</sub>1.2-mediated alterations were recapitulated in arterial myocytes from diabetic mice and these changes were completely absent in diabetic S1928A mice. These results suggest a key role for S1928 phosphorylation in modulating Ca<sub>v</sub>1.2 function and arterial reactivity upon HG and diabetes. We propose that our work may lay the foundation for novel therapeutic strategies with single amino acid accuracy to correct channel function and vascular contractility during pathological conditions.

# Oral Abstracts

## **Heterogenous cyclic AMP signaling in the intact heart is sex dependent**

Jessica. L Caldwell, Eric. I-Ju Lee, Lianguo Wang, Julie Bossuyt and Crystal. M Ripplinger

*Department of Pharmacology*

Cyclic(c)AMP is key for converting autonomic signals into downstream electrophysiological responses. How cAMP signaling, and the resulting functional responses, occur throughout the intact heart is not known. This study aimed to determine the spatiotemporal kinetics of cAMP signaling in the intact heart and the underlying mechanisms. Hearts from cardiac-specific *CAMPER* mice, that report cAMP binding by changes in FRET, were Langendorff-perfused for simultaneous cAMP and membrane-potential imaging. In male hearts, cAMP was uniformly activated and deactivated in response to  $\beta$ -AR stimulation with norepinephrine. In female hearts, norepinephrine led to a greater change in cAMP activity in basal vs. apical regions and faster apical cAMP deactivation, which was associated with a difference in action potential duration between apex and base. Regional differences were also evident following phosphodiesterase inhibition, to inhibit cAMP breakdown, with a greater change in cAMP activity in apical regions. Likewise, phosphodiesterase activity assays showed higher activity in apical regions in female hearts. In conclusion, female hearts display lower maximal cAMP activity and faster deactivation in the apex, in part, due to elevated phosphodiesterase activity in this region. This heterogeneity was not observed in male hearts. These findings may have important implications for electrophysiological responses regulated by the cAMP pathway.

## **Nitrosylation of Cardiac CaMKII at Cys290 Mediates Mechanical Afterload**

Chidera C. Alim, Christopher Y. Ko, Juliana Mira Hernandez, Erin Y. Shen, Sonya Baidar, Ye Chen-Izu, Donald M. Bers and Julie Bossuyt

*Department of Pharmacology*

Cardiac mechanical afterload induces an intrinsic autoregulatory increase in myocyte  $\text{Ca}^{2+}$  (Ca) dynamics to enhance contraction. Both nitric oxide produced by NOS1, and Ca-calmodulin kinase II (CaMKII) activity are required mediators of this mechano-chemo-transduction (MCT). To test whether the S-nitrosylation site CaMKII $\delta$  (Cys290) mediates an afterload-induced increase in sarcoplasmic-reticulum (SR) Ca uptake and release, we developed a novel CaMKII $\delta$  knock-in (KI) mouse with C290A substitution. CaMKII $\delta$ -C290A-KI mouse exhibited normal morphometry and function, basal myocyte Ca transients and  $\beta$ -adrenergic responses. However, compared to wildtype littermates, C290A myocytes prevented increased Ca spark frequency in response to S-Nitrosoglutathione. Using our cell-in-gel system to exert multiaxial-3D-mechanical afterload on contracting myocytes, we found wildtype myocytes exhibited an afterload-induced increase in Ca sparks, Ca transient amplitude and SR Ca uptake, but these affects were prevented in both cardiac-specific CaMKII $\delta$  knockout mice, and CaMKII $\delta$ -C290-KI mutant myocytes. Summarily, CaMKII $\delta$  activation by S-nitrosylation at the C290 site is essential in mediating afterload-induced acute enhancement of myocyte SR Ca uptake, release and Ca transient amplitude. Also, NOS1 activation is upstream of S-nitrosylation at C290 of CaMKII, and this molecular MCT-pathway is beneficial in allowing the heart increase contractility to limit reduction in stroke volume when aortic pressure is elevated.

# Oral Abstracts

Oral Session 3

1:30– 2:20 pm

Session 3A, Conference Room A: *Ecology and Conservation Biology*

## Connected and Extracted: Two sides of the same coin? Understanding how centrality in the global wheat supply chain affects global hunger using a network approach

Subhashni Raj<sup>1</sup>, Catherine Brinkley<sup>1</sup> and John Ulimwengu<sup>2</sup>

<sup>1</sup>Department of Human Ecology, <sup>2</sup>International Food Policy Research Institute

While global food trade has allowed countries to buffer against domestic food production shortfalls and gain access to larger markets, engaging in trade has also opened economies up to shocks and extraction of food resources. With this research, we ask how the amount of arable land per capita, food production and trade networks influence country-level food security. First we model the trade network structure of the global wheat supply chain to measure the centrality or positionality of countries. Followed by spatial autoregressive analysis of the impact of trade characteristics from the social network analysis (SNA) with trade volume, purchasing power, production capacity and geography on undernourishment outcomes. We find that there are a handful of countries that control the wheat supply chain. However, the centrality of these countries as opposed to volume of wheat produced or traded, determines their influence in the wheat supply chain network. The parametric component of our analysis confirms that trade, and centrality in the trade network have significant implications for national levels of nourishment. Our findings suggest that for countries with low purchasing power, trade allows improvements in nourishment levels but for countries with very high purchasing power, trade can increase hunger outcomes.

## Reconstructing Longfin Smelt Life History Using Otolith Geochemical Analysis

Levi Lewis<sup>1,\*</sup>, Christian Denney<sup>1</sup>, Malte Willmes<sup>1</sup>, Leticia Cavole<sup>1</sup>, Justin J. Glessner<sup>2</sup> and James A. Hobbs<sup>1,3</sup>

<sup>1</sup>Wildlife, Fish and Conservation Biology, <sup>2</sup>Interdisciplinary Center for Plasma Mass Spectrometry, <sup>3</sup>Bay-Delta Region, California Department of Fish and Wildlife, Stockton, CA

We combined the analysis of otolith isotope ratios using <sup>87</sup>Sr:<sup>86</sup>Sr (for salinity below 6 PSU) and  $\delta^{18}\text{O}$  (for salinity above 6 PSU) to reconstruct the salinity history of the critically threatened Longfin Smelt (*Spirinchus thaleichthys*) in the San Francisco Estuary. From 142 chemical profiles, we identified four main life-history strategies: three levels of anadromy (A) of slightly different natal salinity histories and a brackish-water residency (BWR) group. While juveniles experience a variety of low-salinity habitats, adults consistently live above salinity 6 PSU, with some individuals exhibiting cyclical movements between brackish and marine waters. Most individuals exhibited variable dispersal ages into brackish waters at around 150 days, suggesting that the increase of freshwater outflow preceding these months could benefit their low-salinity spawning and rearing habitats. The complementarity of the techniques employed here to unravel the salinity history of Longfin Smelts can be applied to other species in the San Francisco Estuary to better understand their natal rearing habitats, residence times, movement patterns, and age at dispersal within this dynamic, albeit highly modified, estuary.

# Oral Abstracts

## **Late-summer temperature anomalies drive population change at avian range margins**

Austin R. Spence<sup>1</sup>, Jacob B. Socolar<sup>2</sup>, Andrew N. Stillman<sup>2</sup> and Morgan W. Tingley<sup>3</sup>

<sup>1</sup>Wildlife, Fish, and Conservation Biology, <sup>2</sup>Cornell Lab of Ornithology, 159 Sapsucker Woods Rd, Ithaca NY, <sup>3</sup>Ecology & Evolutionary Biology, University of California – Los Angeles

Climate-driven range shifts involve differential rates of population growth at leading versus trailing range margins. However, the study of range shifts and their climatic drivers must contend with limited historical data and the difficulty of distinguishing different hypothesized drivers of change. By contrast, monitoring population changes in response to annual weather conditions can isolate the proximate demographic effects of climate, thereby identifying climate induced range shifts. We leveraged data from the North American Breeding Bird Survey to parse the influence of weather on the population changes of 156 bird species across their geographic distributions from 1981–2016. We hypothesized that if temperature has proximate effects on geographic range shifts, then year-to-year temperature anomalies should interact with a species' position within its thermal niche to drive local population dynamics. We tested for such interactions during the nestling stage, the fledgling stage, and the warmest seasonal period in North America. We found a strong signal that temperature affects avian communities, but only during the warmest seasonal period. In contrast to recent evidence that temperature during reproductive periods shape avian geographic ranges, these results suggest that late-summer temperatures are particularly important drivers of the population changes which are precursors to climate-induced range shifts.

## **Session 3B, Conference Room B: Animal Science and Internal Medicine**

### **Vps34 Up-regulation Promotes Smooth Muscle Cell Proliferation and Survival in Pulmonary Arterial Hypertension**

Yuanjun Shen<sup>1</sup>, Dmitry Goncharov<sup>1</sup>, Lifeng Jiang<sup>1</sup>, Derek Lin<sup>1</sup>, Theodore Avolio<sup>2</sup>, Evelyn Okorie<sup>2</sup>, Ana L Mora<sup>3</sup>, Aisha Saiyed<sup>1</sup>, Tatiana Kudryashova<sup>1</sup> and Elena Goncharova<sup>1</sup>

<sup>1</sup>Division of Pulmonary, Critical Care and Sleep Medicine, Department of Internal Medicine, <sup>2</sup>Heart, Lung, Blood and Vascular Medicine Institute, University of Pittsburgh School of Medicine, Pittsburgh, PA, <sup>3</sup>Division of Pulmonary, Critical Care and Sleep Medicine, The Ohio State University College of Medicine, Columbus, OH.

Increased proliferation and survival of resident cells in small pulmonary arteries (PA) are important drivers of PA remodeling and pulmonary arterial hypertension (PAH). Class III phosphatidylinositol 3-kinase (PI3K) vacuolar protein sorting 34 (Vps34), a member of PI3K/Akt/mTOR network, promotes cell hyper-proliferation in cancer, but its role in PAH is unknown. We report that inhibitory phosphorylation of Vps34 at Ser164 (P-Ser164-Vps34) is significantly decreased in smooth muscle layer of small remodeled PAs and early-passage PA vascular smooth muscle cells (PAVSMC) from PAH patients compared to non-diseased controls. This is associated with Akt/mTOR activation, TSC2 deficiency, Vps15 and p62 overaccumulation, increased PAVSMC growth and proliferation. Reduced P-Ser164-Vps34 was also detected in smooth muscle layer of small PAs of mice and rats with experimentally induced PH and was associated with increased PA medial thickness, systolic right ventricular pressure, and right ventricular hypertrophy. siRNA-induced depletion of Vps34 increased TSC2 and decreased Vps15 and p62 in PAH PAVSMC. Pharmacological inhibition of Vps34 by SAR405 and VPS34-IN1 or restoration of P-Ser164-Vps34 by Akt Inhibitor VIII significantly decreased proliferation and induced apoptosis of PAH PAVSMC. In conclusion, Vps34 supports PAH PAVSMC proliferation and survival, and Vps34 inhibition could be considered as potential anti-proliferative approach to treat PAH.

# Oral Abstracts

## **Monkey visual attention does not fall into the uncanny valley**

Sarah B. Carp<sup>1</sup>, Anthony C. Santistevan<sup>1,2</sup>, Christopher J. Machado<sup>1,3</sup>, Alexander M. Whitaker<sup>1</sup>, Brittany L. Aguilar<sup>1</sup> and Eliza Bliss-Moreau<sup>1,2</sup>

*<sup>1</sup>California National Primate Research Center, <sup>2</sup>Department of Psychology, <sup>3</sup>Department of Psychiatry and Behavioral Sciences*

Very humanlike artificial agents can induce feelings of uneasiness in human perceivers. Stimuli that generate this response are said to occupy “the uncanny valley”. There are inconsistent findings in the literature regarding whether nonhuman animals experience the uncanny valley. Therefore, there remain open questions about the evolution of the uncanny valley and degree to which nonhuman primates perceive manipulations to stimuli, like faces, used in experiments. We recorded visual attention of eleven rhesus monkeys as they viewed faces varying in realness of the image and behavior depicted by the face (e.g., lipsmack, threat, bared teeth and neutral, varying affective content). We largely found no support that rhesus monkeys perceive an uncanny valley; however, monkeys alter increase attention to specific areas of the face based on realism. Across all stimuli, monkeys’ attention was drawn to the mouths of images when teeth were visible. Overall, these findings suggest that rhesus monkeys are not sensitive to the uncanny valley effect, but do incorporate affective information in their visual attention to faces regardless of how real those faces appear to be. These findings are important because they provide support for the idea that computer generated images may be useful tools for future experimental paradigms.

## **Early-life Exposure to Wildfire Smoke Results in Dysregulated Pulmonary Immune Responses in Rhesus Macaques**

D.J. You, J. Bassein, A. Rindy and L. Miller

*California National Primate Center*

Wildfires are a public health concern due to the increased frequency of events and generation of particulate matters. The long-term health consequences of wildfire smoke exposure on susceptible human populations are unknown. We have previously reported that rhesus macaque monkeys exposed to ambient wildfire smoke during infancy exhibited decreased lung function and dysregulated innate immune responses in adulthood. The objective of this current study is to investigate whether perturbations of the pulmonary mucosal immune system are detectable in juvenile monkeys following exposure to ambient wildfire smoke during infancy. Lung tissues were collected from two different cohorts of male monkeys that were infants and housed outdoors during the 2018 and 2020 wildfire season in Northern California. Lung tissues collected from age-matched male monkeys from Oregon National Primate Research Center served as controls. Significant decrease in the expressions of genes regulating immune responses were found in both cohorts of wildfire-exposed monkeys compared to the controls. Our results demonstrate that wildfire smoke exposure results in suppression of pulmonary immunity and altered lung development in young rhesus monkeys. This study suggests wildfire smoke exposure in pediatric populations may impair lung development and immune responses, resulting in long-term deleterious effects on the respiratory system.

# Oral Abstracts

## Session 3C, Ballroom A: *Clinical Medicine*

### **Family involvement during older adults' acute hospitalization: Families', patients' and nurses' perceptions**

Orly Tonkikh<sup>1</sup>, Elena Siegel<sup>1</sup>, Ksenya Shulyaev<sup>2</sup>, Amos Rogozinsky<sup>2</sup> and Nurit Gur-Yaish<sup>3</sup>

<sup>1</sup>Betty Irene Moore School of Nursing, <sup>2</sup>The Cheryl Spencer Department of Nursing, University of Haifa, Israel, <sup>3</sup>Oranim College of Education, Israel

Preserving functional and emotional status during acute hospitalization is widely acknowledged as producing better outcomes for older adults. This qualitative descriptive study explored patients', family members' and nurses' perspectives on family involvement in preserving function and emotional support during hospitalization for older adults. Current findings reflect analysis of a subsample of 33 semi-structured phone/Zoom interviews with registered nurses (n=11) and 11 dyads of hospitalized older adults and family members who accompanied them during the hospitalization (n=22). The interviews were conducted in English, Russian or Hebrew, according to the interviewee's preferences. Thematic analysis was used to inductively capture key patterns in data and three key themes emerged. First, patients, family and nurses consider the main role of family as providing emotional support. Second, perceptions regarding the involvement of family in activities of daily living vary. For example, while patients and family members perceive family's involvement as facilitating nurses' work, some nurses spoke about family members as additional patients. Third, nurses commonly rely on their "intuition" to determine a caregiver's preferences and capabilities. The findings provide direction for further exploration of structures and processes needed to support optimal involvement of families accompanying older adults during hospitalization.

### **Inter-joint coordination pattern and variability reveal distinct gait instability in stroke survivors**

Sherveen Riazati<sup>1</sup>, Theresa McGuirk<sup>1,3</sup>, Caitlin L. Banks<sup>1-3</sup> and Carolyn Patten<sup>1-3</sup>

<sup>1</sup>Biomechanics, Rehabilitation, and Integrative Neuroscience (BRaIN) Lab, <sup>2</sup>UC Davis School of Medicine, UC Davis Center for Neuroengineering and Medicine, <sup>3</sup>VA Northern California Health Care System

Understanding the basis of disordered gait following stroke is a challenge. Human walking involves simultaneous coordination of multiple joints in multiple planes of motion. To provide a holistic analysis, we examined the inter-joint coordination pattern (IJCP) and IJCP variability, a signal of instability, of lower extremity joint couplings during gait in stroke survivors compared to healthy individuals. We studied 16 chronic stroke survivors and 8 healthy individuals while walking at their self-selected speed and examined lower-extremity IJCP couplings in sagittal and frontal planes using: Continuous Relative Phase (CRP), Coupling Angle through modified vector coding (CA), and cycle-to-cycle variability ( $C_{var}$ ). Our results reveal discoordination in stroke survivors compared to healthy. CRP revealed differences in mean Knee<sub>sagittal</sub>-Ankle<sub>sagittal</sub> coupling ( $p=0.015$ ) while CA, exhibited a significant overall difference between groups for Hip<sub>frontal</sub>-Knee<sub>sagittal</sub> coupling ( $p=0.041$ ). Stroke survivors also exhibited higher  $C_{var}$  ( $p<0.05$ ), further emphasizing overall gait instability. Discoordination was most prominent at phase transitions within the gait cycle, the most notable distinction occurring at the stance-to-swing transition. Our current analysis of IJCPs identified discoordination behavior within distinct regions of the gait cycle where stroke survivors exhibit instability suggestive of global dysfunction in motor pattern selection or switching.

# Rapid Talks and Poster Abstracts

Poster Session, Combined Ballrooms B + C

2:25 – 3:25 pm

Rapid Talks Session

4:25 – 5:25 pm

Session 4A, Conference Room A: *Agriculture*

## AI-enabled biosensing for rapid identification of pathogens in food and agricultural water

Jiyeon Yi<sup>1,2</sup>, Nicharee Wisuthiphaet<sup>2,3</sup>, Pranav Raja<sup>1,2</sup>, Nitin Nitin<sup>1,2,3</sup> and Mason Earles<sup>1,2,4</sup>

<sup>1</sup>Dept. of Biological & Agricultural Engineering, <sup>2</sup>AI Institute for Next Generation Food Systems (AIFS),

<sup>3</sup>Dept. of Food Science & Technology, <sup>4</sup>Dept. of Viticulture & Enology

Food and agriculture processes are water-intensive, and thus managing microbial water quality is essential for food safety and security. However, timely detection of pathogens is interfered by complex food and environmental matrices. Here, we present an AI-biosensor platform for rapid pathogen identification in food and agricultural water. T7 phage was used to induce *Escherichia coli*-specific cell lysis and generate DNA release patterns detected by an AI model. The model was trained with Faster R-CNN on augmented datasets using *E. coli* monoculture and selected non-*E. coli* bacteria, followed by fine-tuning on a mixed bacterial culture. The model inference was performed on *E. coli* in unseen realistic water samples with a gradient of food and environmental background noise. The results show that our AI-biosensor platform could precisely detect and quantify lysed *E. coli* within 4.5 h (<a single work shift in food production). The model trained on a laboratory-controlled bacterial culture achieved 92–98% accuracy, 76–98% sensitivity, and 83–100% specificity in unseen realistic water samples, depending on the type of background noise (food debris, organic matter, natural microbiota). Overall, this study demonstrates the potential of our AI-biosensor platform to automate and accelerate the monitoring of food and agricultural water.

## Examining the Role of Community and Citizen Science in California's Marine Protected Areas

Harwell, TA <sup>1</sup>, Meyer, RM<sup>1</sup>, Korabik, A<sup>2</sup>, Peterson, N<sup>3</sup> and Ballard, H<sup>1</sup>

<sup>1</sup>Center for Community and Citizen Science, <sup>2</sup>Graduate Group in Ecology, <sup>3</sup>College of Agricultural and Environmental Sciences

Community and citizen science (CCS), which broadly refers to the wide range of ways that nonscientists participate in science processes, has played a prominent role in marine protected area (MPA) implementation and monitoring in the State of California for more than a decade. Led by a team of researchers at the Center for Community and Citizen Science at the University of California, Davis, this presentation highlights the breadth and depth of how CCS efforts have contributed to MPA program priorities and goals along with focusing on participant contributions and outcomes. We will highlight key findings related to the CCS efforts of 10 MPA monitoring projects/programs that received Baseline and/or Long-Term Monitoring funding as part of California's MPA Monitoring Program based on data obtained from program/project managers via publications, reports, databases, and/or responses to questions posed during in-depth conversations with our project team from Spring to Fall 2021. Additionally, we will present a wider view of CCS activities along the California coast by sharing the results of a brief survey that was shared with contacts from over 60 coastal/marine CCS projects and programs identified by various contacts, networks, and results of a broad Internet search in Fall 2021.



# Rapid Talks and Poster Abstracts

## **Structural insights into photoactivation of plant Cryptochrome-2**

Malathy Palayam and Nitzan Shabek

*Department of Plant Biology*

Cryptochromes (CRYs) are evolutionarily conserved photoreceptors that mediate various light-induced responses in bacteria, plants, and animals. Plant cryptochromes govern a variety of critical growth and developmental processes including seed germination, flowering time and entrainment of the circadian clock. CRY's photocycle involves reduction of their flavin adenine dinucleotide (FAD)-bound chromophore, which is completely oxidized in the dark and semi to fully reduced in the light signaling-active state. Despite the progress in characterizing cryptochromes, important aspects of their photochemistry, regulation, and light-induced structural changes remain to be addressed. In this study, we determine the crystal structure of the photosensory domain of Arabidopsis CRY2 in a tetrameric active state. Systematic structure-based analyses of photoactivated and inactive plant CRYs elucidate distinct structural elements and critical residues that dynamically partake in photo-induced oligomerization. Our study offers an updated model of CRYs photoactivation mechanism as well as the mode of its regulation by interacting proteins.

## **Characterization of the organic acids profile on Pinot noir wines from fifteen different vineyards**

Maisa M. M. Lima<sup>1</sup>, Ying Yng Choy<sup>1</sup>, Jandy Tran<sup>2</sup>, Mason Lydon<sup>2</sup> and Ron C. Runnebaum<sup>1,2</sup>

*<sup>1</sup>Department of Viticulture & Enology, <sup>2</sup>Department of Chemical Engineering*

Organic acids influence several wine aspects such as chemical and microbiological stability, appearance, and sensorial properties. The main source of organic acids in wines are grapes and the winemaking process. Among several organic acids, the most present in wines are tartaric and malic acid, with citric acid present in minor proportions. Succinic, lactic, and acetic acids are other existing organic acids, products from the winemaking process. Fifteen different Pinot noir wines from Oregon to southern California were evaluated by organic acids profile by High-Pressure Liquid Chromatography. The grapes were grown from vineyard sites along the Pacific Coast of the United States. In order to standardize the winemaking process, the grapes were processed, and the wines were made at a single location at UC Davis Teaching & Research Winery. Principal component analysis showed correlations with tartaric and malic acids in RRV1, RRV2, RRV3, SNC1, and SNC2 vineyards. While SMV1, SMV2, and CRN1 vineyards were associated with lactic acid. SCN1, OR1 and AV2 vineyards were associated with concentrations of malic, citric and succinic acids. Differences in organic acids profile within an AVA suggest that factors such as unique soil composition or conditions, or microclimate may have an effect.

# Rapid Talks and Poster Abstracts

## Effects of ash aging to the chemical quality of wine

Juliano Toniato, Ignacio Perez, Yan Wen, Bruna Paviani and Anita Oberholster

*Department of Viticulture & Enology*

The incidence of wildfires in grape growing regions of California and the West Coast has highlighted the need for enhanced understanding of the levels of volatile phenols originated from ashes that contribute to the off-flavors associated with smoke taint in grapes and wines. For this study, we want to evaluate the impact of ash with different ages in the phenolic content of wine. Pinewood and hickory were completely burned into ashes and sieved using a 300mesh cheese cloth, phenolic profile of these ashes were obtained using SPME-GC/MS and stored under room conditions. These fine ashes were added to grape must and winemaking followed the standard protocol. It was tested ashes with different ashes (fresh, 1, 3 and 7 days). Wines were analyzed using GC-MS-MS for 4-methylguaiacol, 4-ethylguaiacol, 4-ethylphenol, guaiacol, syringol and o, m, and p-cresol. Ash was also added to model wine to rule out and explain the effect of different matrixes. Preliminary results points that under lab conditions, pinewood produced quantifiable amounts of phenolics that can greatly influence the level of phenolic in wines and that ash age is inversely proportional to the phenolics in wine.

## Session 4B, Conference Room B: *Biomedical Science*

### Trace amounts of antibiotic is detrimental to the health of weaned pigs

Kwangwook Kim and Yanhong Liu

*Department of Animal Science*

Although the administration of antibiotics in farm animals is now restricted for growth promoting purposes, trace amounts of antibiotics may still persist in the environment. Growing evidence demonstrated that exposure to trace amounts of antibiotics might delay the growth and development of young animals and slow down the recovery from diseases. The objective of this experiment was to investigate the potential detrimental effects of trace amounts of antibiotic on weanling pigs' growth performance, systemic immunity, and intestinal health using a disease (enterotoxigenic *Escherichia coli* F18) challenge model. Weaned pigs were randomly allotted to one of the three dietary treatments: 1) control (basal) diet; 2) addition of trace amounts of antibiotic (TRA); or 3) typical therapeutic dose of antibiotic (REC) to the control. Pigs fed the control and TRA had a higher frequency of diarrhea and lower final body weight. Average daily gain and feed efficiency were lowest, whereas serum inflammatory markers were higher in the TRA. Evaluation of fecal samples and intestinal tissue indicated that pigs fed TRA also had increased markers for inflammation. In conclusion, deterioration of disease was likely due to the increased severity of systemic inflammation of pigs in the trace amounts of the antibiotic group.

# Rapid Talks and Poster Abstracts

## **Akt-dependent glycolysis-driven lipogenesis supports proliferation and survival of human pulmonary arterial smooth muscle cells in pulmonary hypertension**

Lifeng Jiang<sup>1</sup>, Dmitry Goncharov<sup>1</sup>, Yuanjun Shen<sup>1</sup>, Derek Lin<sup>1</sup>, Baojun Chang<sup>2</sup>, Andressa Pena<sup>2</sup>, Tatiana Kudryashova<sup>1</sup> and Elena Goncharova<sup>1</sup>

<sup>1</sup>Lung Center, Division of Pulmonary, Critical Care and Sleep Medicine, Department of Internal Medicine, <sup>2</sup>Pittsburgh Heart, Lung, and Blood Vascular Medicine Institute, Division of Pulmonary, Allergy and Critical Care Medicine, Department of Medicine, University of Pittsburgh, Pittsburgh, Pennsylvania.

Pulmonary arterial vascular smooth muscle cells (PAVSMC) proliferation is a key pathological component of pulmonary arterial hypertension (PAH). Lipogenesis is linked with proliferative diseases, including cancer, but its role in PAVSMC proliferation in PAH remains to be elucidated. Here we report that key fatty acids synthesis enzymes ATP-citrate lyase (ACLY), acetyl-CoA carboxylase (ACC) and fatty acid synthase (FASN) were significantly upregulated in early-passage human PAH PAVSMC compared to controls. Using immunocytochemical analysis (BODIPY), cell growth (cell counts) and proliferation (Ki67) assays, we found that accumulation of intracellular lipids and increased proliferation of PAH PAVSMC were preserved in lipid-free conditions but suppressed by non-metabolizable analog of glucose 2-Deoxy-D-glucose and partially restored by addition of pyruvate. 5-tetradecyloxy-2-furoic acid, an allosteric ACC inhibitor, significantly decreased proliferation and induced apoptosis of PAH PAVSMC. Akt was upregulated in human PAH PAVSMC, and Akt inhibitor VIII suppressed phosphorylation of ACLY, increased inhibitory phosphorylation of ACC, reduced proliferation and promoted apoptosis of PAH PAVSMC, suggesting that Akt supports increased cell proliferation and survival in PAH via promoting lipogenesis. In aggregate, our data indicate a link between glycolysis, lipogenesis and proliferation of human PAH PAVSMC and suggest Akt-lipogenesis axis as a potential target pathway for therapeutic intervention.

## **Chitosan Hydrogels Containing MK2 inhibitor peptide-Loaded Nanoparticles to Facilitate Percutaneous Absorption and Dampen Local Inflammation for Atopic Dermatitis Treatment**

Vanessa F.C. Dartora, Claire Hung, Michael Nguyen and Alyssa Panitch

*Biomedical Engineering Graduate Group*

Atopic dermatitis (AD) is a chronic inflammatory skin disorder with limited treatment options. Topical corticosteroids are the first-line treatment to control moderate-to-severe AD; however, their prolonged application can result in dermal atrophy. In this study, the MK2-inhibitor peptide YARA (YARAAARQARAKALNRQGLVAA) was encapsulated into pNIPAM nanoparticles (NP), which were incorporated into chitosan hydrogels to promote local drug delivery, improve moisture and suppress inflammation, while reducing adverse side effects. The NPs showed a mean diameter of  $361.5 \pm 4.6$  nm, negative  $\zeta$  potential (-28.3 mV), high loading efficiency (>50%) and no cytotoxic activity in human fibroblasts and keratinocytes, suggesting their safety for topical applications. Nanoparticles improved the release kinetics of YARA when compared to the nonencapsulated peptide (up to 120 h release). The NPs and hydrogels delivered 2 and 4-fold, respectively, more YARA into viable layers of porcine skin in vitro 12 h post-application than the nonencapsulated compound in intact and impaired barrier conditions. Furthermore, the NPs treatment decreased the levels of IL-1b, TNF-a, INF-a and IL-10 up to 9 times compared to non-treated human keratinocytes after the induction of inflammation. Our data suggest that YARA loaded nanoparticles incorporated into chitosan hydrogel is a promising formulation strategy for topical treatment of AD.

# Rapid Talks and Poster Abstracts

## **Real-Time Kinetic Biofeedback Facilitates Locomotor Learning to Increase Ankle Power During Gait**

David R Young, Theresa E McGuirk, Karen Shlesinger, Ryan L Hobbib, Wilsaan M Joiner and Carollynn Patten

*Physical Medicine and Rehabilitation*

Current gait rehabilitation methods produce inconsistent results and utilization of compensatory strategies rather than recovery of fundamental locomotor patterns. Motor learning principles are increasingly utilized in rehabilitation, however their salience and persistence for gait remains unclear. By providing feedback that reinforces desired behaviors, motor learning increases motivation and behavioral performance, and may induce dopamine-dependent neuroplasticity. Reduced ankle power (A2) is a fundamental cause of gait dysfunction and is commonly observed in stroke survivors. Until now, technical limitations prevented the real-time display of joint kinetics-based feedback. We explored a locomotor learning paradigm designed to target A2 to identify if individuals are capable of learning to increase their A2. Here, our goal was to determine whether real-time kinetic biofeedback facilitates locomotor adaptation through motor learning. Healthy, young participants performed three 15-minute bouts of walking with real-time kinetic biofeedback designed to reward increased ankle power. We observed improved performance in response to A2 biofeedback (Fig 1). Increased ankle power was retained following removal of feedback and after 24 hours. These preliminary results provide evidence that motor learning principles can be used to alter automatically controlled biomechanical mechanisms, such as ankle power production, and may be beneficial in gait rehabilitation for stroke survivors.

## **DDT and DDE attenuate beige differentiation and thermogenic function in adipocytes**

Shenq-Shayng Huang, Aman Singla, Victoria Huang, Chanapa M. Mann and Michele A. La Merrill

*Department of Environmental Toxicology*

Thermogenesis is regulated by adrenergic nerves, brown, and beige adipocytes. The pesticide dichlorodiphenyltrichloroethane (DDT), and its metabolite dichlorodiphenyldichloroethylene (DDE) are associated with the increased risk of type II diabetes and obesity, and reduce adrenergic nerves and body temperature. However, how DDT and DDE impair autonomous adipocyte thermogenesis is not well-understood. We hypothesize that DDT and DDE impair adrenergic function in differentiating beige adipocytes. While DDT and DDE enhanced *Creb1* and *Cebpa* adipogenic expression, DDT and DDE attenuated the expression of key beige and thermoregulatory genes regulated by  $\beta$ 3 adrenergic signaling, *Prdm16* and *Ucp1*, and decreased *Adrb3* expression. Notably, the expression of *Adrb3* negative regulators *Nfat5* and *Dnmt1* were increased upon DDT and DDE treatment. These findings suggest that DDT and DDE impair the thermogenic programming of beige adipocytes directly via NFAT5 and DNMT1 negatively control of the expression of *Adrb3* and consequently *Prdm16* and *Ucp1*. These effects of DDT and DDE on mouse beige adipocytes are independent of their effects on the sympathetic nervous system reported previously in whole mouse studies.

# Poster Abstracts

Poster Session, Combined Ballrooms B + C

2:25 – 3:25 pm

## **Untangling hormone-ErbB receptors interactions in the porcine mammary gland, to explain the complexity of breast morphogenesis.**

Alessia Morato<sup>1</sup>, Josephine F. Trott<sup>1</sup>, Paolo Accornero<sup>2</sup> and Russell C. Hovey<sup>1</sup>

<sup>1</sup>*Department of Animal Science,* <sup>2</sup>*Department of Veterinary Sciences, University of Torino, Italy*

The mammary gland develops after puberty under the effect of reproductive hormones, ultimately becoming a lactating organ. The ErbB family of receptors are common mutants in breast cancers, but also effectors of hormones, in the developing gland. While ErbB1 and its binding factor AREG mediate Estrogen in pubescent mice, the role ErbB role in other species is undefined. Using the porcine mammary gland as reliable model for the human breast, we hypothesized that different ErbB receptors and binding factors contribute to mammary development, downstream of Estrogen. After isolating the mammary epithelium from the stroma, we found high gene expression of many ErbB and binding factors, predominantly in the epithelium. These were mostly induced by Estrogen, in ovariectomized and hormone-treated pigs. Prolactin contributed to regulate factors, that are known to induce later stages of development in mice. High levels of two ErbB-binding factors, not induced by Estrogen, were detected in the fat. Therefore, a diversity of E-effectors, the interaction with Prolactin, and a hormone-independent interplay between fat and parenchyma, might account for a higher level of complexity in the mammary glands of pigs. Untangling ErbB-pathways in the porcine mammary can help to understand endocrine mechanisms in breast cancer.

## **Enhancers of cancer driver genes are enriched in somatic non-coding driver mutation candidates**

Marketa Tomkova, Julie Chow, David Segal and Fereydoun Hormozdiari

*Department of Biochemistry and Molecular Medicine*

Identifying which mutations drive cancer has been of great interest for the last decades. While the coding drivers have been explored extensively, only a rather small number of non-coding driver mutations have been well characterized so far. We hypothesized that non-coding cancer driver mutations are enriched in enhancers and promoters of known cancer driver genes. We tested the hypothesis using over 2,200 whole-genome sequencing (WGS) samples from the Pan-Cancer Analysis of Whole Genomes (PCAWG) dataset and 10 tissue-matched enhancer-gene maps produced by the activity-by-contact (ABC) model. Given the likely large number of passenger non-coding mutations, we focused on mutations with high Combined Annotation Dependent Depletion (CADD) score of pathogenicity. We defined the regulatory space (enhancers and promoter) of a given gene to be a non-coding cancer driver candidate when it is (1) more mutated than expected and (2) predicts expression of the gene that they regulate. We observed a significant enrichment of cancer driver genes in the non-coding regulatory driver candidates across multiple cancer types and pan-cancer. This enrichment correlates with a CADD score cutoff and is strongest when the tissue-matched enhancer-gene maps are used. In conclusion, our results demonstrate how non-coding somatic mutations may contribute to cancer.

# Poster Abstracts

## Mitochondrial ROS-induced stress is a therapeutic target for Rett syndrome

Jacopo di Lucente<sup>1</sup>, Kamil Borkowski<sup>2</sup>, John Newman<sup>2</sup>, Heike Wulff<sup>3</sup>, Gino Cortopassi<sup>4</sup>, Lee-Way Jin<sup>1</sup> and Izumi Maezawa<sup>1</sup>

<sup>1</sup>Department of Pathology and Laboratory Medicine and M.I.N.D. Institute, <sup>2</sup>West Coast Metabolomics Center, <sup>3</sup>Department of Pharmacology, <sup>4</sup>Department of Molecular Biosciences

Rett syndrome (RTT), a devastating neurodevelopmental disorder, is largely caused by loss-of-function mutations in the X-linked gene encoding MeCP2. We hypothesize that MeCP2 controls coordinated expression of bioenergetic genes as part of the recently recognized "mitonuclear signaling pathways" to maintain mitochondrial integrity. We found enhanced mtROS level, and several mitochondrial dysfunctions in the brain of *Mecp2<sup>tm1.1Bird/+</sup>* (*Mecp2-KO*) model of RTT. To test the translational significance of mtROS, we employed the "mCAT" approach, in which catalase, usually not expressed in mitochondria, was engineered to target mitochondria to decompose overproduced H<sub>2</sub>O<sub>2</sub>. mCAT expression extended the lifespan of *Mecp2-KO* mice, and recovered multiple phenotypic parameters, neuronal plasticity, and mitochondrial function to almost wild-type levels. To translate our findings to clinical utility, we screened a library of 1,600 FDA-approved drugs based on their "mitoactive" properties and identified dyclonine as the most promising candidate. Daily intraperitoneal injection of dyclonine at 10mg/kg to *Mecp2-KO* mice showed a therapeutic efficacy parallel to mCAT expression. Together, our data provide proof-of-principle that mtROS-induced mitochondria stress is a therapeutic target and that the FDA-approved drugs able to enhance MSR such as dyclonine are promising clinical candidates for RTT.

## Infinite Complexity: On the Divergence of Predictive State Sets for Hidden Markov Processes

Alex M. Jurgens and James P. Crutchfield

*Department of Physics*

Even simply-defined, finite-state generators produce stochastic processes that require tracking an uncountable infinity of probabilistic features for optimal prediction. For processes generated by hidden Markov chains the consequences are dramatic. Their predictive models are generically infinite-state. And, until recently, one could determine neither their intrinsic randomness nor structural complexity. The prequel to this work introduced methods to accurately calculate the Shannon entropy rate (randomness) and to constructively determine their minimal (though, infinite) set of predictive features. Leveraging this, we address the complementary challenge of determining how structured hidden Markov processes are by calculating their statistical complexity dimension---the information dimension of the minimal set of predictive features. This tracks the divergence rate of the minimal memory resources required to optimally predict a broad class of truly complex processes.

# Poster Abstracts

## **Factors Associated with Habitual Sleep Duration in US Adults with Hypertension: A Cross-sectional Study of the 2015-2018 National Health And Nutrition Examination Survey**

Everlyne G. Ogugu<sup>1</sup>, Sheryl L. Catz<sup>1</sup>, Janice F. Bell<sup>1</sup>, Christiana Drake<sup>2</sup>, Julie T. Bidwell<sup>1</sup> and James E. Gangwisch<sup>3</sup>

*<sup>1</sup>Betty Irene Moore School of Nursing, <sup>2</sup>Department of Statistics, <sup>3</sup>Department of Psychiatry, Columbia University*

**Background:** This study examined factors associated with habitual sleep duration among adults with hypertension in the United States. **Methods:** Data of 5,660 adults with hypertension were obtained by combining the 2015 – 2018 cycles of the National Health and Nutrition Examination Survey (NHANES). Multinomial logistic regression models were fit to examine factors associated with short (<7 hours) and long (>9 hours) sleep duration with adequate sleep duration (7 – 9 hours) as the reference. **Results:** Short sleep duration (compared to adequate sleep duration) was positively associated with history of seeking help for sleeping difficulties, Non-Hispanic Black race/ethnicity, working  $\geq 45$  hours/week, and negatively associated with older age  $\geq 65$  years and female gender. Long sleep duration was positively associated with female gender, chronic kidney disease, moderate depressive symptoms, moderately severe to severe depressive symptoms, being in retirement, and not working due to health reasons or other reasons. **Conclusion:** These findings can help in the development of tailored approaches for promoting adequate sleep duration in adults with hypertension.

## **Predicting environmental and ecological drivers of human population structure**

Evlyn Pless, Anders Eckburg and Brenna Henn

*Department of Anthropology*

Landscape, climate, and culture can all structure human populations, but few methods are designed to disentangle the importance of these many variables. We present a machine learning method for identifying the variables which best explain migration rates, as measured by a coalescent-based program which uses shared identical-by-descent tracts. We apply our method to 30 human populations in eastern Africa with high density SNP array data. The unparalleled diversity of ethnicities, languages, and environments in this region offers a unique opportunity to explore the variables that shape population structure in humans. We explored more than twenty spatial variables relating to landscape, climate, language, and presence of disease vectors. The full model explains ~40% of variance in migration rate – precipitation, minimum temperature of the coldest month, and altitude were found to be the most important variables. We also performed a selection scan on five populations who live in Ethiopia at relatively high altitudes. We did not identify well-known high-altitude genes, but we did find signatures of positive selection related to metabolism and disease. We conclude that environment and landscape shaped the migration and adaptation of human populations in east Africa, but cultural factors not captured in the model likely contributed as well.

# Poster Abstracts

## Enhancing Diagnostics Capacity for Fruit Flies project results

S.V. Korneyev, M. Hauser and S.D. Gaimari

*Department of Entomology and Nematology*

The family Tephritidae or the “true fruit flies”, has nearly 5,000 described species categorized in almost 500 genera in the world fauna. Many Tephritidae species are considered among the most destructive pests as they infest hundreds of different plant species. The goal of Enhancing Diagnostics Capacity for Fruit Flies project is to develop a better picture of tephritid diversity from tropical areas. Fresh collections of materials with known origins are critical to develop tools for rapid identification of intercepted and detected specimens before establishment in the USA, to aid mitigation and eradication efforts to protect US agriculture. From September 2020 till December 2021 approximately 7,700 specimens from Southeast Asia and Africa were identified, mostly from the genera *Bactrocera*, *Zeugodacus*, *Dacus*, *Ceratitis*. Additionally, approximately 6000 specimens of Tephritoidea collected elsewhere, were identified for California State Collection of Arthropods and Bohart museum of Entomology. During this project we have added numerous COI sequences for identified fruit flies. Altogether currently uploaded more than 2200 sequences from 1500 specimens of more than 150 different species. Most of the species were sequenced for the first time and uploaded to a public database known as the Barcode of Life Data System (BOLD).

## Analysis of the offspring of a SRY Knock-in bull produced by embryo-mediated genome editing

Alba V. Ledesma<sup>1</sup>, Thomas F. Bishop<sup>1</sup>, Maci L. Mueller<sup>1</sup>, Joseph R. Owen<sup>2</sup>, Sadie L. Hennig<sup>1</sup>, Bret R. McNabb<sup>3</sup> and Alison L. Van Eenennaam<sup>1</sup>

*<sup>1</sup>Department of Animal Science, <sup>2</sup>University of California San Diego, <sup>3</sup>School of Veterinary Medicine*

In eutherian mammals, the sex-determining region of the Y chromosome (SRY) expresses a protein in early embryogenesis that initiates male sexual differentiation by triggering a cascade of factors necessary for testis development, shutting down the formation of the female gonad. A targeted knock-in of SRY into the safe-harbor H11 locus of chromosome 17 was accomplished using CRISPR-Cas9 genome editing in bovine zygotes. PCR and Sanger sequencing of the resulting bull revealed the biallelic edit of the target location on chromosome 17, resulting in a compound heterozygote with a complex 38 kb knock-in allele with seven concatenated copies of the SRY:GFP template, a single copy of the donor plasmid backbone on one chromosome, and a 26 base pair random insertion on the other, with a XY genotype. Additionally, a subpopulation of cells appeared to carry a smaller (17kb) deletion derivative of the complex 38 kb knock-in allele featuring three copies of the SRY:GFP template, alongside the single copy of the donor plasmid backbone. Blastocysts produced with sperm collected from the bull were individually biopsied to determine the presence or absence of the SRY:GFP template, and the chromosomal sex. Three XX blastocysts that also tested positive for SRY:GFP by PCR were transferred to recipient cows and one pregnancy resulted. Ultrasound analysis at 70 days gestation revealed a female phenotype. The fetus was collected at 90 days and PCR analysis revealed the inheritance of the 38 kb knock-in allele. This allele included a head-to-head inverted repeat configuration of the SRY:GFP template, and we hypothesized that this might have resulted in gene silencing. To test this hypothesis we developed primers that could differentiate between the 38 kb knock-in allele, the 17kb allele that had only head to tail configuration direct repeats of SRY:GFP, and the allele with the small 26 base pair insertion. Blastocysts produced using semen from the bull were phenotyped for GFP expression, and then screened by PCR to determine which of the three alleles they inherited to determine if gene silencing was occurring in any of the blastocysts that inherited the SRY:GFP template, and if this differed between the 38 kb and 17kb knock-in alleles.



# Poster Abstracts

## **Evaluating nitrogen leaching in processing tomatoes for enhanced productivity and groundwater protection**

Iael Raij-Hoffman<sup>1</sup>, William Lennon<sup>1</sup>, Thomas Harter<sup>1</sup> and Isaya Kisekka<sup>1,2</sup>

<sup>1</sup>*Department of Land, Air, and Water Resources,* <sup>2</sup>*Department of Biological and Agricultural Engineering*

Innovative monitoring techniques are needed to assess the effect of irrigation and nitrogen management practices on agricultural nitrate leaching to groundwater. The objective of this study was to measure production and environmental outcomes of a processing tomato cropping system by developing and evaluating monitoring protocols based on deep vadose-zone and groundwater monitoring, and nitrogen balance assessments at the field scale. A monitoring site was established in Yolo County, CA composed of a 34 ha field cropped in a triticale - processing tomato rotation. Historic water and nitrogen mass balances were performed using grower information, remote sensing, meteorological data and nitrogen uptake coefficients. From November 2019, water and nitrogen inputs and outputs have been continuously measured and field level water and nitrogen mass balances performed. In addition, an intensive network of shallow and deep vadose zone as well as groundwater monitoring instruments were installed in the 2020-2021 season and nitrogen movement was monitored from the root zone to the groundwater. In this study, we present a comparison of monitoring approaches for the assessment of nitrogen leaching from irrigated agriculture.

## **Vitamin E and selenium levels of wild donkeys and their diets**

Sara Jerele

*Department of Veterinary Surgery and Radiology*

There is little knowledge on the diet and blood parameters of wild donkeys in the southwest, which limits our capacity to assess their competition dynamics with other species and their health status. We first focused on the study of Vitamin E and selenium from wild donkeys (*Equus asinus*) in Death Valley National Park (DVNC, California). We withdrew blood from sixty-five individuals during October, November, and December of 2020: 20, 37, 6, and 2 samples from females, males, female foals, and male foals, respectively. Median values for serum vitamin E was 461 µg/dL and 474 µg/dL, for adult males and adult females, respectively. Later, we analyzed the diet of the same herds through fecal collection. Our data showed wild donkeys predominantly act as browsers, which might affect their vitamin E levels. This is the first time this kind of data is collected on wild donkeys from the southwest. Outcomes are two-fold: First, it allows to see their vitamin E and selenium levels with possible correlations in diet. Second, it brings information on the dietary choices and health status of wild donkeys and helps with improving the picture of their interaction with the environment they live in.

# Poster Abstracts

## **Weed biomass and forage yield responses to integration of short-term grazing in organic fields**

Oren Hoffman<sup>1</sup>, Nicole Tautges<sup>2</sup> and Kate Scow<sup>1</sup>

<sup>1</sup>*Microbial Ecology Lab, Land Air & Water Resources,* <sup>2</sup>*Micheal Fields Agricultural Institute, East Troy, WI*

Weed control is a problem in organic fields, with possible significant yield loss. Management choices during transition to organic could drive weed community dynamics in ways that affect yields during the transition and into certified organic production. I compared weed cover and biomass responses to management in a field transitioning into organic production. Annual forage crops were compared to alfalfa, with split-plots for sheep grazing during late winter. I measured weed and crop biomass in samples, and cover in transects. Linear models were used to relate weed pressure to yield at sample and plot scales. First-year alfalfa yield was very sensitive to weed pressure, reaching up to 40% yield reduction, driven by two annual weed species. Grazing had no significant effect on abundance, but results suggest some preferential removal of weed biomass in 2nd-year alfalfa. Alfalfa showed lingering effects of 1st-year weed pressure, but later yields were comparable to conventional plots, and weed cover was reduced. Annual cover crops effectively controlled both winter and summer weeds. Growing a perennial crop during the transition period can offer several economic and environmental advantages. However, special attention is needed for weed control during establishment. Sheep grazing could provide this service when strategically employed.

## **Are there host-specific mechanisms that promote *Ralstonia* fitness inside diverse plant hosts?**

Nathalie Aoun, Stratton Georgoulis, Jonathan Beutler and Tiffany-Lowe Power

*Department of Plant Pathology*

*Ralstonia* spp. are one of the most devastating phytopathogens in the world causing severe crop yield losses. Breeding for resistance is the only efficient mean of disease control. However, pathogen virulence evolves constantly, resulting in host switching or expanding, and the loss of crop resistance. Understanding the mechanisms of pathogen virulence and fitness is crucial for developing disease management strategies. Studies have explored the virulence mechanisms of *Ralstonia* but few of them have assessed bacterial fitness inside more than one or two plant hosts. To explore bacterial mechanisms promoting fitness inside the host, we are using a powerful functional genomics approach called random barcoded transposon mutant sequencing (RB-TnSeq). This approach can quantify the fitness of thousands of mutants during their competitive growth in complex naturalistic environments. Using RB-TnSeq on the *Ralstonia*-tomato model system, we expect to unravel diverse bacterial mechanisms enhancing infection in tomato cultivars that impose varying levels of immune pressure. We have also applied this approach across different plant species (i.e., melon and impatiens) and by comparing the RB-TnSeq data we will be able to reveal the presence of common and/or unique mechanisms employed by bacteria across plant species. Findings from this project will deepen our understanding of bacterial behavior under the pressure of the plant immune system.

# Program Outline

8:00 – 8:50 am	Registration, Breakfast, and Poster set up	Triangle Room and Lobby
9:00 – 9:20 am	Opening Remarks by PSA and Associate Deans	Ballroom A
9:25 – 10:25 am	Parallel Oral Session 1	Conference Rooms A and B, Ballroom A
10:30 – 10:45 am	Coffee Break	Ballrooms B + C
10:50 – 11:50 am	Parallel Oral Session 2	Conference Rooms A and B, Ballroom A
12:00 – 12:30 pm	Plenary Speech 1: Dr Prasant Mohapatra	Ballroom A
12:35 – 1:20 pm	Lunch	Conference Center Lobby and Patio
1:30 – 2:20 pm	Parallel Oral Session 3	Conference Rooms A and B, Ballroom A
2:25 – 3:25 pm	Poster Session	Ballrooms B + C
3:30 – 3:40 pm	Coffee Break	Ballrooms B + C
3:45 – 4:15 pm	Plenary Speech 2: Dr Pamela Ronald, Panel Discussion	Ballroom A
4:25 – 5:25 pm	Rapid Talks Session	Conference Rooms A and B
5:30 – 7:00 pm	Award Ceremony and Dinner	Ballrooms A + B + C