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A message from the 2023-2024 PSA Board

The 2023-24 PSA Board would like to express our heartfelt gratitude for your attendance and active participation in the 9th annual UC Davis Postdoctoral Research Symposium. Your support and participation are not just crucial, but they are the very essence of this event. We hope this event inspired you to further engage with the postdoc community at UC Davis. We deeply value and encourage postdoc fellow engagements in additional social events organized by UC Davis Graduate studies such as monthly Postdoc Meet & Greet gatherings and the annual Postdoctoral Appreciation Dinner, both organized by Graduate Studies. We are truly pleased to see such a vibrant participation at different events, ranging from our monthly writing retreats that facilitate your project advancement in a timely manner to our evening socials where postdocs can engage in a relaxed environment, having fun and enjoying life.

We are deeply humbled by the generous financial support from various UC Davis schools and colleges. Your support is what allows us to organize this conference for the UC Davis postdoc community without a cover charge, making it accessible and equitable for all postdocs, not just those with sufficient income. We would also like to thank UC Davis Library and UC Davis Transportation services for their kind support and contributions, which have been instrumental in this event's success.

We are taking the event with a vision to provide a platform for fellow colleagues to present their work to a diverse audience simply yet effectively. The presentations ranged from full-length talks to flash talks and poster presentations to highlight the breadth and depth of the excellent research being conducted at UC Davis by postdocs. The top three winners in each presentation category will be rewarded with a certificate and cash prize as an encouragement for their work.

We would like to thank our plenary Speaker, Lisa Cantrell, for agreeing to share ways to effect storytelling in science. Additionally, we would like to thank Dean Jean-Pierre Delplanque, who will announce the winners of the much-coveted Postdoctoral Excellence Awards before Dinner. This engagement reiterates that the UC Davis leadership is interested in and engaged with our work.

The PSA board would also like to extend their heartfelt thanks to several key Graduate Studies academic staff members, including Executive Director Nicole Rabaud, Associate Dean Ellen Hartigan-O'Connor, and Associate Dean Duncan Temple Lang. We would also like to thank the Graduate Studies support staff, including Rosemary Martin Ocampo, Trina Giardino, Olga Garzón-López, Jacqueline Dosick, and Sara Camara.

Finally, the PSA board would like to thank all the volunteers who made this symposium successful sincerely. We are grateful and overwhelmed by each of your interests and engagement.

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9th Annual Postdoctoral Scholars Research Symposium, April 26, 2024 - UC Davis Conference Center - THEME "One Science"			
8:00 - 9:00 Registration, Breakfast, and Poster setup (Moderator: PSA Relations Officer: Madhura Patankar)			
9:00 - 9:30 Welcome session in Ballroom A			
9:00 - 9:10 Welcome Remarks and Introduction PSA Chair: Ruchika Kashyap			
9:10 - 9:20 Opening Remarks by Dean of Graduate Studies Dean Jean-Pierre Delplanque			
9:20 - 9:30 Felicitations and announcements PSA Chair: Ruchika Kashyap			
9:30 - 10:20 Keynote Talk - Storytelling in Science: The why and how Invited speaker: Dr. Lisa Cantrell			
ORAL TALKS- I			
10:30 - 11:30	Ballroom A (Moderator: Manohar)	Ballroom B (Moderator: Ruchika)	Ballroom C (Moderator: Qing)
10:30 - 10:50	Maternal effects of dietary folate manipulation: Changes in the cortical interneuron markers Arshi Mustafa	Individually in a clonal fish persists despite strong predation threat in early life James Gallagher	Improving nitrogen fixation in chickpea Laura Perilla
10:50 - 11:10	Glyphosate & Glufosinate: Fate in California Almond Orchards Rohith Vulchi	How risky are birds in agriculture? An exploration into the connection between avian communities and food safety Austin Spence	Branched broomrape seed germination response to QAC sanitizers Pershang Hosseini
11:10 - 11:30	An accurate method for the characterization of pathogen activity during infections Hugo Monteiro	Evaluating the impact of sunflower cultivation on nitrate leaching to groundwater in the central valley: a conservation assessment Felix Ogunmokin	Structural Insights into Strigolactone Catabolism by Carboxylesterases Reveal a Conserved Allosteric Regulation Malathy Palayam
11:30 - 11:45 Morning Break			
ORAL TALKS- II			
11:45 - 12:45	Ballroom A (Moderator: Sarah)	Ballroom B (Moderator: Madhura)	Ballroom C (Moderator: Felix)
11:45 - 12:05	Efficacy and safety of psilocybin for peripartum mood disorders in mice and their offspring Cassandra Hatzipantelis	Exploring the Impact of Gene Drive Mosquitoes Released for Malaria Management Through Agent-Based Modeling Approach Sureni Wickramsooriya	Identifying and Quantifying Viruses based on their protein signatures Wenting Li
12:05 - 12:25	Discovery of new clathrates by computational screening, and directed synthesis Frank Cerasoli	Climate-driven risk modeling of zoonotic Arenaviral spillover infection in South America Pranav Kulkarni	Engineering Cyborg Cells as Therapeutic Materials Luis Eduardo Contreras Llano
12:25 - 12:45	Atomistic simulation of thermal transport in FinFETs with near first-principles accuracy: Interplay of bulk, interfacial and geometric properties Carlos Polanco	Ecological niche modeling and functional connectivity of Anopheles couzoui on São Tomé and Príncipe islands Lisa Chamberland	An accurate and rapidly calibrating speech neuroprosthesis Nicholas Card
12:45 - 13:15 Lunch Break			
13:15 - 14:15 BALLROOM A - POSTER SESSION (Lunch continued)			
FLASH TALKS			
14:20 - 14:50	Ballroom A (Moderator: Manohar)	Ballroom B (Moderator: Qing)	Ballroom C (Moderator: Felix)
14:20 - 14:25	Understanding and reducing the genetic reversion mechanism for snap bean pods Burcu Celebioglu	Multigenerational impacts on DNA methylation signatures in autism spectrum disorder. George Kuodza	Development of a peptide-based probe for elucidating the metal-dependent activities of oxytocin Jennifer Park
14:25 - 14:30	Unwelcome Guests: Plant Genes Involved in Root-Knot Nematode Parasitism Bardo Castro Esparza	Silver nanoparticles (AgNPs) bioactive compound from Editan (Lasianthera Africana) and Utazi (Gongronema latifolium) as inhibitors of resistant genes in selected mastitis pathogens Esther Nwanna	Deformations in the Space of Infinite Qubits Daniel Spiegel
14:30 - 14:35	Effective diagnostic approaches: Saving California's wildlands from Phytophthora havocs Ruchika Kashyap	MD Simulation Identifies a Novel and Direct Mechanism for PIP2 Activation of SK2 Channel Ryan Woltz	Counting colored solutions to linear equations Denae Ventura Arredondo
14:35 - 14:40	Analyzing urban soil imperviousness on local tree catchment scale Moreen Willaredt	The link between the gut microbiota and behavior in Hispanic children with autism spectrum disorder Jelissa Reynoso-Garcia	California Prescribed Fire Monitoring Program: Building Credibility Around Prescribed Fire Ruth Domenech-Jardi
14:40 - 14:45	Nutrient Dynamics and Soil pH in Biochar Amended Soil are Influenced by the Time and Rate of Application Omid Zandvakili	The many reliabilities of affective dynamics Sebastian Castro-Alvarez	Slicing convex polytopes Antonio Torres
14:45 - 14:50	-	No haste for food waste: can US state policies meet federal food loss and waste reduction goals? Sarah Kakadellis	Unraveling molecular interactions of vaping cannabinoids with brain drug transporters: Expression and purification of human ABCB1 and ABCG2 transporters via Pichia pastoris for structure-function insights Jagadesha Ganapathy
14:50 - 15:00 Afternoon Break (*Transition to Oral Talks)			
ORAL TALKS- III			
15:00 - 16:00	Ballroom A (Moderator: Madhura)	Ballroom B (Moderator: Ruchika)	Ballroom C (Moderator: Sarah)
15:00 - 15:20	Developing and validating stress transcriptional profiling (STP) chip to assess the resilience of freshwater fishes to changing environments SK Shahinur Islam	Using Contrast Enhanced Computed Tomography to predict hepatic radioembolization dose distribution Brahim Mehadij	Optimizing Reconstruction Parameters allows Dose Reduction in Pediatric Oncology Patients with Delayed Total-Body FDG-PET/CT Clemens Mingels
15:20 - 15:40	Deciphering the Intricate Dance: Pathogen Evolution Meets PRR Immune Signaling Alba Moreno Pérez	Kinetic modeling of [18F]-PI-2620 binding to tau deposits in the brain using an image-derived input function Anjan Bhattarai	Municipal Monkeys Foraging Flexibly: Assessing Innovation in Urban Long-Tailed Macaques (Macaca fascicularis) Josephine Hubbard
15:40 - 16:00	The genetic mechanisms of plant pathogenic Ralstonia host infection Nathalie Aoun	How smoky California was before the European settlement? Andrea Duane	Low to Zero Concentrations of Airborne Bacterial Pathogens and Indicator E. coli in Proximity to Beef Cattle Feedlots in Imperial Valley, California Xiaohong Wei
16:00 - 16:10 Evening Break			
16:10 - 16:30 Workshop and Feedback Session Executive Director: Graduate Studies: Nicole Elizabeth Rabaud, PSA Secretary: Sarah Kakadellis			
16:30 - 17:00 Award Ceremony and Closing Remarks PSA Chair and Vice Chair: Ruchika Kashyap and Qing He			
17:00 - 18:30 Symposium Dinner			

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OMBUDS OFFICE

The UC Davis Ombuds Office is a confidential, independent, impartial, and informal problem-solving and conflict-management resource. They offer individual meetings, mediation, and training to facilitate conflict resolution and invite for all postdocs with university-related issues and concerns to visit their office. The Ombuds can assist by listening to concerns, clarifying issues, identifying policies and resources, and providing coaching and communication strategies.

Postdocs are invited to register for their upcoming session “Complete Conflict Competence Training for Graduate Students and Postdocs” that will take place on Tuesday April 25 9am - 2pm in 1230 Walker Hall (West Conference Room).

Please visit the Ombuds Office stand during the morning break and <https://ombuds.ucdavis.edu/> to find out more.



UC Davis Graduate Studies

cultivating the best learning experience
for students and scholars

Join us at Meet & Greet events to meet over coffee with UC Davis postdocs, PSA, and graduate studies staff! Event dates are announced by email every month.

Graduate studies are organizing every year a Postdoc Appreciation Dinner. Keep an eye on your emails for the 2023 dinner edition!

Other than organizing cool events, graduate studies represent a great support system for UC Davis postdocs. If you have any inquiries related to your employment contract, benefits, conflicts management, etc. feel free to reach out to Graduate Studies.

2024 PRS ABSTRACTS

- I. Flash Talk Presentations
- II. Oral Talk Presentations
- III. Poster Presentations

Flash Talk Presentations

Silver nanoparticles (AgNPs) bioactive compound from Editan (*Lasianthera Africana*) and Utazi (*Gongronema latifolium*) as inhibitors of resistant genes in selected mastitis pathogens

Esther Emem Nwanna*^{1,2} Emmanuel Okello² and Joshua. Nweke¹

¹Department of Biochemistry, Federal University of Technology, Akure, Nigeria ²University of California, Veterinary Medicine Teaching and Research Center, Tulare, CA 93274, USA

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Antimicrobial resistance in food-producing animals is a global threat while the emergence of antibiotic-resistant organisms in bovine mastitis has raised concerns which is mostly due to the resistance genes in the pathogens. Combining organic medicinal plants and inorganic silver nitrate to form nanoparticles (AgNPs) could create nano-drug delivery systems that enhance antimicrobial activity. Green-based (AgNPs) from Editan and Utazi were synthesized. Purification and characterization were carried out using high-performance liquid chromatography (HPLC) scanning electron microscopy (SEM) and Fourier-transformed infrared (FTIR) spectroscopy to determine the phenolics surface morphology functional groups and its formation through sampling at time intervals. The formation of (AgNPs) was displayed within 10 min between 440 and 540 nm with functional groups at peaks between 350nm to 4,400nm. HPLC showed prominent ligands used for the *in-silico* study with Schrodinger Maestro 11.1 software forming complexes with the target resistant genes [encoding biofilm-associated protein (Bap)] of *Staphylococcus aureus* and [encoding laminin-binding protein (eno)] of *Streptococcus agalactia*. It was observed that the drug-likeness of the hit compounds followed Lipinski's rule of five (Rutin>Phlorizin> Procyanidin>Epigallocatechin) with strong binding affinity better than the control drug Cloxacillin. This information could serve as a new scaffold for target-based drug discovery against bacterial pathogens in mastitis.

Understanding and reducing the genetic reversion mechanism for snap bean pods

Burcu Celebioglu* and Travis Parker

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Green “snap” beans and dry beans (e.g. pintos, kidneys, blacks) are members of a single species, *Phaseolus vulgaris*. These categories are distinguished by two critical pod traits. Dry beans require woody fibrous tissue in the pod walls and pod suture “strings” to facilitate removal of seeds, whereas this fiber deposition is unacceptable in green snap beans. Intriguingly, both traits frequently revert from the mutant snap bean form back to the ancestral fibrous form, and this reversion is heritable. Further instability varies depending on climatic conditions and genetic background. The purpose of the project is to characterize the genes and

mutations responsible for distinguishing snap beans and dry beans and to improve their stability. Methods such as fluorescence microscopy, Genome-Wide Association Studies, Whole Genome Shotgun Sequencing, and Real Time quantitative PCR are being used on a panel of 600 unique lineages to better understand the genetic and environmental control of these critical pod traits. Gene duplications related to both pod traits have been identified and may underly reversion of pod traits in some, but not all cases. As a result of the study, plants that are not affected by climatic conditions and have good pod quality will be obtained.

Multigenerational impacts on DNA methylation signatures in autism spectrum disorder.

George E. Kuodza¹, Ray Kawai¹, Yunin J.L. Rodriguez¹, Julia S. Mouat¹, Sophia M. Hakam², Timothy N. Sullivan¹, Cole R. Torvick¹, Viki Haghani¹, Deborah Bennett¹, Irva Hertz-Picciotto¹, Janine M. LaSalle¹

¹University of California, Davis; ²University of California, Berkeley
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The prevalence of autism spectrum disorder (ASD) has been on the rise, and the underlying causes are not fully understood. However, recent research suggests that genetics and environmental factors may play a role in the development of ASD. In order to investigate the potential impact of multigenerational epigenetic inheritance on the development of ASD, our study recruited 349 participants from the CHARGE (Child Autism Risks from Genetics and the Environment), including grandparents, parents, and children. We hypothesize that DNA methylation patterns associated with ASD may be detectable across generations and associated with grandparental environmental exposures. A questionnaire was used to gather information about the participants' exposure to environmental factors, and biospecimen, including saliva samples and dried blood spots, were collected. DNA was extracted from the biospecimens and subjected to whole genome bisulfite sequencing (WGBS) to analyze DNA methylation. We have received sequencing results and we are analyzing it. In the bioinformatics analysis, we will use DMRichR to examine differences in methylation among subjects and Comethyl to compare correlation patterns between methylation marks and selected variables, including grandparental exposures. This research will provide new insights into the underlying etiology of ASD and pave the way for future research in the field.

Unwelcome Guests: Plant Genes Involved in Root-Knot Nematode Parasitism

Bardo Castro Esparza* Shahid Siddique

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Plant parasitic nematodes (PPNs) are a major problem for agriculture, leading to 8-15% loss of total crop yield worldwide. Among PPNs, Root-Knot Nematodes (RKNs) are the most economically devastating due to their wide host range, affecting various crops including tomatoes. During their obligate biotrophic life cycle, RKNs act as unwelcome guests in roots. They penetrate roots systems migrating to the vascular cylinder, where they induce formation

of giant cells. These giant cells have enhanced nutrient uptake and are used for nourishment through the RKN life cycle. Female RKNs lay large numbers of eggs which can survive in the soil for extended periods of time and can lead to further infections. Currently, there are no ideal strategies to combat RKN infections effectively. Some strategies include use of nematicides and resistance genes like Mi-1. These strategies however have drawbacks like enhanced nematode resistance to nematicides and emergence of Mi-1 resistance breaking strains of RKNs. The goal of this project is to identify plant genes involved in the establishment and functioning of giant cells. With this knowledge, we plan to target these genes through gene editing to inhibit the ability of nematodes to establish and maintain feeding sites, thereby interrupting their life cycle.

Effective diagnostic approaches: Saving California's wildlands from *Phytophthora* havocs

Ruchika Kashyap¹, Timothy D. Miles², Frank N. Martin³, and Johanna Del Castillo Munera¹

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²Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI 48824;

³United States Department of Agriculture–Agricultural Research Service, Crop Improvement and Protection Research Unit, Salinas, CA 93905

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California's native plant restoration faces recurrent challenges from *Phytophthora*-induced diseases especially through introductions from nurseries, causing significant damage. Therefore, *Phytophthora* management requires effective on-site diagnostic approaches as it is unclear what methods would be most appropriate considering required expertise, time, and cost. This study compares the effectiveness of five diagnostic methods: leachate baiting, Immunostrips[®], direct root isolations, recombinase polymerase amplification (RPA), and quantitative polymerase chain reaction (qPCR) on both artificially inoculated and naturally infested plants. For RPA and qPCR, genus-specific *trnM-trnP-trnM* locus and *atp9-nad9* locus, respectively were targeted for *Phytophthora* identification. Two native California ornamentals, coffeeberry (*Frangula californica*) and toyon (*Heteromeles arbutifolia*), were inoculated in the greenhouse with three *Phytophthora* species: *P. cinnamomi*, *P. cactorum*, and *P. cryptogea* arranged in a randomized complete block design and sampled thrice, every six weeks post-inoculation. Among the detection assays (excluding the ongoing qPCR), both RPA and leachate baiting had greater *Phytophthora* identification from the artificially inoculated plants, regardless of the host, sampling time, or species ($P < 0.0001$). A comparative diagnostic analysis is underway for naturally infested plants sampled from five distinct nurseries. Thus far, the results indicate that utilizing efficient approaches can enhance *Phytophthora* diagnostics, thereby reducing its introduction risk into wildlands.

Development of a peptide-based probe for elucidating the metal-dependent activities of oxytocin

Jennifer Park, Marie Heffern

Department of Chemistry, University of California, Davis, CA, 95616

Oxytocin, a nine-amino-acid hormone peptide renowned for its role in reproduction and childbirth, has fascinated researchers for its diverse biological functions. Early studies suggested the effect of metal ions on oxytocin's activities, but the molecular details underlying its interaction with metal ions remains elusive. In 2023, our group discovered that oxytocin binding with copper and zinc affects the activation of mitogen-activated protein kinase (MAPK) signaling in kidney cell lines. We hypothesize that extracellular metal-bound oxytocin modulates the interaction of the oxytocin receptor, thereby altering the activation of MAPK pathways. Based on this observation, we propose visualizing oxytocin by appending dyes to strategic sites on the peptide to investigate the oxytocin's activities, understand the interplay between oxytocin receptor and metal ions, and provide insight into metal-dependent oxytocin-derived signaling pathways. Here, we designed fluorescein isothiocyanate (FITC)-labeled oxytocin and observed that Cu-bound FITC-labeled oxytocin exhibited more localization on the cell surface compared to its apo and zinc-bound counterparts in breast cancer cell lines, and this is accompanied by changes in the level of MAPK signaling. We anticipate that this study will both inform on new roles for extracellular metal ions and illuminate the relationship between metals and oxytocin in mediating biological signaling pathways.

California Prescribed Fire Monitoring Program: Building Credibility Around Prescribed Fire

R. Domenech^{1*}, M. T. Putz¹, Melanie Schlueter¹, H. D. Safford^{1, 3}, Joe Restaino⁴

¹Department of Environmental Science and Policy, University of California, Davis, CA. ²Cal Poly-San Luis Obispo, CA. ³Vibrant Planet, Incline Village, NV. ⁴California Department of Forestry and Fire Protection, South Lake Tahoe, CA.

Prescribed fire is a cost-effective tool to facilitate forest resilience restoration through fuel reduction to mitigate large and severe wildfire increasing risk. Through better understanding of effective prescribed fire application, land managers and owners can increase the use of low-intensity fire in the landscape.

The California Prescribed Fire Monitoring Program (CPFMP) is a collaboration between the University of California, Davis and the California Department of Forestry and Fire Protection (CAL FIRE) to assess and inform on prescribed fires best practices to achieve ecological benefits and mitigate extreme wildfire.

Through a network of permanent long-term monitoring plots in forests throughout California, the CPFMP monitors prescribed fire effectiveness (reduction in fuel load and continuity, and reductions in fire behavior), treatment effects (tree mortality, soil surface or aboveground carbon changes) and other variables of interest to collaborators and land managers (air quality impacts or vegetation regeneration).

Now entering its 5th year, the CPFMP encompasses over 30 sites (688 plots) across the state. Plots in each site have been sampled before, during the burn and after at different times. With

such a database, CPFMP can be essential in building credibility around prescribed fire capacity and efficacy for large-scale managed fire programs

No haste for food waste: can US state policies meet federal food loss and waste reduction goals?

Sarah Kakadellis^{1*}, Selena Mao², Asch Harwood² & Edward S. Spang¹

¹ Department of Food Science and Technology, University of California, Davis; ² ReFED

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In 2015, the US introduced its Food Loss and Waste Reduction Goal, which seeks to reduce food waste by 50% by 2030. However, there is limited knowledge on the effectiveness of policies implemented by individual states. Here, we evaluate the effectiveness of state policies and ask:

1. How do individual states align with the federal goal of halving food waste by 2030?
2. How are prevention, rescue and recycling policies prioritized across states?

To address these questions, we estimated per capita food waste diversion potential per state by leveraging on the non-profit ReFED's publicly available database. This included (i) quantifying food waste generation per state to establish a theoretical total food waste target; (ii) identifying relevant food waste reduction strategies and calculating the applicable food waste diversion potential for each policy; and (iii) developing quantitative conversion factor for policy scoring to estimate the likely range of food waste reduction achievable. Results suggested that even in the most optimistic scenario, Arkansas was the only state likely to meet federal ambitions. Findings also showed an overwhelming emphasis on food waste recycling over prevention and rescue, highlighting the need for a re-examination of current policies in the context of the food waste hierarchy.

MD Simulation Identifies a Novel and Direct Mechanism for PIP2 Activation of SK2 Channel

Ryan L. Woltz¹, Woori Choi¹, Khoa Ngo², Brandon Harris², Yanxiao Han², Kyle Rouen², Pauline Trinh¹, Yang Zhang¹, Zhong Jian³, Ye Chen-Izu³, Eamonn Dickson², Ebenezer Yamoah⁴, Vladimir Yarov-Yarovoy^{2,5}, Igor Vorobyov², Xiao-Dong Zhang

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Prescribed fire is a cost-effective tool to facilitate forest resilience restoration through fuel reduction to mitigate large and severe wildfire increasing risk. Through better understanding of effective prescribed fire application, land managers and owners can increase the use of low-intensity fire in the landscape. The California Prescribed Fire Monitoring Program (CPFMP) is a

collaboration between the University of California, Davis and the California Department of Forestry and Fire Protection (CAL FIRE) to assess and inform on prescribed fires best practices to achieve ecological benefits and mitigate extreme wildfire. Through a network of permanent long-term monitoring plots in forests throughout California, the CPFMP monitors prescribed fire effectiveness (reduction in fuel load and continuity, and reductions in fire behavior), treatment effects (tree mortality, soil surface or aboveground carbon changes) and other variables of interest to collaborators and land managers (air quality impacts or vegetation regeneration). Now entering its 5th year, the CPFMP encompasses over 30 sites (688 plots) across the state. Plots in each site have been sampled before, during the burn and after at different times. With such a database, CPFMP can be essential in building credibility around prescribed fire capacity and efficacy for large-scale managed fire programs.

In a Flash: Perovskite and Cherenkov Semiconductors in Gamma Ray Imaging

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CsPbBr and TlBr are high density, high atomic number semiconductors that are unique among those used in gamma ray detection. Each of these materials, in addition to generating an electrical signal from incident gamma rays also generate an additional light signal that can give very precise information about the arrival time of the incident radiation. This unique behavior of these materials bypasses entirely the traditional tradeoffs in gamma ray detection between getting either a very precise energy measurement or a very fast timing measurement. In this brief talk I will outline the interesting physics behind these unique materials. I will then briefly discuss what is meant by energy and timing information. Lastly, I will discuss the potential impact of these materials in health fields from Positron Emission Tomography to radiation therapy.

The link between the gut microbiota and behavior in Hispanic children with autism spectrum disorder

Jelissa Reynoso-García^{1,2,3}, María Jimena Salcedo-Arellano^{1,2,3}, Robert W. Li⁴, Blythe Durbin-Johnson⁵, Verónica Martínez-Cerdeño^{1,2,3*}

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The disparity in autism spectrum disorder (ASD) prevalence between Hispanic and non-Hispanic white children is significant. Social determinants of health, including overall health status and nutrition, may play a role in the pathogenesis of ASD among these two populations, but remain poorly understood. Recent studies in the US have linked the gut microbiota to ASD. However, none of them analyzed ethnical differences, with only one including Hispanics. Hence, we propose to determine whether racial/ethnic differences in Hispanic and non-Hispanic white children impact the gut microbiota and associated metabolites in children with ASD; and determine whether there is a correlation between gut microbiota and microbiota-derived metabolites with behavioral deficits, socioeconomic status (SES), health status, and nutrition. We will extract and analyze DNA from fecal samples using 16S rRNA sequencing and metabolomics. We will statistically correlate microbiome data with data obtained from questionnaires about general clinical history, behavior, SES, and nutrition. We expect to see differences in the gut microbiota of Hispanic children with ASD compared to non-Hispanic white due to nutritional differences related to SES. The data we will obtain regarding gut.

Analyzing urban soil imperviousness on local tree catchment scale

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Imperviousness is a feature of paved urban environments, which can impact urban tree growth and performance. Despite its significance, assessing the impact of imperviousness on individual trees remains challenging due to the coarse scale of imperviousness data.

To address this gap, we leverage a rare high-resolution dataset of impervious surfaces mapped for the city of Berlin to analyze its effect on local tree catchment scale (i.e., meters). We classify tree catchments according to the reduction of infiltration of mean annual precipitation and assess their distribution across the city and among tree species. Based on the classification we test whether the results using the novel spatial approach are reflected within the Copernicus urban imperviousness dataset at a resolution of 10 m. Further, we investigate the relation between diameter at breast height (DBH) and age of ten species across a gradient of imperviousness to estimate the effect of imperviousness on tree growth. Our hypothesis posits a negative correlation between tree growth and imperviousness, with variations observed among species. By gaining a deeper understanding of how imperviousness might affect tree water supply and physiological responses, our research aims to inform effective water management strategies for urban trees under increased urbanization and climate change.

Deformations in the Space of Infinite Qubits

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A shape A is said to be “contractible” in a shape B that contains A if A can be shrunk to a point in B without ripping A apart. For example, a circle is contractible in a 2-dimensional plane, but a circle on the outer edge of a donut is not contractible within the donut. One can play this game with infinite-dimensional shapes too, the likes of which arise in the study of quantum systems with a large number of particles. I will discuss how an arbitrary finite-dimensional shape A can always be contracted when B is taken to be the “shape” of all possible configurations of a string of quantum bits (a.k.a. qubits). Quantum entanglement between the bits allows us to transport A down the string until it eventually disappears at infinity.

Optimizing Reconstruction Parameters allows Dose Reduction in Pediatric Oncology Patients with Delayed Total-Body FDG PET/CT

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Background: The aim of the study was to define a lower limit of reduced injected dose in delayed [¹⁸F]FDG TB PET/CT in pediatric oncology patients.

Methods: In this single-center study, 19 children (12 y/o (5-17y), 54.53±19.75kg) were scanned for 20 min with TB PET/CT, 120 min after administration of 4.07±0.49 MBq/kg [¹⁸F]FDG intravenously. Five low-count reconstructions were generated using 1/4th, 1/8th, 1/16th, 1/32nd of the counts of the randomly resampled list-mode reference standard acquisition (20 min), to simulate dose reduction. Tumor lesions were quantified. Coefficient-of-variation (COV), tumor-to-background ratio (TBR), and contrast-to-noise ratio (CNR) were calculated. Three physicians assessed the image quality using a 5-point Likert scale.

Results: 113 malignant lesions were identified. 87.6% of the lesions were quantifiable. Lowest COV was detected in the 20 min reference standard. All low-count reconstructions obtained significantly higher COV ($p < 0.0001$). Tumor uptake (SUV_{max}), TBR, and total lesion count were significantly lower in the reconstructions with 1/16th and 1/32nd counts ($p < 0.05$). CNR and clinical image quality were significantly lower in all low-count reconstructions.

Conclusion: Dose reduction with delayed [¹⁸F]FDG TB PET/CT imaging in children is possible after optimizing TB PET/CT reconstruction parameters. Our results indicate that PET centers should not reduce the dose below 0.5 MBq/kg (1/8th of 4.07MBq/kg).

Counting colored solutions to linear equations

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Ramsey theory is the study of the appearance of unavoidable monochromatic patterns in large enough arbitrarily colored structures. This can be studied on the positive integers where a natural question arises: how large must the integer n be so that any coloring of the positive integers from 1 to n contains a certain monochromatic substructure? One such structure can be a solution set of a given equation.

In 1927, Van der Waerden proved that any coloring of the positive integers must admit a monochromatic solution to the equation $x+y=2z$. Later on, Schur proved that there exists a minimum positive integer s such that for any 2-coloring of the integers from 1 to s there is a monochromatic solution to $x+y=z$. We call (x,y,z) a Schur triple if it is a solution to $x+y=z$. An interesting problem is to count the number of monochromatic Schur triples in any 2-coloring of the integers from 1 to a large enough n . Long-standing computation tools and techniques have been used to optimize this number. We employ some of these techniques along with Datskovsky's method to minimize the number of monochromatic triples associated to the equation $ax+ay=z$ in the interval 1 to n , where n is large enough and a is at least 2.

The many reliabilities of affective dynamics

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Reliability is a key concept in psychology that has been broadly studied since the introduction of Cronbach's alpha, which is a measure of the internal consistency of a test. Despite its importance, this is a topic that is relatively understudied when dealing with intensive longitudinal data. In particular, when studying the psychological dynamics of affective states, there is no warranty that the measurements are reliable. Given this, empirical researchers need tools to study and report the reliability of the scales used in intensive longitudinal research. In recent years, different approaches to estimate the reliability of the scales and the items used when studying psychological dynamics have been proposed. However, the advantages and

disadvantages of each of these methods are unclear, making it difficult to determine when a certain approach would be preferred over the others. For example, while some methods suggest estimating one reliability index for the scale, others estimate specific reliability indices for each individual in the sample. This wide variety of approaches can provoke some confusion for empirical researchers. In this talk, we give an overview of the available methods and highlight their advantages and disadvantages. We also showcase their use with empirical data.

Nutrient Dynamics and Soil pH in Biochar Amended Soil are Influenced by the Time and Rate of Application

Omid R. Zandvakili, Emily J. Cole, Baoshan Xing, Masoud Hashemi, Allen V. Barker, Stephen J. Herbert, Rafael Clemente, Sanjai J. Parikh

Our primary goals were to assess the impact of sugar maple wood biochar on soil properties after it had been in the field soil for 12 years. We examined factors such as soil pH, nutrient levels, sweet corn and edamame yields, and the surface characteristics of the biochar as it aged in the soil. The experimental design consisted of a Randomized Complete Block Design layout with five replications. The plots received different application rates of biochar in 2012, which included a control with 0% biochar and four other rates of 2%, 4%, 6%, and 8% by weight (equivalent to 0, 40.5, 81.1, 121.5, and 162.0 Mg/ha, respectively). Sweet corn was planted between 2012 and 2014, while edamame was grown from 2016 to 2018. Following a 12-year period in the field soil, we examined both fresh and aged biochar using Scanning Electron Microscopy (SEM), X-ray Electron Microscopy (XPS), and analyzed the composition of elements.

Unraveling molecular interactions of vaping cannabinoids with brain drug transporters: Expression and purification of human ABCB1 and ABCG2 transporters via *Pichia pastoris* for structure-function insights

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The transport proteins ABCB1 (P-glycoprotein) and ABCG2 (breast cancer resistance protein) play pivotal roles in the blood-brain barrier (BBB) by actively effluxing various substrates, including drugs and toxins, out of the brain. Cannabis, a widely used psychoactive substance, contains cannabinoids that interact with the endocannabinoid system in the brain, exerting psychoactive effects. Adolescent cannabis use with vaping has seen a remarkable increase in recent years. However, the mechanisms governing the entry of vaping cannabinoids into the brain and their interaction with the protective ABCB1 and ABCG2 transporters remain poorly understood. This study focuses on elucidating the structural mechanisms underlying the interaction between cannabinoids and their vaping derivatives with mammalian ABCB1 and

ABCG2 transporters. To this end, pPICZ plasmids harboring Human ABCB1, Human ABCG2, Mouse ABCB1, or Mouse ABCG2 transporter proteins were constructed. Efforts are being made to express and purify these transporters using the Pichia system, employing various transformation techniques and different strains of *Pichia pastoris*. Through this investigation, our goal is to enhance our understanding of how vaping cannabinoids interact with ABCB1 and ABCG2 transporters, with potential implications for designing a new class of cannabinoids to improve human health.

Oral Talk Presentations

How risky are birds in agriculture? An exploration into the connection between avian communities and food safety

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Wild birds pose a unique food-safety risk to agriculture as they carry zoonotic pathogens, are difficult to exclude, and are federally protected. As a result, farmers have few strategies for reducing bird fecal contamination. Here, we evaluate the food-safety risks of wild birds, from the point of entering farms through harvest via three complementary approaches. First, we collected feces from wild birds and assayed them for three enteropathogenic bacteria. Second, we conducted bird surveys on leafy-green farms across the Central Coast. Finally, we conducted experiments examining *E. coli* survival in avian feces. Our results indicate pathogen prevalence in birds is limited, with pathogens found in less than 2% of the ~1,300 samples. Importantly, not all species carried the same risk. Fecal mass was the strongest predictor for how long *E. coli* survives, with increased survival in larger fecal samples. By investigating which birds harbor pathogens, which birds occupy agricultural habitat, and how long pathogens survive in feces after defecation, our work contributes to a more holistic understanding of the risk wild birds pose to food safety. These results will better inform farmers and policy makers on how to co-manage agricultural lands for both conservation and human health.

Using Contrast Enhanced Computed Tomography to predict hepatic radioembolization dose distribution

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Purpose:

Radioembolization consists in injecting glass or resin microspheres covered or infused with Y-90 atoms as close as possible to the targeted tumor via the hepatic artery. The treatment requires two Interventional Radiology (IR) day-long procedures spaced by several days. The first IR intervention costs 17 000\$ and consists of a work-up to anticipate the efficacy of the treatment. We propose here a new method of predicting treatment efficacy for small and well delimited tumors using a four-phase liver Contrast Enhanced Computed Tomography (CECT) scan.

Materials and methods:

The CECT arterial phase is subtracted by the non-injected CT to obtain the iodine arterial phase distribution. The targeted liver segments are selected according to the IR forecast injection point.

Results:

Three first patients have been tested using the method and results show a good concordance between predicted and delivered Y-90 distribution with less than 10 % difference in terms of mean dose.

Conclusion:

Using CECT instead of IR workup to predict Y-90 distribution seems promising for small and well delimited tumors for which the lung shunt fraction is expected to be negligible. This would hence allow to treat more patients and to reduce the treatment costs.

Engineering Cells as Therapeutic Materials

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Many advanced chronic or critical diseases lack effective long-term therapeutic options. This is particularly critical when the required stability and sustained activity are beyond what materials-based approaches or cell therapies can offer. Thus, there is a persistent need to develop new therapeutic paradigms that help address these unmet clinical needs. We have developed a platform combining principles of materials science, synthetic biology, and cell therapy, that allows the creation of semi-synthetic cellular systems with living cell capabilities and synthetic material behavior. This new class of chassis that we call Cyborg Cells can be derived from virtually any bacterial species or mammalian cell line making it suitable for a wide range of potential applications. Our system leverages the preservation of core capabilities of the native cell lines including secretion profile, metabolic activity and cell physiology and enhances them with tolerance to lethal stressors and increased stability. Cyborg Cells are created by assembling a

synthetic polymer network inside each cell, rendering them incapable of dividing and providing enhanced mechanical support. Our platform establishes a new archetype in the fields of cell engineering and therapeutic biomaterials with ongoing applications as semi-living bacterial vaccines, anti-cancer treatments, and enhanced cell therapies.

Ecological niche modeling and functional connectivity of *Anopheles coluzzii* on São Tomé and Príncipe islands

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The mosquito vector-borne disease, malaria, is responsible for over 500,000 annual deaths, and the stability of mosquito species distributions are critical to assess in the face of changing climate conditions. Here, we used an ecological niche modeling (ENM) approach to test the relationship between environmental variables, including topology, climate, and landscape composition, to *Anopheles coluzzii* mosquito larval occurrences within São Tomé and Príncipe (STP) islands. We implemented high-resolution models of both current and future larval distributions under a range of climate change scenarios. Furthermore, we assessed functional connectivity of *An. coluzzii* on STP using least-cost and circuit theory-based approaches to identify areas of flow (movement) potential. Results from the ENM revealed higher habitat suitability and movement potential in the northeastern regions of both islands, characterized by higher human population densities and lower elevation. Furthermore, distributions under future climate models predicted instability and significant range expansions on Príncipe Island. In addition to highlighting the dynamic interplay of environmental factors influencing suitable larval habitats and movement corridors of *An. coluzzii* on STP, this research identifies areas of these small islands that are most at risk for range expansions and should be considered when implementing future vector control strategies.

The genetic mechanisms of plant pathogenic *Ralstonia* host infection

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The increasing severity of plant disease threatens global food security and environmental sustainability. To effectively manage disease, it is crucial to understand how the evolution of pathogen populations contributes to their spread. Pathogen growth and reproduction within the host are critical fitness traits that affect disease outcomes. However, the fitness mechanisms required for plant pathogens to successfully infect and colonize plant hosts remain poorly understood. Here we investigate genetic traits of plant pathogenic *Ralstonia* that affect host infection. To identify these genetic traits, we used high-throughput forward genetic screening using a random barcode transposon mutant sequencing approach to quantify the fitness of thousands of mutants in complex naturalistic environments. We inoculated tomato cultivars with the library of barcoded mutants. Using Illumina sequencing, we quantified the change in the relative abundance of bacterial mutants before and after growth in tomato cultivars. This quantification allowed us to identify the presence of efflux pumps with paradoxical contributions to *Ralstonia* growth across diverse tomato cultivars. Our next step is to validate these genes and understand their involvement in resistance or susceptibility to toxic chemicals, such as phytochemical defenses that pathogens encounter in plants.

Maternal effects of dietary folate manipulation: Changes in the cortical interneuron markers

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Folate is an essential micronutrient and prenatal folate deficiency is known to cause neural tube defects and altered neurogenesis. Recently, it has been shown that both maternal folate deficiency and excess folate intake delays prenatal cerebral cortical neurogenesis and favors late born projection neurons. However, nothing is known about the effect of prenatal folate deficient/excess diet intake in context of changes in the expression of interneuron markers. In this study wild type C57BL/6N mice were on different folate diets. The expression of interneuron markers was analyzed in the cortical region of brain. Compared to controls, we found reduction in the number of Parvalbumin, Calretinin and Somatostatin expressing interneurons mouse that had been pre and postnatally subject to deficient, excess and super excess diets. Maternal folate intake alters the expression of interneuron markers in the offspring. Both deficient and excessive folate intake negatively affects neurogenesis.

Individuality in a clonal fish persists despite strong predation threat in early life

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Early life predator experiences can have profound effects on behavior, including the development of individuality. However, their impact on individual behavioral variation and the timing of its emergence is largely unknown. Although previous work has linked predator exposure to the emergence and maintenance of individual variation, predation may instead collapse variation if there is an optimal survival response. We test these alternate hypotheses using a naturally clonal fish, the Amazon molly (*Poecilia formosa*), removing confounding genetic effects on behavioral variation. We reared individuals in standardized environments that differed only in the presence or absence of predatory cues, and tracked individual behavior, all day, every day, for the first month of life. We found that predation pressure does not collapse behavioral variation. Newborns were highly responsive to predators on day one of life and maintained these responses throughout their early lives. We then allowed these fish to interact with a live predator and found that their behaviors during development predicted their response to the predator, suggesting likely adaptive value. This powerful model system allowed us to fully isolate the effects of predation on behavior and track behavioral responses in intimate details, giving us deep insight into the developmental trajectories of individuality.

Developing and validating stress transcriptional profiling (STP) chip to assess the resilience of freshwater fishes to changing environments

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While most research on climate change effects on biodiversity has concentrated on the terrestrial and marine realms, relatively few studies, however, have investigated these effects on freshwater species, especially in the context of genomic basis of physiological adaptation. Freshwater fish resources contribute to Canada's economy both directly and indirectly. Yet Canadian freshwater fish species are under threat with various stressors (e.g., invasive species, climate change). Understanding the health status and coping capacity of fish species is therefore

crucial for rapid adaptation to increasing stressors. Thus, there is a need for genomic tools that can address a broad range of biotic responses to multiple stressors. Here, we have developed a panel of quantitative PCR (qPCR) assays for use in a high-throughput nanofluidic OpenArray Stress Transcriptional Profiling Chip (STP-Chip) capable of simultaneous qPCR at multiple gene loci representing responses to various stressors. We have optimized qPCR assays for the 112 multiple stressors genes using cDNA from multiple populations of 42 target freshwater fish species and using in nanofluidic STP-Chips. This chip can be used in the framework of quantifying stress in fish, improving health through more accurate diagnostic tests for disease, and monitoring adaptation to accelerated climate change regionally and globally.

Exploring the Impact of Gene Drive Mosquitoes Released for Malaria Management through Agent-Based Modeling Approach

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The classical vector control mechanism for malaria has shown limitations in effectively managing vector-borne diseases including malaria. A novel alternative approach involves the release of genetically engineered mosquitoes (GEMs) capable of blocking the malaria parasite. This innovative strategy aims to prevent the transmission of malaria, particularly by targeting vectors. This study introduces an agent-based model (ABM) focusing on the release of GEMs to modify the local *Anopheles coluzzii* population. The simulation is applied to the West African island of Príncipe, utilizing empirical data from laboratory and field studies. The model aims to forecast the dynamics of mosquito populations, with a specific focus on devising effective strategies for GEM release. The primary objective is to analyze the time required for GEMs to reach a frequency of 0.95 in the target area. This research provides valuable insights into the integration of GEMs and their potential in controlling malaria vectors. By simulating the introduction of GEMs in a real world context, the study contributes essential information for the development of successful strategies to combat malaria transmission in the affected region.

Improving nitrogen fixation in chickpea

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Wild chickpea relatives (*Cicer* spp.) demonstrate more efficient nitrogen-fixing symbiosis compared to cultivated genotypes, particularly with native *Mesorhizobium* spp., in a genotype-dependent manner. Understanding the genetic control of this symbiotic efficiency holds the key to breeding for enhanced nitrogen fixation, ultimately reducing the need for fertilizers in legume production. Highly compatible host symbiont genotypes in wild counterparts yield a substantial 30% to 100% increase in biomass compared to less efficient symbiotic pairs. This project focuses on evaluating symbiotic efficiency in segregating biparental populations of wild *C. reticulatum* crossed with domesticated *C. arietinum*. Phenotypic quantification of plant biomass across four biparental populations, testing approximately 100 Recombinant Inbred Lines (RILs), coupled with genetic analysis, reveals the heritability of the wild Nfix efficiency trait. Identifying high Nfix performance genotypes, exhibiting around 40% higher biomass gain than progenitors, serves as a crucial outcome. Ongoing data analysis using quantitative genetic methods aims to identify genetic regions in the chickpea genome associated with nitrogen fixation efficiency. These findings will introduce beneficial traits into domesticated cultivars of *C. arietinum*, with future research focusing on field testing and refining genetic analysis precision.

Kinetic modeling of [¹⁸F]-PI-2620 binding to tau deposits in the brain using an image-derived input function

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Background: This study utilized a non-invasive Image-Derived Input Function (IDIF) from a total-body EXPLORER PET/CT scanner to quantify tau binding in the brains of elderly individuals at risk of dementia.

Methods: Dynamic total-body ¹⁸F-PI-2620 PET images from elderly individuals (N=15), with or without dementia, were acquired over 90 minutes. Grey matter regions of interest (ROIs), including the medial temporal (MT), posterior cingulate (PC), and lateral parietal (LP) cortices, were parcellated from T1-weighted images. A two-tissue compartmental model (2TCM) with the descending aorta IDIF was used for kinetic modeling. Kinetic parameters, including tracer delivery rate (K_1), total distribution volume (V_T), and non-displaceable binding potential (BP_{ND}), were estimated. Logan graphical analysis was also used to estimate V_T .

Results: K_1 was significantly reduced in MT. All kinetic parameters remained stable after the 60-minute scan window. Notably, K_1 stability was observed after 30 minutes. A strong correlation was observed between V_T estimated using 2TCM and Logan plot analysis across all ROIs (MT: $r=1.00$, LP: $r=0.96$, PC: $r=1.00$). Additionally, a negative correlation was observed between BP_{ND} and K_1 in all ROIs ($r=-0.40$).

Conclusion: This study highlights the utility of a non-invasive IDIF derived from the total-body PET scanner to quantify ^{18}F -PI-2620 grey matter kinetics.

An accurate method for the characterization of pathogen activity during infections

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Next-generation sequencing has remarkably advanced microbial discoveries within microbiomes, especially of pathogens that can be causative of diseases. However, the development of effective disease treatment strategies remains reliant on accurately characterizing pathogen activity within a microbiome so targeted approaches can be developed. Here, we developed an accurate method to characterize pathogen activity using a horse placentitis model, inoculating *Streptococcus equi subs. zooepidemicus* into six mares at 272 days of gestation, while six others served as negative controls. After placentitis progression was confirmed through inflammatory markers, placentas were collected and analyzed for dual-RNA sequencing and metabolomics. A PNAS-validated mock microbiome community was used to calibrate our identification models at 100% accuracy, while an RNA aligner was used for further validation of our findings. Except for *S. zooepidemicus*, 10 microbes formed the mares' placenta microbiome. Genome-guided RNA alignment and *de novo* transcript assembly with *S. zooepidemicus* further unraveled this pathogen expressed 699 genes during infection within the microbiome. Among those, galactose degradation genes were upregulated, which were validated with lower galactose concentration in placentitis. Several host immune response-expressed genes further validated these findings. Thus, a calibrated multi-omics approach shows promise to accurately characterize pathogen activity in the development of preventive treatments.

Municipal Monkeys Foraging Flexibly: Assessing Innovation in Urban Long-tailed Macaques (*Macaca fascicularis*)

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Many animals make behavioral adjustments in response to increasing overlap with humans. One adjustment includes the ability to solve novel problems introduced into the environment. Long-tailed macaques (*Macaca fascicularis*) are urban adapters that use behavioral flexibility to adjust to environmental changes. Here we assess how individual monkeys' interactions with the urban environment and exploratory behaviors influenced their ability to solve novel foraging problems such as opening a puzzle box. Overall, we found that macaques who were more exploratory were more likely to solve the puzzle box ($\beta = 0.45$, $p = < 0.001$). Social context played an important role in solving behaviors, where individuals who were tested alone were more likely to solve ($\beta = 2.3$, $p = < 0.001$) and had higher exploratory behaviors compared to those who were tested in a group setting ($\beta = 0.33$, $p = 0.002$). Finally, we found that aspects of the urban environment also influenced solving behaviors, where individuals who fed more on human foods were less exploratory with the puzzle box ($\beta = 0.39$, $p = < 0.001$). This study highlights the importance of correlating urban interactions with innovation in urban adapters and has important insights for measuring behavioral flexibility in macaques.

The genetic landscape of hypervirulent *Salmonella* Strains

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Hypervirulence refers to the enhanced ability of pathogens to cause severe disease, characterized by a significant increase in morbidity and mortality accompanied by a reduction in the infectious dose. This study focused on a comparative genomic analysis of 18 hypervirulent strains with *Salmonella enterica* serovars Bovismorbificans and Choleraesuis to delineate the genetic landscape contributing to the enhanced virulence during in vivo infection, as compared to *S. Typhimurium* 14028. Illumina and PacBio sequencing produced high-quality genome assemblies and enabled a high-resolution comparison of gene content associated with hypervirulence. The analysis revealed variability in the presence of specific genes, notably *avrA*, *gogB*, and *sseK2*, which are effector genes of the Type III Secretion System (T3SS), crucial for the bacterium's ability to initiate infection. Additionally, the presence of genes conferring resistance to 24 antimicrobials was found, highlighting a significant repertoire of efflux-mediated drug resistance genes. This discovery signals a strains' potential for multidrug resistance, a concerning trait that complicates treatment strategies. These findings elucidate the sophisticated relationship between virulence factors and antimicrobial resistance mechanisms that, collectively, exacerbate infection and disease severity. This study underscores

the need for ongoing surveillance and research directed at these pathogens, accentuating their considerable implications for public health.

Structural Insights into Strigolactone Catabolism by Carboxylesterases Reveal a Conserved Allosteric Regulation

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Strigolactones (SLs) play a crucial role as plant hormones, coordinating various growth and developmental processes while also functioning as signaling molecules in the rhizosphere. This enables communication with both symbiotic fungi and parasitic plants. The levels of phytohormones are regulated through specialized enzymes, participating not only in their biosynthesis but also in post-signaling processes for signal inactivation and cue depletion. It has been recently proposed that carboxylesterases (CXE15 and CXE20) play key role in SL depletion through catalysis and/or sequestering. In this study, we elucidated the crystal structures of CXE15 (both apo and SL intermediate bound) and CXE20, providing new insights into the mechanisms of SL perception and catabolism mediated by carboxylesterases. CXE15 and CXE20 reveal distinct secondary structures in their N-terminal region, playing pivotal roles in their function both in vitro and in planta. We present a model proposing that a dynamic transition of open-closed N-terminal helix domain in CXE15 facilitates robust SL hydrolysis. This study not only illuminates the distinctive process of phytohormone breakdown in plants but also uncovers a novel molecular architecture and mode of plasticity within a specific class of carboxylesterases.

Identifying and Quantifying Viruses based on their protein signatures

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Wastewater-based epidemiology (WBE) is a cross-disciplinary field that accelerated from theory to practice during the Coronavirus Disease 2019 (COVID-19) pandemic. WBE utilizing Polymerase Chain Reaction (PCR) has emerged as a promising tool for monitoring the prevalence of viral infections in a population. However, due to frequent viral genetic mutations, PCR test may fail to detect novel variants of high-concerning viruses. In this study, we developed a method using nano-liquid chromatography and high-resolution mass spectrometry (nano LC-MS/MS) that identifies peptides generated from influent wastewater extracted viral proteins. We used centrifugal filtering device following by S-trap (in-column trypsin digestion) for viral peptide extraction and C18 Solid Phase Extraction (SPE) cartridges for free-flowing peptides that are pre-digested by the enzymes in the sewage. We used data dependent acquisition (DDA) method and data independent acquisition (DIA) data for spectra search and quantification. In addition to prevalent bacterial and human proteins, we identified specific viral proteins, including three variants of SARS-CoV-2 spike proteins and enterovirus proteins. The semi-quantification was achieved by using mass-labeled internal standards and human

biomarker, alpha amylase. This study laid the roadmap for nontarget WBE as a surveillance tool to better prepare and prevent future pandemic.

Efficacy and safety of psilocybin for peripartum mood disorders in mice and their offspring

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Current treatment options for peripartum mood disorders (PMDs) are either only effective in 30% of patients or cost \$35,000 USD. Psilocybin (PSI) has shown antidepressant efficacy, with patients taking PSI describing increased connectedness with loved ones, self-compassion, and remission of depressive symptoms. Therefore, there is strong rationale for using PSI to treat feelings of maternal disconnect, personal shame, and blunted affect seen in PMD. Here, we used a psychosocial stress model of PMD to assess the efficacy and safety of PSI in parous mice and their offspring. Postpartum mice were repeatedly exposed to infanticidal male mice, which dramatically destabilized caregiving behavior, induced maternal withdrawal and avoidance from pups, and increased anxiety-like behaviors – none of which were prevented by PSI treatment. In fact, weeks following injection, PSI-treated dams were more anxious and had increased vulnerability to stress-induced depressive phenotypes. Pups were raised to adulthood where they were tested using a battery of standardized behavioral tests. Interestingly, just a single postnatal exposure of offspring to PSI through breastmilk increased depressive-like phenotypes in adult males. Our data suggest that PSI may not have as broad transdiagnostic utility as predicted, and may pose a major health risk for both parous parents and their offspring.

Discovery of new clathrates by computational screening and directed synthesis

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Charge-balanced inorganic clathrates are semiconducting materials with unique properties, such as ultra-low thermal conductivity, superconductivity, and high-density ion storage. They consist of covalent frameworks constructed from nanometer-sized polyhedral cages encapsulating metallic guest atoms. While the frameworks of conventional clathrates consist of group-IV elements (Si, Ge, Sn), we have recently discovered new stable intermetallic clathrates with III-V frameworks and enticing transport properties. In this work, we combine Zintl compositional predictions, high-throughput density functional theory calculations, and machine learning to screen several thousands of compositions of III-V and II-VI type-I clathrates, mixed with transition metals, to identify stability trends and families of potentially stable compounds. In particular, a novel workflow is developed, which uses transfer learning to refine convolutional graph neural networks for predicting the site ordering of clathrate superstructures, as well as their equilibrium density and decomposition energy. Theoretical

predictions are tested by ex-situ synthesis and crystal growth, which have revealed new clathrates and clathrate-like compounds. Single-phase synthesis and first-principles calculations enable the joint theoretical and experimental exploration of their transport properties, revealing promising properties for thermoelectric energy conversion.

Climate-driven risk modeling of zoonotic arenaviral spillover infection in South America

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New World Arenaviruses (NWA) cause viral hemorrhagic fever in humans, with high potential burden in terms of mortality and morbidity in susceptible populations. Primarily a spillover risk from rodent reservoirs to humans, the risk of infection is significantly affected by distribution of the rodent hosts and the movement patterns of humans. The aim of this study was to model the climate-change driven risk of zoonotic spillover of NWA by species distribution modelling (SDM) of the rodent reservoir species (*Calomys musculinus*, *Zygodotomys brevicauda* and *Sigmodon alstoni*). SDMs were developed using ensembles of four tree-based machine learning techniques trained on current bioclimatic and landscape data of the area under study. Shared Socioeconomic Pathways (SSP) of moderate and extremely negative type (SSP2 and SSP5 resp.) projections of climate change for year 2050 and 2070 were used as future scenarios for climate-change. Based on the two scenarios, predicted changes in the risk patterns and hotspots for zoonotic outbreaks were investigated. SDMs of rodent reservoirs of Junin virus in Argentina and Guanarito virus in Venezuela and Colombia yielded high precision in predicting species habitats ranging from 83% to 91%. Our study provides valuable insights into potential shifts in rodent habitat suitability and patterns.

Atomistic simulation of thermal transport in FinFETs with near first-principles accuracy: Interplay of bulk, interfacial and geometric properties

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The performance of transistors is tightly related to their temperature of operation, which is dictated by their thermal transport properties. For current FinFET transistors, which have characteristic sizes below 10 nm, thermal energy propagation depends on bulk properties, material interfaces, and geometric constraints. Understanding the correlation and contribution of these factors is crucial to designing better strategies to mitigate heat dissipation problems. We present molecular dynamics simulations of thermal energy propagation in FinFETs with near-first-principles accuracy. These simulations use a single machine-learning interatomic potential trained with an evolutionary methodology to fit energy, forces, and stress values

computed from first principles using density functional theory. We show thermal conductance calculations at single interfaces (Si-SiO₂, Si-HfO₂, Si-SiGe, and Si-Co) and unveil the relationship between these values, bulk thermal conductivities, low dimensionality, geometric constraints, and the thermal properties of the full FinFET. We also present some of the challenges of fitting an accurate machine learning potential for multicomponent systems as well as the trade-offs to achieve thermal transport simulations for multi-million atom systems.

Low to Zero Concentrations of Airborne Bacterial Pathogens and Indicator *E. coli* in Proximity to Beef Cattle Feedlots in Imperial Valley, California

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This study characterized the effect of distance from beef cattle feedlots, environmental factors, and climate on the occurrence of airborne bacterial indicators and pathogens. Three hundred air samples were collected over 6 months from five feedlots, with each air sample comprising 6000 L of air. Air samples were processed onto TSB-enriched air filters, qPCR-screened, and then qPCR-confirmed for suspect positive colonies of *E. coli* O157, non-O157-Shiga-toxin-producing *E. coli* (STEC), *Salmonella*, and *E. coli*. Direct enumeration of *E. coli* was also collected. Although no bacterial pathogens were qPCR-confirmed for the 300 samples, *E. coli* was detected in 16.7% (50/300) of samples, with an overall mean concentration of 0.17 CFU/6000 L air. Logistic regression analyses revealed a higher odds of *E. coli* for samples in close proximity compared to >610 m (2000 ft) distance from feedlots, along with significant associations with meteorological factors, sampling hour of day, and the presence of a dust-generating activity such as plowing a field or nearby vehicular traffic. The lack of bacterial pathogen detection suggests airborne deposition from nearby feedlots may not be a significant mechanism of leafy green bacterial pathogen contamination; the result of our study provides data to inform future revisions of produce-safety guidance.

Evaluating the impact of sunflower cultivation on nitrate leaching to groundwater in the central valley: a conservation assessment

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Across California, many rely on clean groundwater for drinking, but nitrate contamination is a widespread concern, especially in agricultural areas. This pollution stems largely from excess nitrogen used in agriculture, which leaches into groundwater. To address this issue, various policies have been implemented to evaluate the impact of conservation practices. This study

evaluates the cultivation of sunflower (*Helianthus annuus*) on nitrate leaching to groundwater. We investigated nitrate dynamics through soil pore water, irrigation water, well water, soil samples, and plant biomass analyses. Total applied water and crop water use were determined from irrigation and evapotranspiration records. Irrigation and porewater analysis indicate higher concentrations of nitrate than allowed by the EPA in drinking water while soil samples indicated very low concentrations. Mass balance analysis indicated acceptable nitrogen use efficiency, suggesting legacy nitrates in the unsaturated zone, not sunflower cultivation, were the primary source of groundwater nitrate. Excessive irrigation and atmospheric rivers contributed to significant nitrate leaching into deeper soil profiles. While sunflower cultivation did not contribute significantly to nitrate leaching, this study highlights the complex interplay between irrigation, precipitation, and legacy nitrogen in groundwater contamination. Further research is needed to optimize water management and refine nitrate mitigation strategies.

An accurate and rapidly calibrating speech neuroprosthesis

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Brain-computer interfaces (BCIs) can provide a rapid, intuitive way for people with paralysis to communicate by transforming the cortical activity associated with attempted speech into text. Despite recent advances, communication with BCIs has been restricted by requiring many weeks of training data, and by inadequate decoding accuracy. Here we report a speech BCI that decodes neural activity from 256 microelectrodes in the left precentral gyrus of a person with ALS and severe dysarthria. This system achieves daily word error rates as low as 1% (2.66% average; 9 times fewer errors than previous state-of-the-art speech BCIs) using a comprehensive 125,000-word vocabulary. On the first day of system use, following only

30 minutes of attempted speech training data, the BCI achieved 99.6% word accuracy with a 50 word vocabulary. On the second day of use, we increased the vocabulary size to 125,000 words and after an additional 1.4 hours of training data, the BCI achieved 90.2% word accuracy. Our participant used the speech BCI in self-paced conversation for over 32 hours to communicate with friends, family, and colleagues. These results indicate that speech BCIs have reached a level of performance suitable to restore naturalistic communication to people living with severe dysarthria.

Branched broomrape seed germination response to QAC sanitizers

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A study was conducted to develop strategies for preventing the spread of branched broomrape seeds, a parasitic weed, in California's processing tomato fields. This weed is notorious for its vast host range and the production of thousands of tiny seeds, which can easily be spread via farm machinery. The study explored the efficacy of quaternary ammonium compounds (QAC) in various doses (0-2.5% w/v) and exposure durations (1, 3, and 5 minutes) to inhibit seed germination. It involved three phases: the first tested QAC's impact on preventing germination, the second assessed the effect of three commercial sanitizers containing QAC at a recommended dose (1% v/v) for a short exposure, and the final phase examined the influence of adding plant and soil debris to the sanitizers. Results indicated that certain QACs significantly reduced broomrape germination, with the effective dose for a 50% reduction ranging significantly. The study also found that at low concentrations, commercial sanitizers were effective, but their efficacy was quickly neutralized by the presence of plant and soil debris. Consequently, it was determined that machinery must be thoroughly cleaned before sanitizer application, and higher doses of QAC sanitizers are necessary when debris is present to prevent seed germination effectively.

Glyphosate & Glufosinate: Fate in California Almond Orchards

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In recent studies by the University of California researchers, 3-methylphosphinopropionic acid (MPPA), a glufosinate metabolite of regulatory importance was detected in some kernel samples above the European Union tolerance limits. In this context, to understand the fate and transformation of glyphosate, glufosinate and their metabolites in the soil in an orchard environment, two sets of treatments were evaluated in a micro-sprinkler irrigated orchard and an adjacent unirrigated non-crop area. One set of treatments included monthly application of

two rates of glyphosate and glufosinate tank-mixes to a new plot from April through July to evaluate herbicide fate in soil relative to different spring/summer application timings. Another set of treatments included the application of two rates of glyphosate and glufosinate tank-mixes in April looking at the half-life in soil. Leaf and kernel samples were collected to understand the correlating levels of parent compounds and metabolites to various spring/summer applications for both sets of treatments. Soil, leaf, and kernel samples were analyzed in commercial laboratory. MPPA in the non-irrigated site suggests substantially different rates of degradation in irrigated and non-irrigated portions of almond orchards. Future research should include year-round sampling and multiple applications during the year as is common in conventional almond orchards.

How smoky California was before the European settlement?

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Under an increasing high intensity fires scenario, reducing negative impacts of smoke is becoming crucial under a harsher climate, but when Californian regional agencies are committing for a greater use of fire as a fire management tool, targeting a non-smoke region is nonrealistic. A good way to address how much smoke is enough smoke is looking at the baselines. Here, we aim to estimate historical annual wildfire emissions (pre-1850) in the whole state of California according to historical fire burnt area estimates. Here, we update Stephens et al 2007 estimates by using used advanced burnt area calculations (fire rotation periods) and up-to-date FOFEM simulations to provide an updated value. Our provisional results show that total CO₂ emissions averaged 22.87 Tg per year, whereas fine particulates were 0.41 and 0.35 Tg per year for 10 and 2.5 particulates respectively. In California, since 2000 only five years have surpassed this amount of carbon dioxide emitted from wildfires (2008, 2017, 2018, 2020 and 2021), and the average for the 2000-2022 period is 21.44 Tg per year according to the California Air Resources Board. The results here point to California being a smoky region as it has been witnessed in recent years.

Deciphering the Intricate Dance: Pathogen Evolution Meets PRR Immune Signaling

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Plants are continuously exposed to attack by diverse pathogens. Plants possess an innate immune system comprised of germline-encoded immune receptors capable of recognizing all classes of pathogens. Surface-localized immune receptors known as pattern recognition

receptors (PRRs) activate immunity upon recognition of microbe-associated molecular patterns (MAMPs), leading to PRR-triggered immunity (PTI). PTI plays a crucial role in curtailing pathogen invasion. However, pathogens employ various strategies, including immune evasion and antagonism, to overcome PTI. The impact of epitope diversity on MAMP function, immune outcomes and pathogen restriction remains largely unexplored. In this study, we characterized the immunogenic outcomes of a bacterial MAMP, the Elongation Factor Tu (EF-Tu) epitope elf18. Our findings reveal that some elf18 epitopes can elicit early immune responses, such as the generation of reactive oxygen species, but not late immune responses. These elf18 epitopes with bifurcating responses are termed deviant epitopes. Our results will detail the capacity of deviant epitopes to bind to their respective plant immune receptor/co-receptors, restrict bacterial colonization, and retain protein function within bacteria. We hypothesize that deviant epitopes represent a general pathogen adaptation strategy and can serve as a tool to dissect PRR signaling.

POSTER PRESENTATIONS

Breastfeeding Goals, Experiences, and Infant Formula Perceptions Among Parents Affected by the 2022 U.S. Infant Formula Shortage

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This study examined the breastfeeding goals, experiences, and perceptions of infant formula among parents affected by the 2022 U.S. infant formula shortage. An anonymous cross-sectional survey collected data from 178 respondents across 37 states, predominantly female (93.3%). Eighty-one percent of females planned to breastfeed exclusively, yet 87% did not meet this goal. Eighty-six percent of females received lactation support postpartum and 18% paid out-of-pocket for lactation support. Half of females participated in prenatal and 35% participated in postpartum breastfeeding support groups. Before the shortage, 89% of parents relied on U.S. infant formula brands but decreased to 79% during the shortage. Imported infant formula increased from 2% to 7% and use of social media to purchase formula increased from 3% to 10%. Parents' dependence on U.S. shipments from friends or family increased from 11% to 25%. Twenty-seven percent of parents received recommendations on switching formulas, 25% obtained formula samples, and 16% received lactation and breastfeeding information. Parents were concerned what they would feed their infants if they stopped breastfeeding (83%) and about their infants' tolerance to a new formula (91%), parents introduced solid food earlier than planned (16%). The study highlights the urgent need for policy changes to stabilize formula supply, enhance breastfeeding education, and improve access to lactation support services.

Renewable Energy siting: Anticipating Future Conservation Risks and opportunities for Vulnerable Species

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As anthropogenic climate change progresses, attention is increasing on climate change mitigation, including a dramatic increase in renewable energy (RE) development. Simultaneously, the Biden Administration's 30x30 / America the Beautiful vision sets ambitious targets for conservation. Despite the promise of these goals for addressing conservation issues, conflicts between wildlife conservation and RE are of increasing concern. In this research, we are identifying conflicts between wildlife conservation and solar and wind siting by intersecting models of species' climate-change-induced range shifts with maps of RE potential. We are developing an integrated methodology for reducing conflicts between RE installations and conservation, both now and in the future. We aim to enhance RE capacity while reducing biodiversity impacts and facilitating research-related activities that enhance equity and energy democracy without compromising wildlife conservation goals. To identify target species, we conducted a systematic literature review. Additionally, we are considering costs and benefits to frontline communities and using a translational science approach to engage with and assess stakeholder attitudes, including semi-quantitative approaches to understand values and perceptions towards RE siting and its outcomes for wildlife towards identifying typologies of environmental injustice. Overall, we identify current and future impacts of RE siting scenarios on vulnerable wildlife populations towards a unified goal of Climate-Smart Siting to achieve best outcomes for climate mitigation, biodiversity, and local communities.

Unravelling the role of CaMKII δ S-nitrosylation in cardiac contractility and arrhythmias during ischemia-reperfusion

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Background: Ca²⁺/Calmodulin-dependent protein kinase II delta (CaMKII δ), a protein that plays key roles in cardiac function, is regulated via S-nitrosylation at two sites, C273 (inhibitory) and C290 (excitatory). S-nitrosylation of the excitatory site has been linked to cardiac arrhythmias. Since CaMKII is activated during early ischemia-reperfusion (I-R), it is possible that CaMKII δ S-nitrosylation during I-R may worsen left ventricular developed pressure (LVDP) recovery and lead to arrhythmias, but direct evidence is lacking.

Methods: Hearts from male C57BL/6 WT and C273S Knock-in mice (with excitatory site only) were Langendorff-perfused and subjected to 20 mins of global ischemia and 40 mins of reperfusion. We evaluated the effects of beta-adrenoceptor (B-AR) stimulation on LVDP recovery post-reperfusion and arrhythmias in early reperfusion.

Results: WT hearts exposed to B-AR stimulation had reduced LVDP recovery and increased arrhythmia duration in early reperfusion. However, hearts from C273S mice revealed no significant change with LVDP recovery and arrhythmias duration in early reperfusion.

Conclusions: Although CaMKII δ contributes to early I-R arrhythmias and reduced LVDP recovery, hearts from C273S mice that lack the inhibitory site, had similar LVDP recovery and duration of arrhythmias compared to WT hearts, suggesting that S-nitrosylation of CaMKII δ at C273 is insufficient to provide protection.

Qualification and quantification of mono/oligo/polysaccharides naturally occurring in pomegranate pomace via microfluidic chip-Q-TOF and QQQ platforms.

Han Peng and Daniela Barile

Pomegranates are often consumed in separated fresh arils or processed into juice and sauce, while the non-edible pomace are discarded, accounting for more than 50% of the whole fruit by weight. This research was to characterize and quantify the main functional carbohydrates in the pomegranate pomace, including monosaccharides, oligosaccharides, and polysaccharides, using a series of extraction, purification, derivatization, and MS (mass spectra) analysis methods.

Free oligosaccharide compositions were separated and analyzed using LC-**chip**-Q-TOF MS. The MS/MS results reveal 89 naturally occurring oligosaccharides with a diverse composition (from 3 to 8 units) in pomegranate pomace. Meanwhile, the QQQ MS results show that fructose ($46.24 \pm 2.43\%$) and glucose ($35.79 \pm 0.16\%$) are the richest free monosaccharide building blocks of these oligosaccharides, following by arabinose ($6.71 \pm 0.18\%$), galactose ($5.11 \pm 0.06\%$), and mannose ($2.01 \pm 0.03\%$). The total oligosaccharide content quantified by the QQQ method is 17.48 ± 0.39 mg/g raw material. Similarly, fructose ($50.33 \pm 0.62\%$) and glucose ($37.51 \pm 3.48\%$) are two major compounds of the free monosaccharides in the pomegranate pomace. The total content of free monosaccharides obtained by the QQQ method is 147.63 ± 6.25 mg/g raw material. The hydrolysis result of pomace residues providing the highest total monosaccharide contents (~ 200 mg/g raw material) is around 4-7h, which shows that the pomace is an excellent source of pomegranate polysaccharides.

Blocking Serine 1928 phosphorylation of $\text{Ca}_v1.2$ to rescue Long Term Potentiation (LTP) downstream β -Amyloid ($\text{A}\beta$) signaling

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Introduction: Alzheimer Disease (AD), the most common cause of dementia in the elder population, is characterized by irreversible loss of memory and cognitive function. The early stage is indicated by a high concentration of soluble β -Amyloid ($\text{A}\beta$) peptide. In the hippocampus, $\text{A}\beta$ increases $\text{Ca}_v1.2$ activity by activating the β_2 Adrenergic Receptor ($\beta_2\text{AR}$), through Serine 1928 phosphorylation. This activity alters synaptic plasticity, characterized by the loss of Long-Term Potentiation (LTP), leading to memory decay.

Method: LTP was recorded in hippocampal brain slices of WT or S1928A KI mice. During recording of the baseline, concentrations of $\text{A}\beta$ ranged from 100nM to 1 μ M. Additionally, nimodipine ($\text{Ca}_v1.2$ unspecific blocker) and ICI118,551 ($\beta_2\text{AR}$ blocker) have been perfused to treat slices.

Results and Perspectives: In WT mice, blocking either $\text{Ca}_v1.2$ or $\beta_2\text{AR}$ can restore LTP-impairment (160.9% and 128% of the baseline, respectively) caused by $\text{A}\beta$ (116.8% of the

baseline). Moreover, LTP is not affected in S1928A KI mice (159% with 200nM of A β), confirming that the phosphorylation site has a key role on A β toxicity and can be targeted for AD therapy.

The next step is to use MyrPEP2, a peptide developed by our lab, which displaces Cav1.2 and β 2AR directly to the S1928 phosphorylation site.

Structural investigation of A-to-I editing by Human Adenosine Deaminases Acting on RNA 1 (ADAR1) complexed with dsRNA using Cryo-Electron Microscopy (Cryo-EM)

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Adenosine deaminases acting on RNA (ADARs) are editing enzymes that convert adenosine (A) to inosine (I) in duplex RNA, a modification reaction with wide-ranging importance in RNA function. In humans, two active ADARs are known: ADAR1 and ADAR2. Mutations in gene encoding ADAR1 cause Aicardi–Goutières syndrome and the skin disorder dyschromatosis symmetrica hereditaria. Although X-ray crystal structure of ADAR2 bound to different RNA duplexes have been solved, there is no high-resolution structure of the ADAR1. Hence, a structure of ADAR1 with the help of cryo-EM is necessary to understand the RNA binding and editing mechanism of the protein. Recently, we have overexpressed and purified active ADAR1 protein using yeast expression. We have synthesized the target RNA, with the nucleoside analog 8-azanebularine at the edited site of duplex RNAs, forming a stable complex for structure determination. Cryo-EM grids were screened on the Glacios microscope (200 kV), and image processing was done using cryoSPARC 4.0. Iterative rounds of 2D classification produced several classes of ADAR1-RNA bound complexes and best classes were selected for an ab-initio reconstruction. Currently we have an electron density map of 7.0 Å resolution. Additional data will be collected on the Titan Krios at S²C² in the future.

Computational characterization of decision making in a visual perception task

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Moving the eyes to sample the environment disrupts the flow of incoming visual information and subsequently the perception of a continuous scene. Compensating for these disruptions across eye movements is hypothesized to be aided by the integration of external sensory and internally-generated information. In this project, we developed a drift diffusion model (DDM) to capture this integration process in a visual perception task. We recruited healthy control subjects ($N = 30$) to track a screen target that changed position along the horizontal plane during eye movements. We monitored eye movements and the direction subjects reported for the target change (“left” vs. “right”). Responses were made by pressing one of two buttons indicating the target shift direction. The button press reaction time, precision of eye movements (i.e., saccades), and manual response directions were used as model inputs to predict the perceptual accuracy (i.e., the reported target shift change compared to the actual change). We show how different model parameters can mechanistically explain the perceptual decisions during the task. Our operationalization of the DDM acts as a unified computational model that may later be implemented in clinical contexts to provide an explanatory account of patients’ perceptual deficits (e.g., schizophrenia).

**Unraveling drought resistance mechanisms at root level in various monkey flowers
(*Mimulus Guttatus*) populations.**

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Drought is a major problem for California agriculture. Last year, summer drought cost the state over a billion dollars in crop losses. Understanding how plant can cope with this stress is a challenge, but various species in nature are already adapted and have their own mechanisms for combating drought. In this study, we use a remarkable plant, *Mimulus guttatus*, as model. Native to the American west coast, this plant can survive in Mexican desert, on serpentine rocks, or snow-covered peaks. This suggests that different populations have evolved various resistance mechanisms. Using 22 different populations harvested across California and Oregon before and after the huge drought of 2015, we plan to carry out a genome-wide association study. We want to compare the SNPs present in these populations with their root system architecture phenotype, an analyze of differentially expressed genes and a histological analysis focusing on cell wall compounds such as lignin and suberin. All these traits will be measured in normal condition and in response to drought stress, using PEG8000 which mimic drought *in vitro* by reducing water availability. We hope to find new genes involved in drought resistance and even shed light on mechanisms never observed in other species.

PROMISE II – Image-based high-throughput quantification of lignin, suberin and aerenchyma in *Sorghum bicolor*

Stefan Sanow¹, Tamera Taylor¹, Dustin Hadley^{1,2}, Randy P. Carney², Siobhan M. Brady¹

Sorghum bicolor, a key cereal crop globally and vital staple in sub-Saharan Africa, faces significant yield loss due to *Striga hermonthica* infestation, a devastating plant parasite with dormant seedbanks in African soils. Modifying root anatomy, including increasing lignin, suberin, and aerenchyma content, may reduce susceptibility to *Striga hermonthica*. Microbes of the genera *Arthrobacter* and *Pseudomonas* and fungi, isolated from African soils (Ethiopia, Senegal, Tanzania), are being evaluated for their potential to enhance cellular barriers. *Sorghum bicolor* will be imaged via confocal microscopy for machine learning-based high-throughput analysis, enabling quantification of lignin, suberin, and aerenchyma within the same image. In future experiments, the aforementioned microbes and fungi, which can be cultivated in labs and show no pathogenicity, will undergo screening in various *Sorghum bicolor*, *Oryza sativa*, and *Pennisetum glaucum* genotypes, conducted at both laboratory and greenhouse levels. Promising candidates will subsequently undergo field trials for further evaluation.

Tailored Sialosides with 8-N-Substituted Sialic Acid: Selective Substrates for Bacterial and Influenza Virus Sialidases

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Sialosides, featuring C8-modified sialic acids, present formidable challenges in synthesis but hold immense promise as diagnostic tools for profiling sialidases and elucidating sialic acid-protein interactions. In this study, we unveil efficient chemoenzymatic pathways for synthesizing para-nitrophenol-tagged α 2–3- and α 2–6-linked sialyl galactosides with C8- N-acetyl, C8-azido, or C8-amino derivatized N-acetylneuraminic acid (Neu5Ac). Our comprehensive substrate specificity assays unveil a striking shift in recognition by sialidases from humans, diverse bacteria, and influenza A and B viruses induced by the C8 modifications. Notably, sialosides adorned with C8-azido modifications exhibit remarkable tolerance across all tested sialidases. Conversely, those with C8-N-acetyl modifications exclusively engage selective bacterial sialidases. Most intriguingly, sialosides featuring C8-amino modifications are targeted by a synergistic array of bacterial and influenza A virus sialidases. These findings underscore the potential of sialosides terminated with C8-amino or C8-N-acetyl modified sialic acids as pivotal components in diagnostic profiling of pathogenic sialidase-producing agents. By leveraging these modified sialosides alongside traditional counterparts, we chart a course towards enhanced diagnostic precision in combating sialidase-associated diseases.

Investigating the Roles of E3 Ubiquitin Ligases Regulating Poplar Wood Development under Drought

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Angiosperm wood contains highly lignified tube-like cells called vessel elements whose dimensions and distribution affect water transport and growth rates, as well as susceptibility to hydraulic failure during drought. Despite their crucial role in determining the hydraulic physiology of trees, the molecular components responsible for vessel element development remain unclear. In a dosage-dependent genome-wide screen we detected the height adjusted mean vessel diameter and frequency significantly correlated to genes that code for E3 ubiquitin ligases. Here, we selected vessel trait-related E3 ligase candidates for further functional characterization of ubiquitin-proteasome regulation in poplar wood forming tissue. To achieve this goal, CRISPR-Cas9 mutants targeting poplar E3 ligase candidate genes have been generated to assess alterations in wood phenotype, gene expression, protein abundance, and ubiquitinomes. Additionally, TurboID transgenic lines are being generated to elucidate protein interacting partners for our candidate proteins through proximity labeling. In anticipation of poplar E3 ligase datasets, we examined the interactome of similar components in Arabidopsis transgenic lines subjected to drought and ABA treatments, revealing substantial treatment-induced alterations in the UPS compared to controls. These approaches aim to enhance our understanding of the role of the ubiquitin-proteasome system in wood formation and tree responses to environmental stressors.

The R2R3-MYB transcription factor AtMYB49 modulates salt tolerance in Arabidopsis by modulating the cuticle formation and antioxidant defence

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Salt stress activates defence responses in plants, including changes in leaf surface structure. Here, we showed that the transcriptional activation of cutin deposition and antioxidant defence by the R2R3-type MYB transcription factor AtMYB49 contributed to salt tolerance in *Arabidopsis thaliana*. Characterization of loss-of-function *myb49* mutants, and chimeric AtMYB49-SRDX-overexpressing SRDX49 transcriptional repressor and AtMYB49-overexpressing (OX49) overexpressor plants demonstrated a positive role of AtMYB49 in salt tolerance. Transcriptome analysis revealed that many genes belonging to the category “cutin, suberin and wax biosyntheses” were markedly up-regulated and down-regulated in OX49 and SRDX49 plants, respectively, under normal and/or salt stress conditions. Some of these differentially expressed genes, including MYB41, ASFT, FACT and CYP86B1, were also shown to be the direct targets of AtMYB49 and activated by AtMYB49. Biochemical analysis indicated that AtMYB49 modulated cutin deposition in the leaves. Importantly, cuticular transpiration, chlorophyll leaching and toluidine blue-staining assays revealed a link between increased AtMYB49-mediated cutin deposition in leaves and enhanced salt tolerance. Additionally, increased AtMYB49 expression elevated Ca²⁺ level in leaves and improved antioxidant capacity by up-regulating genes encoding peroxidases and late embryogenesis abundant proteins. These results suggest that genetic manipulation of AtMYB49 may provide a novel way to improve salt tolerance in plants.

Incidental myocardial infarction on routine thoracic Computed Tomography.

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OBJECTIVES: Myocardial infarction (MI) is a major health concern worldwide. This study aim to evaluate the prevalence, characteristics, and clinical implications of incidental MI findings on routine non-gated thoracic CT.

METHODS: We retrospectively assessed all individuals aged 18 or above who underwent routine non-gated thoracic CT scans as outpatients at University of California Davis in 2015. We evaluated the presence and location of incidental MI on non-gated thoracic CT and compared major adverse cardiac events (MACE) and overall survival in infarct patients with a control group.

RESULTS: We reviewed non-gated thoracic CT scans of 1157 individuals and identified 12 individuals with incidental MI. The mean age was 71.4 ± 14.1 years, and 50% were female. All patients with incidental MI had coronary calcification. Patients with incidental MI had a higher rate of MACE endpoint (92% vs. 28%, p=0.0001), number of MACE events (1.1 vs. 0.3, p<0.001), and lower overall survival (median survival of 67 months, p=0.023) than those without incidental MI.

CONCLUSIONS: Incidental MI can be detected on routine non-gated thoracic CT scans and is associated with worse cardiovascular outcomes and overall survival compared with absence of infarction.

Development of recombinant nanobodies against Connexin 43 hemichannels

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Connexin-43 (Cx43) is the main connexin isoform found in the heart. They assemble as hexamers to form hemichannels, which, at the plasma membrane, dock with an hemichannel from an adjacent cell to form a gap junction channel (GJC). GJC are essential for proper heart functioning via metabolic and electric coupling. In many cardiac diseases, however, undocked Cx43 hemichannels are remodeled to the lateral side of cardiomyocytes, where they open upon cardiac stress leading to disruption of cardiac excitability. Due to their medical relevance and lack of proper tools, we aimed to develop anti-undocked hemichannel nanobodies, targeting the second extracellular loop of Cx43 (EC2-nAb). Peptides corresponding to EC2 were used for llama immunization, resulting in a serum with high reactivity towards EC2. The llama's B-cells were used as source of nAb-coding RNA to produce a nAb-Phage library. After three selection cycles, bacteria infected by EC2 nAb-Phages were individually cultivated, and the recombinant EC2-nAb production was induced by IPTG. More than 80% of the tested colonies produced EC2-nAbs with at least a 3-fold higher reactivity towards EC2, compared to the control. This work resulted in 7 different nAbs with potential to recognize and prevent the opening of Cx43 undocked hemichannels.

Synergizing composting and biochar: Setting the stage for a sustainable tomorrow

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Composting is hailed as a cornerstone of sustainable waste management, facilitating the conversion of organic materials into valuable resources. However, challenges such as greenhouse gas emissions, nutrient leaching, and organic matter loss can compromise its sustainability objectives. Recently, biochar has emerged as a promising additive for composting, offering a range of benefits including mitigating greenhouse gas emissions, enhancing microbial activity, improving composting efficiency, and immobilizing pollutants. The study examined the

co-composting process, focusing on changes in greenhouse gas emissions and nutrient contents. Dairy manure and rice straws were co-composted with different ratios of biochars (derived from walnut shells and wood chips) and FeCl₃-modified biochars. Additionally, various pristine and modified biochars were screened for their efficiencies to adsorb various nutrients, which could be crucial for subsequent potential applications. Embracing composting with biochar holds significant potential for achieving objectives of environmental and agricultural sustainability. The outcomes of the study could assist in mitigating climate change, fostering cleaner environments, healthier soils, and a more resilient food system, ultimately paving the way for a sustainable tomorrow.

Revealing the Arabidopsis SCF Ubiquitin Ligases Interactome through TurboID-based Proximity Labeling

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Protein ubiquitination, a vital post-translational modification, plays diverse roles in numerous cellular processes. To gain a comprehensive understanding of the dynamic interactome within the ubiquitin pathway, we employed TurboID-based proximity labeling as a powerful investigative tool in plants. By genetically fusing TurboID to Skp1-Cullin-F-box (SCF), we successfully captured and identified neighboring proteins involved in the ubiquitination process. Utilizing mass spectrometry-based proteomics, we identified both well-known components of the ubiquitin pathway and novel interactors, collectively forming an intricate map of the ubiquitin pathway network. Notably, this study unravels previously unexplored protein-protein interactions and sheds light on potential regulatory mechanisms. Our findings highlight the immense potential of TurboID-based proximity labeling in elucidating the functional roles of proteins engaged in protein ubiquitination and related cellular processes and other related cellular processes.

Validation of Endopep-Mass Spectrometry method for qualitative detection of botulinum toxin serotype C in animal sera using spiked and archived animal botulism case samples

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Botulinum toxins (BoNTs) are potent neurotoxins produced mostly by *Clostridium botulinum* and cause flaccid paralysis in humans and animals. *C. botulinum* and its toxins are classified into seven types, A through G. The standard method for identification of BoNTs is the mouse bioassay (MBA) which is a lethal test and requires many mice per sample. The end goal of this work is to replace the MBA currently performed at CAHFS with an alternative *in vitro* assay – Endopep-Mass Spectrometry (Endopep-MS). This method utilizes proteolytic properties of the BoNTs to cleave a synthetic peptide containing a cleavage location specific to each BoNTs serotype. A positive result can be confirmed by the detection of two peptide cleavage products using mass spectrometry. The initial phase of this work focuses on development of the Endopep-MS for detection of botulinum toxin serotype C (BoNT/C) in animal sera. Partial validation suggests this method can detect BoNT/C in chicken and duck sera at the level of 10 mLD₅₀ with 100% probability and at the level of 2 mLD₅₀ with 50% probability. Next steps will include the validation of this method with MBA using BoNT/C spiked samples and archived samples collected from natural botulism cases.

Investigating metabolic sensitivity and renal cell carcinoma organization: to improve therapies and patient survival.

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Background: Renal cell carcinoma (RCC) is the 6th (in men) and 9th (in women) most common cancer in the United States. RCC tissues are metabolically dysfunctional. Current therapies, including immune checkpoint inhibitors and tyrosine kinase inhibitors, have shown improvements in the outcomes of patients with RCC, however, there are no biomarkers clinically available to predict the efficacy of these drugs.

Aim: We aim to investigate changes in metabolic adaptation in RCC from kidney cancer cell lines and primary cells isolated from human cancer sites using live biosensor assay.

Methods: We have built cell lines with metabolic reporters and using a novel biosensor-based technique developed in the Albeck lab to identify the dependence of live RCC cells on specific metabolic pathways tested for standard-of care (SOC) pathway inhibitors.

Results & Conclusion: Our preliminary results show an association of high oxidative phosphorylation (OXPHOS) with primary tumors from early relapse after nephrectomy than the relapsed late tumors. In addition, heterogeneity in genetically homogeneous cell populations

can influence usage of OXPHOS and glycolysis to supply ATP for cell growth. The knowledge will not only improve tumor prognosis but will enable designing therapeutic trials to optimize the use of targeted or metabolic inhibitors.

Genotyping-By-Sequencing on an Iranian Cannabis Collection to Identify Genetic Variants Associated with Unique Characteristics in Cannabis

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Future breeding and selection of *Cannabis sativa* L. for drug production and industrial purposes require a source of germplasm with wide genetic variation, such as that found in wild relatives and progenitors of highly cultivated plants. Limited directional selection and breeding have occurred in this crop, especially informed by molecular markers. Here, we investigated the population genomics of a natural cannabis collection of male and female individuals from differing climatic zones in Iran. Using Genotyping-By-Sequencing (GBS), we sequenced 228 genotypes from 35 populations. The results obtained from GBS were used to perform association analysis identifying links between genotype and important phenotypes, including inflorescence characteristics, flowering time, plant morphology, tetrahydrocannabinol (THC) content, cannabidiol (CBD) content and sex. Approximately 23,266 significant SNPs of high quality were detected to establish associations between markers and traits, and population structure showed that Iranian cannabis plants fall into five groups. A comparison of Iranian samples from this study to global data suggests that the Iranian population is distinctive and, in general, is closer to marijuana than to hemp, although some populations in this collection are closer to hemp. The GWAS results showed that novel genetic loci, not previously identified, contribute to sex, yield and chemotype traits in cannabis and are worthy of further study.

Deciphering the form and function of Transcription Factors in *Giardia duodenalis*

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Giardia duodenalis is a protozoan parasite of interest as it's a human pathogen and a highly divergent protist from an understudied supergroup. *G. duodenalis* have a simple life cycle, cycling between the immotile but environmentally hardy cyst, and the flagellated trophozoite.

While in a host, trophozoites are challenged by host immunity and microbiome, as well as oxygen/food fluctuations. Surviving must require robust and precise systems to regulate gene expression. Sequence specific Transcription Factors (TFs) are DNA binding proteins involved in gene expression regulation but are poorly described in *G. duodenalis*, with just 16 TFs annotated in the genome, and only 6 experimental studies in the literature. Here I will describe our efforts to characterize TFs in *G. duodenalis* using novel reverse genetic approaches, and to identify additional TFs using computational methods. Our newly developed Cas9 mediated knockout strategy has yielded some of the first ever complete tetraploid knockouts in *G. duodenalis*. The responses to condition changes in knockout strains are being assessed by multiple molecular methods including Immunofluorescence and RNA-Seq, with particular focus on life-cycle changes. Preliminary data suggest we have identified an agonist and antagonist to encystation, and additional TFs that seemingly are not involved in encystation at all.

Molecular snapshots of the mitochondrial machinery in *Diplonema papillatum*.

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Respiring organisms utilize a structurally and functionally conserved set of mitochondrial respiratory protein complexes I to IV (CI to IV) as electrochemical wires and proton pumps for ATP synthase (CV) to produce ATP. Despite similarities between mitochondrial respiratory protein complexes across species, there are variations in composition and higher order assemblies. Differences in assembly and regulation are also observed across species. However, the impacts of these structural variations on function remains elusive, partly due to a lack of available structural and biochemical data from a diverse set of organisms. Here we show snapshots of the mitochondrial machineries in *Diplonema papillatum* (*D. papillatum*), a planktonic protist. Using a cryogenic electron microscopy (cryoEM) based bottom-up structural proteomics approach, we isolated mitochondria complexes directly from *D. papillatum* mitochondrial membranes and classified them *in silico*. Through this approach, we visualized structures of CIII₂, CV, and a yet unidentified complex. Our results attest to the molecular diversity of mitochondrial proteins, as well as suggest the degree of variation across eukaryotes, most of which remains to be unveiled. We anticipate further optimizations will provide additional structural insight of other protein complexes and offer further insight into the structural-functional diversity and plasticity of mitochondrial respiratory proteins.

Protein-Based Rechargeable and Replaceable Coatings: Antimicrobial and Anti-fouling Solutions for Hydrophobic Food-Contact Surfaces

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The growing concerns regarding foodborne illnesses related to fresh produce accentuate the necessity for innovative material solutions, particularly in surfaces that come into close contact with foods. This study introduces a sustainable, efficient, and removable antimicrobial and antifouling coating, ideally suited for hydrophobic food-contact surfaces such as low-density polyethylene (LDPE). Developed through a crosslinking reaction involving tannic acid (TA), gelatin, and soy protein hydrolysate (SPH), these coatings exhibit proper stability in aqueous washing solutions and effectively combat bacterial contaminations and prevent biofilm formation. The unique surface architecture promotes the formation of halamine structures, enhancing antimicrobial efficacy with rapid contact killing effect, reducing microbial contamination by up to 5 Log₁₀CFU·cm⁻² against both *Escherichia coli* (Gram-negative) and *Listeria innocua* (Gram-positive). Notably, the coatings are designed for at least five recharging cycles under mild conditions and can be easily removed with hot water or steam to refresh depositions. This removal process not only conveniently aligns with existing sanitation protocols in fresh produce industry but also facilitates the complete eradication of potential developed biofilms, outperforming uncoated LDPE coupons. Overall, these coatings represent a sustainable, cost-effective, and practical advancement in food safety and are promising candidates for widespread adoption in food processing environments.

Genetic underpinnings of the persistent phenotype in *Listeria monocytogenes*

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Listeria monocytogenes is a particularly lethal pathogen that can exist long-term in harsh environments through the induction of a physiologically distinct persister state marked by substantially reduced growth rate and increased stress tolerance. Persistent *Listeria* have been associated with recurrent outbreaks from singular sources across many decades. Consumption of foods contaminated with these populations causes irreparable host harm, including spontaneous abortion in humans and animals. While broadly understood that extracellular stressors like antibiotic pressure and starvation expose persistent populations of *Listeria*, the intracellular signals that prompt entry into this state and the reemergence to active growth remain unknown, making detection and treatment of persister populations difficult. To better understand genetic regulation of the persistent phenotype, *Listeria monocytogenes* EGDe grown in carbohydrate-depleted medium was subsequently revived in serum and longitudinally profiled using gene expression analysis. Differential gene expression revealed environment-sensing two-component systems, such as *LisRK*, were important for both induction into the persistent phenotype and resuscitation to active replication. Such findings suggest persistent

Listeria are genetically exquisitely poised to sense and respond to metabolic conditions in the host that favor *Listeria* to quickly expand infection, supporting that persister pathogen populations are a pertinent yet understudied threat to public and animal health.

Towards Measuring Toxic Volatile Organic Compounds in Environmental Justice Communities

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Air pollution causes significant health issues and environmental concerns. Small atmospheric particles and toxic volatile organic compounds (VOCs) are key contributors to air pollution, damaging wildlife, vegetation, and increasing global mortality rates, thereby affecting the prosperity of agriculture. VOCs originate from both natural sources like smoke from wildfires, volcanic eruptions or decomposition of organic materials, as well as anthropogenic sources such as vehicle emissions, burning of fossil fuels, industrial by products, and solvents. The US Environmental Protection Agency has listed over 180 compounds as hazardous air pollutants which need to be monitored for protecting public health and the environment. As a result, determination of air pollutants that populations and vegetation are exposed to are of primary concern, yet portable, real-time instruments for measuring these pollutants are too expensive for routine deployment. A common method for measuring the VOCs is gas chromatography mass spectrometry (GC-MS), which can detect and quantify VOCs in both indoor and outdoor environments. In this work, we will show the working principle, application areas, and our progress developing a low-cost, light-weight, battery-powered portable GC-MS intended to be more accessible to broader audience.

Timing of red LED supplementation on tomato plants to manipulate preference and performance of *Tetranychus urticae* (Acari: Tetranychidae)

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Light-emitting diodes (LED) are being used in greenhouses to improve crop production and pest management strategies, and most studies have focused on continuous LED treatments. Here, we investigated direct and indirect effects of supplementing tomato plants (with a daily 3-hour red LED during either daytime or nighttime) on populations of two-spotted spider mites (TSSM)

(*Tetranychus urticae* Koch). Nighttime red LED supplemented-plants significantly increased glandular trichome densities. Two-choice preference bioassays (leaf discs from untreated control tomato plants and from tomato plants subjected to red LED) revealed that TSSM significantly avoided settling on red LED treated leaf discs. Additionally, we observed a significant avoidance of settling and oviposition by TSSM on leaf discs from nighttime red LED supplemented plants when compared to daytime plant treatment. Life table studies showed a slower development time and a significant reduction in fecundity and longevity of TSSM on leaf discs from plants supplemented with red LED at nighttime. Our results support the hypothesis that supplementing tomato plants with timed red LED supplementation significantly reduces their suitability as hosts for TSSM.

Horizontal Gene Transfer into Poxviruses is Mediated by LINE-1 Retrotransposons

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Horizontal gene transfer (HGT) is an important driver of the evolution and functional diversity of all major life forms, including viruses. Bioinformatic analyses have indicated that poxvirus genomes contain a substantial number of genes that have been likely acquired from their hosts. However, the mechanism(s) by which host genes can be acquired by poxviruses remained elusive. We developed an experimental system to investigate HGT in a laboratory setting by harnessing the selective pressure imposed by protein kinase R (PKR) on vaccinia virus (VACV) replication. VACV contains two genes (E3L and K3L) that allow it to evade a host defense mechanism mediated by PKR. We generated rabbit cells that stably express VACV E3L and infected them with PKR-sensitive VACV mutants that lacked both E3L and K3L. With this system, we found a total of 27 cases of poxviruses that acquired E3L from the host. The integration sites were distributed throughout the VACV genome with a transfer rate of 1 in 23 million viable virions. All isolates displayed hallmarks of RNA-dependent LINE-1 retrotransposon-mediated integrations, including spliced-out introns, the presence of target side duplications and poly(A) tracts at the 3' end. Overall, we elucidated a mechanism of HGT from hosts to poxviruses.

Characterization of the role of NHIP in oxidative stress

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Autism spectrum disorder (ASD) is a neurodevelopmental disorder with a complex etiology involving genetic, environment, and gene-environment interactions. We recently discovered a

novel gene, NHIP (neuronal hypoxia inducible, placenta), which has decreased expression in ASD placenta and brain. NHIP is transcribed as a long non-coding RNA that encodes a nuclear-localized, 20 amino acid-long peptide predicted to contain a 9 amino acid transactivation domain. Its transcript levels increase in the neuronal cell line LUHMES following differentiation and exposure to hypoxia. To test the hypothesis that NHIP plays a protective role in response to oxidative stress, we measured reactive oxygen species (ROS) levels in undifferentiated and differentiated LUHMES and HEK293T cells that were treated with NHIP peptide. We found that NHIP treatment decreases ROS levels in HEK293T cells and undifferentiated LUHMES, which have low endogenous levels of NHIP, but does not have a significant effect on ROS levels in differentiated LUHMES, which have high levels of NHIP. This supports the hypothesis that NHIP plays a protective role in oxidative stress. Characterization of NHIP will allow for evaluation of its potential use as a neuroprotective therapeutic in neurodevelopmental disorders such as ASD.