



# UC Davis Summer Research Symposium

Friday, 11 August 2023, 1:00-3:15pm

Gibeling Room, Walker Hall

## 1:00-1:30 Presenter group 1A

- A.1 **Marie D Delcy**, Z. Mostofinejad, E. Cremonini, D. Milenkovic, and P. Oteiza  
Differential postprandial responses to a high fat meal in healthy humans with a focus on individual's hypertriglyceridemia
- A.2 **Naomi Becks**, Tatiana Diacova, Francene M. Steinberg  
Validation of a Calprotectin ELISA assay
- A.3 **Maraé M. Woodson**, Aya S. Ead and Gerardo G. Mackenzie  
Investigating potential molecular targets for diet induced obesity in early stages of pancreatic carcinogenesis in mice
- A.4 **Srinivas Rao Voruganti**, Duncan Sylvestre, Kirsten J. Roslund, Carolyn M. Slupsky and Ameer Y. Taha  
Role of ketone ester supplementation on hippocampal lipid metabolism in aged mice
- A.5 **Celaya J. Murray**, T. Bolt, A.Palkovic, J. Adaskaveg, C. Diepenbrock  
Evaluating hundred-seed weight and nutritional quality traits in lima beans for California

## 1:30-2:00 Presenter group 1B

- B.1 **Patrick H Roehling**, A. Padvannil, and J. Letts.  
Functional characterization of plant mitochondrial complex II
- B.2 **Hannah Herron**, Heddy Menendez, and Crystal D. Rogers.  
Defining the stage specific role of SOX9 in avian neural crest cell development
- B.3 **Nancy S. Diaz**, Camilo V. Echeverria, Jr., and Crystal D. Rogers.  
Spatiotemporal characterization of tissue-specific tubulin subunits during avian development
- B.4 **Donnie Ca**, N. Aoun, R. Chen, N. Guillome, N. Bonagura, L. Repetto, V. Elmgreen, T Lowe-Power  
Investigating genetic factors that contribute to *Ralstonia*'s fitness

- B.5 **Jaequon M Henderson**, ST Traxler, MK Mary Kable  
Honey does not affect the virulence gene expression of Enterotoxigenic *E. coli* (ETEC) in mock small intestine communities.
- B.6 **Helen M Noroian**, AN Martin, RL Vannette.  
Pollen has differential effects on the growth of nectar-inhabiting microbes

**2:00-2:15 break**

**2:15-2:45 Presenter group 2A**

- A.1 **Jala C Rice**, O Sharifi, D Yasui, J LaSalle  
snRNA-seq integration enables accurate cell-type labeling in the Hypothalamus of Rett Syndrome mouse model
- A.2 **Christy Wheatley**, J Ross-Ibarra, AR Phillips.  
Genome size variation does not affect anatomy and growth in *Tripsacum dactyloides*
- A.3 **Claudia M. Perez** and Jeffrey Ross-Ibarra.  
Ethnolinguistic influence on maize genetic diversity
- A.4 **Eryse L. White**, Alan Urquidi, Fallon Ely, Beth Forrestel  
Unveiling cultivar resilience: physiological indicators for sustainable viticulture in a changing climate
- A.5 **Marisha Towner**  
Plant partners

**2:45-3:15 Presenter group 2B**

- B.1 **Samantha P. Hubbard**, J. P. Michielini, E. E. Crone  
Why didn't the butterfly cross the road?
- B.2 **Cailin M. Kessen**, L.H. Yang  
Effect of host plant on pyrrolizidine alkaloid collection in monarch butterflies (*Danaus plexippus*)
- B.3 **Kenneth Damper**, S. Khan, K. Laskowski  
Do clonal fish spend more time with closely related clones?
- B.4 **LaCommare-Soto, A; Duchild, PH**; Bay, RA; Stachowicz, JJ.  
No significant effect of eelgrass genotype on wasting disease lesion severity
- B.5 **Nargis Karamatova**, Anthony Tercero, Anne Todgham.  
How does EE2 affect both physiology and cognitive health in Mangrove Killifish?

Please also join us for refreshments in the adjoining conference room and enjoy the EERREC videos

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## ABSTRACTS

**Naomi Becks**, Tatiana Diacova, Francene M. Steinberg. Validation of A Calprotectin ELISA Assay (1A.2)

Calprotectin is a zinc- and calcium-binding protein that is usually found within neutrophils. The presence of calprotectin in feces can be a sign of neutrophil migration into the gastrointestinal tissue due to inflammatory processes. An increased concentration of fecal calprotectin has been detected in individuals with chronic diseases like cardiovascular disease, ulcerative colitis, and irritable bowel disease. Walnut consumption has shown potential to decrease intestinal inflammation in mice likely due to ellagitannins being converted to urolithin metabolites by gut microbes. Urolithins have demonstrated anti-inflammatory effects in the gut in vivo and in vitro. However, the effect of daily walnut consumption on fecal calprotectin levels has not been investigated in human subjects yet. Steinberg lab is aiming to explore this by conducting a randomized crossover clinical trial where generally healthy individuals between the ages of 45 and 70 yo, BMI >25 kg/m<sup>2</sup> and elevated LDL-cholesterol are asked to consume 2 oz of walnuts daily for 3 weeks. Hypothesis: One of the overall trial hypotheses is that daily walnut consumption will decrease calprotectin concentration in feces relative to control diet. The summer subproject was to develop and validate fecal calprotectin measurement protocol. Methods: Steps from various relevant manual kits were consolidated and developed into a step-by-step protocol. This protocol was then adjusted based on feedback from other researchers in the department who do similar work. Four experiments utilizing fecal samples from three different human donors were conducted. Appropriate fecal sample collection materials, protein extraction tools, and a commercially available ELISA kit were used. Optimal sample dilution was determined by testing various dilution factors spanning from 100 to 2500. The obtained results were multiplied by the appropriate dilution factor to get the actual calprotectin concentrations in the original sample. Calibration curve was constructed at each experiment using Prism 10. Samples, controls, and standards were plated in duplicates. Results: The calibration curve was constructed with the following standards: 0, 13, 52, 210 and 840 ng/ml. Our goal was to determine a dilution factor that would produce an assay concentration falling in the middle of the calibration curve (between 52 and 210 ng/ml). The dilution factor of 2500 suggested by the ELISA kit manual did not produce a desirable result for either of the three samples tested. Lower dilution factor of 500 worked for one out of the three samples where the assay concentration was 67.359 ng/ml. Dilution factor of 200 produced a desirable result for two out of the three samples, where the assay concentrations were 135.148 ng/ml and 80.295 ng/ml. Conclusion: The dilution factor of 200 was determined as optimal to be used for the overall trial sample analysis. While it did not work for one of the samples tested, that could be due to the fact that this particular sample was donated by an individual younger and healthier than the actual trial population. The other two samples were representative of the population of interest. Calprotectin concentrations of 27.03 ug/ml (1 ml = 1 g) and 16.06 ug/ml in the original samples is appropriate for the age group and consistent with what is being reported in the literature.

**Donnie Ca**, N. Aoun, R. Chen, N. Guillome, N. Bonagura, L. Repetto, V. Elmgreen, T Lowe-Power. Investigating genetic factors that contribute to *Ralstonia*'s fitness (1B.4)

*Ralstonia* are plant pathogens that cause wilting of plants and they are known to infect around 400 different plant species. However, *Ralstonia* adaptation mechanisms to plant species are poorly understood. To investigate *Ralstonia* adaptation mechanisms we used a Random-Barcoded Transposon Mutant sequencing (RB-Tnseq) approach which is a forward genetic screening of thousands of bacterial transposon mutants. This screening allows us to study *Ralstonia* gene function in various conditions. In this study, we found that transporters seem to be involved in *Ralstonia* adaptation to tomato cultivars. The goal of my project is to functionally validate an ABC transporter by creating a knockout mutant and then testing it in planta conditions for disease severity.

**Kenneth H. Damper**, S. Khan, K. Laskowski. Do clonal fish spend more time with closely related clones? (2B.3)

Amazon Mollies are an all-female, clonal and gynogenetic species that are a result of a hybridization between Atlantic and Sailfin mollies. A result of their gynogenetic nature is that they are sperm parasites and are obligated to group together with their parental species. As per kin selection theory (Hamilton WD), Amazons should display more cooperative behavior towards other amazons rather than their parental species. Kin selection also predicts that cooperation should scale with relatedness, so Amazons should modulate their behavior towards other Amazons based on the degree of kinship between them. However, given that Amazons are clones, it may be difficult or even redundant for them to differentiate between sister and non-sister clones. In our project, we aimed to test this. We gave an Amazon from the Scharf line a choice between a stimulus fish, which would be a different clonal line or different species, and a control fish, which would be a fish from the same clonal line as the focal. The non sister clones were from the AM 11 and San Ignacio clonal lines, while the different species was a Sailfin Molly. If the Amazons prefer to associate with closely related individuals, we would expect to see that the focal fish interacts more with the sister clone than the stimulus fish. We would also expect the non-sister clones to receive more interaction from the focal fish as compared to the sailfin molly, which is a different species.

**Marie D Delcy**, Z. Mostofinejad, E. Cremonini, D. Milenkovic, and P. Oteiza. Differential postprandial responses to a high fat meal in healthy humans with a focus on individual's hypertriglyceridemia (1A.1)

Postprandial dysmetabolism is a condition that occurs after eating that is defined by abnormal glucose and lipid metabolism. More specifically, it is characterized by high levels of glucose and lipoproteins, including triglycerides (TG). It has been observed that around 30% of young, healthy individuals do not experience a substantial rise in plasma TG after consuming a high-fat meal within a 5-hour timeframe. Thus, in this study, our aim is to characterize potential

differential responses in those participants who exhibit low or high postprandial cumulative plasma TG increase over the course of 5 hours. The objective of this study is to investigate the effects of a high fat meal (HFM) on 1) parameters of lipid and carbohydrate metabolism in plasma and 2) genomic variations in peripheral blood mononuclear cells (PBMCs), in healthy humans with low and high postprandial hypertriglyceridemia. We have observed significant differences in the effects of HFM consumption on postprandial hyperlipidemia between participants with low and high postprandial hypertriglyceridemia.

**Nancy S. Diaz**, Camilo V. Echeverria, Jr., and Crystal D. Rogers. Spatiotemporal characterization of tissue-specific tubulin subunits during avian development (1B.3)

Neural crest cells (NCCs) are dynamic vertebrate stem cells. They form in the dorsal neural tube and undergo an epithelial to mesenchymal transition (EMT) to migrate to distant sites where they differentiate into various adult tissues. To allow for these dynamic changes, NCCs alter their cell adhesion by modulating the expression and localization of cadherin proteins, which are calcium-dependent adhesion proteins. The precise localization of cadherin proteins is crucial for NCC migration and differentiation. Disruptions in proper NCC cadherin localization causes developmental disorders like cleft palate and deafness. Cadherins are post translationally trafficked to and from the cell membrane via microtubules. Microtubules are composed of alpha and beta tubulin heterodimers and serve as highways for intracellular transport. Our lab has identified that  $\beta$ -III tubulin (TUBB3) is upregulated in NCCs during EMT, and that perturbations in its expression affect NCC migration due to alterations in cadherin localization. We hypothesize that TUBB3 has a specific alpha subunit partner expressed in NCCs during EMT and that other tubulin subunits have tissue-specific expression during development. Single-cell RNA sequencing of NCCs identified potential TUBB3 partners, but their spatial expression remains unknown. This study utilizes *in situ* hybridization chain reaction (HCR) to characterize the spatiotemporal expression of multiple alpha and beta tubulin subunits and directly compares their expression to *Tubb3* during early development. We have identified that *Tubb2a* and *Tuba4a* may co-localize with *Tubb3* in the NCCs during specification and EMT while the other subunits are expressed in the neural tube and mesodermally-derived cells. Future work will identify the role of these subunits in NCC development.

**Jaequon M Henderson**, ST Traxler, MK Mary Kable. Honey does not affect the virulence gene expression of Enterotoxigenic *E. coli* (ETEC) in mock small intestine communities. (1B.5)

Previously, the Kable lab has shown that in an *in vitro* gastric digestion of honey, the food pathogen ETEC displays a significant decrease in survival as compared to a matched simple sugar control. Here, we explored whether honey consumption can impact the expression of the heat-stable enterotoxin, Sta2, in an *in vitro* small intestine fermentation in the presence of a mock community. An *in vitro* gastric digestion and fermentation of sterile filtered clover honey, a matched sugar control (42% fructose, 35% glucose, 23% water), or media alone in a small intestine microbial mock community. The mock community fermentations were inoculated with 1 mL of gastric-digested ETEC in media alone. Samples were taken every 2 hrs. during fermentations and plated on selective MacConkey agar to assess *E. coli* survival. DNA was extracted for qPCR to assess levels of relative expression of the virulence factor Sta2 via the house-keeping gene *arcA*. Our data suggest honey does not decrease the expression of the virulence factor Sta2 in ETEC when compared to a matched sugar control and media. Through statistical analysis, there are no significant differences in the relative expression of Sta2 via the house-keeping gene *arcA* in honey when compared to the sugar control and media. The Kable lab's research suggests honey may promote the growth of small intestine microbial communities in comparison to a sugar control however, this growth has not enhanced resistance to ETEC within the context of an *in vitro* small intestine environment. Further research is ongoing to explore changes in community composition and impacts on intestinal cell health.

**Hannah Herron**, Heddy Menendez, and Crystal D. Rogers. Defining the stage specific role of SOX9 in avian neural crest cell development. (1B.2)

Neural crest (NC) cells are a population of stem-like, transient, multipotent cells originating from the dorsal side of the neural tube in developing embryos. After undergoing an epithelial to mesenchymal transition (EMT), where the cells transition from tightly bound to migratory invasive cells, they travel long distances and differentiate into craniofacial structures and other derivatives. However, errors in NC development and function results in the formation of defects such as craniofacial cleft or the development of lethal congenital disorders such as Campomelic Dysplasia. Our project focuses on defining the role of SOX9, which is a transcription factor linked to NC EMT. Preliminary work from our lab identified that *Sox9* transcripts are limited to premigratory NC cells, but that SOX9 protein expression is maintained throughout NC migration in two avian species. To determine the role of SOX9 in multiple phases of NC development, we performed SOX9 knockdown at two unique developmental stages in chick embryos, prior to NC specification and at the onset of NC EMT. We then used immunohistochemistry and histological analysis to observe the effects of SOX9 perturbation on various NC transcription factors and cell adhesion markers involved in NC EMT. We found that loss of SOX9 at early stages led to a robust increase in *Sox9* and *Sox10* gene expression and altered the localization of cell adhesion markers. In later developmental stages, SOX9 knockdown resulted in shorter NC cell migration distances. This work will illuminate the molecular mechanisms that drive NC cell formation and increase our understanding of how cells transition from epithelial to migratory, invasive, and mesenchymal. Our future work will help to determine the conservation of SOX9 function across species and how congenital defects caused by abnormal SOX9 expression may occur.

**Samantha P. Hubbard**, J. P. Michielini, E. E. Crone. Why didn't the butterfly cross the road? (2B.1)

Artificial barriers such as roads have been observed to impair the movement of larger vertebrates and flightless insects, but it's difficult to quantify the effects roads play on flying invertebrates, such as butterflies. One factor that may affect whether they cross roads is how attractive the habitat they're leaving is as they encounter a road. Therefore, we observed the effects of roads on butterfly movement when adjacent to habitat (gardens) and non-habitat (lawns) by releasing butterflies at garden-road and lawn-road interfaces. Four sites of each boundary type were identified, from which butterflies were caught, cooled down, and released, noting flight angles and side each butterfly chose, among other things. 214 butterflies were released, of which 85 stayed in the garden and 24 crossed the road for the garden-road sites, while 65 stayed in the lawn and 40 crossed the road for the lawn-road sites. Butterflies released at gardens significantly avoided roads, but didn't notably avoid them when released at lawns; however, there was no significant difference in the proportion of butterflies that crossed the road between the two types of boundaries. Although we controlled the habitat for releases, the habitat across the roads was not controlled for, and throughout the experiment, we noticed they would often fly across roads if there was a garden on the other side. In the future, evaluating the impacts of flowers located across roads for butterflies and other flying insects may provide clearer insight into how severely roads impact movement and dispersal.

**Nargis Karamatova**, Anthony Tercero, Anne Todgham. How does EE2 affect both physiology and cognitive health in Mangrove Killifish? (2B.5)

17 $\alpha$ -Ethinylestradiol (EE2) is a birth control hormone that is a contaminant in our water. EE2 is difficult to detect and remove during waste water treatment and thus poses a large risk to human and ecological health. EE2 perturbs fish physiology, affecting traits such as reproduction and behavior. While EE2 exposure is known to disrupt neuroendocrine processes sensitive to estrogen, the effects of embryonic exposure on early-life cognition is less well studied. We measured the effects of EE2 on the Mangrove Killifish to understand the persistent consequences of developmental exposure to EE2. Mangrove Killifish are clonal self fertilizing hermaphrodites with short generation times. This model system enabled us to examine the effects of pollution exposure on behavior while controlling for genetic variation. Fish were exposed to either control or EE2 treatments as embryos (4 ng/L, and 120 ng/L). Upon hatching, they were transferred to clean EE2 free conditions and reared towards adulthood. Fish were sampled at 34 days post hatch (dph) and assessed for changes in anxiety, aggression, and boldness. We measured anxiety using a thigmotaxis assay on an open field arena. Thigmotaxis is a well validated index of anxiety in animals and humans. After the thigmotaxis assay, a mirror was revealed to the fish, and boldness was measured as the latency of the fish to approach the mirror. Aggression was scored by characterizing the total duration of aggressive posturing that a fish would make towards their mirror image. Our results indicate a significant difference in boldness behavior between the control and 4 ng/L treatment, indicating that developmental EE2 disrupts the establishment of exploratory behavior. Early embryogenesis is a key stage in which neurological development takes place. Possibly representing a critical stage sensitive to endocrine disrupting compounds. Future work should examine whether these effects are persistent into juvenile and adulthood and whether these behavioral results are transgenerationally inherited in unexposed progeny.

**Cailin M. Kessen**, L.H. Yang. Effect of host plant on pyrrolizidine alkaloid collection in monarch butterflies (*Danaus plexippus*) (2B.2)

Monarch butterflies (*Danaus plexippus*) are known to use host plant cardenolides as a defense against predators. As adults, monarchs have also been observed to collect pyrrolizidine alkaloids (PAs) from dead and decaying plants, but the utility of these PA compounds remains uncertain. In other species, PAs are thought to play a role in defenses against predators or parasitoids, or in male courtship. We hypothesized that monarchs reared on low cardenolide milkweed would collect PAs more than monarchs reared on high cardenolide milkweed, as the PAs could compensate for low defensive cardenolide content. We also hypothesized that males would be more likely to engage in PA collecting behavior than females, because in other *Danaus* species the males gather PAs for use in courtship pheromones. In part 1 of the study, we ran 52 pilot trials to determine which PA sources the butterflies were attracted to and under what conditions they would engage in the collection behavior. We found that in experimental conditions, butterflies do not readily engage in collection behavior, as only 6% of all butterflies tested responded positively. In all the trials with positive responses the butterflies were held directly to a PA source with their feet touching it, and there was some form of moisture present in/on the PA. In part 2, we reared monarch caterpillars on narrowleaf milkweed (*Asclepias fascicularis*), which has low cardenolide content, and tropical milkweed (*Asclepias curassavica*), which has high cardenolide content. Adult monarchs were then allowed to collect from powdered and rehydrated *Amsinckia menziesii* as a source of PAs. We measured collection behavior as proportion of butterflies that extended their proboscis, proportion of the butterflies that engaged in collecting behavior, latency to proboscis extension, latency to proboscis contact with the PA source, duration of collecting behavior, and duration of probing behavior. In general, monarchs reared on low cardenolide milkweed were 12% more likely to extend their proboscis ( $p=0.40$ ) and 6% more likely to engage in active collecting behavior than monarchs reared on high cardenolide milkweed ( $p=0.40$ ), though neither effect was statistically significant. Additionally, females were 2% more likely to extend their proboscis than males ( $p=0.59$ ), but males were 11% more likely to engage in active collection behavior ( $p=0.59$ ), though neither effect was statistically significant. We did not observe a statistically significant interaction between the effects of host plant and sex, though we did observe a pattern of stronger host plant effects in males than in females ( $p=0.30$ ). These results suggest that monarchs reared on low cardenolide milkweed are more incentivized to collect PAs, possibly to compensate for low cardenolides for defense. Male monarchs also have greater incentive to collect PAs than females.

Further studies into the use of PAs for defense, as well as how PA use varies by sex is recommended.  
Keywords: monarch, butterfly, pyrrolizidine alkaloids, behavior, collection, defense, *Danaus plexippus*

**Angelo LaCommare-Soto, Philip H Duchild**, Bay, RA; Stachowicz, JJ. No significant effect of eelgrass genotype on wasting disease lesion severity (2B.4)

The purpose of this study was to determine if there is a relationship between the susceptibility of eelgrass (*Zostera marina*) to wasting disease (*Labyrinthula zosterae*) based on genetic differences. Eelgrass is a foundational marine flowering plant with a global distribution across coastal habitats. Wasting disease outbreaks are known to increase in frequency and severity with respect to warming temperatures, leading to black necrotic lesions on individuals and widespread population declines within eelgrass meadows. We collected 180 genets from Blake's Landing, Tomales Bay, CA and grew them in a single mesocosm tub at Bodega Marine Laboratory (BML) for 17 days. We then transferred the surviving genets to cold-room aquaria at UC Davis Campus and conducted PCR and Hind III digest to determine their inversion genotype. Genotypes for each individual were based on preliminary data suggesting that a large chromosomal inversion might affect individual eelgrass performance, including disease susceptibility. Based on this inversion region, we categorized individuals as "northern" (originating from the northern west coast of North America), "southern" (from the southern west coast), and "heterozygote" (a hybrid of northern and southern individuals). Using quantitative scoring techniques, we found that eelgrass genotype had no significant effect on lesion coverage across all individuals. This study demonstrates that the supposed chromosomal inversion in eelgrass likely does not affect disease susceptibility differently across genotypes.

**Celaya J. Murray**, T. Bolt, A. Palkovic, J. Adaskaveg, C. Diepenbrock. Evaluating hundred-seed weight and nutritional quality traits in lima beans for California (1A.5)

Lima bean (*Phaseolus lunatus* L.) genotypes have differing seed coat patterns and either baby- or large-seeded sizes. However, we do not know how those traits relate to overall seed composition (nor how compositional traits co-vary) in genotypes relevant to California. We characterized at-harvest nutritional quality traits in 35 lima bean genotypes grown in Davis, CA, in 2018, 2019, and 2021.

**Helen M Noroian**, AN Martin, RL Vannette. Pollen has differential effects on the growth of nectar-inhabiting microbes (1B.6)

Floral nectar is a carbohydrate-rich and nitrogen-poor resource inhabited by bacteria and yeasts. Certain microbes are able to overcome nutrient limitations by utilizing another floral resource – pollen. Pollen granules can be found in nectar, and certain specialist microbes break down the pollen granules in order to access the nitrogen inside. This project aims to investigate how the addition of pollen to nectar changes the density of nectar-inhabiting microbes over time. Two microbes known to break down pollen granules (*Acinetobacter pollinis* and *Metschnikowia reukauffii*) and one additional nectar-inhabiting microbe (*Lactobacillus kunkeei*) were simultaneously grown in artificial nectar solution with and without pollen. The nectar was plated on three types of growth media (TSA, YM, and MRS) immediately after nectar inoculation and two days after. The difference in cell density for each microbe was calculated based on plate counts. For *L. kunkeei* and *M. reukauffii*, the addition of pollen significantly increased cell density over time; however, there was no effect on *A. pollinis*. By investigating the impact of nutrient availability on the growth of nectar-inhabiting microbes, we can better understand the environmental conditions that impact patterns of microbial community assembly.

**Claudia Perez** and J. Ross-Ibarra. Ethnolinguistic Influence on Maize Genetic Diversity (2A.3)

Genetic differences in plants can be influenced by both environmental and geographic factors. However, in the case of cultivated plants like maize, where seed movement is mainly facilitated by human intervention, the likelihood of seed exchange is closely linked to economic, social, and cultural interactions between human populations. We propose that language could act as a barrier to the genetic exchange of seeds, meaning that communities speaking different languages are less inclined to trade or exchange seeds. Furthermore, we aim to explore whether specific language groups have developed unique adaptations or genetic distinctions. To investigate this, we conduct a Genome-Wide Association Study (GWAS) using maize and Mayan and Uto-Aztecan language data to analyze the correlation between language and genetics. We find a number of associations, including a key developmental gene associated with Yucatec Maya, suggesting selection by Maya groups for novel plant forms.

**Jala C Rice**, O Sharifi, D Yasui, J LaSalle. snRNA-seq integration enables accurate cell-type labeling in the Hypothalamus of Rett Syndrome mouse model (2A.1)

Rett Syndrome (RTT) is a rare metabolic disease and neurodevelopmental disorder that primarily affects about 1 in 10,000 girls due to mutations in the MECP2 gene, which is an X-linked gene. Symptoms include developmental regression at about 18 months of age, loss of purposeful hand skills, language and communication difficulties, cognitive impairment, motor regression, etc. Females have two copies of the MECP2 gene present, one in the paternal X-chromosome and the other in the maternal X-chromosome and are heterozygous for MECP2 mutations. Random X-chromosome inactivation leads to a mixture of WT or mutant MECP2 expressing cells, creating a mosaic brain in RTT. The LaSalle Lab engineered a novel RTT mouse model inducing a point mutation in the 5' end of MeCP2 ablating the translation site of the MeCP2-e1 protein (Yasui D, et. al 2013). We have utilized snRNA-seq 5' to analyze the gene

expression patterns of each cell type individually in the hypothalamus to parse out the cells as mutant or wild-type based on the induced point mutation. Since RTT is a metabolic disorder, we focused on the hypothalamus because it controls metabolism and other functions related to RTT-like symptoms. Here, we have accurately labeled cell types present in the hypothalamus of a RTT mouse model based on integration of cells with (Steuernagel L, et al. 2022) dataset. Further, we have validated the accurate cell type labeling by doing a cell type marker test.

**Patrick H Roehling**, A. Padvannil, and J. Letts. Functional Characterization of Plant Mitochondrial Complex II (1B.1)

Complex II (CII) is a multi-subunit integral membrane protein complex essential to plant metabolism and stress response. Therefore, functional and structural characterization of CII in plants impacts both agriculture output and plant adaptation to climate change. Isolation of stable plant CII has yet to be done. Isolation for detailed characterization is dependent on a stable extraction of CII from the mitochondrial membranes. Plant CII is inherently more unstable than that of mammals and bacteria when extracted from the membrane using standard detergents. While an additional 4 subunits (subunits 5-8) have been identified in plant CII compared to more well studied species, an actual protein structure has yet to be produced. We hypothesize that using the styrene malic acid (SMA) polymer, we can extract a stable CII that can be used for these studies. Here, we compare the SMA polymer to common detergents to determine its effectiveness. The assay used determines CII activity by utilizing the oxidoreductive properties of CII and quinone. By better understanding its structural and functional characteristics we can specifically increase plant growth, design better pesticides, and help plants better adapt to biotic and abiotic stresses.

**Marisha D. Towner**. Plant partners. (2A.5)

This research was conducted to determine how the addition of phosphorus reacts to the roots and arbuscular mycorrhizal fungi of organic versus conventional practices. There were originally two sites, Fulton 1 and 2 Vineyards (Pinot Noir and Chardonnay), Sonoma County, California. Soil samples were collected from nine vines from each vineyard underneath drip lines. The results from the first experiment were not finished, so I used results from a similar experiment by Bowles et al. 2016 for the poster. Bowles, T.M., Jackson, Loeher, M., Cavagnaro, T.R., 2016. Ecological intensification and arbuscular mycorrhizas: a meta-analysis of tillage and cover crop effects. *J. Appl. Ecol.*

**Srinivas Rao Voruganti**, Duncan Sylvestre, Kirsten J. Roslund, Carolyn M. Slupsky and Ameer Y. Taha. Role of ketone ester supplementation on hippocampal lipid metabolism in aged mice (1A.4)

Ketone ester supplementation has gained attention for its potential impact on brain health and metabolism. Yet, little is known about its effects on brain lipid metabolism, which is key for maintaining neuronal structure and viability during aging. The aim of this study was to examine the role of ketone ester supplementation on hippocampal lipid metabolism in old male and female C57BL/6 mice. At 24 months of age, mice were randomly assigned to a semi-purified control diet group and a treatment group with 21.5% kcal of carbohydrates replaced with 21.5% kcal of the (R)-3-hydroxybutyl (R)-3-hydroxybutyrate ketone ester. Intervention diets were administered until the mice reached 26 months of age, at which point they were sacrificed, and the hippocampi were collected for lipid analysis using gas chromatography. There were no significant changes in hippocampus fatty acid composition in male and female mice. This study adds to the growing body of knowledge surrounding ketone ester supplementation and its potential effects on brain physiology in aging mice. Further investigation is warranted to explore potential effects on other brain regions, such as the cortex.

**Christy Wheatley**, J Ross-Ibarra, AR Phillips. Genome size variation does not affect anatomy and growth in *Tripsacum dactyloides* (2A.2)

Genome size – the amount of DNA in a cell – varies among individuals within a species. This phenomenon is widespread throughout the natural world, but is especially common among plants. There are many unknown impacts of genome size variation. Studies have shown that as genome size increases, so does stomatal cell size. However, the impacts of this increase on carbon assimilation and photosynthesis are unknown. In domesticated maize and its wild relatives (*Zea mays*), a previous study demonstrated that genome size varies along an altitudinal cline due to selection pressure on flowering time. Previous research within the Ross-Ibarra lab found that this association between altitude and genome size was not found in eastern gamagrass (*Tripsacum dactyloides*), sister species to *Z. mays*. The species does exhibit genome size variation. Here, we measured leaf growth rate, stomatal cell size and density, and genome size of eastern gamagrass (*Tripsacum dactyloides*), sister species to maize, to determine the impacts of genome size on functional traits. We evaluated 24 individuals from 8 populations along a 1590 meter altitude cline. We used linear mixed models to test if altitude and genome size affect these traits. Here, we will present our findings on the relationship between genome size and functional traits. This study provides insight into the physiological impacts of genome size variation and will help determine how widespread they are amongst maize and its relatives.

**Eryse L. White**, Alan Urquidi, Fallon Ely, Beth Forrestel. Unveiling Cultivar Resilience: Physiological Indicators for Sustainable Viticulture in a Changing Climate (2A.4)

Climate change has had a significant impact on viticulture, and has led to the consideration of changing cultivars across wine growing regions. To date, most research on cultivar choice has been related to reproductive traits or phenological traits (i.e, choosing later ripening cultivars in response to a warming climate). The assumption has been made that these later ripening varieties will have been assumed will also harbor desirable physiological traits to adapt to higher

temperatures, but that assumption has not been broadly tested. Across the growing season, 18 cultivars from different climates and wine regions were monitored. We selected a subset of 5 of these cultivars ranging in their timing in ripening or flowering to test whether reproductive traits are efficient indicators of adaptability in relation to Climate Change. We evaluated the stomatal conductance responses and photosynthetic rates of Tempranillo, Cabernet Sauvignon, Vermentino, and Chardonnay cultivars to rising temperatures using a LICOR 6800 instrument. Some cultivars displayed reduced stomatal conductance under higher temperatures, indicating susceptibility to heat-induced water stress, while others showed resilience by sustaining or enhancing stomatal conductance levels. In controlled environmental chambers, Tempranillo, Cabernet Sauvignon, Vermentino, and Chardonnay cultivars were exposed to incremental temperature elevations while their gas exchange responses were monitored. Stomatal conductance, a key physiological process regulating water loss and CO<sub>2</sub> uptake, serves as a crucial indicator of a plant's ability to withstand heat stress and maintain proper water balance. These findings highlight promising cultivars with inherent mechanisms to cope with climate change challenges and supporting sustainable viticulture practices. Overall, the research underscores the significance of physiological research in viticulture and demonstrates how modern instrumentation like the LICOR system can facilitate in-depth analyses of plant responses to environmental stressors. The outcomes of this research can aid viticulturists in making informed decisions to foster the resilience of vineyards and promote sustainable growth in the face of climate change.

**Maraé M. Woodson**, Aya S. Ead and Gerardo G. Mackenzie. Investigating potential molecular targets for diet induced obesity in early stages of pancreatic carcinogenesis in mice (1A.3)

Pancreatic ductal adenocarcinoma (PDAC) is an exceedingly threatening neoplasia due to the insufficiency of early diagnosis and insubstantial response to treatments. Despite several advances in recent years, PDAC remains one of the deadliest cancers with a five-year survival rate of 12%. In previous studies, alterable risk factors such as obesity, high-fat diet (HFD), and high caloric intake all have been linked to an increased risk of developing PDAC. However, the precise role and cellular mechanisms played by HFD in the early stages of pancreatic cancer development continues to be difficult to elucidate. Previous studies in the lab have shown that intake of a HFD accelerates the development of initial stages of pancreatic carcinogenesis in LSL-KrasLSL-G12D/+; Ptf1-Cre (KC) mouse model, compared to KC mice fed a control diet (CD). After 8 weeks on HFD, Hematoxylin and Eosin (H&E) histology staining revealed there was a significant difference in the amount of acinar cell loss in the pancreas of both male ( $p < 0.05$ ) and female ( $p < 0.05$ ) mice fed HFD compared to mice fed a CD. While HFD-fed female KC mice had a 2-fold increase in the percent of pancreatic acinar cell loss, HFD-fed male mice had a 29-fold increase of compared to mice fed a CD. However, the mechanisms of how HFD enhances pancreatic carcinogenesis remains unclear. For this purpose, we sought to investigate various molecular targets that have been implicated previously in obesity and cancer. Immunohistochemistry analysis revealed that female KC mice on the HFD had significantly higher levels of phosphorylated-Signal Transducer and Activator of Transcription 3 (p-STAT3), a 2-fold increase ( $P < 0.05$ ) compared to female CD fed mice. Moreover, HFD fed KC mice had no significant change in levels of phosphorylated Epidermal Growth Factor (p-EGFR) or phosphorylated 4E-Binding Protein (p-4EBP1), compared to CD fed KC mice. Out of these markers evaluated so far, only p-STAT3 is critical for early stages of pancreatic carcinogenesis induced by HFD, at least in females. For future studies, we aim to identify additional potential targets related to tumor proliferation.