Department of Biology
New Mexico State University
Biosymposium

BE BOLD. Shape the Future.
College of Arts and Sciences

Saturday, April 20, 2024

TABLE OF CONTENTS

ORAL PRESENTATIONS

Presenter name*	Session, Talk	Time	Title
Abeykoon, Lakshani	S1, T4	10:15-10:30	Establishing an algae-bacteria pest model system
Dai, Jingyu	S1, T1	9:30-9:45	The interactions between the environment and plant functional type in controlling global maximum forest height
Karki, Anjali	S2, T7	11:15-11:30	Bloodless blood: Developing an artificial blood meal alternative for Anopheles mosquito culture
Landfair, Taylor	S3, T11	2:00-2:15	Studying myosin II organization and recruitment into the contractile ring of adherent cells
Mendoza, Joshua	S1, T3	10:00-10:15	Bee-lining conservation: addressing trap waste and seasonal dormancy in bee Research
Muzammil, Aqsa	S3, T14	2:45-3:00	Exploring role of Nep1 and Nepl15 in *Drosophila melanogester* adult muscle
Nelson, Ian	S2, T10	12:00-12:15	Measurements of the rate of insect DNA degradation in field-deployed passive traps
Pantoja, Angie	S3, T13	2:30-2:45	Tracing muscle cell lineage during sea star development
Rivero, Jorge	S3, T12	2:15-2:30	Validation of vaginal cytology to assign reproductive stages in captive Jamaican fruit-eating bats (*Artibeus jamaicensis*)
Romero, Abril	S2, T9	11:45-12:00	The effect of warming on decomposition rates of dryland fungi
Sellers, Scarlet	S1, T5	10:30-10:45	Do functional traits in bees predict landscape genetic patterns? A meta-analysis of genetic differentiation
Villalba, Alondra	S3, T15	3:00-3:15	Effects of chronic stress on the physiological stress response and glucocorticoid and mineralocorticoid receptor expression in budgerigars over time
Wickramarathne, Poorni Da Silva	S2, T8	11:30-11:45	Low sugar supply affects survival rate and vector competence against Plasmodium in mosquitoes
Zhou, Lawrence	S2, T6	11:00-11:15	Who's flying this thing? Investigating potential insect vectors of vesicular stomatitis virus in its endemic and outbreak regions
Zimba, Heather	S1, T2	9:45-10:00	Habitat selection of translocated juvenile Bolson tortoises

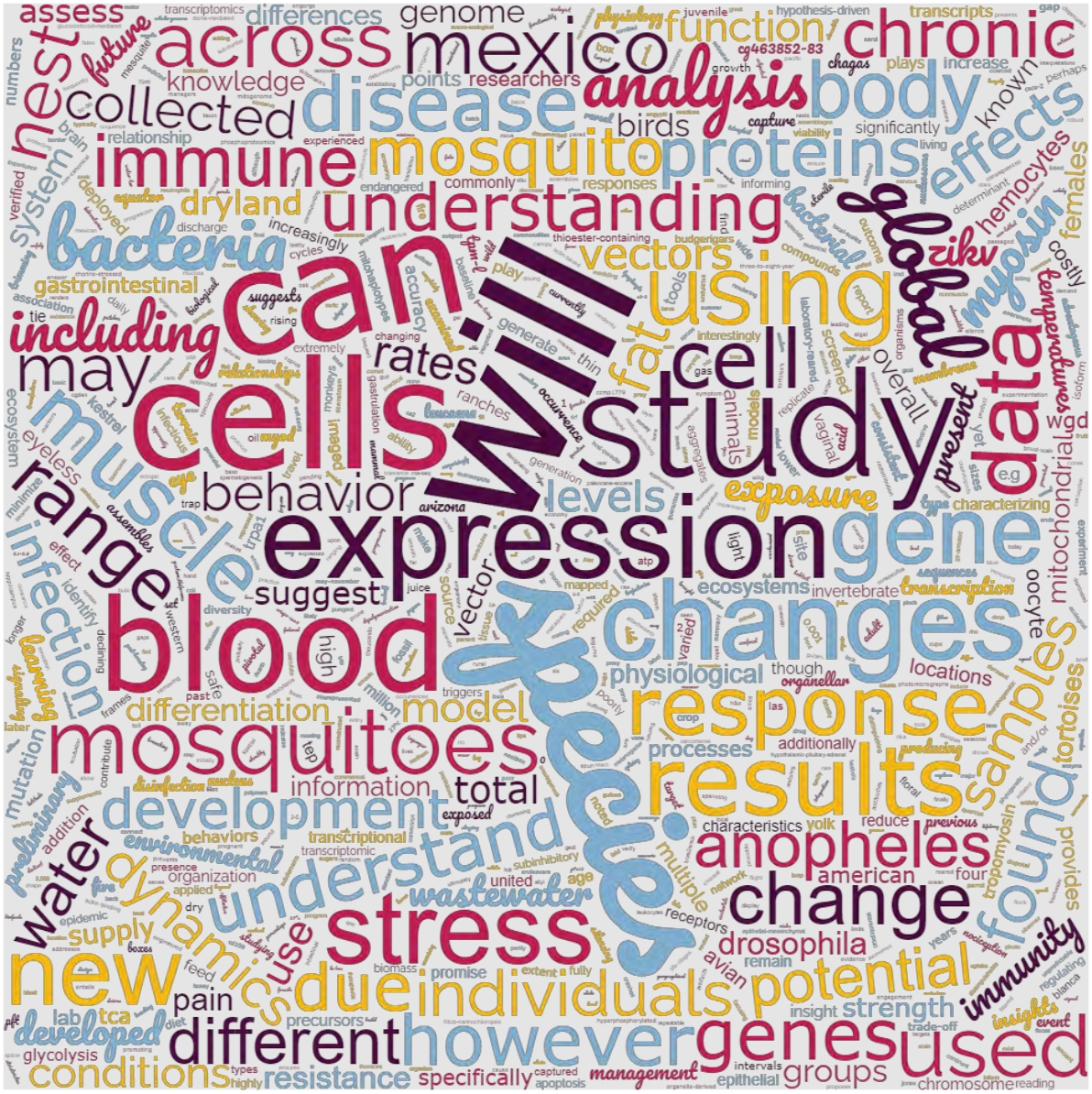
***Listed alphabetically by presenter surname**

POSTER PRESENTATIONS

Presenter name*	Poster	Title
Al-Nouman, Abdul	P1	The *Drosophila melanogaster* TENT5 homolog is required for individualization of spermatids during spermatogenesis
Ahmed, Shakil	P2	Investigating the evolutionary trajectories of organelle-derived DNA in the nuclear genome of Fabaceae
Aswad, Fateh	P3	Molecular characterization of thioester-containing proteins (TEPs) in the sepiolid squid *Euprymna scolopes*
Baca, Gabrielle	P4	Detection of *Trypanosoma cruzi* in triatomine vectors in New Mexico
Baquera, Victor	P5	The effects of early life stress on adult social networks in budgerigars
Crowl, Leona	P6	Is nest defense behavior in American Kestrels associated with higher nest success?
Dickson, Meig	P7	Avian range response to paleogene global warming
Esmaeili, Delaram	P8	Phosphoproteomics analysis of *Aedes aegypti* abdominal fat body after a blood meal reveals phosphorylation changes in a majority of ribosomal proteins
Grooms, William	P9	Verification of Peñasco least chipmunk persistence in novel habitat on Nogal Peak
Hesser, Andreya	P10	Reproductive dynamics of two *Physella acuta* mitohaplotypes displaying differential invasive capabilities
Iloba, Ogochukwu	P11	Exploring the influence of chromatin structure on homoeologous gene expression in the tetraploid *Leucaena trichandra*
Marquez, James Jonathan	P12	A Comparative analysis of thioester-containing proteins expression in hemocytes of the *Biomphalaria glabrata* snails in response to *Schistosoma mansoni* products
Montoya, Andrew	P13	Comparison of replication dynamics of human endemic and Sylvatic Zika and Dengue Virus in Cynomolgus Macaques
Ortiz, Alexis	P14	The health condition of Mexican free-tailed bats (*Tadarida brasiliensis*)
Pearson, Elena	P15	The impact of Ect2 on the mechanical functions in the cytoskeleton in sea star oocytes during meiosis
Salazar, Jaxon	P16	Exploring the immunomodulatory role of Nep15 in *Drosophila melanogaster*
Sanchez, Jocelyn	P17	Behavioral responses driven by TRPA1 channels in AITC induced behaviors of *Drosophila melanogaster*
Silva, Carleen	P18	Investigating the relationships between wildfire, pathogen prevalence, and management practices in *Peromyscus maniculatus* in northern New Mexico, USA
Weerasinghe, Piyumi	P19	Understanding the impact of subinhibitory concentrations of disinfectants on bacterial risk in wastewater
Wijekoon, Senuri	P20	Evaluating toxicity induced by treated produced water on human cell lines

***Listed alphabetically by presenter surname**

WORD CLOUD OF ABSTRACTS



EVENT SCHEDULE

Foster Hall, Saturday April 20, 2024.

9:00-9:30 AM	**Breakfast/coffee (Foster Hall room 137) and setup posters (Foster Hall rooms 243 and 244)**
9:30-10:45 AM	**Oral Presentations Session 1 (Foster Hall room 231)** 9:30-9:45 – Jingyu Dai 9:45-10:00 – Heather Zimba 10:00-10:15 – Joshua Mendoza 10:15-10:30 – Lakshani Abeykoon 10:30-10:45 – Scarlet Sellers
10:45-11:00 AM	**Short Break**
11:00-12:15 PM	**Oral Presentations Session 2 (Foster Hall room 231)** 11:00-11:15 – Lawrence Zhou 11:15-11:30 – Anjali Karki 11:30-11:45 – Poorni Da Silva Wickramarathne 11:45-12:00 – Abril Romero 12:00-12:15 – Ian Nelson
12:12-12:30 PM	**Short Break and setup lunch (Foster Hall room 137)**
12:30-2:00 PM	**Poster session (Foster Hall rooms 243 and 244)**
2:00-3:15 PM	**Oral Presentations Session 3 (foster Hall room 231)** 2:00-2:15 – Taylor Landfair 2:15-2:30 – Jorge Rivero 2:30-2:45 – Angie Pantoja 2:45-3:00 – Aqsa Muzammil 3:00-3:15 – Alondra Villalba
3:15-3:30 PM	**Wrap up/Conclusion** Remove posters

Abstracts (in alphabetical order by presenter surname)

T4. Establishing an algae-bacteria pest model system

Lakshani Abeykoon[1] and Alina A. Corcoran[2]

[1]Department of Civil Engineering, New Mexico State University; [2]Department of Biology, New Mexico State University.

Algae is a sustainable raw material for producing biofuels, human food and supplements, animal feed, polymers, and fertilizer. Algae are typically grown in outdoor ponds and are subject to external pest invasions that reduce or destroy biomass. Predatory bacteria infect a variety of strains and, if conditions are right, can decimate a crop. Researchers do not currently understand the mechanisms by which bacteria infect algal cultivars, partly because few bacterial pest models have been established for production strains. Establishing model systems is crucial to building foundational knowledge that can be used for crop protection. *Bdellovibrio* and like organisms (BALOs) are gram-negative bacteria that prey on other gram-negative bacteria. FD111 is a BALO-like organism discovered in outdoor raceways in Las Cruces, NM. Here, we describe efforts to re-establish an FD111-*Nannochloropsis* model system. Field samples of putative FD111 collected in 2023 were passaged in the lab and back frozen. These aliquots were then used to replicate a crash phenotype within two *Nannochloropsis oceanica* strains, P7C12 (a field-adapted cultivar) and CCMP1779 (a culture collection strain). In all experiments, bacterial attachments were visible under the microscope; however, crashes, as previously documented, were not observed. Flask-scale experiments suggested that infection success depended on temperature and nitrogen (N) source. Results were not repeatable across experimental formats (e.g., well plates vs. flasks). Moreover, adding the pest samples to the culture collection strain enhanced biomass production when cultivated on a new (to that strain) N source. Ongoing work focuses on understanding the optimal conditions for infection.

P1. Investigating the evolutionary trajectories of organelle-derived DNA in the nuclear genome of Fabaceae

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. Throughout evolutionary processes, the functional copies of organellar genes have been lost or transferred to the nucleus, leading to a reduction in the genome size of the plastome and mitogenome. This process involves nuclear integrants of mitochondrial DNA (NUMTs) and plastid DNA (NUPTs). Despite their frequent occurrence, the evolutionary dynamics of NUPTs and NUMTs in Fabaceae and their relationship to organismal phylogeny remain largely unexplored. Leveraging nuclear and organellar genomic resources across the Fabaceae, this study aims to elucidate the evolutionary trajectories of NUPTs and NUMTs. These may undergo diverse evolutionary fates, including elimination, mutation, rearrangement, fragmentation, and/or proliferation. Integrated organellar DNAs play pivotal roles in augmenting genetic diversity, driving gene and genome evolution, and contributing to sex chromosome evolution. By employing available chromosomal-scale legume genomes and BLAST analysis with mitochondrial and plastid genomes, we seek to quantify the extent of ongoing DNA transfer from organelles to nuclear chromosome. Secondarily, we will assess whether the putative integrants may be artifacts of genome assembly. Based on the analyzed data, we will construct phylogenetic interpretations to delineate the evolutionary patterns of integration in Fabaceae. Subsequently, we will assess gene expression, distinguishing between expression from organelle DNA and nuclear DNA. This research endeavors to provide valuable insights into the evolution of NUMTs and NUPTs. Moreover, it will give a clear conception of the dynamic evolutionary patterns shaping organelle-derived nuclear DNA in the Fabaceae.

P2. 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

The transcription factor Eyeless can induce the formation of an ectopic eye in other tissues when mis-expressed. Previously this lab mis-expressed Eyeless in the wing and a transcriptomics analysis was done to look for which eye specific transcripts were upregulated. In conjunction with data from an Eyeless CHiP-seq, the gene *CG46385* appeared in both data sets, suggesting that *CG46385* is a direct transcriptional target of Eyeless and plays a role in the eye determination network. *CG46385* is predicted to be a non-canonical poly-A polymerase and its orthologs have poly-A polymerase activity and physically interact with transcription factors involved in Bone Morphogenetic Protein (BMP) signaling. Here we have used the CRISPR-Cas9 system resulting in generation of three different mutations in *CG46385*. None of these mutations have obvious effects on eye development; however, a mutation in the catalytic domain of *CG46385* (*CG46385*$^{2\text{-}83}$) renders homozygous males sterile. In-situ hybridization reveals that *CG46385* transcripts are present during elongating spermatids and localizes in a "comet" expression pattern. Antibodies against actin and caspase-3 shows *CG46385*$^{2\text{-}83}$ homozygous mutants have defects with individualization as waste bags are absent and the actin cones that travel down the axonemes display a scattered configuration. Together this work demonstrates that *CG46385* is essential during *Drosophila* spermatogenesis and loss of function of *CG46385* prevents the individualization process from progressing normally rendering *CG46385*$^{2\text{-}83}$ completely sterile.

P3. Molecular characterization of thioester-containing proteins (TEPs) in the sepiolid squid *Euprymna scolopes*

Fateh Aswad[1], Thujitha Thuraisamy[1], Tathagata Debnath[1], and Maria G. Castillo[1]

[1]Department of Biology, New Mexico State University

Thioester-containing proteins (TEPs) are critical pattern recognition receptors in the innate immune system. The engagement of these receptors by pathogens initiate signal transduction pathways that activate defense and pro-inflammatory mechanisms in innate immune cells. Researchers have taken a keen interest in the conservation of these genes coding for TEPs amongst various species, including both vertebrates and invertebrates. Preliminary analyses of tissue samples have characterized eight TEP molecules in *Euprymna scolopes*, a species of bobtail squid native to the central Pacific Ocean. The aim of this project is to complete the coding sequences for these molecules, characterize putative amino acid sequences and protein motifs associated with the sequences, and outline molecular commonalities with TEP molecules in other species. Potential open reading frames encoding for *E. scolopes* TEP molecules have been identified through gene alignments with separate invertebrate species. To outline transcripts and proteins stemming from these open reading frames, nucleotide and amino acid sequence analysis will be undertaken through the use of standard and quantitative PCR along with specialized bioinformatics tools. Furthermore, gene expression levels of TEPs in various squid tissues will be quantified, providing insights into their roles in cephalopod immune responses. This research holds promise for advancing our understanding of innate immunity in cephalopods and contributing to broader knowledge of immune system conservation amongst invertebrate species.

P4. Detection of *Trypanosoma cruzi* in triatomine vectors in New Mexico

Gabrielle Baca[1], KavitaAdhikari[2], Alvaro Romero[2], Maria G. Castillo[1]

[1]Department of Biology, [2]Department of Entomology, Plant Pathology, and Weed Science

Triatomines, commonly known as “kissing bugs”, are blood feeding insects that are vectors for the protozoan parasite *Trypanosoma cruzi,* the causative agent of Chagas disease. Triatomines are found in the United States, with higher prevalence in the southwest region of the country. These insects feed on blood, and while feeding on a mammalian host, they deposit feces that can be contaminated with the metacyclic trypomastigote stage of the parasite, which later enter through the bite wound or mucosa. *T. cruzi* can live for decades in asymptomatic individuals, but some chronic cases can result in death due to cardiac and gastrointestinal complications. Due to the presence of triatome insects in the US-Mexico border, including Arizona, New Mexico, Texas, and northern states of Mexico, the human population in these areas can be at risk for contracting Chagas disease. In this study we aim to test for the presence of *T. cruzi* infection in triatomines collected in rural and urban areas in Las Cruces, New Mexico. To detect *T. cruzi*, the midgut of triatomine insects were dissected and homogenized for DNA extraction, followed by amplification of parasite targets using PCR and gel electrophoresis analysis. The screening of *T. cruzi* in triatomines is an essential step in promoting public health and awareness about the potential risks of *T. cruzi* infection and preventing the spread of Chagas disease in the U.S.

P5. The effects of early life stress on adult social networks in budgerigars

Victor M. Baquera [1], Alex Hernandez [2], Alondra Villalba [1], Timothy F. Wright [1]

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

Chronic stress is widely believed to have profound and lasting negative effects on health and well-being. We investigated how stress experienced during early life in budgerigars affects their social interactions as adults, with the aim of determining whether such stress compounds or counteracts negative effects experienced later life. Using a fully crossed experiment, we subjected groups of budgerigars to either high or baseline stress as juveniles and again as adults. This approach allowed us to examine the interactions between early life and adult chronic stress and observe how stress levels impacted their strength of ties to other conspecifics. We used an automated tracking program developed for this project and video recordings, to track individuals wearing QR code backpacks to create proximity-based social networks. Measuring the distance to an individual's next nearest neighbor allowed us to quantify the strength of ties to the other individuals. We found that there was no clear difference between treatments in terms of tie density or strength among individuals. Tie density was generally high across all treatments, and social groups, indicating that most individuals interacted with all of their flock mates. Tie strength showed some differences between treatments, but the strength and direction of these differences was inconsistent across replicate flocks. The absence of consistent differences in social network metrics suggests that our stress treatments did not significantly impact the social dynamics or relationships within the group. Future work entails characterizing affiliative and agonistic behaviors to examine any changes brought on by chronic stress.

P6. Is nest defense behavior in American Kestrels associated with higher nest success?

Leona S. Crowl[1], Kristin P. Davis[1], Abigail J. Lawson[2]

[1]Department of Wildlife, Fish, and Conservation Ecology, New Mexico State University, Las Cruces, NM, USA
[2]U.S. Geological Survey, New Mexico Cooperative Fish and Wildlife Research Unit, Las Cruces, NM, USA

Nest defense is a common behavior among raptor species. While deterring nest predators may prevent depredation of young, it is energetically costly and could result in mortality for the parent. Thus, displaying nest defense behaviors may be advantageous at certain points of the nesting cycle. Our study is investigating whether nest defense behavior varies across the nesting cycle and correlates with nest success for the American Kestrel (*Falco sparverius*), a widespread but declining falcon species in the western United States. We will analyze nesting data collected from 1990 to 1994 from nestbox studies across the Front Range of Colorado. We are using a constructed scale from 1 to 4 to quantify nest defense behavior, where higher numbers represent increasingly aggressive behavior. During the study period, 87 nest boxes were occupied by American kestrels. We will use generalized linear models to determine whether nest defense behavior varies across the nesting cycle (e.g., egg incubation vs. nestling phases) and to evaluate whether nest defense behavior correlates with nest success. As nest boxes are a common monitoring and management tool for American Kestrel populations, it is important for researchers to understand how nest box monitoring affects kestrel reproduction over the course of the nesting cycle. Understanding defensive behavior will help researchers to minimize disturbance to nesting birds and could inform nest box placement.

T1. The interactions between the environment and plant functional type in controlling global maximum forest height

Jingyu Dai[1], Qiuyan Yu[1], Guangdao Bao[1], Michael G. Ryan[2], Niall. P. Hanan[1]

[1]Department of Plant & Environmental Sciences, New Mexico State University

[2]Natural Resource Ecology Laboratory, Colorado State University

Forest maximum height is a critical determinant of ecosystem structure and function, but the relative importance of genetic and environmental controls on maximum individual tree heights at macro-ecological scales have not been fully elucidated. Specifically, it remains unknown how the mechanical and physiological limits to tree height associated with plant genetics and plant functional type (PFT) interact with critical resources impacting tree physiology and growth (e.g., water, light, and soil nutrient availability) at regional scales (determined by large scale climate patterns and geomorphology) and local-scales terrain complexity (impacting landscape resource distributions). Here we disentangled the contribution and interaction of environmental determinants and broad-scale PFT in controlling global patterns in maximum tree height (Hm). We use data from the Global Ecosystem Dynamics Investigation (GEDI) lidar instrument on the International Space Station and a combination of ensemble random forest and structural equation algorithms. While at global scale water availability positively contributes ~75% to Hm variations, terrain complexity is surprisingly the most important non-water determinant on Hm. Complex terrain increases Hm in arid regions, perhaps because of resource redistribution and accumulation in depressions, while Hm is suppressed in flat landscapes in wetter environments, perhaps due to poor drainage. PFTs play a relatively small role in regulating Hm globally. Instead, they follow the global water-Hm relationship, with different PFTs occupying different segments of climate space.

P7. Avian range response to paleogene global warming

M. Dickson[1]

[1]Department of Biology, New Mexico State University

Past examples of dramatic climate change in Earth's history remain one of our best ways to understand the long-term consequences of modern-day climate change. The Paleocene-Eocene Thermal Maximum (PETM) is the most recent instance of rapid warming like present conditions. The reactions of mammal and plant groups to this event have been studied extensively. The response of birds, however, is poorly known. Modern day birds have shifted range as climates have warmed in the past epoch. As such, the ranges of birds before and after the PETM require examination for similarities to present behavioral changes; with long-term response potentially informing how birds will react to anthropogenic climate change in the future. I examined range shift via overall change in latitude and longitude as well as change in reconstructed fossil range based on associated species. I then correlated these findings with climatic shifts seen during the PETM. I found a global avian range shift into higher latitudes due to the PETM. Furthermore, individual clades such as Gastornithiformes and Sphenisciformes show evidence of range shifts into new hemispheres. Range expansions across clades were accompanied by increases in taxonomic diversity and number of fossil occurrences. These changes may be unique to avian fossils, though some may also be related to global taphonomic trends, pending further study. This indicates that avian response to climate change has remained consistent during the Cenozoic. Further work will look for other changes that may have accompanied range shift in birds during this time.

P8. Phosphoproteomics analysis of *Aedes aegypti* abdominal fat body after a blood meal reveals phosphorylation changes in a majority of ribosomal proteins

Delaram Esmaeili[1], Keyla R. Salas[1], Matthew Pinch[2], Hailey A. Luker[1], Immo A. Hansen[1]

[1]Department of Biology, New Mexico State University; [2]Department of Biological Science, The University of Texas at El Paso

The uptake of a vertebrate blood meal by a mosquito triggers a series of events that culminate in vitellogenesis, the synthesis, secretion, and receptor-mediated endocytosis of massive amounts of yolk protein precursors. Yolk protein precursors are synthesized by the fat body tissue and transported to the developing oocytes. Vitellogenesis is tightly repressed in the fat body before a blood meal. After a blood meal is taken, several cellular signaling pathways that regulate the expression of vitellogenesis-related genes are activated within the cells of the fat body. This study is focused on dynamic changes in ribosome numbers and composition in the fat body during vitellogenesis. The structure and size of nucleoli in fat body cells were mapped using confocal microscopy. Total RNA levels in fat body cells were measured at different time points after a blood meal to assess relative changes in ribosome abundance. Lastly, we mined a fat body phosphoproteomics dataset to detect dynamic changes in the phosphorylation of ribosomal proteins during vitellogenesis. We found dynamic changes in the overall size of the nucleoli and the amounts of RNA in fat body cells at different time points after a blood meal. We identified 129 specific phosphorylation sites on 48 ribosomal proteins. The protein with the highest number of phosphorylated residues was ribosomal protein S6 which is hyperphosphorylated during the progression of vitellogenesis. Our findings suggest that after a blood meal, ribosome quantity increases and specific ribosomal proteins undergo changes in phosphorylation.

P9. Verification of Peñasco least chipmunk persistence in novel habitat on Nogal Peak

William Grooms[1], Jennifer Frey[1]

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

The Peñasco least chipmunk (*Neotamias minimus atristriatus,* PLC) historically occurred throughout the Sierra Blanca and Sacramento Mountain ranges in southern New Mexico. The PLC is listed as endangered by the state of New Mexico and has been proposed for federal listing as endangered. Despite extensive survey efforts, as of 2017 the chipmunk was only verified to persist in one population near Lookout Mountain in the Sierra Blanca sub-range. The Lookout Mountain population exists in shrubby, subalpine meadows with scattered old growth Engelmann spruce. In 2018 a new population was discovered on Nogal Peak, approximately 11 km away from the known population and separated by an apparently unsuitable environment. The chipmunks on Nogal Peak occur at lower elevations and in a novel vegetation type dominated by Gambel oak (*Quercus gambelii*). Using motion-detecting cameras, we verified the continued occurrence of PLC on Nogal Peak. We deployed cameras at 179 sites for a total of 9,242 camera days collecting approximately three million photos. Each photo was viewed by an observer with specialized training in identifying PLC. Multiple observers reviewed potential photos of PLC to ensure accuracy. We preliminarily verified the occurrence of PLC at 10 camera sites and collected habitat characteristics at a total of 96 used or available sites. Our findings verify that PLC persists on Nogal Peak and contribute to the conservation of this taxon by ensuring that all potential habitat is considered when designating critical habitat and through a better understanding of the microhabitat preferences of the Peñasco least chipmunk.

P10. Reproductive dynamics of two *Physella acuta* mitohaplotypes displaying differential invasive capabilities

Hesser Andreya[1], Navarrete Priscila[1], Castillo Maria G.[1]

[1]Department of Biology, New Mexico State University

Physella acuta is a hermaphroditic snail native to the North American continent and found in New Mexico. Natural habitats of *P. acuta* are freshwater bodies where they feed on aquatic vegetation. In favorable environments, *P. acuta* can thrive and potentially outcompete local snail populations becoming invasive. Previous studies described different *P. acuta* populations based on mitohaplotypes (mitochondrial genomes). This study utilized two *P. acuta* snail groups (A and B), where group A is considered a globally invasive species. The aim of this study was to investigate the reproductive capacity of these two snail mitohaplotypes in laboratory settings, including the number of egg masses laid and embryos per egg mass. To answer this question, 30 snails of each *P. acuta* population were placed in cups with 75mL of pond water, 10 of them were paired with a mate of the same group, and the other 10 remained as single individuals. Snails were fed twice a week, while water changes were done once weekly. The number of egg masses and embryos per mass were counted weekly during a 70-day period. Statistical analysis using Kruskall-Wallis Rank Sum test showed that *P. acuta* group A produced a significantly higher number of egg masses (p-value: 0.01489), but not embryos per egg mass (p-value: 0.453) when compared to group B. Overall, results indicated that *P. acuta* group A had a greater fecundity compared to group B. These results suggest a possible link between mitochondrial genome function and increased fecundity, and therefore invasive potential.

P11. Exploring the influence of chromatin structure on homoeologous gene expression in the tetraploid, *Leucaena trichandra*

Ogochukwu Iloba[1], Katie Banga[2], Robert J. Schmitz[3], C. Donovan Bailey[1]

[1]Department of Biology, New Mexico State University; [2]Department of Biology, Brown University; [3]Department of Genetics, University of Georgia

Whole-genome duplication is a significant evolutionary event that can lead to both advantageous and challenging outcomes for plants. Polyploid plants have developed sophisticated genomic and epigenetic mechanisms contributing to genomic stability and adaptation after WGD, although our understanding of these phenomena remains limited. Chromatin structure can play a crucial role in WGD-related gene regulation, with nucleosome organization directing chromatin accessibility and gene expression. *Leucaena trichandra*, a tetraploid with a history of ancient WGD, provides a unique model to explore the complex nature of plant genome evolution following WGD. By employing ATAC-seq (Assay for transposase accessible chromatin) to analyze nucleosome occupancy, we aim to elucidate the influence of chromatin dynamics on gene regulation in polyploids post-WGD, focusing on comparing homoeologous gene expression regulation. We sequenced five ATAC-seq libraries, tested three trimming tools, and found Trimgalore to be optimal. We aligned the reads to the *Leucaena* genome using BWA and filtered the data through SAMtools. After removing PCR duplicates, we used MACS2 for peakcalling. One dataset was excluded due to low percentage of mapped reads, the remaining were merged and analyzed from trimming to peakcalling. For further downstream analysis, DiffBind will be used to calculate merged peak locations for differential accessibility analysis, while RNA-seq data will connect changes in accessibility to gene expression. DESeq2 will be used for differential expression analysis. The outcome of this study will provide insights into the degree chromatin structure affects gene regulation following WGD in *Leucaena trichandra*.

T7. Bloodless blood: developing an artificial blood meal alternative for Anopheles mosquito culture

Anjali Karki[1] and Immo A. Hansen[1]

[1]Department of Biology, New Mexico State University, Las Cruces, NM, United States

Mosquitoes are reared in research laboratories to study their physiology and vector-borne disease transmission. Blood meals are necessary to maintain laboratory-raised mosquito cultures of anautogenous species. Blood is often sourced from live animals which can be costly and have a short shelf life. In addition, there are ethical, economic, and safety challenges for using blood in laboratory settings. Hence, there is a demand for alternatives to bloodmeals that are easy to use, have long shelf lives, and can effectively support mosquito culture. SkitoSnack is a blood meal replacement that has been previously developed to rear *Aedes* mosquitoes. SkitoSnack's nutritional content is analogous to that of vertebrate blood and can stimulate physiological processes in *Aedes* mosquitoes such as engorgement, oogenesis, and egg deposition. However, *Anopheles* mosquitoes do not engorge on this SkitoSnack recipe. Therefore, in this study, we modified SkitoSnack for the rearing of *Anopheles* mosquitoes. By changing single components of the original recipe, we developed several variations of this diet that are suitable for *Anopheles stephensi* culture. We measured engorgement rates, egg numbers, and hatch rates to identify an optimized version of SkitoSnack for *Anopheles*. We present a modified SkitoSnack as a cruelty-free, sustainable, effective, and affordable blood meal alternative that can support laboratory-reared *Anopheles* mosquitoes.

T11. Studying myosin II organization and recruitment into the contractile ring of adherent cells

Taylor Landfair[1], Gabriela Reyes[1] and Charles B. Shuster[1]

[1]Department of Biology

In animal cells, cytokinesis is accomplished through the assembly of a contractile ring that forms at the cell equator to pinch the cell into two. The force-generating motor for ring constriction is Myosin II (MII), which forms 300 nm bipolar minifilaments that assemble from individual MII hexamers. In large embryonic cells, MII initially assembles at the cell equator as radial aggregates or “nodes”, but it is unclear how MII assembles in mammalian cells in culture. In an effort to observe MII in living cells, fluorescent protein-tagged fusions of myosin regulatory light chain (MRLC) were imaged live using Total Internal Reflection Fluorescence (TIRF) microscopy, which selectively illuminates fluorescent molecules within 200 nm of the coverslip. This affords the ability to visualize MII assemblies at the plasma membrane, where the ring assembles at the cell equator. However, the low expression rates associated with transient transfections makes it difficult to capture cells during mitosis and cytokinesis. To generate cell lines that stably express MII markers, mApple-MRLC was subcloned into a vector system that uses CRISPR/Cas9 to integrate the insert into the AAVS1 safe harbor locus on human chromosome 19 using Homologous-Directed Repair (HDR). Cells transfected with mApple-MRLC and Cas9/gRNA plasmids will be screened for puromycin resistance and then screened for expression. With these engineered cells in hand, MII dynamics can be quantitatively measured to determine if contractile ring formation in adherent cells forms in a manner similar to- or distinct from large embryonic blastomeres.

P12. A Comparative analysis of thioester-containing proteins expression in hemocytes of the *Biomphalaria glabrata* snails in response to *Schistosoma mansoni* products

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Schistosomiasis, also known as snail fever, is caused by the parasite **Schistosoma mansoni**. Due to its prevalence and people at risk of infection, schistosomiasis is a significant global health concern. Our research focuses on the immune response of the parasite's intermediate host, the snail *Biomphalaria glabrata*. This species serves as a model to better understand host-parasite interactions due to the existence of snail strains with varied levels of resistance to the parasite. Previous studies have identified the snail blood cells, or hemocytes, as the primary immune cell in the host's immune responses. In this study, we analyzed the differential expression of thioester-containing proteins (TEPs) in hemocytes of two *B. glabrata* strains, one showing resistance to *S. mansoni* infection (BS90), and the other susceptibility (BB02). Hemocytes were collected from laboratory-reared snails and exposed to the secretion product of *S. mansoni* miracidia called Larval Transformation Products (LTPs), and then compared to controls (buffer-only exposure). To quantify the expression of 11 previously characterized TEPs, we utilized nucleic acid-hybridization techniques. We hypothesized that a subset of TEPs will be upregulated in response to exposure to parasite products. Preliminary results showed that several snail TEPs, notably A2M-1, C3-3, C3-1, and CD109 were upregulated in hemocytes of both strains, with the highest change observed in hemocytes of BS-90, suggesting a possible association between these TEPs and the resistance phenotype. This investigation aims to improve our understanding of snail host immunity and examine if TEPs could be used as potential biomarkers for resistance.

T3. Bee-lining conservation: addressing trap waste and seasonal dormancy in bee research

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Solitary bees make up an estimated 70 percent of the over 20,000 known bee species globally, yet their life-histories beyond direct pollinating behaviors, such as seasonal dormancy, remain understudied. Global data suggests that many bee species are decreasing in abundance and range. Information about the life-histories of these species is needed to conserve remaining populations. Tools to study solitary bees include passive trapping methods, which are commonly used but criticized for being too indiscriminate. Furthermore, successful methods for studying solitary bees during their dormant life-stages have not yet been developed. We are working to fill these informational gaps within native bee research in two ways: (i), by modifying an established lethal passive trapping method to minimize non-target captures, and (ii), by developing a novel method to trap living solitary bees and coerce them into dormancy. We deployed 12 modified lethal traps at 5 sites in southern New Mexico to assess their ability to exclude invertebrate species of conservation concern. We also deployed prototypes of eight live ground-nesting traps at one site in southern New Mexico to determine if solitary ground-nesting bees could be coerced to build nests in them. Calibration and successful application of our novel non-lethal nesting traps will allow us to gather physiological and survivorship data from a previously unstudied life-stage for most solitary bees. The two approaches described here, if successfully applied, will greatly improve our understanding of solitary bees, which make up the bulk of bee species but are the least studied group.

P13. Comparison of replication dynamics of human-endemic and Sylvatic Zika and Dengue Virus in Cynomolgus Macaques

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Zika (ZIKV) and dengue (DENV) are arthropod-borne viruses that infect hundreds of millions of people worldwide, causing substantial morbidity and mortality. Both viruses spilled over into human circulation from sylvatic cycles maintained in monkeys and canopy-living mosquitoes in Old World forests. However, it has been difficult to predict the likelihood of future spillover events of these viruses due to a lack of information on within-host dynamics in their monkey hosts. In this study, we quantified daily viremia in cynomolgus macaques infected with the sylvatic ecotype of ZIKV or DENV or the human-endemic ecotype of DENV or ZIKV. In particular, we investigated whether these viruses manifested a trade-off between magnitude (i.e. peak titer) of viremia and how quickly the virus was cleared by the immune response. The clearest difference in viral replication dynamics in this study was the substantially (≥4 days) longer duration of replication of DENV, irrespective of ecotype, relative to ZIKV. The second notable finding was the extremely high magnitude of replication of sylvatic ZIKV relative to the other three viruses. Finally, among individual monkeys, we detected a significant negative association between magnitude and duration of viremia for sylvatic ZIKV. Thus, this study reveals a trade-off in magnitude and clearance of replication both within individual viruses and between viruses. However, human-endemic ZIKV replication dynamics contradicted this general pattern, showing both low magnitude and brief duration of replication. We speculate that this could reflect adaptation of human-endemic ZIKV to human hosts.

T14. Exploring role 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. Based on our transcriptomic analysis, we expect that Nep1 and Nepl15 flies will have less muscle protein and therefore will have less muscle. The basic subunit of muscle is the sarcomere which is made of actin (thin filament) and myosin (thick filaments). Each muscle fiber has many sarcomeres arranged side by side. When muscles contract thin filaments slide over thick filaments. Flies have skeletal muscle for instance in thoraces that control the wings, and they also have cardiac muscles and smooth muscles that line the gut. To determine which muscles are affected in Nep1 and Nepl15 mutants we will conduct cryosectioning of whole flies and measure the sizes of different muscle types. Additionally, we will stain with fluorescent phalloidin which stains actin thin filaments to see sarcomere structure. We will also perform behavioral assays such as climbing assays and flight assays to see the functionality of muscles.

T10. Measurements of the rate of insect DNA degradation in field-deployed passive traps

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Passive trapping is one of the most efficient, and often only practical, methods of gathering data on insect populations and communities. Blue vane traps (BVTs), passive traps commonly used to capture native bees, may be set for periods of hours to months, resulting in lethal capture of tens to thousands of small invertebrates. While valuable information about insects within the sampled environment is collected, the data is often not applied to molecular ecology studies, due to the perception that DNA degradation is too great. Currently, there is little data on the rate of DNA degradation of samples in these traps. The purpose of this study is to understand the tradeoff between time in the trap and DNA quality of the collected specimens. We measured the effects of environmental exposure on DNA for insect samples left in BVTs for 12 treatments varying in exposure time, which ranged from six hours to four weeks. To simulate field conditions, honeybees were placed in field-deployed traps in an arid desert environment before collection. DNA was extracted from each bee, quantified, and assessed for quality. We predict that DNA degradation will be highest when the samples are exposed for longer time periods, and the rate of degradation will increase over time, with intermediate times between 48 hours and two weeks producing sufficient DNA for some molecular studies. This experiment will improve understanding of environmental impact on DNA quality and expand applications of passive trapping to molecular ecology of arthropods.

P14. The health condition of Mexican free-tailed bats (*Tadarida brasiliensis*) from Southern New Mexico and Southern Arizona

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Bats are unique disease reservoirs compared to other organisms given their abilities to travel long distances, their seemingly robust immune systems, and their varied social structures ranging from solitary roosting bats to aggregates of over a million individuals. This study sought to understand how overall body condition ('health') including immunological profiles differ between the sexes and age in the Mexican free-tailed bat (*Tadarida brasiliensis*). Further, we asked if there are geographical differences between animals in New Mexico and Arizona in immune profiles. We captured bats at two sites in the summer of 2022 and 2023. Once captured, blood samples were collected for blood smears, body mass, relative skeletal sizes, sex and approximate age were all noted. Blood remaining was spun to measure hematocrit a proxy for hydration status. Blood smears were stained using Hematoxylin and Eosin (H&E), and imaged light microscope. Using the resulting photomicrographs, we were able to identify cells and estimate differential white blood cell counts. Precedently, we have observed key types of immune cells, including the relative prevalence of neutrophils and leukocytes. We present data from a total of 72 blood smears corresponding to 20 males, 20 females from New Mexico, 24 males 8 females from Arizona. We noted that Hematocrit varied by sex (females: 0.63 +_0.001 males: 0.61 +_0.001). However, body condition relative to the neutrophil (N) to lymphocyte (L) ratio is highly conserved (0.1-0.6 N:L) across the individuals we have examined thus far suggesting bats maintain a consistent immune profile despite location, age, and sex.

T13. Tracing muscle cell lineage during sea star development

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Differential gene expression is the principal driver of cell fate decisions, and differential expression of cytoskeletal proteins helps determine cell shape and function. Tropomyosin (Tpm) is an actin-binding protein with a multitude of effects on filament branching, actin depolymerization and myosin contractility. Tropomyosin undergoes alternative splicing, generating multiple isoforms that presumably influence cell function. Recent work in the lab has focused on Tpm isoform expression and function in sea stars, which have a single Tpm gene with a limited set of long and short isoforms. Interestingly, Tpm long isoforms (Tpm-L) appear to be expressed exclusively in muscle cell (esophageal and dorsal) populations, which contrasts with vertebrate cells, where long and short isoforms are co-expressed in muscle and nonmuscle cells alike. To better understand Tpm isoform expression and muscle development, we will perform *in situ* hybridization analysis on *Patiria miniata* embryos between gastrulation and the onset of larval feeding (spanning days 2-5). In the sea star, mesodermal cell populations are derived from the top of the archenteron, where cells undergo an epithelial-mesenchymal transition and migrate into the blastocoel. Initial efforts will focus on the expression patterns of Tpm-L and MyoD, a conserved transcription factor that drives muscle gene expression. If MyoD is involved in sea star muscle differentiation, then we predict that MyoD and Tpm-L will be co-expressed in mesenchymal cells late in gastrulation. These data will help develop novel hypothesis-driven lines of experimentation to determine how muscle determining factors and tropomyosin splice forms contribute to embryonic and larval muscle development.

P15. The impact of Ect2 on the mechanical functions in the cytoskeleton in sea Star oocytes during meiosis

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Female meiosis represents a highly asymmetric cell division that results in a single gamete. Meiotic re-entry also triggers several changes that prepare the oocyte for fertilization and development. In starfish, oocytes are arrested in G2 of meiosis I, and upon stimulation with a hormone, undergo M phase entry within 30 minutes. Interestingly, G2-arrested oocytes have the highest cortical tension levels measured for any cell type; but following hormone addition, cortical tension levels drop as the oocyte enters meiosis. We hypothesized that the changes in the mechanical properties of oocytes is driven by Myosin II activity and organization. Towards these ends, Patiria miniata oocytes were injected with Lifeact-GFP and iMyo-Scarlet mRNA to label actin and myosin II respectively, and oocytes were imaged prior to and following hormone stimulation. In the inactivated oocyte, actin was observed as an isotropic layer of short microvilli and cortical actin. Myosin II was also found at the cortex, but was organized into broad patches as opposed to being evenly dispersed throughout the cortex. These subdomains did not move or demonstrate any wave-like pulses in contrast to what has been observed in other species or stages. Immediately following hormone stimulation, actin-based projections were observed, with Myosin II enriched in the cortex at the base of each projection. Current efforts are focused on further measuring changes in the cortical Myosin II organization as the oocyte re-enters meiosis, as well as identifying the upstream factors that maintain Rho (and thus Myosin II contractility) prior to hormone stimulation.

T12. Validation of vaginal cytology to assign reproductive stages in captive Jamaican fruit-eating bats (*Artibeus jamaicensis*)

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Understanding reproduction in wild animals provides information for conservation such as variation in population size and viability. However, it is important to examine the accuracy of different approaches used to detect the reproductive stage of individuals. Many historical studies of bat reproduction have been done using lethal collection or indirect proxies such as examining external morphology. We sought to validate the use of vaginal cytology for characterizing reproductive cycles in a captive colony of Jamaican fruit-eating bats (*Artibeus jamaicensis*). Vaginal cytology has been used in several mammals including rodents, carnivores, artiodactyls, and some bats. Here we assess the accuracy of this method in a controlled setting and describe cellular changes in vaginal aspirations from female bats. From September 2023 to January 2024, we took longitudinal samples from 8 individual females which were left to breed for 2 weeks in a mating cage and then transferred them into a post-breeding cage. Epithelial cells were categorized as parabasal, intermediate, superficial nucleated, and cornified using Papanicolau (PAP) staining. Using the resulting ratios of superficial to non-superficial epithelial cells, reproductive stages (proestrus, estrus, metestrus, and diestrus) were distinguishable using linear discriminant analysis. We compare variation over time in these stages for 3 pregnant and 5 non-pregnant females. We discuss the promise of cytology for detecting cryptic reproductive stages and how these methods may facilitate future studies of reproductive biology in free-living animals.

T9. The effect of warming on decomposition rates of dryland fungi

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Global climate change profoundly impacts ecosystems worldwide, yet one crucial and understudied effect of climate change is the effect of increasing temperatures on fungal decomposition, especially in dryland ecosystems such as the Chihuahuan Desert. Therefore, in this study, I aim to quantify how rising temperatures affect decomposition rates in dryland fungi. I measured decomposition rates of mesquite leaves by eighteen species of dryland fungi exposed to two different temperatures of 27ºC (control) and 37ºC to simulate rising temperatures. Preliminary decomposition results under control conditions showed species-specific decomposition rates of mesquite leaves. Under warming, I anticipate species-specific increased decomposition rates compared to control conditions. My findings are pivotal to understanding the extent of climate change in dryland ecosystems and can help us predict the adaptive capacities of dryland fungi to changing environments. Additionally, exploring the decomposition rates of these fungi under higher temperatures can help us better predict greenhouse gas emissions from dryland ecosystems under global climate change.

P16. Exploring the immunomodulatory role of *Nep1*^{5} in *Drosophila melanogaster*

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Neprilysins are peptidases that cleave peptide hormones, playing a crucial role in various biological processes. Here, we report the generation of a loss-of-function mutation in the Nep1 gene, which encodes a Neprilysin in fruit flies. Transcriptomic analysis of Nep1 mutants reveals a significant enrichment of upregulated genes in pathways related to immunity, suggesting a role for the Nep1 gene in immune regulation. To validate these findings, we are conducting qPCR on the identified genes. Furthermore, we aim to assess the immune response of Nep1 mutants by challenging them with different commensal and pathogenic bacteria. Specifically, we will use the gram-positive bacterium E. faecalis to challenge the Toll pathway and the gram-negative bacterium S. marcescens to challenge the IMD pathway. Subsequently, we will quantify the bacterial load and monitor fly survival. This research not only enhances our understanding of biological processes but also holds promise for informing novel therapeutic approaches to immune-related disorders.

P17. Behavioral responses driven by TRPA1 channels in AITC induced behaviors of *Drosophila melanogaster*

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The transient receptor potential ankyrin 1 (TRPA1) channel is a promising target for drug development and treatment of chronic pain, cancer, and diabetes (PMID: 29207921, 36135016, 37729917). Allyl isothiocyanate (AITC), found in plants such as wasabi and mustard, is an allosteric activator of TRP channels. This binding allows an influx of Ca2+ ions to stimulate peripheral sensory neurons and is interpreted as a pungent numbing sensation (PMID: 37729917). When these sensory neurons malfunction, stimuli are misrepresented, and can lead to chronic pain (PMID: 21041958). Development of new interventions for treatment of chronic pain is urgently needed, considering that 70% of individuals managing chronic pain report inadequate relief (PMID: 28009082). *Drosophila melanogaster* expresses two TRPA1 channels in their peripheral nervous system; *dTRPA1* and *painless*. Mutation of these genes reduces nociception in larvae, delaying the response to flee from harmful stimuli (PMID: 12705873, 31735672). In *Drosophila* adults, mutations in both *painless* and *dTRPA1* reduce behavioral avoidance to AITC (PMID: 30018539). In larva, *dTrpA1* is required for nociceptive response to AITC (PMID: 31735672), but the requirement of *painless* has not been tested. Previous work in the lab has found that full deletions of the gene *painless* do not disrupt thermal nociception, in contrast to partial mutations. We hypothesized the behavioral responses of *Drosophila* larvae to AITC stimuli do not require *painless* and depend solely on dTRPA1 function. Studying how mutations in TRPA1 channels affect AITC response provides insights to the specific mechanisms of pain perception, paving the way for new pain treatments.

T5. Do functional traits in bees predict landscape genetic patterns? A meta-analysis of genetic differentiation

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Conservation ecology increasingly focuses on multi-species approaches to understand declines in abundance of entire communities or assemblages. Often these approaches reveal that functional traits, for example body size or foraging distance, are related to conservation metrics such as extinction vulnerability. As species traits are often shaped by ecological relationships, we also expect genetic structure of populations to be affected by environmental change, knowledge that is critical for conservation. Landscape genetics, a field developed in recent decades, specifically addresses the influence of landscape features on genetic differentiation, and has recently moved to focus on generalizations of patterns across taxa. While insects are not frequently studied in landscape genetics, bees, with over 20,000 species worldwide, provide a diverse model for trait-based studies, displaying a wide range of functional traits related to behavior and physiology. We conducted a meta-analysis of 100+ papers in bee landscape genetics with the goal of generalizing patterns of genetic differentiation across functional traits of species, including size, sociality, diet, and nest-building behavior. We expect to find differences in geographic genetic differentiation across groups of functional traits, as well as other patterns related to spatial scale and total area of study. Patterns we predict to find include less genetic differentiation in larger-bodied, eusocial, and generalist species, and more differentiation in small, solitary, and specialist species. In addition to motivating hypothesis-driven research in landscape genetics, results from this analysis may also identify for conservation purposes taxa likely to be sensitive to landscape changes.

P18. Investigating the relationships between wildfire, pathogen prevalence, and management practices in *Peromyscus maniculatus* in northern New Mexico, USA

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Disease ecology, and wildlife reservoirs of disease, have been placed on a global stage. Globally, we are witnessing the emergence of infectious diseases at an unprecedented rate (Jones et al. 2008). Global change can exacerbate the severity of wildlife diseases and alters relationships between vectors, pathogens and hosts (Ogden et al. 2008; Price et al. 2019). Wildfires are a major symptom of global change, and our world is becoming increasingly fire and disease prone. However, little research has been conducted to elucidate the relationship between fire and zoonotic infectious disease. Even less understood is how post-fire management practices may interact with host and pathogen dynamics to influence a disease outcome in wildlife systems. Our research will address if re-seeding post-fire can result in higher prevalence rates of Sin Nombre Virus (SNV), an orthohantavirus with significant public health implications and a case fatality rate of ~30% in humans. We hypothesize that the post-fire management practice of re-seeding for erosion control affects the prevalence of SNV. To this end, our objective is to quantify SNV prevalence in *Peromyscus maniculatus*, through serological assays, across burned areas that have been re-seeded after a wildfire event, burned sites that have not been re-seeded, and sites that have not burned nor been re-seeded. Not only will this provide critical knowledge for wildlife disease ecologist, but the results from this study can provide insight into where and when infection risk of SNV is higher for forest managers post-fire.

T15. Effects of chronic stress on the physiological stress response and glucocorticoid and mineralocorticoid receptor expression in budgerigars over time

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Stressful events lead to the release of glucocorticoids, which are products of the activation of the hypothalamic-pituitary-adrenal axis. While glucocorticoids such as corticosterone (the main avian stress hormone) are necessary for survival, studies have shown that a prolonged stress response can have detrimental effects on behavior and cognition, including vocal learning. However, how chronic stress impacts the expression of glucocorticoid and mineralocorticoid receptors (GR and MR) in vocal learning regions is poorly understood. The budgerigar (*Melopsittacus undulatus*), a small parrot, is an excellent model to better understand such chronic effects because it is a lifelong vocal learner. We developed a chronic stress protocol that presents stressors at unpredictable intervals to adult males over the course of 3 weeks. We measured the physiological stress response and changes in *GR* and *MR* expression in the brain over time. Brain regions include the magnocellular nucleus of the medial striatum (MMSt), a region associated with vocal learning, the ventral striato-pallidum (VSP), a region not associated with vocal learning, and the hippocampus, which is involved in the negative feedback loop of the stress response. We found changes in the glucocorticoid-mediated stress response resulting in an increase in baseline corticosterone and a decrease in stress response levels in the stress treatment. We also found a lower expression of *GR* in the MMSt of stressed individuals that was not mirrored in the other brain regions. Our results suggest that there may be a buffering mechanism protecting a vocal learning region from the impacts of prolonged chronic stress.

P19. Understanding the impact of subinhibitory concentrations of disinfectants on bacterial risk in wastewater

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Disinfection is the final stage of the wastewater treatment process, which removes pathogens from treated water, ensures its safe discharge to the ecosystem, and protects public health from waterborne diseases. Even though the disinfection process helps eliminate most pathogenic bacteria in wastewater, some bacteria still exist even after disinfection due to their resistance to the disinfectants. Recent studies have found that the subinhibitory concentrations of disinfectants can increase the hazardous characteristics of surviving bacteria in treated wastewater. Therefore, this study proposes to analyze the tolerance of chlorine-stressed wastewater bacteria under simulated gastrointestinal conditions to understand the risk associated with the exposure of treated wastewater discharges. Chlorine-stressed bacterial samples were prepared by using enriched bacteria in secondary effluent bacterial samples after exposure to an available chlorine concentration of 0.05 mg/l, 0.1 mg/l, and 0.5 mg/L. The gastrointestinal tract model consists of the digestive compartments of the mouth, stomach, and small intestine, which were used to simulate the in vitro digestion of humans. The survival of chorine-stressed bacteria was tested at 37 °C after successive incubations with artificial saliva, gastric juice, and bile juice. Results show that the chlorine-stressed wastewater bacteria can be grown in each tested digestion compartment. Even though stomach acid acts as a barrier to inhibit model bacteria *E. coli* effectively, wastewater bacteria, after exposure to a subinhibitory concentration of chlorine, can tolerate the harsh gastrointestinal conditions more.

T8. Low sugar supply affects survival rate and vector competence against *Plasmodium* in mosquitoes.

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Malaria is a mosquito-borne disease caused by the parasite *Plasmodium sp*. Mosquitoes obtain sugars, including glucose, mannose, galactose, fructose, and gulose, from plants usually as floral and extrafloral nectar. Energy production in mosquitoes requires glycolysis and TCA cycle to generate ATP. Immunity is costly, which requires energy support. Glucose plays a vital role as a daily nutrient requirement for mosquitoes. In this study, we used *Anopheles stephensi* and *Anopheles gambiae* as our mosquito models. We hypothesize that low sugar supply will have an impact on both survival rate and malaria infection pattern. According to our results, low sugar supply decreases the malaria infection against *Plasmodium berghei* in the mosquito *Anopheles gambiae* while low sugar supply favored *Plasmodium berghei* development in *Anopheles stephensi*. The mortality comparison revealed that *Anopheles stephensi* are resistant to low sugar supply , linking their capabilities as an invasive species. In contrast, *Anopheles gambiae* does not share this similarity. These results suggest that low sugar supply have an influence on vector competence for malaria parasites. Additionally, the data provides some insight into *A. stephensi's* vector superiority.

P20. Evaluating toxicity induced by treated produced water on human cell lines

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Abstract: Shale oil and gas extraction significantly impacts the global energy landscape and is the main driver for the country's economy. However, the extraction process generates large volumes of produced water (PW) due to hydraulic fracturing. PW has a complex composition and constitutes high levels of total dissolved solids, oil, grease, radionuclides, heavy metals, dissolved organic matter, salinity, and hydraulic fracturing chemicals. Thus, improper management or disposal of PW can have a wide range of impacts on the environment and human health. We must treat and reuse PW for beneficial reuse in locations where water scarcity is a concern. Even with the most sophisticated water treatment technologies, we cannot guarantee the safe discharge and reuse of PW without comprehensive toxicity assays as the treated water still contains organic compounds which cannot be identified and quantified. This study investigated the effects of untreated and PW treated from thermal desalination technology from the Permian basin. The impacts of produced water on cellular metabolic activities, plasma membrane damage, apoptosis, and endocrine-disrupting effects were assessed using human intestinal epithelial (Caco-2) cells, human breast cancer cells (MCF-7), and human embryonic kidney cells (HEK293). In summary, the results indicate that exposure to treated PW showed no significant impact on cell viability and membrane integrity, whereas untreated PW showed a significant effect on human cells. It was also found no oxidative stress and apoptosis induced by the treated produced water. Overall, we demonstrated that PW, after appropriate treatment, has good potential to be discharged or reused safely.

T6. Who's flying this thing? Investigating potential insect vectors of vesicular stomatitis virus in its endemic and outbreak regions

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Vesicular stomatitis virus (VSV) emerges from its focus of endemic transmission in southern Mexico to cause epizootics in livestock across the western USA at three-to-eight-year intervals. A dearth of information on the relative role of the many possible arthropod vectors of VSV in the endemic and outbreak regions hampers efforts to predict future incursions into the US. As part of a larger effort to understand and anticipate VSV emergence, we sampled potential vectors in both VSV endemic (Chiapas, Mexico) and epidemic (New Mexico, USA) regions and screened a subset of these for virus. In New Mexico, VSV RNA was detected in four species of black flies collected along the Rio Grande during a 2020 outbreak in the state. In contrast, black flies were extremely rare in vector collections across five ranches in Chiapas compared to other potential vector taxa, like sand flies, mosquitoes, and biting midges, and VSV RNA was detected in all four groups of vectors. Intriguingly livestock VS cases were not reported during the dry season at the five sample ranches, but the virus was detected in vectors on these ranches in the dry season. These results suggest that different insect vectors are involved in VSV transmission in the endemic region compared to the epidemic region and suggests that non-livestock hosts and/or vertical maintenance in vectors may explain continuous circulation of VSV in its endemic region.

T2. Habitat selection of translocated juvenile Bolson tortoises

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The Bolson tortoise (*Gopherus flavomarginatus*; hereafter tortoise) is the largest tortoise species in North America. This tortoise's range once extended throughout the Chihuahuan desert during the Pleistocene, however, today the tortoise is extirpated from the wild in the United States. Furthermore, the remaining extant tortoises in Mexico (~2,500 individuals) are declining due to multiple threats. In 2021 we initiated a translocation project of captive-bred juvenile tortoises to investigate the feasibility of restoring the species to their historic range. Since the species has been absent from the translocation site for over 10,000 years, there is a gap in our understanding of habitat requirements of this species. To address this knowledge gap, we began a habitat selection study with the objective of characterizing burrow sites of translocated juvenile tortoises in a resource selection modeling framework. For this study we examined the effects of vegetation, soil, and topographic characteristics on burrow site selection for 45 tortoises. From May–November 2023, we collected data at 136 burrow locations and 272 randomly generated available locations and compared this data at a 1:2 use to availability ratio. Preliminary results indicate that tortoises are positively selecting burrow sites with higher vegetation cover (β: 0.729 ± 0.138 SE), higher canopy cover (β: 0.514 ± 0.214 SE), and more small mammal burrows (β: 1.377 ± 0.252 SE). We will present the study design, methods, and summarize preliminary results. Ultimately, through this research we plan to provide best practices for selecting future Bolson tortoise translocation sites in the Chihuahuan Desert.