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Research Experience for Undergraduates

Summer 2021
Symposium

Integrating Biology
from molecules to ecosystems

The NSF REU Biology Site in Berkeley is designed to expose participating students to core concepts of Cell, Developmental and Evolutionary Biology. The many participating faculty provide a broad range of research options in these areas. They also share a strong commitment to working with undergraduates and promoting diversity in the biosciences community at Berkeley.

Under the direction and guidance of a UCB faculty mentor and a graduate student or post-doctoral co-mentor, students gain first-hand research experience and training in state-of-the-art research facilities, working on individual summer projects. Through seminars, professional development workshops, and interactions with faculty, post-doctorate fellows, graduate and undergraduate students, program participants are familiarized with research and the graduate school experience, from the application process, to career Ph.D. possibilities, and everything in between.

This program showcases participants' accomplishments for the summer.

Summer Research Experience for Undergraduates
Final Symposium

Welcome & Refreshments — 9:00

I. Pedro X. Medina — 9:15
Developing an analysis pipeline to study gut resident T cell subset specificity to commensal microbes during homeostasis

II. Zonyha M. Vélez-Ferrer — 9:30
Regulation of effector-triggered immunity by the nuclear transport receptor KA120 in Arabidopsis — 9:45

III. Fernando Bolio — 10:00
Investigation of a potential molecular mechanism behind cortical circuit deficits in autism spectrum disorder

IV. Lance Li — 10:15
Characterizing Allosteric Regulation of PFKFB

V. Den Arthur Lipata — 10:30
Examining spindle morphology with expansion microscopy of Xenopus laevis egg extracts

BREAK — 10:45

VI. Lizet Reyes Rodas — 11:00
Understanding the Mechanisms of Ume6 Degradation in *Saccharomyces cerevisiae*

VII. Sofia G. Beskid — 11:15
Investigating the origins of chemical defense in the Drosophila melanogaster model system

VIII. Diana Gao — 11:30
Do kangaroo rats act as ecosystem engineers? Potential Evidence from increased nitrogen uptake by plants

IX. Daniel Ibañez IV — 11?45
Female choice as an isolating mechanism within the genus Habronattus

X. Anay Ochoa — 12:00
It's about to be a fish fight: the role of aggression during trophic specialization in an adaptive radiation of Cyprinodon pupfish

Close

Pedro X. Medina

Pedro X. Medina[1], Jessica N. Witchley[2], Gregory M. Barton[2]

[1]Department of Microbiology University of Puerto Rico at Arecibo, Acecibo, PR
[2]Division of Immunology and Pathogenesis, Department of Molecular and Cell Biology, University of California, Berkeley CA

Developing an analysis pipeline to study gut resident T cell subset specificity to commensal microbes during homeostasis

Mammalian gut commensal bacteria play an important role in the development and function of the immune system. While most of these microbes are not targeted by the host defenses, some may trigger differential immune responses that could have far-reaching effects on host fitness. For instance, previous studies have shown that specific commensals can be recognized by the immune system, but the mechanisms by which immune cells interact with these microbes remain largely unknown mainly due to the lack of appropriate study systems. In this project, we developed a system and analysis pipeline that enabled us to study T cell cognate responses to commensals during homeostasis in mice colonized with an *Akkermansia muciniphila*-containing microbiota. Our lab has previously demonstrated that a specific peptide from commensal *A. muciniphila* (Akk OMP) induces T cell-dependent immunity, so Akk OMP will serve as the stimulus for T cell-commensal specificity screening in our system. To develop and test the system that would allow us to study T cell cognate responses to commensals, we stimulated a green fluorescent protein (GFP) reporter cell line expressing a T cell receptor (TCR) reactive to Akk OMP with an antigen-presenting cell exposed to Akk OMP. We then incubated the cells for 24 hours and stained them with a fluorescent antibody for subsequent cytometric analysis. Preliminary results showed that 30.7% of cells that were stimulated with Akk OMP expressed GFP, suggesting specificity between the TCR and Akk OMP. We further built on these findings by testing whether adding CD3, a surface marker involved in signal transduction and activation of T cells, could increase the percentage of cells expressing GFP when stimulated with Akk OMP. Our data showed that the addition of CD3 slightly increases the percentage of cells expressing GFP when stimulated with Akk OMP in comparison with cells that do not contain CD3, implying that incorporating CD3 could increase the identification of TCR-Akk OMP cognate responses in our system. Taken together, these results could shed light on the study of T cell cognate responses to commensals by providing a reliable system to analyze T cell-commensal interactions.

Pedro Medina *is a rising senior at the University of Puerto Rico at Arecibo. He intends to graduate in May 2022 with a Bachelor's degree in Microbiology. He has worked with Dr. Margaret MacDonnell at Argonne National Laboratory and with Proffesor Cynthia Cardona at his home institution where he characterized antimicrobial resistance in the muli-drug resistant Acinetobacter calcoaceticus.*

"You discover yourself through the research of your work." - Carine Roitfeld

Zonyha M. Vélez-Ferrer

Zonyha M. Vélez-Ferrer[1,2], Jia Min[2,3], Yangnan Gu[2,3]

[1]Department of Agro-Environmental Sciences, University of Puerto Rico, Mayaguez, Mayaguez, PR
[2]Department of Plant and Microbial Biology; University of California, Berkeley CA
[3]Inonovative Genomics Institute, University of California, Berkeley CA

Regulation of effector-triggered immunity by the nuclear transport receptor KA120 in Arabidopsis

The nucleotide-binding, leucine-rich repeat (NLR) immune receptors recognize effector proteins secreted by pathogens and activate effector-triggered immunity (ETI) in plants. However, ETI activation needs to be tightly controlled in the absence of pathogens to prevent autoactivation. The activation of a subgroup of NLR proteins (TIR-NLRs) depends on their nuclear transport. Specifically, karyopherin-βs are importins and exportins that facilitate the transport of proteins in and out of the nucleus, respectively. Previously, it was reported that an Arabidopsis karyopherin KA120 is required to maintain nucleocytoplasmic homeostasis of the TIR-NLR protein SNC1, and KA120 negatively regulates immunity partially through constrains in SNC1 nuclear activity. Nonetheless, loss of SNC1 cannot fully suppress *ka120*-induced autoimmunity, suggesting that other KA120 substrates are involved. In this project, we analyzed the functional importance of potential KA120 substrates using genetics. Then, we will cross loss-of-function mutants of potential KA120 substrates obtained by proximity labeling proteomics with the *ka120* mutant and observe potential genetic interactions, which can help narrow down functional KA120 cargo. Moreover, we studied if overexpressing KA120 can compromise ETI and if so, whether it is linked with disruption in the nucleocytoplasmic homeostasis of other NLRs. To this end, *KA120* overexpression transgenic plants and wild-type plants were infected with bacterial pathogen *Pseudomonas syringae* carrying effector protein AvrRps4 or AvrRpt2. RPS4 is a TIR-NLR receptor that recognizes AvrRps4 and it is subject to nucleocytoplasmic regulation, whereas RPS2 is a membrane-anchored NLR that recognizes AvrRpt2 and does not function in the nucleus. *KA120* overexpression plants infected with AvrRps4 and AvrRpt2 showed high and low levels of bacterial growth, respectively. This indicates that KA120 overexpression compromises R protein-mediated defense, but does not disrupt basal defense response. This project will further strengthen our understanding of KA120's role in regulating TIR-NLR nuclear activity and provide a molecular basis for modulating its activity to control plant immunity.

Zonyha M. Vélez-Ferrer *is a rising senior at the University of Puerto Rico, Mayagüez (UPR-M) majoring in Horticulture with a minor in Plant Biosecurity. At UPR-M, she works in Dr. Lydia I. Rivera-Vargas's lab studying pathogenic fungi associated with soursops in the South of Puerto Rico. After her undergraduate career, Zonyha plans to pursue graduate studies in Plant Pathology because she believes that trough the work of applied research a paradigm for agricultural development and humanity's needs can be reached.*

"Science knows no country, because knowledge belongs to humanity."

Fernando Bolio

Fernando Bolio[1,2], Hannah Monday[2,3], Daniel Feldman[2,3]

[1]Department of Molecular Biology Pomona College, Claremont CA
[2]Department of Molecular and Cell Biology; University of California, Berkeley CA
[3]Helen Wills Neuroscience Institute; University of California, Berkeley CA

Investigation of a potential molecular mechanism behind cortical circuit deficits in autism spectrum disorder

Autism spectrum disorder (ASD) is characterized by social and sensory processing deficits and repetitive behaviors. Three common neurobiological defects proposed to underlie ASD are an increased excitation to inhibition (E-I) ratio, parvalbumin (PV) circuit hypofunction, and dysregulated protein synthesis. PV interneurons monitor local activity and adjust their inhibition to maintain a constant network firing rate, termed PV circuit homeostasis. We hypothesize that the increased E-I ratio underlying ASD stems from impaired PV circuit homeostasis. Our lab has shown that whisker deprivation leads to robust homeostasis of PV circuits in S1. PV circuit homeostasis involves reduced intrinsic excitability of PV interneurons through increased potassium currents (presumed Kv1.1 channels), but its molecular mechanisms are unknown. One candidate, transcription factor Er81, promotes Kv1.1 channel expression in an activity-dependent manner. We will test the hypothesis that PV circuit homeostasis requires Er81 and Kv1.1 expression and this expression is impaired in ASD mice due to its dysregulated protein synthesis and leads to impaired network activity. We will measure levels of Er81 and Kv1.1 in PV cells using immunohistochemistry in response to brief whisker deprivation in wild-type and ASD mice. Our mouse model, $Tsc2^{+/-}$ is a well-established ASD model of numerous sclerosis complex, a disorder in humans characterized by intellectual difficulties, behavioral difficulties, and epilepsy. As Tsc2 is part of a complex that inhibits mTOR, our $Tsc2^{+/-}$ mouse model should demonstrate increased activity-dependent protein synthesis. We found a strong trend towards decreased ER81/Kv1.1 expression levels in $Tsc2^{+/-}$ sham and whisker-deprived mice compared to wild-type. Although surprising given the proposed function of TSC2, these results are consistent with previous literature demonstrating decreased $Tsc2^{+/-}$ protein synthesis and highlight a potential mechanism of impairment of PV circuit homeostasis in ASD mice. This could explain sensory processing difficulties, potentially elucidating targets for treatment of ASD symptoms.

Fernando Bolio *is a rising senior at Pamona College. He intends to graduate in May 2022 with a Bachelor's degree in Molecular Biology. He has studied directed evolution of E. coli endonucleases with Professor Lenny Seligman at Pomona College and a conducted a remote literature curation project with a focus of creating a GO-CAM model of interactions between various neurons and the dauer decision process in C. elegans with Professor Paul Sternberg at CalTech.*

Lance Li

Lance Li[1,2], Megan Kober[2], Denis Titov[2]

[1]Department of Biology, Georgetown University, Washington, DC
[2]Department of Molecular and Cell Biology, University of California, Berkeley CA

pedro.medina5@upr.edu

Characterizing Allosteric Regulation of PFKFB

Fructose-2,6-bisphosphate (F-2,6-BP) is a metabolite that regulates mammalian glycolysis through allosteric activation of the rate-limiting enzyme phosphofructokinase-1 (PFK1). F-2,6-BP levels are solely determined by the activity of a single, bifunctional enzyme, 6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase (PFKFB). The PFKFB kinase domain synthesizes F-2,6-BP by phosphorylating fructose-6-phosphate (F-6-P), while the phosphatase domain dephosphorylates F-2,6-BP and regenerates F-6-P. We are establishing a mechanistic model to predict the activity of every glycolytic enzyme, using the Michaelis-Menten equation to represent near-equilibrium enzymes and the Monod-Wyman-Changeux equation to represent the allosterically regulated enzymes. However, our existing kinetic equations based on purified PFKFB enzyme led to the production of F-2,6-BP levels orders of magnitude higher than its intracellular concentrations. Therefore, the regulation of PFKFB activity is incompletely understood. To generate a model that would allow a more accurate prediction of PFK-1 activity, we will be optimizing an *E. coli* recombinant protein expression system for the purification of PFKFB isoenzymes. We will use the purified PFKFB to screen numerous regulatory conditions and assess effects on relative enzymatic activity. Specifically, I will characterize the effects of allosteric regulators on PFKFB kinase activity by measuring ADP production. By characterizing PFKFB kinase domain regulation, we will gain a greater understanding of the cellular conditions that promote F-2,6-BP synthesis to enhance glycolysis.

Lance Li *is a rising junior at Georgetown University. He intends to graduate in May 2023 with a Bachelor's degree in Biology. He has worked to identify unknown microbial communities in the soil of wineries with Professor Heidi G. Elmendorf at Georgetown University and conducted bioinformatics research measuring the effectiveness of thin-layer deposition restoration techniques on salt marshes by analyzing plant and arthropod data using R with Professor Gina Wimp at Georgetown University.*

"Everyday. I just want to cry. Everyday."

Den Arthur Lipata

Den Arthur Lipata[1,2], Maiko Kitaoka[2], Rebecca Heald[2]

[1]Department of Biology California State University Stanislaus, Turlock CA
[2]Division of Cell and Developmental Biology, Department of Molecular and Cell Biology, University of California, Berkeley

Examining spindle morphology with expansion microscopy of *Xenopus laevis* egg extracts

During the process of cell division, the microtubule-based mitotic spindle faithfully segregates chromosomes to daughter cells. Although it has a universal function and conserved components across eukaryotes, spindle structure varies widely across species and is adaptive to cell size. Notably, the relationship between spindle microtubule arrangement and the fidelity of spindle function is unclear. To begin investigating the relationship between spindle morphology and the accuracy of chromosome segregation, we set out to compare the detailed structure of the spindle using extracts prepared from eggs of the African clawed frog, *Xenopus laevis.* Because the spindle has high microtubule density, its organization and the localization of specific spindle proteins is difficult to analyze by conventional light microscopy. In this study, we utilized expansion microscopy to increase the physical size of spindles isotropically to increase resolution and provide new structural details, an approach that has not previously been applied to a cell-free system. We compared the structure of unexpanded and expanded meiotic spindles assembled in egg extracts of *X. laevis,* using rhodamine-labeled tubulin and Alexa Fluor 488-EB1 to visualize microtubules and growing microtubule plus ends, respectively. We find that expansion microscopy allows spindles to reach 4 times its original size in a cell free environment. Currently, we are using these techniques in conjunction with immunofluorescence to elucidate the nature of the mitotic spindle assembly and morphology across different species and cell types to begin correlating spindle structure with function.

Den Arthur Lipata *is a general biology major attending California State University, Stanislaus. There, he also works as a supplemental instruction leader for both general biology and molecular and cell biology. This summer at UC Berkeley, he is learning microscopy techniques by looking at the spindle structure of African clawed frogs in Rebecca Heald's lab with his mentor Maiko Kitaoka. His love of science fiction has led him to pursue a PhD in biology.*

Lizet Reyes Rodas

Lizet Reyes Rodas[1,2] ,Anthony Harris[2], Elcin Ünal[2]

[1]Department of Natural Sciences and Mathematics, Dominican University of California, San Rafael, CA

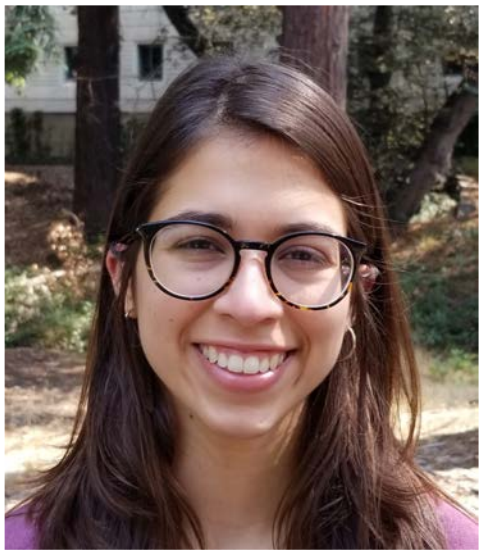
[2]Division of Genetics, Genomics and Development, Department of Molecular Cell and Biology, University of California, Berkeley, CA

Understanding the Mechanisms of Ume6 Degradation in *Saccharomyces cerevisiae*

Meiotic differentiation is a highly conserved and tightly regulated cellular program that results in the production of genetically distinct haploid gametes. In *Saccharomyces cerevisiae,* progression through this cellular program is coordinated at two major points. Entry into and activation of early meiotic events like DNA replication and recombination are coordinated by two transcription factors (TFs), Ume6 and Ime1. Once the early events are completed, another TF called Ndt80 becomes active to trigger middle meiotic events such as chromosome segregation. However, it remains unclear how transcripts that are activated by Ume6 and Ime1 are down-regulated once cells transition into mid-meiosis. It is known that Ume6 is degraded during meiosis, but the timing of this has been unclear. Previous research from our lab suggests that the timing of Ume6 degradation occurs following Ndt80 activation. We posit that Ndt80-dependent degradation of Ume6 is necessary to stop early meiotic events such as DNA replication and recombination. The goals of this project are: 1) to determine whether Ume6 degradation occurs in mitosis upon *NDT80* induction and 2) to identify which regions within Ume6 are necessary for its degradation. To address the first question, *NDT80* was ectopically expressed during mitosis and Ume6 protein levels were monitored. We found that *NDT80* induction was not sufficient to cause Ume6 degradation in mitosis and thus additional factors must be required. We also built five constructs that carry deletions within Ume6 to determine the residues critical for its degradation. These will be tested in the future. Altogether, our findings will give us a better understanding about the mechanism of Ume6 degradation and how cells transition from early to middle meiotic events.

Lizet Reyes Rodas *is a rising senior at Dominican University of California, where she studies Music and Biological Sciences with a minor in Chemistry. At DUC, she works at Dr. Meredith Protas lab studying Asellus aquaticus, a species of crustacean with cave and surface forms, to understand their different characteristics through developmental biology and evolution. She intends to continue her education by pursuing a Ph.D. in biology. In her free time, she enjoys playing the piano and exploring the outdoors.*

“There’s beauty in the yeast experiments”



Sofia G. Beskid

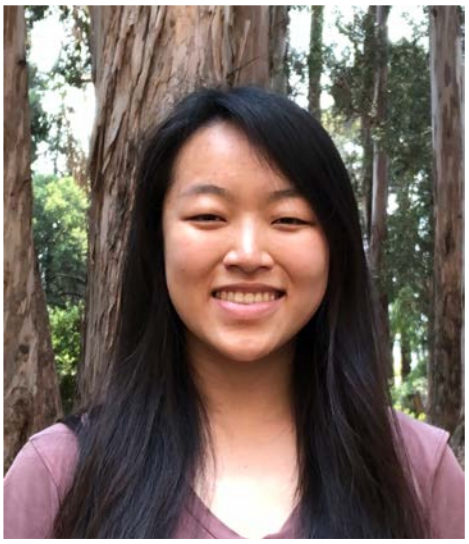
Sofia G. Beskid[1,2], Tyler Douglas[2], Rebeccas Tarvin[2]

[1]Department of Environmental Science University of Texas, Austin TX
[2]Department of Integrative Biology, University of California, Berkeley CA

Investigating the origins of chemical defense in the *Drosophila melanogaster* model system

Chemically defended organisms utilize toxins to ward off predators without poisoning themselves by balancing toxin resistance and sequestration. The simultaneous presence of these two adaptations, that is resistance and sequestration, raises a challenge in understanding the evolutionary origins of chemical defense. Specifically, one of the primary mechanisms of toxin resistance, metabolic breakdown of toxin, is expected to inhibit sequestration by promoting toxin elimination. In contrast to this theoretical expectation, we have found that one strain of *Drosophila melanogaster* that is known to have upregulated detoxification enzymes also maintains relatively high levels of toxins when raised on a toxic diet. We therefore hypothesize that increased metabolic toxin breakdown may actually facilitate toxin sequestration by offsetting the cost of toxin ingestion and allowing for an overall increased toxin intake. We suggest that this *Drosophila* strain, and chemically defended organisms in general, balance toxin metabolic breakdown and sequestration by increasing toxin feeding rate. In our study, we used the *Drosophila melanogaster*, the parasitic wasp *Leptopilina heterotoma*, and nicotine as a model to investigate the dynamics of sequestration and resistance in the origin of chemical defense. To test feeding rate, we parasitized nicotine-resistant and nicotine-sensitive strains of *Drosophila* with *Leptopilina*, and then fed them nicotine-free or nicotine-treated food. We predict that parasitized, nicotine-resistant *Drosophila* have higher feeding rates of nicotine-treated food than nicotine-sensitive *Drosophila*. Ultimately, this study will determine whether increased toxin resistance drives rather than precludes the evolution of toxin sequestration by allowing for increased toxin consumption.

i**Sofia G. Beskid** *is a rising senior at the University of Texas at Austin majoring in environmental science with an emphasis in biology. For the past two years, she has worked in Dr. Matz's lab first helping a graduate student with lab work – DNA extractions, gels, and library prep – and then taking on her own computational project investigating coral adaptation to different environments. This summer, she is working in Dr. Tarvin's lab with her mentor, Tyler Douglas, studying the origins of chemical defense in the Drosophila model system. After graduating, Sofia plans to pursue a PhD focusing on genetics, evolution, and bioinformatics.*



Diana Gao

Diana Gao[1,2], Danielle Perryman[2], Steven R. Beissinger[2]

[1]Department of Biology University San Francisco, San Francisco CA
[2]Department of Environmental Sciences, Policy and Management; University of California, Berkeley

Do kangaroo rats act as ecosystem engineers? Potential evidence from increased nitrogen uptake by plants

Ecosystem engineers are species that modify their habitats in a significant way in order to better suit their needs. This modification is great enough to strongly affect other species in the area. Small burrowing mammals, such as kangaroo rats (*Dipodomys spp*.), have been shown to affect the plant composition in their microhabitats due to rapid turnover of the soil. This process is important in desert ecosystems, where bioavailable nitrogen is the most limiting factor for biological productivity after water. Here we hypothesize that the engineering effects of four species of kangaroo rats will alter the surface nitrogen (N) content of the soil and increase N uptake in associated plants (e.g. *Larrea spp, Atriplex spp.*) of the Mojave Desert. We tested this hypothesis by determining how N uptake varied with kangaroo rats' presence or absence at sixteen sites, eight with kangaroo rats and eight without. This was done using stable isotope analysis to determine the elemental composition of associated plants, specifically to see how much N each plant contained. Stable isotope analysis provides a quantitative metric for noting the impact of kangaroo rats on plant health and composition. We predict to find higher N in plants in areas with kangaroo rats present than in areas without kangaroo rats, after taking into account background levels of nitrogen deposition. Studies of the interdependence of ecosystem engineers, like kangaroo rats, on plant communities can elucidate mechanisms of coexistence and inform future efforts for species management.

Diana *Gao* *is a senior at the University of San Francisco majoring in biology and minoring in chemistry. In her free time, Diana enjoys drawing, swimming, and bird watching. Growing up in Hawaii surrounded by nature sparked her interests in zoology. Her previous research experience is with Dr. Marguerite Butler's lab at the University of Hawaii at Manoa, where she worked to study the biogeographic history and resolve the phylogeny of Papuan microhylid frogs.This summer, she worked under Danielle Perryman in Dr. Steve Beissinger's lab studying the effects of kangaroo rats on plant distribution in Death Valley.*

Daniel Ibañez IV

Daniel Ibañez IV[1], Malcolm Rosenthal[2], Damian Elias[2]

[1]Department of Biology. New Mexico State University, Las Cruces NM
[2]Department of Environmental Sciences, Policy and Management, University of California, Berkeley CA

Female choice as an isolating mechanism within the genus *Habronattus*

Habronattus is a diverse genus of spiders in the family Salticidae, known for a high degree of variation in vibratory signaling and male ornamentation. Suspected high rates of speciation during recent evolutionary history have produced several closely related species that readily hybridize. Mating preference variation within the genus make *Habronattus* an interesting model for studying how behavior serves as a mechanism for reproductive isolation. Here we seek to understand how mate choice plays a role in pre-zygotic reproductive isolation of this genus. Previous work suggests that males display courtship indiscriminate of species, thus we focus instead on female choice. To examine this question, we paired males and females of the species *Habronattus americanus* and *Habronattus johnsonae* in no-choice mating trials where we record all interactions for 15-minute periods. During trials, we record the presence of male courtship and copulation as well as record vibratory signals for further analysis. Observing conspecific preferences by females of these species indicates that female choice plays a key role as a pre-zygotic isolating mechanism. By understanding behavior between these two species and comparing them to interactions across the genus *Habronattus* we can develop a more complete picture of the evolution of this taxon.

Daniel Ibanez *is a senior at New Mexico State University where he is majoring in Biology with minors in Chemistry, Biochemistry, Molecular Biology, and Human Anatomy. He has been involved in undergraduate research for three years in which he has studied plant physiology, bat organismal physiology and behavioral ecology as well as jumping spider mating behaviors here at UC Berkeley. He is a MARC scholar as well as president of the American Society of Biochemistry and Molecular Biology chapter at his home institution where he works to guide undergraduate students into research positions. He has an eventual goal of attaining his PhD in Biology and pursuing academic research as a career.*

"I never thought a sofa could become my best friend"

Anay Ochoa

Anay Ochoa[1,2], Emilie Richards[2], Christopher Martin[2]

[1]Department of Biological Sciences California State University San Marcos, San Marcos CA
[2]Department of Integrative Biology, University of California, Berkeley CA

It's about to be a fish fight: the role of aggression during trophic specialization in an adaptive radiation of *Cyprinodon* pupfish

There are many ways that a population may adapt to new ecological niches including shifts in behavior, morphology, or a combination of the two. However, the relative importance of behavior versus morphology in these transitions is still unknown. Here we investigate the importance of aggression in a radiation of *Cyprinodon* pupfishes that displays several ecological shifts. This radiation includes a wide-spread algae-eating generalist living in sympatry with three trophic specialists; including a recently discovered intermediate scale-eating specialist called the 'wide-mouth'. A previous study found that two specialists in the radiation, molluscivore (*C. brontotheroides)* and scale-eater (*C. desquamator),* were more aggressive than the generalist (*C. variegatus)*, suggesting that shifts in aggression underlie trophic specialization in this system. However, little is known about aggression in the 'wide-mouth' species. If shifts in aggressive behavior were important for trophic specialization, we expect that the 'wide mouth' specialist is aggressive like the other two specialists. Additionally, all three specialists should be more aggressive than the generalist. We tested these hypotheses using mirror assays that measured three aspects of aggressive behavior: latency to approach, latency to attack, and total number of attacks. We found that 'wide-mouths' were equally as aggressive as the other two trophic specialists. However, we also discovered that some generalist individuals from nearby New Providence Island also displayed aggressive behavior. Our results suggest that elevated aggression alone does not explain trophic specialization in this system but rather suggests that an interaction between behavior and trophic morphology may better explain these ecological transitions.

Anay Ochoa *is a* first generation, rising senior in Biological Sciences at California State University San Marcos (CSUSM). She was a Bridges Scholar at Palomar College and in the Scientific Enhancement (U-RISE) and Louis Stokes Alliance for Minority Participation (LSAMP) programs at CSUSM. She was a part of Dr. John Eme's comparative physiology lab where she focused on the effect of egg mass, hatchling size and clutch on growth of body masses and lengths of female American alligators (Alligator mississippiensis). She presented this independent study at the CSUSM Symposium on Student Research, Creative Activities, & Innovation and became a finalist for the CSU-wide Student Research Competition. She also presented this work at the Experimental Biology meeting in April 2021. This summer she was part of Dr. Christopher Martin's lab focusing on the role of aggression during trophic specialization in an adaptive radiation of *Cyprinodon* pupfish. She plans on pursuing a PhD after obtaining my bachelor's in Biological Sciences. Her desire to obtain a doctorate degree stems from her passion in research as well as promoting diversity in sciences.

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