Department of Biology
New Mexico State University
Biosymposium

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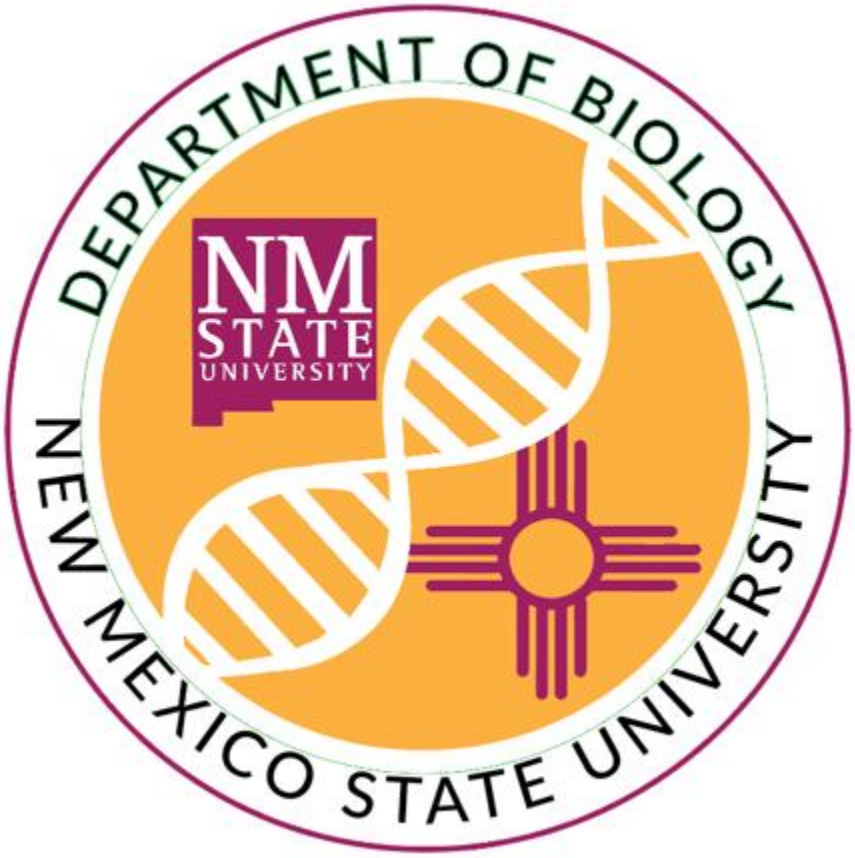
College of Arts and Sciences

Saturday, March 29, 2025

TABLE OF CONTENTS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ORAL PRESENTATIONS

Presenter name*	Session, Talk	Time	Title
Agbetsi, John	S3, T11	2:15-2:30	The role of *Anopheles stephensi* 's leg in odor detection: how gravid mosquitoes make decisions
Ahmed, Shakil	S1, T3	10:10-10:15	Investigating the evolutionary trajectories of organelle-derived DNA in Fabaceae nuclear genomes
Al-Nouman, Abdul	S2, T8	11:30-11:45	The *Drosophila melanogaster* TENT5 homolog is required for individualization of spermatids during spermatogenesis
Baca, Gabrielle	S2, T10	2:00-2:15	Molecular testing of triatomine insects for *Trypanosoma cruzi* infection and bloodmeal analysis in Las Cruces, New Mexico
Dickson, Meig	S3, T14	3:00-3:15	Filling the gaps: Determining ranges of fossil birds using machine learning
Dozier, Nicole	S1, T1	9:30-9:45	Devising an eDNA assay for critically endangered butterfly *Euphydryas anicia cloudcrofti*
Iloba, Ogochukwu	S3, T13	2:45-3:00	Exploring the influence of chromatin accessibility on homeologous (duplicate) gene expression in the tetraploid plant, *Leucaena trichandra*
Karki, Anjali	S2, T9	11:45-12:00	Small mosquitoes – large Implications: Effects of larval crowding and starvation on locomotor activity, adult biting frequency, and insecticide resistance in two strains of *Aedes aegypti*
Landfair, Taylor	S1, T4	10:15-10:30	PI3K activity influences cell fate in response to mitotic arrest
Nelson, Ian	S2, T6	11:00-11:15	Identifying the evolutionary relationships among lichenized fungi populations in gypsum soil
Osterhaus, Dylan	S1, T2	9:45-10:00	Demographic variation in speed and timing of Fall migration shapes community composition of migrating North American passerines
Plante, Jakob	S1, T5	10:30-10:45	Incubation in low radiation environment increases oviposition, slows growth, reduces longevity in *D. melanogaster*
Silva, Carleen	S2, T7	11:15-11:30	Burning down the mouse: Fire effects on deer mouse abundance and carriage of Sin Nombre Virus
Villalba, Alondra	S3, T12	2:30-2:45	Impacts of early life stress on the physiological stress response and glucocorticoid receptor distribution in the brains of juvenile budgerigars

***Listed alphabetically by presenter surname**

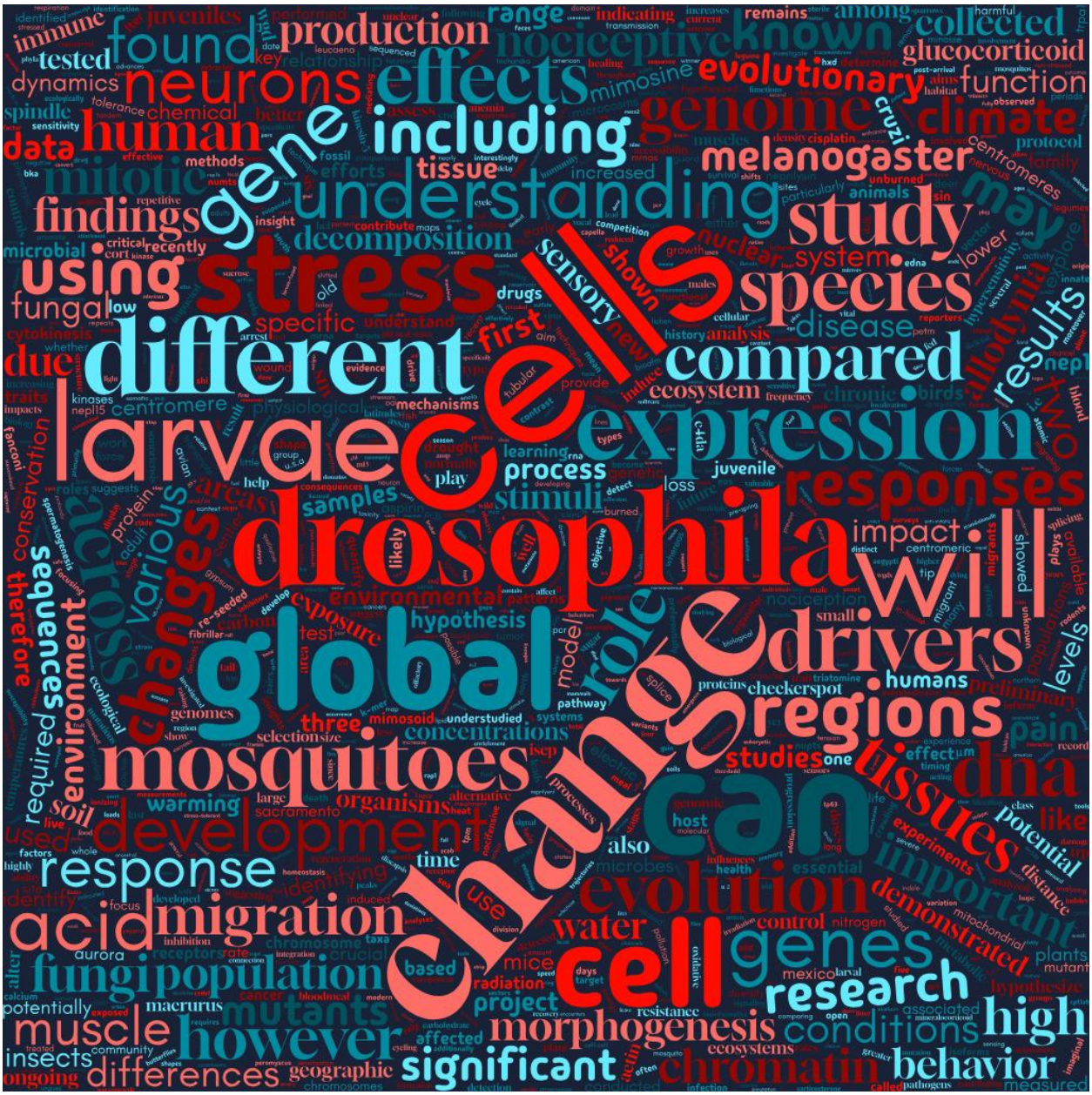
POSTER PRESENTATIONS

Presenter name*	Poster	Title
Araiza, Alan	P1	Doing the job of two: dissecting the function of Aurora kinase in echinoderms
Arroyo, Jaime	P2	Neurogenetic dissection of sensory states in an acid nociception assay of *Drosophila melanogaster*
Borg, Gabriel	P3	Effects of hormetic ethanol treatment on locomotion and gene expression of X-ray irradiated *Aedes aegypti*
Brazil, Samantha	P4	Using time-lapse microscopy during *Drosophila melanogaster* eye development to determine the role of the small GTPase Rap1 in morphogenesis
Cisneros, Esai	P5	Optimizing bio-afm for force spectroscopy of *Brassica* guard cells
Clausen, Maya	P6	Fungal responses to global change: Assessing growth under warming, drought, and nitrogen pollution
Collins, Jade	P7	Evolutionary history of mimosine production in agriculturally significant legumes
Da Silva, Poorni	P8	Investigating the effect of lower sucrose on the development of malaria parasites in *Anopheles stephensi* mosquitoes
Jafari, Delaram	P9	Understanding the role of Neprilysin on cell competition
Salmon, Grace	P10	Fluctuations of the innate immune system of migratory white-crowned sparrows on their wintering grounds in New Mexico
Farrar, Lauren	P11	Exploring the processes of wound healing that contribute to chemical allodynia in *Drosophila melanogaster* larvae
Gomez, Janet	P12	Effects of low and high aspirin dose in the development of *Drosophila l*arvae
Gottwald, Kate	P13	Impact of global change drivers on dryland microbes: Implications for public health and biodiversity
Hernandez, Eliha	P14	Detection of cancer-associate genes in the regeneration blastema of *Sternopygus macrurus*
Jayasundara, Inoka	P15	Microbial community responses to global change drivers: A large-scale analysis across global change experiments in the USA and Puerto Rico
Negin, Jazi	P16	Early life stress and corticosterone receptor concentrations across various tissues in Budgerigars (*Melopsittacus undulatus)*
Jimenez, Caleb	P17	Fungal responses to environmental stress: A decomposition experiment
Kaur, Snehpreet	P18	Localization of centromeres in the *Leucaena trichandra* genome using CentIER
Lopez, Celia	P19	Taxonomic verification of *Peromyscus sonoriensis* for Sin Nombre Virus research via DNA barcoding

Muzammil, Aqsa	P20	Exploring the roles of *Nep1* and *Nepl15* in *Drosophila melanogaster* adult muscle
Navarrete, Priscila	P21	Developing novel reporters to explore cellular mechanics in living cells
Ortega, Franchesca	P22	Alternative splicing (AS) patterns differ in cell types of the same myogenic lineage
Pando, Vanessa	P23	TRPA1 and painless: A comparative analysis of sensory modulation
Rojo, Karim	P24	Global climate change factors effect on fungi respiration and biomass
Salazar, Jaxon	P25	Developing a *Drosophila* model for Neprilysin's role in cisplatin resistance
Victorian, Kaitlin	P26	Measuring the neurological and developmental responses to acid re-exposure in *Drosophila melanogaster* larvae

***Listed alphabetically by presenter surname**

WORD CLOUD OF ABSTRACTS



EVENT SCHEDULE
Domenici Hall (rooms 102 and 106), Saturday March 29, 2025.

9:00-9:30 AM - Breakfast/coffee (Domenici Hall room 102) **and setup posters** (in hallway, front of Domenici Hall 102-106)

9:30-10:45 AM - Oral Presentations Session 1 (Domenici Hall 106)
9:30-9:45 – Nicole Dozier
9:45-10:00 – Dylan Osterhaus
10:00-10:15 – Shakil Ahmed
10:15-10:30 – Taylor Landfair
10:30-10:45 – Jakob Plantae

10:45-11:00 AM Short Break

11:00-12:00 PM Oral Presentations Session 2 (Domenici Hall 106)
11:00-11:15 – Ian Nelson
11:15-11:30 – Carleen Silva
11:30-11:45 – Abdul Al-Nouman
11:45-12:00 – Anjali Karki

12:00-12:15 PM Short Break and set up lunch

12:15-2:00 PM Poster session (in hallway, front of Domenici Hall 102-106)

2:00-3:15 PM Oral Presentations Session 3 (Domenici Hall 106)
2:00-2:15 – Gabrielle Baca
2:15-2:30 – John Agbetsi
2:30-2:45 – Alondra Villalba
2:45-3:00 – Ogochukwu Iloba
3:00-3:15 – Meig Dickson

3:15-3:30 PM Wrap up/Conclusion and remove posters

Abstracts (in alphabetical order by presenter surname)

T11 - The role of *Anopheles stephensi* 's leg in odor detection: how gravid mosquitoes make decisions.

John Agbetsi[1], John Xu[1]

[1]Department of Biology, New Mexico State University.

Transmission of vector borne disease depends on the mosquito population. Complex olfactory and gustatory sensing systems, distributed across various appendages, antennae, palps, and legs, equip mosquitoes to detect various chemical signals in their surroundings. However, the role of the sensing systems in oviposition site selection is understudied. In this study, we used *Anopheles stephensi* to study the role of legs in habitat selection for oviposition. First, odorant binding protein OBP56d was regulated at 24- and 48-hours post-blood meal, indicating olfactory genes are responsive to a blood meal. We found that gravid mosquitoes preferentially deposit eggs in water with first instar larvae (OAI mean: 0.662), whereas water with fourth instar larvae exhibits a repellent effect (OAI mean: -0.2661). Since larvae-fused water harbors bacteria that produce indoles as a metabolite, we tested how gravid mosquitoes respond to indoles in water for oviposition. Water with indole at 10 µM, 30 µM, and 50 µM were tested in triplicates. Water with 10 µM indole showed the best attractiveness to gravid mosquitoes, with a *P* value of 0.1733 (One way ANOVA).

T3 - Investigating the Evolutionary Trajectories of Organelle-Derived DNA in Fabaceae Nuclear Genomes

Shakil Ahmed[1] and C. Donovan Bailey[1]

[1]*Department of Biology, New Mexico State University, Las Cruces, NM, USA*

Plant cells contain three different genomes, the nuclear, mitochondrial, and plastid. Through the process of endosymbiosis, mitochondria evolved from α-proteobacteria while plastids originated from cyanobacteria. Once combined into eukaryotic cells, these organellar genomes have undergone dynamic changes, including both the massive loss of organellar DNA and the transfer of mitochondrial (NUMTs) and plastid (NUPTs) DNA to the nucleus. Several research studies have provided evidence indicating that DNA transfer is an ongoing process, yet there remains limited understanding regarding the frequency and evolutionary dynamics of NUMTs and NUPTs. Nuclear integrants may undergo diverse evolutionary fates including elimination, mutation, rearrangement, fragmentation, and/or proliferation. Integrated organellar DNAs play pivotal roles in augmenting genetic diversity as well as driving gene and genome evolution. Leveraging the extensive nuclear and organellar genomic resources available for economically and ecologically important Fabaceae, this study aims to elucidate the evolutionary trajectories of NUPTs and NUMTs by quantify ongoing organelle-to-nucleus DNA transfer, assessing integration authenticity, and constructing phylogenetic interpretations of organelle-derived nuclear DNA integration. To quantify the ongoing DNA transfer from organelles to nuclear chromosomes, we will utilize available chromosomal-scale legume genomes. Our research will focus on identifying organelle-derived nuclear DNA (NUMTs and NUPTs) and analyzing its evolutionary patterns. By examining the integration patterns across various lineages, we aim to gain insights into the mechanisms that drive the evolution of these sequences in the nuclear genome. This investigation will contribute to a deeper understanding of how organelle DNA fragments become integrated and evolve within nuclear genomes across the Fabaceae family.

T8- The *Drosophila melanogaster* TENT5 homolog is required for individualization of spermatids during spermatogenesis

Abdul Al-Nouman[1], Kyle Helms[2], Jennifer Curtiss[1]

[1]Department of Biology, New Mexico State University; [2]Department of Neurology, Columbia University

TENT5s are non-canonical poly(A) polymerases (PAPs) that add non-templated adenines to mRNAs post-transcriptionally. Orthologs of TENT5 are important for reactivation of translationally repressed mRNAs in oocytes and in dendrites of neurons and are required for long term memory. Human TENT5s have been implicated in multiple diseases and cancers suggesting a tumor suppressive role. TENT5D has been linked to human male infertility and TENT5C has also been shown to be essential during spermatogenesis in mice. However, the mechanisms by which TENT5s polyadenylate mRNAs remain elusive and they may have other biochemical roles besides poly(A) polymerase activity.

Drosophila melanogaster has one *TENT5* ortholog, *isep*. We have generated a loss of function allele of *isep* and have demonstrated that homozygous males are sterile with defects arising during spermatid individualization. Individualization is the last stage of spermatogenesis where a syncytium of 64 spermatids must be resolved to encase each spermatid in its own plasma membrane and strip away unneeded organelles and cytoplasm. Restricted localization of caspase-3 and synchronous actin cone progress along the axoneme is disturbed in *isep* loss of function. *Isep* is also required for localized accumulation of *scotti*, a key regulator of individualization. Our *in situ hybridization* reveals that *isep* is transcribed in two distinct stages: during the miotic division of spermatocytes and post-mitotically in elongating spermatids where it localizes in a “comet” pattern. Our ongoing work aims to identify the mechanism by which *isep* operates by identifying its mRNA targets and RNA binding protein cofactor(s) in the context of spermatogenesis.

P1 - Doing the job of two: dissecting the function of Aurora kinase in echinoderms.

Alan Araiza[1], Gabriela Reyes[1], John Henson[2] and Charles B. Shuster[1]

[1]Department of Biology, New Mexico State University; and [2]Department of Biology, Dickinson College

Cell division in eukaryotic cells is orchestrated by mitotic kinases that regulate chromatin condensation, spindle assembly, chromosome segregation and cytokinesis. The Aurora kinases A and B play critical roles in organizing the mitotic spindle, ensuring the fidelity of chromosome segregation and initiating cytokinesis. And while these kinases share significant homologies, they are activated by different scaffolding proteins and target distinct substrates. Interestingly, while nearly all metazoans contain both aurora kinases, two deuterostome phyla (echinoderms and ascidians) contain a single Aurora gene, raising the possibility that these phyla have undergone a gene loss, with the remaining kinase assumes the function of both A and B. To better understand how sea urchin Aurora regulates spindle assembly and cytokinesis, the open reading frames of *Lytechinus pictus* Aurora will be tagged with the fluorescent protein Staygold, and preliminary expression studies performed in both human cultured cells and sea urchin embryos to confirm that LpAurora localizes to both spindle poles and centromeres. Mutations known to convert human Aur A into AurB will be introduced as well as mutations in an AurB sumoylation site, effectively turning these mutants into either Aurora A or Aurora B. Introduction of a second, kinase-dead mutation into the catalytic domain should then create a kinase that will exert a dominant-negative effect on mitotic structures where these mutants localize. Using this battery of mutants, we hope to understand how these organisms are capable of executing cell division with a single kinase whereas the rest of metazoa requires two.

P2 - Neurogenetic dissection of sensory states in an acid nociception assay of *Drosophila melanogaster*

Jaime Arroyo, Raul Chavez, Jacob Jaszczak

Department of Biology, New Mexico State University

Animals rely on nociceptive sensory systems to detect and escape to potentially damaging stimuli. *Drosophila* larvae use multidendritic (md) neurons in their peripheral nervous system to respond to a wide range of nociceptive stimuli, and concentrated hydrochloric acid can induce nociceptive behavior of *Drosophila* larvae. A specific type of md neuron, the class IV dendritic arborization (c4da) neurons, are sensors for mechanical, thermal, and acid nociception. We find that nociceptive behavior in response to acid can differ based on the larva's physical state. Larvae are more likely to show a nociceptive response when suspended than when crawling, but a TRP channel mutant disrupts behavior only when larvae are crawling. To access the contribution of sensory neurons to this physical-state dependent response, we used the GAL4/UAS system to temporally block sensory function by expressing Shibire^ts (Shi^ts) in the c4da neurons. Shi^ts is a temperature-sensitive dynamin mutant that blocks synaptic transmission at restrictive temperatures (29°C). We surveyed whether silencing md and c4da neurons alter acid induced nocifensive rolling behavior during different physical-states. At permissive temperatures (22°C), all larvae responded normally to acid exposure, and at restricted temperatures, we observed a loss in the rolling behavior when either group of neurons were silenced. This indicates the necessity of these neurons in acid nociception in both crawling and suspended physical-states, in contrast to the TRP sensory channel results. This study provides insight into the neuronal circuits mediating acid pain sensation and suggests new sensors may be involved during different physical-states.

T10 - Molecular Testing of Triatomine Insects for *Trypanosoma cruzi* Infection and Bloodmeal Analysis in Las Cruces, New Mexico

Gabrielle Baca[1], Kavita Adhikari[2], Isaiah Gallosa[1], C. Scott Bundy[2], Maria G. Castillo[1]

[1]Department of Biology, [2]Department of Entomology, Plant Pathology, and Weed Science. New Mexico State University.

Triatomine insects of the family Reduviidae, or "kissing bugs," are vectors for transmitting the parasitic protozoan *Trypanosoma cruzi*, the causative agent of Chagas disease. Triatomine insects are found in the Southwest U.S., particularly in Arizona, California, Texas, and New Mexico. Infection with *T. cruzi* can induce severe health complications and can be fatal. There is no available vaccine for Chagas disease and chronic infections may not be effectively treated. Prevention efforts include avoiding insect bites and use of insecticides. Triatomines are hematophagous and transmit *T. cruzi* to hosts after taking a bloodmeal by depositing contaminated feces that enter through skin abrasions or mucous membranes. Triatomine insects feed on various mammals, including humans, dogs, cats, and rodents. In this study, we collected triatomine insects from urban and suburban sites in Las Cruces, New Mexico. Insects were tested for *T. cruzi* infection. Additionally, an analysis on collected insects was performed to identify the bloodmeal source. For these purposes, DNA was extracted from the insects' hindguts and used for PCR using primers specific to *T. cruzi* and vertebrate/mammalian targets. Positive samples were identified on agarose gels, compared to positive controls, and sequenced. Results showed that 60% of samples tested were infected with *T. cruzi*. Currently, bloodmeal source(s) are being tested. The detection of *T. cruzi* in triatomines and identification of their preferred bloodmeal sources are essential steps in monitoring and preventing Chagas disease in New Mexico.

P3 - Effects of Hormetic Ethanol Treatment on Locomotion and Gene Expression of X-ray Irradiated Aedes aegypti

Gabriel Borg and Immo Hansen

Department of Biology, New Mexico State University, Las Cruces, NM

Mosquitoes pose a significant risk to health as vectors of various pathogens. Past studies have shown the Sterile Insect Technique (S.I.T.) to be effective at reducing vector populations. These advances, however, have also illuminated major drawbacks, primarily the weakening of male mosquitos that results from the radiation required to sterilize them. The radiation's effects on the somatic cells result in less competitive males, which is a critical factor in the S.I.T. Studies have shown a strong case for the effectiveness of ethanol hormesis to induce radioprotectants when fed to Aedes aegypti mosquitos prior to radiation. With this in mind, we performed transcriptomics on irradiated Aedes aegypti mosquitos that had been fed ethanol for a week and compared them to a control group. RNAseq at three, one-hour interval time points from ethanol-fed radiated males allowed us to create a list of possible radioprotectant genes based on the most upregulated expression and demonstrated the peak time of early gene expression following irradiation. Analyzing these genes can be an important step in optimizing the sterile insect technique by providing a means to understand how mosquito cells protect themselves from irradiation.

P4 - Using time-lapse microscopy during *Drosophila melanogaster* eye development to determine the role of the small GTPase Rap1 in morphogenesis

Samantha Brazil[1], Jennifer Curtiss[1]

[1]Department of Biology, New Mexico State University

Morphogenesis is the process by which cells and organisms develop their shape and structure, essential for proper physiological function. Having a better understanding of how cells and tissues undergo morphogenesis can lead to advancements in wound healing, origin and treatment of birth defects, and tissue engineering. A classic example of morphogenesis is the development of a frog, which transitions from a spherical egg to an elongated tadpole with an oval-shaped head and long tail. In epithelial tissues, morphogenesis is driven by cell adhesion and contractile forces, with E-cadherin playing a key role in cell-to-cell adhesion and allowing cells to move and change shape. *Drosophila melanogaster*, commonly known as the fruit fly, serves as a valuable model. Their compound eyes exhibit a precise pattern of cell shapes to function properly, providing insight into how morphogenetic processes are regulated. The small GTPase Rap1 is like an “on and off switch” and is involved in signaling pathways related to cell adhesion and actomyosin contractility, which both play a critical role in morphogenesis. We are using time-lapse microscopy to observe wild-type and Rap1 mutant cells undergoing morphogenesis in the Drosophila eye to determine Rap1’s role in morphogenesis. We aim to collect initial data to develop a hypothesis about the molecular mechanisms behind morphogenesis.

P5 - Optimizing BIO-AFM for force spectroscopy of *Brassica* guard cells

Esai Cisneros[1], Stanley Cheng[1], Tatiana Kardashina[2], E.E. Serrano[1]

Department of Biology, New Mexico State University[1]; Department of Mechanical Engineering, Washington University at St. Louis[2]

The mechanical properties of plant guard cells, such as elasticity and stiffness, are essential for regulating stomatal pore opening and closing in response to environmental stimuli. We aim to explore guard cell development using methods applicable to live tissue biomechanics. Biological Atomic Force Microscopy (BioAFM) is a powerful tool for measuring stiffness, elasticity, and deformation of live cells, but it requires sample-specific optimization. In this pilot study, we optimized experimental conditions and tip selection for acquiring force maps and Young's modulus (YM) measurements from guard cells using a Bruker Nanowizard 4 XP BioAFM. Brassica juncea seeds were aseptically germinated and grown at 24°C. Live cell measurements were made from whole 1-3 week-old seedlings with intact stems and roots, with water added to prevent dehydration. This preparation allowed the acquisition of up to six force maps per stoma in about two hours. We tested three tips with varying shapes and force constants: PPP-FMAuD-10, TESPA-V2, and Biosphere B100-NCH-1. After optimizing scan settings for each tip, we analyzed data in Atomic J. The Biosphere B100-NCH-1 tip produced the most reproducible measurements, smoothest force curves, and YM values with lower standard deviations (0.1-1.5 MPa). These results establish a foundation for future research into the viscoelastic properties of guard cells during development.

P6 - Fungal Responses to Global Change: Assessing Growth and Pigment Production Under Warming, Drought, and Nitrogen Pollution

Maya Clausen[1], Caleb Jimenez[1], Karim Rojo[1], Shad Abubaker[1], Adriana L. Romero-Olivares[1]

[1]Department of Biology, New Mexico State University

Fungi are a diverse group of eukaryotic organisms that play essential roles in our ecosystem. For example, they mediate biogeochemical cycles and interact with all plants and animals. Like all other organisms, fungi are vulnerable to the harmful effects of global climate change, yet little is known about their specific responses to different global change drivers. In this project, we wanted to assess how three global change drivers (i.e., warming, drought, and nitrogen pollution) affected growth rate and pigment production in fungi. These two traits are of special interest in the context of global change as they indicate how much energy fungi are investing towards growing and towards producing important molecules for protection (i.e., pigment). To this end, we measured growth rate and pigment production of 48 different fungal species under global change drivers and under control conditions. We conducted one-week incubations followed by measurement of colony size and assessment of pigment using a computer software. We hypothesized that we would see differences in fungal trait responses based on global change drivers and based on fungal species. Ultimately, our research aims to deepen our understanding of fungal trait ecology under global change drivers to better understand the consequences of our ecosystems to global climate change.

P7 - Evolutionary history of mimosine production in agriculturally significant legumes

Jade Collins[1] and Donovan Bailey[1]

[1] Department of Biology, New Mexico State University

Mimosine is an amino acid-like substance produced by plants in the mimosoid clade of the legume plant family. The mimosine chemical pathway is thought to have evolved as a defense mechanism against insects and other herbivores as it has toxic effects when digested. Mimosoid legumes are important plants in the wild and to humans due to their geographic range, agricultural significance, and scientific contributions. Many legumes, including the taxa used here, have a nitrogen-fixing ability, which can revitalize farmlands and other depleted soils. The mimosoid clade of legumes are scientifically significant due to their multiple whole genome duplications (WGDs), which make them great for genetic studies, as WGDs create copies of genes which evolution can act on for more/faster adaptations. However, the evolution of mimosine production in legumes remains unclear. The objective of this project is to explore the evolutionary history of the genes involved in mimosine production. This will be done through the collection of relevant genomes, determining orthologous groups, and characterizing the evolutionary history of mimosine genes to show the origin of mimosine. The progress to date includes the collection of 15 mimosoid genomes, 1 outgroup, and 8 sequences of genes related to mimosine production, and preliminary data on the presence of mimosine-related genes in mimosoid genomes/plants. Future directions include finding the possible reason for mimosine evolution from cystathionine β-lyase (CBL) and connecting the evolutionary history of the mimosoid clade to other agriculturally important plants of the time.

P8 - Investigating the effect of lower sucrose on the development of malaria parasites in *Anopheles stephensi* mosquitoes

[1]Poorni De Silva and [1]Jiannong Xu
[1] Department of Biology, New Mexico State University

Mosquito-borne illnesses represent a major public health challenge and can have severe socio-economic consequences. Malaria is a mosquito-borne disease caused by the parasite *Plasmodium sp*. Mosquitoes rely on plant-derived sugars for daily energy supply. Glucose plays a vital role as a daily nutrient requirement for mosquitoes which influences their survival, immunity and vector competence. However, the effect of sugar metabolism on the immunity of vector mosquitoes is understudied. In this study, we used *Anopheles stephensi* as a model to investigate the effects of sugar supply on survival and susceptibility to *Plasmodium berghei* infection. Our results revealed that approximately 50% of mosquitoes could survive on lower sugar diets (0.5% sucrose meal). Therefore, 0.5% sucrose diet selection was implemented to enrich genotypes with low sucrose tolerance. In the first four generations post-selection, these mosquitoes exhibited higher parasite loads compared to wild-type mosquitoes. Interestingly, an intriguing shift occurred after the fifth generation, with selected mosquitoes showing reduced parasite loads compared to wild type mosquitoes. This suggests a genetic connection between carbohydrate metabolism and *Plasmodium* susceptibility. Gene expression analysis revealed metabolic shifts due to selection pressure. Upregulation of Acetyl CoA carboxylase indicated increased fatty acid biosynthesis, while downregulation of trehalose transporter suggested reduced glucose transport. These findings demonstrate significant alterations in lipid metabolism and carbohydrate utilization resulting from selection.

P9 - Understanding the role of Neprilysin on cell competition

Delaram Jafari[1], Jennifer Curtiss[1]

Department of Biology[1], New Mexico State University[2]

Cell competition is a vital biological process that maintains tissue homeostasis by eliminating less fit or abnormal cells ("losers") while allowing metabolically superior cells ("winners") to dominate. This phenomenon was first shown in mosaic Drosophila melanogaster imaginal cells mutant for ribosomal proteins, but mirrors the ways in which subclones of tumor cells drive cancer progression via cell-cell interactions. Recently, systemic metabolic changes have been shown to affect cell competition. For instance, hyperinsulinemia has been shown to change “loser” cells that would normally be eliminated by cell competition into tumor cells. In addition, “winner” cells have been shown to have increases in glycolysis and protein synthesis, and to trigger a reduction in oxidative phosphorylation in “loser” cells. Therefore, the metabolic environment can impact the behavior of loser cells. We have been studying a Drosophila melanogaster peptidase called Neprilysin1, which is conserved in humans, and for which a transcriptomic analysis has demonstrated that mutants have reduced expression of genes encoding proteins involved in oxidative phosphorylation. We hypothesize that by altering the metabolic environment, Neprilysin1 will alter the competitive advantage of winner cells in the Drosophila imaginal cells, and that human Neprilysin might have the same effect in subclones of tumor cells in humans, impacting whether they drive cancer progression. We will test this hypothesis by conducting cell competition experiments in Neprilysin1 mutant flies.

P10 - Fluctuations in the Innate Immune System of Migratory White-crowned Sparrows on their Wintering Grounds in New Mexico

Grace M. Salmon[1], Julianna K. Diaz[2], Jodie M. Jawor[3], Timothy F. Wright[4]

[1]Department of Fish, Wildlife, and Conservation Ecology, New Mexico State University;
[2]Department of Biology, New Mexico State University

Migration in birds is a strenuous activity that requires constant modulations and tradeoffs of physiological traits to maintain optimal fitness. Among these traits, the innate immune system likely plays a vital role in migratory success, as birds migrating from breeding areas may face novel pathogens during stopovers and at overwintering grounds. This work aims to observe the fluctuations of the innate immune system as long-distance migrants transition across annual stages. To do this, we compared the strength of the innate immune system of overwintering White-crowned Sparrows (*Zonotrichia leucophrys*), a long-distance migrant, during two periods: post-arrival from fall migration (November-December) and pre-spring migration (March-April). We captured birds and collected blood and morphometric data from White-crowned Sparrows during these two periods. Collected blood was used in bacterial killing assays (BKA) to measure the strength of their innate immune response. We noted a slight immune response decrease from the post-arrival period to the pre-spring migration period, changing from a mean BKA percentage of 50.41% (SE=3.52) to 43.4% (SE=5.83). This may suggest that sparrows have a lower immune response right before they leave for spring migration, potentially due to energetic trade-offs. Conversely, they may have an enhanced immune response post-arrival as a carry over from migration.

T14 - Filling the Gaps: Determining Ranges of Fossil Birds using Machine Learning

Meig Dickson

Department of Biology, New Mexico State University

Geographic range is a key ecological trait of any given organism. The heightened mobility of birds makes range one of the first parameters to change in response to environmental shifts like modern global warming. Range changes evident in the fossil record have the potential to inform predictions about the effects of modern climate change. The Paleocene-Eocene Thermal Maximum (PETM), 56 mya, is the most recent rapid warming event comparable to modern conditions. However, the PETM is understudied in birds due to their poor Paleocene fossil record. Machine learning algorithms can potentially impute gaps in the fossil record with methods like correlating occurrences of more frequently preserved ecologically related taxa to predict the range of a target taxon. I use one such algorithm, Massively Interpolated Occurrences for Species Spatial Estimation (MInOSSE), in tandem with traditional range reconstruction methods to estimate the ranges of birds known across the PETM. This work uses data from fossil occurrences of avian clades including the extinct Gastornithiformes, penguins, mousebirds, and owls. Increased holistic study of prehistoric ecosystems and collaboration among specialists of different paleotaxa will be required to realize the full potential of MInOSSE and other machine learning algorithms. Techniques like MInOSSE will allow researchers to impute more information from the fossil record than previously possible, increasing the utility and importance of paleontology in biological research of contemporary neotaxa.

T1 - Devising an eDNA Assay for Critically Endangered Butterfly *Euphydryas anicia cloudcrofti*

Nicole M. Dozier, Ashley T. Rohde, Brook G. Milligan

Department of Biology, New Mexico State University

The Sacramento checkerspot butterfly (*Euphydryas anicia cloudcrofti*) is federally endangered and endemic to the Sacramento Mountains near Cloudcroft, New Mexico. It has the smallest known geographic range of any butterfly in North America. Furthermore, visual population surveys have shown steep population declines over the last three decades, likely in response to habitat destruction and fragmentation; no sightings were reported in 2023 or 2024. This suggests that population density is below the threshold of detection for visual surveys, and it is unclear if the last known extant populations have been entirely extirpated. Resourced managers wish to supplement visual surveys with recently developed methods to detect pollinator environmental DNA (eDNA) from host flowers to detect remaining individuals and assess the conservation status of surviving populations. We are developing an eDNA assay specific to the Sacramento checkerspot and a closely related conspecific, the capella checkerspot (*E. anicia capella*). We will identify promising genomic regions for assay design by comparing published and newly sequenced mitochondrial DNA in all available sequences of these taxa and test the specificity of potential markers by comparing them to sequences from non-target butterflies co-occurring with the Sacramento checkerspot. Regions common to target and non-target butterflies will be excluded. We will use eDNA from the capella checkerspot to hone the assay's reaction conditions and quantify the protocol's precision once established. We will then test the eDNA collected from throughout the Sacramento checkerspot’s known habitat to quantify the occurrence of the target taxa, which will serve as baseline data for recovery efforts.

P11 - Exploring the Processes of Wound Healing that Contribute to Chemical Allodynia in *Drosophila melanogaster* Larvae

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Would healing is a critical process in multicellular organisms that sustains the integrity of the epithelial barrier following tissue injury. During this process, sensory neurons become hypersensitized to protect the tissue while it heals. This heightened sensitization is called allodynia and can be described as pain due to a stimulus that does not normally provoke pain. For example, when we get a sunburn, it can later be painful to put on a T-shirt; something that would normally be innocuous. *Drosophila* larvae also experience allodynia during wound healing, due to sensitization of the class IV peripheral sensory neurons, which are located directly below the epidermis. Previous literature has identified 0.5% hydrochloric acid to be subthreshold and does not cause aversive behaviors in *Drosophila* larvae. However, hours after larvae have been puncture-wounded, they become sensitive to subthreshold acid concentrations. After puncture-wounding, a plug forms in the wound gap to stop the larvae from bleeding, which then melanizes over the next few hours, forming a scab, which promotes the process of re-epithelialization. We hypothesize that specific steps within the wound-healing process contribute to allodynia. To test this, I have determined the different categories of wounds associated with sensitized larvae. Preliminary results suggest that larvae with more developed scabs are more sensitive to allodynia. Ongoing work is further categorizing the timing of scab formation with allodynia sensitivity. This research aims to elucidate the mechanisms of pain during wound healing, potentially identifying novel factors to enhance patient care.

P12 - Effects of Low and High Aspirin Dose in the Development of *Drosophila* Larvae

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Non-steroidal anti-inflammatory drugs (NSAIDs) such as aspirin are commonly known for their benefits in relieving pain and reducing fever. However, at high doses these drugs have been found to have harmful impacts, such as gastrointestinal bleeding, bleeding disorders, and liver disease. At low doses, aspirin increases cell viability by decreasing inflammation and oxidative stress (Jorda et al., 2020). The impact of NSIADs and painkillers on health during development is less well understood, and the long-term effects of use during pregnancy has recently become a concern (Bührer et al. 2021). In this research project, the effects of aspirin on *Drosophila* larvae development are analyzed. The medication was mixed in food and administered to three-day, four-day, and five-day old larvae for evaluation. High and low dosages of aspirin were used. We then measured the development of larvae into their pupa stage as reflection of how the toxicity of these drugs may lead to larval death. We find that larvae of all ages are sensitive to high doses of aspirin. In contrast, only three-day old larvae are sensitive to low doses of aspirin. Future experiments will determine which tissues contribute to this developmental sensitivity. By examining the pathophysiological effects of analgesic medications during larval development, we can consider the effects of toxic interventions. This study will enhance our understanding of effective pain management and provide greater insight into the toxicity of pain medications in developing animals.

P13 - Impact of global change drivers on dryland microbes: Implications for public health and biodiversity

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Global climate change has caused extreme conditions of heat and drought in the Southwest United States that are projected to worsen over time. In fact, these changes are impacting entire ecosystems and may be contributing to the emergence of disease. However, there is little research on how global change drivers are impacting microbial ability to tolerate stress. Understanding these responses is important, as there is evidence suggesting that increased stress tolerance can impact the onset of pathogenicity in microbes, especially in microbes that are known to be facultative pathotrophs. Therefore, the objective of this project was to assess how the community of soil microbes was affected by global change drivers over time. We collected top-soil samples from the Jornada Basin LTER site in the northern extent of the Chihuahuan Desert in southern New Mexico. We added soil in microcosms and placed them into three treatment groups (heat, drought, and their interaction (i.e., hxd) and one control group. Heat and control microcosms were watered weekly, and drought and hxd microcosms were watered every three weeks. Microcosms were harvested at 3, 6, 9, and 12 months after the onset of treatments. We extracted DNA from all samples and conducted ITS and 16S metabarcoding to identify fungi and bacteria, respectively. We hypothesized that there would be a greater abundance of pathogenic and facultative pathogenic microbes in treatment groups compared to the control. Our findings help to inform on potential consequences of microbial responses to global climate change to public health and ecosystem biodiversity.

P14 - Detection of Cancer-Associate Genes in the Regeneration Blastema of *Sternopygus macrurus*

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The South American electric fish Sternopygus macurus can regenerate all tissues including skin, cartilage, skeletal muscle (SM), the muscle-derived electric organ (EO), and the spinal cord following tail amputation (Unguez, 2013). Repetitive removal of its tail leads to a robust stem-cell based regeneration of SM and EO tissues (Unguez, 2013). To date, there is no reported evidence of uncontrolled growth or tumor formation during regeneration in S. macrurus. Further, the relationship between tissue regeneration and cancer has not been tested in electric fish as it has been in mammals (Maggiore and Zhu, 2023). We test the hypothesis that genes associated with human cancers are detected in S. macrurus tissues in the absence of uncontrolled growth. Using standard molecular biology techniques, we characterized the presence of transcripts for genes csde1, eno1a, usp2a, cpt1ab, and tp63. Our data (n=1) support our hypothesis in that mRNAs for csde1, eno1a, usp2a, cpt1ab, and tp63 genes were detected in all tissues. Specifically, qualitative PCR showed band intensities for all 5 transcripts in the regeneration blastemas at 7- and 14-days post amputation to be stronger than those observed in mature SM and EO tissues. Interestingly, studies in mammals report that splicing variants for these genes may impact cancer formation differently. Characterization of these variants in S. macrurus tissues are now underway.

T13 - Exploring the Influence of Chromatin Accessibility on Homeologous (Duplicate) Gene Expression in the Tetraploid Plant, *Leucaena trichandra.*

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Whole genome duplication (WGD) leads to polyploidy in plants, triggering gene expression changes, epigenetic modifications, and often extensive duplicate gene loss through diploidization. This study examines the impact of chromatin accessibility on gene expression variation among retained homeologous gene pairs following WGD in tetraploid genome of *Leucaena trichandra* (Leguminosae). The genome of *L. trichandra* is intriguing because it underwent an ancestral WGD over 10 million years ago but has experienced little diploidization, raising questions about genome and gene expression evolution in the aftermath of the WGD.

We used Assay for accessible chromatin regions (ATAC-seq) to identify accessible chromatin regions. We performed quality checks with Trimgalore, aligned reads with BWA, called peaks with MACS2, and assigned open chromatin peaks to genomic features using in-house scripts. After normalizing open chromatin peaks by genomic region size, we found the highest peak densities in the 5'UTR and upstream regions, suggesting their functional importance. This pattern was consistent across all duplicated chromosomes, indicating stable chromatin accessibility in this polyploid. We analyzed TPM values from RNA-seq and ATAC-seq peak lengths to investigate the correlation between gene expression and chromatin accessibility focusing on pairs where one gene's TPM was at least twice its homeolog's. Preliminary results of this analysis between two duplicated chromosomes show no consistent correlation chromatin accessibility and gene expression, suggesting the involvement of additional regulatory mechanisms. Future analyses will expand our pipeline to all homeologous chromosome datasets, identify significant differences between duplicate chromosome pairs, and explore transcription factor binding motifs in open chromatin regions.

P15 - Microbial community responses to global change drivers: A large-scale analysis across of global change experiments in the USA and Puerto Rico

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Global change drivers, such as drought, warming, and increased soil nitrogen levels, are disrupting ecosystems-scale processes. Although microbes play a crucial role in mediating ecosystem processes, the impact of global change drivers on the microbial community, and how these compare across ecosystems remains an understudied area. Therefore, our aim was to assess microbial community responses across global change experiments in multiple Long-Term Ecological Research (LTER) sites in the United States and Puerto Rico. We received 400 soil samples from nine LTER sites from drought, warming, and nitrogen addition studies. We hypothesized that stress-tolerant microbes will be more abundant under global change drivers compared to control conditions regardless of ecosystem type. We extracted DNA and conducted bioinformatics and statistical analysis to assess responses. Our findings are shedding light to the large-scale impacts of global change drivers on microbial communities, offering valuable insights into their unified responses. These insights are valuable in improving the current understanding of microbial responses to climate change and are crucial for developing solutions for climate change mitigation.

P16 - Early Life Stress and Corticosterone Receptor Concentrations across Various Tissues in Budgerigars (*Melopsittacus undulatus)*

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Early life stress triggers the release of glucocorticoid (GC) hormones which can profoundly impact the development and function of various physiological systems. Chronic stress can also alter the expression of the glucocorticoid and mineralocorticoid receptors *(GR* and *MR)* that bind corticosterone (CORT), the primary avian stress hormone, and mediate the body's response to stress. Several studies have explored how chronic stress alters *GR* and *MR* expression in the brain, but the impact of chronic stress on peripheral *GR and MR* remains poorly understood. In this study, we compared *GR* and *MR* expression across both reproductive and non-reproductive tissues in female and male budgerigars *(Melopsittacus undulatus)* that were exposed to either a 3-week chronic stress protocol or a non-stressed control protocol during the juvenile period and adulthood in a fully crossed design. We then used qPCR to measure the expression of GC receptors *GR* and *MR* in various tissues including kidney, liver, pectoralis muscle, pancreas, and testes or ovary. Based on the hypothesis that chronic stress can increase tissue sensitivity to CORT, we predict increased *GR* and/or *MR* expression in these tissues in individuals subjected to the stress treatments, and that there will be an additive effect in individuals stressed in both the juvenile and adult stages. Understanding the differential expression of GC receptors in both nongonadal and gonadal tissues of budgerigars will provide a comprehensive understanding of how stress influences glucocorticoid signaling across multiple physiological systems.

P17 - Fungal Responses to Environmental Stress: A Decomposition Experiment

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Amidst global change, studying fungi can help scientists gain an understanding of how biogeochemical cycles, such as the carbon cycle, will be impacted by environmental changes. Since fungal metabolism is highly vulnerable to changes in the environment, the rate at which they produce decomposition enzymes is affected by changes in the environment. Therefore, decomposition rates and the amount of carbon stored in the soil, the amount of carbon available for plant, animals, and other microbes, and the amount of carbon released to the atmosphere as CO_2, is highly affected by environmental stress. To this end, our objective was to determine how decomposition rates by different fungi are affected by global change drivers. We conducted a decomposition experiment using mesquite shrub (*Prosopis* sp.) litter and 48 different fungal species. Specifically, we inoculated mesquite litter with each fungus under three different global change drivers, warming, water stress, and nitrogen pollution. We measured decomposition after six weeks exposed to these global change drivers. Our results shed light on how decomposition rates of different fungal species are affected by different global change drivers. This type of work is important as it can help us to better understand how the global carbon cycle will be impacted by global climate change.

T9 - Small Mosquitoes – Large Implications: Effects of Larval Crowding and Starvation on Locomotor Activity, Adult Biting Frequency, and Insecticide Resistance in Two Strains of *Aedes aegypti*

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Stress during the larval phase of their post-embryonic development can result in reduced-size imagoes in mosquitoes. Water temperature, salinity, food availability, crowding, and predation are factors that affect larval development timing and adult size. In an earlier study we compared the transcriptomes and metabolomes of adult mosquitoes that were raised under standard conditions (large) with mosquitoes raised under stress conditions (small) and found significant changes. Continuing this line of inquiry, we compared the general activity, biting frequency, and insecticide resistance in small and large *Aedes aegypti*. We found that small and large mosquitoes have different activity and biting patterns over a two-week time course, however, the cumulative number of engorgements was not different. After pyrethroid exposure, mortality curves of small and large mosquitoes were similar in the susceptible UGAL strain but different in the insecticide-resistant Puerto Rico strain. Our results highlight the large knowledge gaps regarding the effects of mosquito size on vectorial capacity.

P18 - Localization of Centromeres in the *Leucaena trichandra* Genome Using CentIER

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Centromeres are constricted region of chromosomes that play essential roles in during cell division, including acting as the central attachment point of spindle fibers during cytokinesis. Centromeric regions are composed of repetitive sequences called tandem repeats (satellites) and transposons. Identifying centromere locations is crucial for studying genome organization, chromosome stability, and evolution. These regions have been identified historically using cytogenetic techniques like C-banding which has low specificity, FISH which is labor-intensive, and ChIP which is antibody-dependent and incomplete coverage. While centromeric regions are visually known, their DNA sequences remain unclear. Due to their high complexity, it has been difficult to obtain high-quality centromeric sequences, limiting the research on centromere function, evolution, and variation. Additionally, most full genome sequencing project ignore the annotation of centromeric regions, further limiting our understanding of their locations and molecular evolution. To address these challenges, bioinformatics tools use computational methods, including k-mer frequencies and repetitive element detection, to provide a more efficient approach for centromere identification. In this project we are locating centromeres in the *Leucaena trichandra* genome. *Leucaena* plays a significant role in fuel wood production, fodder supply, and soil fertility. Identifying centromeres will help in comparing with other legume species and to understand centromere evolution and hybridization. We are using a software called CentIER, this is designed to detect centromeres in whole genome using computational methods via k-mer frequency, repetitive regions like TRs (tandem repeats) and LTRs (long terminal repeats). The key principle behind CentIER is that centromeres have distinct patterns, such as lower sequence specificity and continuous low k-mer signal intensity, compared to other genomic regions. By analyzing these patterns, CentIER identifies candidate centromere regions. The tool uses a statistical aggregation method to combine results from different analyses and highlights the most likely centromeric regions. CentIER has been installed on linux by setting up dependencies which includes genome tools, LTR_retreiver and python packages. After installation, system was tested using an *Arabidopsis* test data, confirming its accuracy. By applying CentIER to the *Leucaena* genome, we aim to generate high-resolution centromere maps, contributing to the broader understanding of centromere evolution and genome organization in leguminous trees.

T4 - PI3K activity influences cell fate in response to mitotic arrest

Taylor Landfair, Naghmana Ashraf, Roaa Kassim, Edward Goldstein and Charles B. Shuster

Anti-mitotic drugs that induce mitotic delay and eventual cell death are commonly employed as chemotherapeutic drugs. However, there is a high degree of heterogeneity in tumor cell responses to mitotic arrest, both between cell lines as well as between individual cells. There are also differences in cellular responses based on the mechanisms by which drugs interfere with mitotic progression. Work in the lab has focused on cellular responses to kinesin-5 inhibitors, which prevent cells from forming a bipolar spindle and cause eventual cell death in cancer cells. And while cells treated with kinesin-5 inhibitors cannot successfully complete mitosis and cytokinesis, they have not proven to be as effective as taxanes and vinca drugs in the clinic. Experiments in HeLa cells demonstrated that simultaneous inhibition of Kinesin-5 and PI3K/AKT/mTOR induced apoptosis more effectively than mitotic arrest or PI3K/AKT/mTOR inhibitors alone. Cells subjected to combinatorial treatment were less able to sustain mitotic arrest, dying significantly sooner than cells subjected to Kinesin-5 inhibition alone. Moreover, we found that PI3K inhibition dramatically shifted the dynamics of cell death such that cells that normally died during mitotic slippage underwent apoptosis during mitotic arrest. Comparison of Hela cell responses with noncancerous cells and other cervical carcinomas demonstrated a range of sensitivities, ranging from no sensitivity to PI3K inhibition to cells dying during interphase. Current efforts are focused on understanding the basis for PI3K dependence between cell lines as well as identifying the effectors of PI3K signaling that help promote survival during mitotic delay.

P19 - Taxonomic Verification of *Peromyscus sonoriensis* for Sin Nombre Virus Research via DNA Barcoding

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Sin Nombre Virus (SNV) is transmitted among rodents in the genus *Peromyscus*, particularly the deer mouse *Peromyscus maniculatus,* which has recently been split into two species, *P. maniculatus and P. sonoriensis*. SNV occasionally spills over into humans who have contact with aerosolized rodent feces and can cause hantavirus cardiopulmonary syndrome (HCPS). HPCS has a 30-35% human case fatality rate. Thus, identifying the ecological factors that shape SNV transmission in its rodent reservoir is critical for better safeguarding humans against infection. To investigate the impact of wildfire on Sin Nombre Virus transmission in deer mice, we collected a total of 430 mice from northern New Mexico – 245 mice from recently burned areas, 105 mice from unburned control areas, and 80 mice from areas that had been burned and subsequently re-seeded – in 2023 and 2024. All 430 of these specimens were morphologically identified as *P. sonoriensis*. To corroborate these morphological identifications, we are genetically barcoding a subset of samples from each of our three site types (30 from burned, 17 from unburned, and six from reseeded), including adult males, adult females, and sub-adults of both sexes in each area. To do so, we will amplify and sequence part of the cytochrome b gene and compare it to published reference sequences in GenBank. This study will advance our understanding of the specific relationship between reservoir species and pathogens in an ecologically altered system.

P20 - Exploring the roles of *Nep1* and *Nepl15* in Drosophila melanogaster adult muscle

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Neprilysins, members of the M13 metalloendopeptidase family, cleave and thereby regulate physiological homeostasis of many peptide hormones, including neuropeptides. While neprilysins have been extensively studied in various disease contexts and homeostasis, a role in muscle development and function remains unknown. Nepl15 is a Drosophila specific neprilysin that is probably catalytically inactive but is conserved over 35 million years of Drosophila evolution, and is required for carbohydrate and lipid storage. Nep1 is a stereotypical transmembrane neprilysin expressed in insulin producing cells. We performed transcriptomics studies of Nep1 loss-of-function and Nepl15 knockout mutants revealing an enrichment of genes encoding muscle proteins among downregulated genes. In many insects there are two types of somatic muscles, fibrillar(flight) and tubular(leg) muscles. Tubular muscles are similar to human skeletal muscle in structure and each contraction is triggered by a signal from a neuron. In contrast fibrillar muscles contract several times for every neuron signal, enabling high frequency wing beats. In Drosophila melanogaster, fibrillar and tubular muscles differ in part due to alternative splice forms of muscle proteins. We have data showing that Nep1 and Nepl15 mutants have different alternative splice forms in muscle gene transcripts compared to controls. We hypothesize that Nep1 and Nepl15 affect tubular and fibrillar muscle gene expression differently. To test this hypothesis, we will map alternate splice isoform observed in Nep1 and Nepl15 mutants to the muscle gene exon map for tubular and fibrillar muscles to determine which splice isoforms are present in mutants.

P21 - Developing novel reporters to explore cellular mechanics in living cells

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The actin cytoskeleton is the primary determinant of cell shape and the driver of shape change in animal cells. There are a variety of live cell approaches to explore cellular mechanics, ranging from biophysical techniques to the expression of fluorescently-tagged cytoskeletal elements or FRET reporters. Our goal is to develop simple fluorescent reporters that will preferentially label actin filaments under tension so that changes in cellular mechanics can be easily measured in either single cells or multicellular tissues. Towards these ends, we have developed two candidate tension reporters based on the THATCH domain of sea urchin Talin and the LIM domains of human Zyxin. Each of these actin-binding domains have demonstrated the ability to form “catch” bonds, where binding to actin is stronger when tension is applied to the filament. Preliminary experiments in mammalian cultured cells suggest that the Talin reporter bound to all actin structures when expressed at high levels, whereas the Zyxin-LIM domain bound to focal adhesions and cell-cell contacts, suggestive of mechanosensitivity. Moreover, if cells were cultured on increasingly softer substrates, cytoskeletal Zyxin-LIM localization was reduced. Current efforts to further validate these reporters involve the expression of these constructs in the *Drosophila* imaginal disc, where the forces acting on cells during morphogenesis is well-characterized, and in the fission yeast *Schizosaccharomyces pombe*, where the assembly and constriction of the contractile ring may be temporally and functionally unlinked. Once validated, we hope to use these probes to study forces acting on cells during the cell cycle and embryonic development.

T6 - Identifying the evolutionary relationships among lichenized fungi populations in gypsum soil

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Extreme environmental conditions promote endemism through evolution of site-specific adaptations. One example is soil biota native to gypsum, which must survive high concentrations of calcium sulfate dihydrate. In this study, we considered the evolutionary history of gypsophilic lichens. Lichens are composite organisms made of a fungal component, or mycobionts, and a photosynthetic component, or photobionts; they are often found in early successional habitats. Gypsophilic lichens are adapted to cope with harsh soil chemistry, but the relationship between genetic diversity and the physiological tolerance of calcium sulfate has not been studied. We hypothesized that lichen population genetic distance increases as geographic distance increases, but genes for tolerance of high calcium sulfate concentrations are relatively conserved. We investigated the relationship between geographic distance and genetic distance and between geographic distance and phenological trait observations among lichen populations. We sampled gypsum deposits in four southwestern U.S.A and 23 Iberian Peninsula (IP) plots and identified five mycobiont species in the U.S.A and 15 in the IP; three species were found in both. We compared phenological traits including water holding content, specific thallus mass, chlorophyll content, and nutrient composition (carbon, hydrogen, nitrogen, and sulfur ratios) for IP samples (*Diploschistes diacapsis, D. ocellatus, Psora saviczii,* and *P. decipiens*), and U.S.A samples (*D. diacapsis, P. decipiens,* and *P. crenata*). We sequenced the internal transcribed spacer region for the mycobiont portion and compared the genetic diversity across populations. This experiment will expand our understanding of lichen evolution and of how gypsum soils direct their evolutionary trajectories.

P22 - Alternative splicing (AS) patterns differ in cell types of the same myogenic lineage

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Skeletal muscle cells (*SMs*) display extraordinary phenotypic plasticity that allows them to differentiate, dedifferentiate, and/or regenerate depending on environmental cues, injury and disease. This highly plastic capability is crucial for animals to maintain optimal performance. With complementary advances in RNA biology and technology, there has been a growing focus on the role of mRNA alternative splicing (*AS*) in tissue-specific functions. *Herein, we explore the role that AS may play in the extreme plasticity of the muscle program to produce the specialized, non-contractile electrogenic cells of electric organs (EOs) unique to electric fishes.* Using in-house software, we detected disproportional splicing events which we subsequently verified through qualitative PCR in the *EOs* and *SMs* in the knifefish *Sternopygus macrurus* (n=2). Our preliminary data show *AS* patterns in *EOs* that diverge from those detected in *SMs*. Specifically, genes with differential *AS* included those that modulate calcium handling, are sarcomere constituents, and act as transcription factors which switch transcript variants during myogenesis. These findings add to the growing sentiment that *AS* contributes to muscle development and function. In *S. macrurus*, AS may contribute not only to the development of different cell types, but also to the evolution of highly specialized cell types.

T2 - Demographic Variation in Speed and Timing of Fall Migration Shapes Community Composition of Migrating North American Passerines

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Avian migrants face numerous threats during their journeys, leading to high mortality, especially among juveniles on their first migration. Human impacts have worsened these risks, contributing to widespread declines in migrant populations. Conservation efforts are increasingly focused on aiding juveniles through their first migration to promote population recovery. The identification of specific locations or time periods when juvenile migrant density is high would allow for targeted conservation efforts, potentially increasing efficacy. To this end, we used a dataset of ~7 million bird banding encounters from 69 species of North American passerine migrants to analyze migration speed and timing differences between juveniles and adults across taxa and determine if variation results in shifting demographics throughout migration. We found significant differences in speed for 35% of species, with adults migrating faster than juveniles in nearly all cases. For timing, adults migrated first in 26% of species, while juveniles migrated first in 35% of species, with differences primarily explained by molt strategy. Our analysis of migrant community composition revealed that at northerly latitudes, juvenile density was at its highest early in migration, while further south juvenile densities peaked later. Lastly, we found that demography has shifted across years, with juvenile density increasing at higher latitudes and decreasing at lower latitudes, potentially as the result of climate mediated shifts of wintering distributions. From these findings, we recommend conservation efforts targeted to juvenile migrants focus on higher latitudes early in the migration season, and lower latitudes later in the season to maximize effect.

P23 - TRPA1 and Painless: A Comparative Analysis of Sensory Modulation

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The transient receptor potential (TRP) channels are a family of ion channels that serve as sensors for environmental stimuli. The TRP channels aid in sensations, such as taste, touch, heat, and chemical stimuli, which are crucial in sensory perception (Song & Yuan, 2010). The transient receptor potential ankyrin 1 (TRPA1) is a protein channel on most animal cells' cell membranes. TRPA1 has five isoforms that have been studied to identify which are required from different stimuli. Alternative splicing suggests that alternative protein isoforms contribute to the complexity of the nervous system (Li, Lee, & Black, 2007). This project explores a system for nociception in *Drosophila melanogaster* with a multiple-acid exposure protocol. *Drosophila* larvae display a nociception behavioral response to harsh stimuli (Lopez-Bellido et al., 2019). Cd4a neurons are suggested to be required for nociceptive behavior. TRPA1 and its isoforms are found in C4da neurons. In this project, we are exploring various modalities for nociception and repeated exposure. The data collected suggests that the loss of the pain gene(dTRPA1) has the strongest effect in comparison to the loss of the TRPA1 gene and the wild type. Due to TRPA1’s involvement in human pain disorders, the findings provide an insight into potential targets for treating chronic pain. Exploring and understanding how painless (dTRPA1 gene) functions in *Drosophila* can specify pain modulation and drug development.

T5 - Incubation in Low Radiation Environment Increases Oviposition, Slows Growth, Reduces Longevity in *D. melanogaster*

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Ionizing background radiation has been a component of natural environments for as long as life has existed. The current dose-response model of ionizing radiation, the linear no-threshold model, claims that there is a proportional linear relationship between its harmful effects and total dose over time. Further, it implies that below-background dose-rate levels become comparatively beneficial as there exists no threshold where a dose is considered 'safe'. This model has been challenged in recent history by experimental evidence indicating that deprivation of typical background radiation leads to negative effects on model organisms. Our recent research in a low-background environment with ionizing radiation levels below detection limits found a reduction in the growth of *D. melanogaster* during incubation, as well as in the climbing ability of their offspring. Additionally, a temporary reduction in survival rate was observed in the first generation brought into the environment, though this change was negated in their offspring. These phenotypic changes suggest that there is some lower threshold above complete removal of background radiation, below which detrimental effects occur for *D. melanogaster*.

P24 - Global Climate Change Factors Effect on Fungi Respiration and Biomass

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Fungi play a crucial role in ecosystem functions, particularly in nutrient cycling, such as the cycling of carbon. These roles are essential for maintaining ecosystem stability and facilitating nutrients to plants, animals, and other microbes. Fungi, like any other organism on Earth, are being affected by global climate change, but little is known about how different global change drivers affect their production of key functional traits, such as biomass and respiration. Understanding these is crucial for developing effective conservation strategies and mitigation plans that can inform ecological and societal impacts. Therefore, I investigated how fungal biomass and respiration is impacted by various global change drivers, warming, water stress, and nitrogen pollution. I conducted an experiment measuring fungal respiration and biomass in 48 distinct species and how they are influenced by global change drivers. The fungi were incubated under global change driver conditions, to assess their impact on these key functional traits. When these traits are put under stress, crucial ecosystem services like the cycling of organic matter, such as decomposition and CO2 emissions can be disrupted. Our findings provide insights into the role of fungi in desert ecosystems under future climate scenarios and inform conservation efforts aimed at preserving fungal diversity and function in a changing world.

P25 - Developing a Drosophila model for Neprilysin's role in cisplatin resistance

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Cisplatin is a chemotherapeutic drug that creates DNA crosslinks. These crosslinks can be repaired by the Fanconi anemia pathway, such that an upregulation of the Fanconi anemia pathway can result in cisplatin resistance. Neprilysin (Nep), part of the M13 family of metallopeptidases has been linked to increased resistance to cisplatin in ovarian cancer stem cells. We created a Nep1 mutant model in *Drosophila melanogaster* using CRISPR/Cas9. RNA sequencing of these mutants, followed by functional enrichment analysis, showed significant upregulation of genes in the Fanconi anemia pathway (7.8-fold enrichment, P=0.00019), indicating a possible regulatory connection. We hypothesize that Neprilysin upregulates the Fanconi anemia pathway, generating cisplatin resistance. To test this hypothesis we are administering cisplatin to the Nep1 mutants and evaluating DNA damage and repair processes, changes in gene expression, and phenotypic outcomes.

T7 - Burning down the mouse: Fire effects on deer mouse abundance and carriage of Sin Nombre Virus

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Wildfires can exacerbate the severity of wildlife diseases by altering relationships between environment, pathogens, and hosts. Yet, the relationship between fire and zoonotic infectious disease remains understudied. This study investigates the wildfire effects on host and pathogen dynamics, focusing on Sin Nombre Virus (SNV), an orthohantavirus with a human fatality rate of ~30%. We hypothesize that wildfire-mediated changes in the environment alter dynamics of SNV in its reservoir host, the deer mouse (*Peromyscus sonoriensis*), through changes in host population dynamics and variations in within-population prevalence due to host stress. We live-trapped deer mice (n=423) across two fires in northern New Mexico, USA. ANOVA was used to assess differences in population dynamics of deer mice between burned, unburned, and post-fire re-seeded areas. Our findings indicated no significant differences in host population dynamics. Comparison between re-seeded and unburned densities approached significance ($p=0.07$), likely due to small sample size. However, mice in re-seeded areas were in better body condition than mice in burned areas that had not been re-seeded, assessed through linear regression residuals of log-transformed weight and hindfoot lengths ($p=0.004$). Future research will utilize RT-qPCR and ELISA to evaluate differences in SNV carriage between burned and unburned areas and fecal glucocorticoid metabolites, respectively, and incorporate these findings along with habitat variables and host population dynamics into GLMMs to further understanding of wildlife disease in the context of wildfire.

P26 - Measuring the Neurological and Developmental Responses to Acid Re-exposure in *Drosophila melanogaster* larvae

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Nociception is the process in which the nervous system detects and responds to harmful stimuli. Almost all animals, including *Drosophila melanogaster* larvae experience nociceptive responses to harmful stimuli. Somatosensory neurons (SSN) in *Drosophila* larvae are responsible for nociceptive behaviors. The most important SSN stimulating nociceptive responses are class IV dendritic neurons. Inactivating these neurons prevents *Drosophila* larvae from experiencing nociceptive responses. Exposure to acid activates class IV dendritic neurons. At low concentrations of hydrochloric acid (HCL), *Drosophila* larvae do not experience nocifensive behavior. When increasing the concentration of acid, *Drosophila* larvae begin to experience nocifensive behaviors and roll. It is known that in *Drosophila* larvae, stimuli that cause tissue damage can induce hypersensitivity. It is unknown if re-exposure to chemical stimuli can induce hypersensitivity or chemical allodynia. It is also unknown how tissue damage induced by acid exposure influences the development of *Drosophila* larvae. This study encompasses whether chemical allodynia or hypersensitivity can be induced through exposing *Drosophila* larvae to different concentrations of acid and re-exposing them to acid. To test whether chemical allodynia or hypersensitivity can be induced through repeated acid exposure, *Drosophila* larvae were exposed to various concentrations of HCL at 3 days old. At 5 days old, the larvae were re-exposed to varying concentrations of HCL. The larvae were also measured at 5 days old to evaluate developmental consequences when exposed to acid.

T12 - Impacts of early life stress on the physiological stress response and glucocorticoid receptor distribution in the brains of juvenile budgerigars

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Stressful events experienced early in life can have long-lasting influences on physiology and behavior, particularly in the cognitive domains of learning and memory. It remains unclear, however, whether early-life stressors impact the distribution of glucocorticoid receptors in brain regions important for vocal learning. The budgerigar (*Melopsittacus undulatus*) is an excellent model to better understand such effects as both sexes learn vocalizations throughout their life. We developed a 21-day chronic stress protocol that presented stressors at unpredictable intervals to birds as juveniles. We then measured the circulating corticosterone (CORT, main avian stress hormone) weekly and changes in the mRNA expression of glucocorticoid (GR) and mineralocorticoid receptors (MR) in the brains of stressed birds and unstressed controls. Brain regions included areas associated with vocal learning and production, adjacent regions not associated with vocal learning or production, and an area associated with the negative feedback loop of the stress response. We found an increase in baseline CORT levels and a decrease in the stress response CORT levels in stressed juveniles relative to non-stressed controls, supporting the efficacy of our stress protocol. Analyses on the GR and MR receptor mRNA levels in ongoing. These findings will provide valuable insight into the effects of early-life stress on communication and learning across species, including humans.