DEPARTMENT OF
BIOLOGY

34th Annual Research Days

A Presentation of Student Research
Celebrating Discovery and Education in the Biological Sciences

April 3-4, 2025

Committee Members

Co-Chair: Seth Newsome
Co-Chair: Syed Mubarak
Tayli Lam
Joanne Kuestner
Jade Knight
Jessica Belmares Ortega, BGSA
Kourtney Zimmerly, BGSA

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34th Annual Research Days

April 3-4th, 2025
Castetter Hall

Killing in the name of science: The ethics and effects of scientific collecting

Thursday Speaker

Dr. Steven Poe
Professor,
Department of Biology,
University of New Mexico

Research in my lab is focused on Anolis lizards. In the course of our work, we have collected (i.e., captured, killed, and preserved) thousands of lizards for scientific study. Museum collections of preserved specimens are indispensable for many areas of science, including studies of climate change and evolutionary relationship. However, collecting specimens is heavily regulated, and much of the public is understandably uncomfortable with the process of collecting. Here I examine collecting from philosophical and conservation viewpoints. I show that, for some organisms, many of the restrictions placed on collecting by governing bodies may lack strong justification based on either ethical or practical grounds. Also there will be some cool lizard photos.

Day: Thursday, April 03
Time: 3:30 PM
Venue: Castetter 100

Effect of social experience on gene expression, circuit function, and behaviors

Friday Speaker

Dr. Pelin Volkan
Associate Professor,
Department of Biological,
Sciences,
Duke University

In many animals, social experience alters various behavioral and physiological responses. Notably, chronic social isolation is associated with adverse effects on our mental and physical health. My lab aims to unravel genetic and neural circuit mechanisms mediating the impact of social experience using Drosophila as a model system.

Day: Friday, April 04
Time: 3:30 PM
Venue: SMLC 102

Schedule of Events

Thursday April 3rd			
All day	Judges preview posters		
12:30-1:30 p.m.	**GRADUATE STUDENT LUNCH**		**CAST Room 1420 (PiBBs)**
1:30-3:30 p.m.	Poster Printing and Hanging		**CAST Room 40**
3:30-4:30 pm.	**SEMINAR - Dr. Steven Poe**		**CAST Room 100**
4:30 pm	**Hausammann Brewhouse Social**		**2004 Central Ave SE**
Friday April 4th			
8:30-9:30 a.m.	**SESSION I**	**Level**	**CAST Room 100**
8:30-8:45 a.m.	Connor Burgin	GR	
8:45-9:00 a.m.	Jessica Belmares	GR	
9:00-9:15 a.m.	Trinity Griffus	UG	
9:15-9:30 a.m.	Thomas Bulger	UG	
9:30-10:30 a.m.	**SESSION 2**		**CAST Room 100**
9:30-9:45 a.m.	Emily Reynebeau	GR	
9:45-10:00 a.m.	Anejelique Martinez	GR	
10:00-10:15 a.m.	Hannah Bradley	UG	
10:15-10:30 a.m.	Adina Ataran	PB	
10:30-10:45 a.m.	**COFFEE BREAK**		**CAST Greenhouse**
10:45 a.m. - 12:00 p.m.	**SESSION 3**		**CAST Room 100**
10:45-11:00 a.m.	Esteban Rosario-Sanchez	GR	
11:00-11:15 a.m.	Chris McDaniels	GR	
11:15-11:30 a.m.	Kourtney Zimmerly	GR	
11:30-11:45 a.m.	Noah Castro	UG	
11:45 a.m. - 12:00 p.m.	Ariana Pritha	UG	
12:00-1:00 p.m.	**LUNCH**		**CAST Basement**

1:30 - 3:30 p.m.	**Open Laboratory Visits**		
	Center for Stable Isotopes		PAIS 1315
	Syed Lab		CAST 207
	Salinas Lab		CAST 2564
	Takacs-Vesbach Lab		CAST 3517
	Cook Lab		CAST 157, 159
1:00–2:00 p.m.	**POSTER SESSION I**		**CAST** **1st Floor** **AND** **CAST** **Basement**
	Narmin Musayeva (1)	RS	
	Savannah Sanchez (2)	GR	
	Josh Lopez-Binder (3)	GR	
	Rachael Auer (4)	GR	
	Michael Fragua (5)	GR	
	Patrick Baca (6)	GR	
	Shayne Halter (7)	GR	
	Natalia Chavez (8)	GR	
	Lexi Baca (9)	GR	
	Isabel Robertson (10)	HS	
	Conner Mertz (11)	GR	
	Garrett Wondra (12)	UG	
	Maia Hizny (13)	UG	
	Raul Salas (14)	UG	
	Ethan Lombardi (15)	UG	
	Kian Hill (16)	UG	
	Sunnie (Ares) Repka (17)	UG	
	Josiah Kingston (18)	UG	
	Patricia Sotelo Chavira (19)	UG	
	Rene Archiga (20)	UG	

	Shristey Tamang (21)	PB	
	Kane Anaya (22)	UG	
	Thailia Stallings (23)	UG	
	Lito Appell (24)	UG	
	Sophia Rivera (25)	UG	
	Isabelle Gurney (26)	UG	
	Noah Castro (27)	UG	
	Christiana Concepcion (28)	UG	
	Michael Robinson (29)	UG	
2:00-3:00 p.m.	**POSTER SESSION II**		**CAST** **1st Floor** **AND** **CAST** **Basement**
	John Korbin (30)	GR	
	Tulaib Azam (31)	GR	
	Shweta Agarwal (32)	GR	
	Noelle Mason (33)	GR	
	Eva Tipps (34)	GR	
	Dale Fastle (35)	GR	
	Caitlin Zimmer (36)	GR	
	Abigail Granath (37)	GR	
	Josiah Lavender (38)	GR	
	Jian Xiong David Tan (39)	GR	
	Joshua Cortez (40)	GR	
	Rosemary Cochran (41)	HS	
	Maximus Youngman (42)	HS	
	Sophia Griego (43)	HS	
	Alto Bridges (44)	HS	
	Janna Martinez (45)	UG	
	Julianna Ford (46)	UG	

	Joshua Abraham (47)	UG	
	Kamren Decker (48)	UG	
	Alan Ibarra (49)	UG	
	Andrea Ibarra (50)	UG	
	Kristen Estill (51)	UG	
	Rachel Smith (52)	UG	
	Serena Helewicz (53)	UG	
	Nicolette Brite (54)	UG	
	Ari Rothschild (55)	UG	
	Job Flores (56)	UG	
	Lelia Yane and Ada Kieweg (57)	HS	
	Alissa Jones (58)	UG	
	Collis Bousliman (59)	UG	
	Mike Velasquez (60)	UG	
3:00-3:30 p.m.	**COFFEE BREAK**		**CAST Greenhouse**
3:30-4:30 p.m.	**SEMINAR - Dr. Pelin Volkan**		**SMLC 102**
4:30-5:30 p.m.	**SCHOLARSHIPS & AWARDS**		**SMLC 102**
5:30-6:30 p.m.	**RECEPTION**		**SMLC Lobby**
6:30 p.m.	**BOSQUE BREWING SOCIAL**		**106 Girard Blvd SE**

Oral Presentations Abstracts

How many mammal species are there? A synthesis of current taxonomic, nomenclatural, and geographic knowledge.

Connor J. Burgin, Department of Biology, UNM

The Mammal Diversity Database (MDD) is an open-access resource providing up-to-date taxonomic, nomenclatural, and geographic data for global mammal species. Since its launch in 2018, the MDD has transformed the traditionally static process of updating mammalian taxonomy into regular online releases reflecting the latest published research. To build on this foundation, I present version 2.0 of the MDD (MDD2), which catalogues 6,759 living and recently extinct mammal species, respectively representing net increases of 4.1% and 24.8% over the 2018 release of MDD (version 1.0) and 2004 publication of Mammal Species of the World, 3rd edition (MSW3). Here, I investigate trends in global mammal biodiversity using taxonomic, geographic, and nomenclatural metadata of the MDD. I emphasize lagging mammal conservation assessments: 25% of the MDD2-recognized mammal species allocated to the ‘understudied’ conservation threat categories of Data Deficient (11%) or Not Evaluated (14%), underscoring the need for greater taxonomic integration with international conservation efforts. MDD2 includes the release of a cross-platform application that provides offline access to the MDD taxonomy. By providing up-to-date mammalian taxonomic and nomenclatural data—including links to the published text of original name descriptions, type localities, and type specimen collections—the MDD provides an integrative resource for biologists and conservationists to more easily investigate the systematics and conservation status of focal organisms.

Understanding how IL-36γ shapes immune responses to *Toxoplasma gondii*

Jessica Belmares-Ortega, Cory Henn, Fatouma Kapran, Miriam Shin, Lindsay Snyder, Eric Denkers, Department of Biology, UNM

IL-36γ is part of a family of molecules involved in inflammation, but its role during infection is still being uncovered. Our research investigates how IL-36γ affects the immune response to *Toxoplasma gondii*, a common parasite that first establishes in the gut. We found that human intestinal cells increase IL-36γ levels during infection and respond to it by activating signaling pathways linked to inflammation. Mouse immune cells like macrophages also respond to IL-36γ by producing inflammatory signals. In mice lacking IL-36γ, we saw a heightened susceptibility during infection—higher parasite levels, more inflammation, and lower survival—despite no major changes in gut bacteria. We also identified a small cell subset of lamina propria immune cells that express IL-36γ and are currently investigating their broader gene expression profile and function. Together, we hypothesize that IL-36γ plays a critical role both at baseline and during infection. These insights may inform future therapeutic strategies for controlling inflammation and maintaining immune balance in the gut.

Remediating Sunflowers Grown in Extraterrestrial Regolith through the use of Mycorrhizae Fungi and Supplemental Nutrients

Trinity Griffus, Department of Biology, UNM

In situ resource utilization will be essential to self-sufficiency for astronauts in future space missions on extraterrestrial planets. The unconsolidated rock and dust known as regolith will be the most abundant resource that can be used to establish gardens for food sustainability. While plants can germinate in regolith, their growth is often stunted. A question to ask is how we can improve the conditions of the regolith to be better suited for plant cultivation. The research questions for this project are: Will the mycorrhizae Rhizophagus irregularis assist in plant resource acquisition, water stress reduction, and improved growth for Helianthus annuus grown in simulated Martian and Lunar regolith and will the second generation of Helianthus annuus grown in previously used regolith with Rhizophagus irregularis have improved growth compared to the first generation. The cultivation occurs in a controlled laboratory environment. Factors such as temperature and light are maintained at fixed levels. Using measurements to monitor growth rates and plant physiology, progress can be tracked for each plant within three different substrates (soil, synthetic Martian regolith, and synthetic Lunar regolith) with two treatments (inoculated and non-inoculated) between the generations of H. annuus. Preliminary results show that R. irregularis assisted differently in each substrate: improved root development in Martian regolith, and improved growth rates in Lunar regolith. Further measurements are needed to fully understand the fungi's impact. If effective, mycorrhizae could improve plant resource acquisition and reduce water stress, benefiting not only extraterrestrial agriculture but also boosting food productivity in drought-affected regions.

Identifying insect collection bias in New Mexico with a special focus on butterflies

Thomas Bulger, Simon Doneski, Quinlyn Baine, Department of Biology, UNM

The state of New Mexico contains a high amount of insect biodiversity. This is due to the state’s diverse ecoregions and highly variable topography, especially mountain ranges. However, insect sampling collection efforts are underrepresenting the state's true insect biodiversity. Uncovering collection bias within the state is key to understanding New Mexico’s true insect biodiversity and determining where future collection efforts should be focused. This study examined all insect occurrences from New Mexico that were listed in the Global Biodiversity Information Facility records and compared collections efforts by total records and diversity of taxa across ecoregions, mountain ranges, land managed for natural resources by federal agencies, and proximity to roads. This study also examined butterfly collection due to their relative abundance of population data compared to other insect groups. The results showed a bias towards mountain ecoregions, mountain ranges near urban centers, and land managed by the US Forest Service. The results also showed a bias toward underrepresentation on New Mexico’s Great Plains ecoregions, mountain ranges near state borders, land managed by the Bureau of Land Management and Tribal entities. Additionally, results revealed that nearly 80% of all insect and butterfly occurrence records occur within one kilometer of a road. With this knowledge in mind, detailed collection recommendations are provided, insect surveys and collecting across unrepresented lands will better inform biodiversity and the conservation status of New Mexico’s insects.

Microbial Dynamics in the Polar Night

Emily Reynebeau, Kodi Haughn, Brandon Briggs, Rachael Morgan-Kiss, and Cristina Takacs-Vesbach, Department of Biology, UNM

High latitude ecosystems experience phenologically driven extremes in temperature and sunlight and biological activity is believed to be largely dormant during the polar winter. However, recent studies conducted at the poles have demonstrated dynamic and active microbial communities in both freshwater and marine systems. Yet due to logistical limitations, few of these studies include multi- and full-year sequencing data. Lake Bonney in the McMurdo Dry Valleys, Antarctica is microbially dominated and maintains a stable and diverse bacterial community as recorded during the last thirty years. Here we analyze prokaryotic and eukaryotic communities over four years by sequencing community 16S and 18S rRNA genes to estimate microbial dynamics during the polar night and in contrast to the plankton composition during the austral summer. Indicator species analysis was used to determine if communities varied with season and year. We found that a few prokaryote and eukaryote ASVs were indicative of certain months, and had a consistent periodic increase in relative abundance for every year of the study. There is evidence that some of the detected ASVs may be chemolithoautotrphic or predatory explaining how this community survives the long dark winter of the polar night.

Nutrient Acquisition in Arid Environments: The Gut Microbiome's role in Essential Amino Acid Synthesis for Granivorous Rodents.

Anejelique J. Martinez, Alexi C. Besser, Seth D. Newsome, Department of Biology, UNM

The mammalian gut microbiome performs many functions for the host that directly affects fitness, immunity, and development. One of the most important functions is the conversion of recalcitrant dietary molecules (e.g., cellulose) into compounds that are more easily assimilated by the host (e.g., amino acids) for sources of energy or to maintain tissues. Recent laboratory and field experiments have shown that gut microbes synthesize essential amino acids (AAESS) utilized by their host to maintain protein balance and emerging isotopic evidence suggests herbivores and omnivores faced with seasonal or persistent protein limitation assimilate microbially derived AAESS. We use carbon isotope (d13C) analysis of AAESS in red blood cells from granivorous desert rodents (Dipodomys) to quantify seasonal and annual variation in the relative contributions of AAESS derived from gut microbes versus dietary plant sources. We present longitudinal data for 24 individuals that were captured at least three separate times across three consecutive years (2021-2023). Our findings suggest that rodents assimilate greater proportions of AAESS from C4 plants (e.g., grasses) in years with higher C4 seed production and greater proportions of AAESS from gut microbes during seasons and years with less C4 seed production. Future work incorporating 16S rRNA gene sequencing will allow us to characterize how the composition and function of the mammalian gut microbiome interact with variation in resource availability to influence host protein metabolism.

Snake Fungal Disease: How long has it been here?

Hannah D. Bradley, Daniele L.F Wiley, Lisa N. Barrow, Department of Biology, UNM

Snake mortality across North America has been linked to the fungal pathogen Ophidiomyces ophiodiicola (Oo), which causes Ophidiomycosis, or Snake Fungal Disease (SFD). Susceptible hosts exhibit skin lesions, scale necrosis, and lethargy, with infection confirmation and intensity determined via visual examination and quantitative PCR (qPCR). While SFD has been detected in museum specimens dating back to 1945, its introduction timeline in the U.S., particularly the West, remains unclear. The first documented case in New Mexico occurred in 2021, though the fungus may have been present earlier. This study aims to determine whether Oo was present in New Mexico snakes before 2021. To answer this, I will swab and screen museum specimens (n = 532) collected between 2006-2024, using established qPCR protocols. So far, I have found pathological signs of SFD in 104 specimens, with the earliest potential case from 2006. Pending confirmation, these findings suggest an earlier timeline of fungal migration into the Southwest than previously thought. Establishing an accurate timeline of Oo introduction is crucial for understanding its spread and informing conservation strategies to mitigate negative impacts on already vulnerable Southwestern snake species.

Epistasis as a balancing mechanism in changing environments

Adina Ataran

Balanced polymorphism is a fundamental yet elusive phenomenon in population biology, with profound implications for evolution in changing environments. Recent theory proposes that epistasis may promote balanced polymorphism in temporally varying environments, although under a restrictive model of phenotypic plasticity or infinite population settings. It remains unclear whether epistasis can foster balanced polymorphism in finite populations. We explore the effects of reinforcing, diminishing, and sign epistasis on levels of genetic polymorphism at two selected loci in a population inhabiting temporally changing environments. First, we argue that at least one of the two interacting loci needs to experience sign interactions for epistasis to promote balanced polymorphism. Next, we show that selection needs to be strong for such polymorphism to be protected in finite populations. Finally, we demonstrate that reinforcing epistasis, combined with the balancing effects of spatial heterogeneity in temporally varying environments, can enhance polymorphism in finite populations, even in the absence of strong selection. This describes a new balancing mechanism that significantly broadens the conditions under which epistasis promotes polymorphism. Intuitions for the effect involve a combination of indirect negative frequency dependence and the reinforced effect of rare alleles under reinforcing epistasis. Using analytical approximations and an extensive set of stochastic Monte Carlo simulations, we comprehensively examine and quantify this effect across a wide range of parameters in Write-Fisher finite populations. Therefore, this research highlights the underexplored role of epistasis, specifically reinforcing and strong sign epistasis, as a mechanism of balancing selection in finite populations.

Investigating the Effects of Invasive Species and Climate Change in the Populations of Freshwater Turtles in the Southwestern United States

Esteban O. Rosario-Sánchez, Lisa N. Barrow, Mariah King, Marin Romero, Department of Biology, UNM

Increasing global temperatures, with an average increase of 1.28°C in the last century, are anticipated to induce significant alterations in wildlife habitats and populations around the world. Ectothermic organisms like reptiles, which rely on external temperatures for thermoregulation, are projected to be disproportionately affected by these climatic shifts. This research aims to explore the impacts of climate change and habitat loss on freshwater turtles in New Mexico, focusing on their dietary patterns. Employing stable isotope analysis (δ15N and δ13C), we studied the dietary habits of turtle populations across four sites, correlating these with varied habitat and environmental conditions. We also conducted a temporal dietary comparison between present-day isotopic values of Western Painted Turtles (Chrysemys picta bellii) and those from the 1960s-1980s using museum specimens. The site-to-site analysis showed differences in isotopic values between species at Elephant Butte and the Rio Grande Nature Center. The historical comparison of Chrysemys picta bellii showed differences in isotopic values between present and historical turtles at the Sevilleta National Wildlife Refuge and the Rio Grande Nature Center State Park. Next season, we will assess the genetic structure of the turtle populations across the Rio Grande. Genetic data will allow us to study the genetic structure and potential hybridization between the native Big Bend Slider (Trachemys gaigeae) and the invasive Red-eared slider (Trachemys scripta elegans).

Lineage Boundaries of Six-lined Racerunner Lizards

Chris X. McDaniels, Kadie N. Omlor, Robert C. Thomson, Anthony J. Barley, Lisa N. Barrow, Department of Biology, UNM

Understanding species diversity is a fundamental goal in systematic biology, and identifying taxonomic units is important for conservation efforts. Geographic features and environmental variation are associated with population structure and diversification in a variety of taxa. Six-lined Racerunners (Aspidoscelis sexlineatus) are a species of lizard ranging across much of the eastern and central United States and into northern Mexico. Several subspecies have been described based on morphological features and associated with different ecoregions: Eastern Six-lined Racerunners (A. s. sexlineatus) associated with the Eastern Temperate Forests, Prairie Racerunners (A. s. viridis) associated with the Great Plains, and Texas Yellow-Headed Racerunners (A. s. stephensae) associated with the Texas Coastal Sand Plain. The sexlineatus and viridis subspecies were also described as having a large zone of clinal intergradation west of the Mississippi River. However, comprehensive geographic and genetic sampling has not been used to validate these subspecies or patterns. Using thorough geographic and taxonomic sampling and thousands of nuclear genetic loci, we investigate the evolutionary relationships between racerunner subspecies and populations. Preliminary analyses of both population structure and phylogenetic relationships reveal that all three subspecies form distinct populations and clades. Samples in the “intergrade” zone are found within the viridis clade, with little evidence of admixture between viridis and sexlineatus. Further work will test species hypotheses by comparing species delimitation models and incorporating demographic history and gene flow.

The Developing Gut Microbiome and its Circadian Rhythm in a Model Marsupial

Kourtney M. Zimmerly, Tiffany Garcia, Hailey Aragon, Jordan M. Sampson, and Robert D. Miller, Department of Biology, UNM

Key bacterial species contributing to a healthy gut microbiome are established early in life. Recently, it has been shown in mice and humans that the gut microbiome has a circadian rhythm, which is important for both metabolic and immune health. Marsupials are a lineage of mammals that diverged from placental mammals nearly 160 million years ago. They are characterized by giving birth to highly altricial young. Since most of their postnatal development occurs ex utero, they heavily rely on milk for maternal antibodies and nutrients critical for growth. Indeed, marsupial milk changes both immunologically and nutritionally at key moments of neonatal development. Using the marsupial model Monodelphis domestica, we first investigated the source of the developing gut microbiome. At birth, the neonatal gut microbiome appears more like the microbiome of maternal mammary tissue. When the neonates begin intermittently suckling instead of full-time teat attachment, the neonatal gut microbiome starts to diverge from the mammary microbiome. To investigate the development of the circadian rhythm of the gut microbiome, we first had to establish that there is a circadian rhythm to the M. domestica gut microbiome. Here, we present the first evidence that the gut microbiome of a marsupial has a circadian rhythm. Next, we aim to investigate how the milk microbiome could regulate the circadian rhythm of the developing gut microbiome throughout lactation.

Exploring the Therapeutic Potential of Dexpramipexole in Neuropathic Pain and Inflammatory Cytokine Modulation

NA Castro*, CJ Tomicek*, MS Sun, AK Fernandez-Oropeza, JR Zimmerly, SD Gomez-Medina, ZM Dominguez **, JR Maxwell **, ED Milligan

* Equal contribution of these authors

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Introduction: Dexpramipexole (DPX), an investigational drug approved for clinical trials to treat inflammatory conditions, has demonstrated effectiveness in pain alleviation, possibly through anti-inflammatory properties. However, it remains unknown whether DPX, acting within the central nervous system (CNS), can reduce neuro-immune proinflammatory actions induced by peripheral sciatic nerve chronic-constriction-injury (CCI) in a mouse model. CCI leads to pathological sensitivity to light touch, referred to allodynia. The current study evaluated the spinal action of DPX on CCI-induced allodynia in mice to determine whether DPX acts by suppressing spinal proinflammatory actions. The spleen produces pro- and anti-inflammatory cytokines; thus, splenic cytokine levels were analyzed. Hypothesis: spinal DPX controls CCI-induced allodynia via spinal anti-inflammatory actions leaving peripheral cytokine expression levels intact.

Methods: The von Frey fiber test was applied to assess light touch sensitivity of the hindpaws before and after CCI or SHAM surgery in female C57BL/6 mice. On day 14 post-surgery, mice received intrathecal vehicle (saline; 10ul) or DPX (500ng/10ul) followed by hindpaw reassessment 1hr later. CNS (spinal cord, brain) and spleen were collected. Splenic mRNA gene expression of IL-10 (anti-inflammatory), IL-1B and TNF-a (pro-inflammatory) were assessed.

Results: Vehicle-treated CCI mice remained fully allodynic at 1-hr after injection. Mice with CCI given DPX exhibited full allodynia reversal 1hr later. Splenic-cytokine mRNA expression did not differ between treatment groups. Analyses of cytokine protein levels in CNS tissues are underway. Results suggest that intrathecal DPX reverses neuropathic pain by acting in the spinal cord, while leaving peripheral splenic cytokine expression intact.

CIRCVOPP1 MAY ACT AS NOVEL REGULATOR OF LONG-TERM PERIPHERAL AND CENTRAL NERVOUS SYSTEM IMMUNE DYSFUNCTION DUE TO PRENATAL ALCOHOL EXPOSURE

Ariana N. Pritha, Andrea A. Pasmay, Michaela Dell'Orco, Joshua J. Sanchez, Jacob E. Sanchez, Suzy Davies, Dan D. Savage, Nikolaos Mellios, Erin D. Milligan, Shahani Noor

Affiliations:

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Prenatal alcohol exposure (PAE) increases the risk of pathological touch sensitivity (allodynia) after minor peripheral nerve injury, likely due to heightened proinflammatory immune activation. However, the role of spinal gene expression and non-coding circular RNAs (circRNAs) in this process remains poorly understood. CircRNAs modulate mRNA expression and may regulate neuroimmune function in response to adult challenges.

In a rat model of PAE with sciatic nerve injury or sham controls, we analyzed circRNA expression in circulating immune cells using a microarray (Arraystar Inc) with 14,145 probes. We identified 18 significantly differentially expressed circRNAs ($p < 0.05$, >1.5-fold change) in PAE rats. Ingenuity Pathway Analysis (IPA) revealed involvement of NF-κB, a key proinflammatory pathway activated by TLR4 signaling.

Notably, our data identified circVopp1, derived from the Vopp1 gene, which regulates NF-κB transcription. Using real-time PCR and melting curve analysis, we designed primers to detect circVopp1 specifically, differentiating it from linear Vopp1 mRNA. We are now validating our rat data in mice by screening primer candidates for circVopp1 and other circRNA targets.

These findings suggest circRNA dysregulation may underlie PAE-induced neuroimmune dysfunction. Ongoing research has translated this model into mice and may identify circVopp1 as a clinical biomarker for fetal alcohol spectrum disorder (FASD) and a potential therapeutic target for mitigating immune dysfunction associated with PAE.

Funding: This work was supported by R01 AA025967, R21 AA023051, T32-AA014127, P50 AA022534 and R01AA029694.

Poster Presentations Abstracts

Investigating the role of T cells in maintaining olfactory structure and function and their implications for smell disorders in the context of immunodeficiency

Narmin Musayeva, Benjamin J Garcia, Irene Salinas, Department of Biology, UNM

The olfactory nerve (ON) is the first cranial nerve, which connects the nasal cavity to the central nervous system (CNS) and plays a key role in our ability to smell. Therefore, ON can serve as a direct pathway for various pathogens to invade the CNS. Olfactory dysfunction affects approximately 22% of U.S. adults, with heightened prevalence among immunocompromised populations. While substantial evidence links impaired adaptive immunity to disturbances in olfactory function, yet the underlying neuroimmune mechanisms for this phenomenon are not well understood. Utilizing adult zebrafish (Danio rerio) as a model organism, we discovered that not only macrophages, but also mature T cells reside along the ON at the steady state. Out of the total ON resident T cell population, 20% are foxp3a+ regulatory T cells (Tregs). In response to in vivo peripheral olfactory inflammation or neurotropic viral infection, mature T cells are recruited to the ON by day 1 following an earlier macrophage recruitment wave. Notably, immunodeficient zebrafish lacking mature T cells (zap70-/-) exhibited increased neuronal apoptosis within the olfactory bulb (OB) in response to olfactory inflammation compared to their wild-type immunocompetent counterparts. Our data reveals for the first time the essential role that mature T cells play in maintaining ON homeostasis and responses to inflammation and uncover new potential therapeutic targets for smell disorders.

AUTOTROPHIC AND HETEROTROPHIC CONTRIBUTIONS TO SOIL CO2 EFFLUX IN A CHIHUAHUAN DESERT GRASSLAND

Savannah Sanchez, Department of Biology, UNM

Marcy Litvak, Department of Biology, UNM

Megan Rae Devan, Department of Biology, UNM

Jennifer Rudgers, Department of Biology, UNM

Drylands are crucial drivers of interannual variability of the terrestrial carbon sink. Their influence will likely increase as hotter and drier conditions in the coming decades predict expansion of drylands. The consequences of these shifts are difficult to predict as ecosystem models are currently biased towards mesic systems, which have more water and nutrients, faster decomposition, higher respiration, and different microbial communities compared to drylands. The goal of my research is to improve our understanding of carbon cycling models in drylands by focusing on one component, soil CO2 efflux through respiration. Soil CO2 efflux is a large source of terrestrial CO2 emissions, and in drylands is driven primarily by plant root respiration, microbial decomposition of organic matter, and to a lesser extent by UV decomposition. In particular, I focus on understanding the drivers of soil respiration in one ecosystem at the Sevilleta National Wildlife Refuge, Desert Plains Grassland. To achieve this, I measured soil hourly fluxes from May to September in 2023 and in 2024 in an experimental manipulation with three distinct treatments: bare ground and trenched, bare ground and trenched with litter addition, and over Bouteloua eriopoda with litter addition. I paired these data with meteorological data from the eddy covariance tower at the site to understand the specific climatic controls driving these fluxes.

Piñon and juniper water use in response to both soil moisture and atmospheric dryness

Josh Lopez-Binder, Marcy Litvak, Will Pockman, Rae DeVan, Department of Biology, UNM

I am investigating how soil moisture and atmospheric dryness interact to influence tree water use in Pinus edulis (piñon) and Juniperus monosperma (one-seed juniper). The “interaction effect” is defined as the scenario where the relationship between two variables (atmospheric dryness and tree water use) is influenced by a third variable (soil moisture). Species differences in the interaction effect indicate if long-term drought or sudden heat-waves are more stressful. I hypothesize that 1) the interactive effect will be significant for both species, because both variables contribute to elevated within-plant water tension, which can result in mortality and 2) the interaction effect will be significantly different between the two species because juniper can withstand higher within-plant water tension than piñon. Tree water use data, recorded by sap-flux sensors, was collected for piñon (n=13) and juniper (n=6) trees for up to 16 years during the growing season, logged every 30 minutes, along with soil moisture and atmospheric dryness. A linear mixed effects model was fit to the data with “individual-tree” corresponding to random effects. The interactive effect was found to be significant for all trees. Currently species differences in the interactive effect are being investigated. This information will help us understand patterns in past mortality events across the Southwestern US and contribute to more confident predictions of future mortality events in the context of climate change.

Differing Phenological Plasticity of Black Grama (Bouteloua eriopoda) Across Population Range

Rachael Auer, Dr. Marcy Litvak, Dr. Megan Devan, Department of Biology, UNM

With climate change driving hotter temperatures and variable precipitation, plant ranges are expected to shift toward their preferred climatic niches. Phenological plasticity—the ability to adjust life cycle timing to environmental conditions—can offer a competitive advantage, enabling species to adapt to new conditions at the trailing or leading edge of their range, or a competitive disadvantage, reducing or slowing advancement. The role of phenological plasticity in range shifts remains understudied, especially in dryland ecosystems.

At the Sevilleta National Wildlife Refuge, black grama (Bouteloua eriopoda) is expected to replace blue grama (Bouteloua gracilis), while Creosote (Larrea tridentata) replace black grama. This study examines black grama's phenological plasticity at its trailing edge (Creosote Shrub site), central range (Desert Grassland site), and leading edge populations (black grama/blue grama ecotone site). Using phenocams to track seasonal timing of growth, we found that black grama phenology is highly plastic, with variation in number of growing seasons per year, and significantly different variation in phenological timing between sites. We further found that black grama has a longer growing season length due to a later end of season at its trailing edge compared to its central range, which may be enabling black grama to maintain its trailing edge population. Our findings suggest that blue grama growing season length plasticity may help sustain trailing-edge populations, offering insight into how phenological flexibility shapes range shifts in dryland ecosystems.

Sky Islands Provide Natural Tests of the Relative Importance of Green vs Brown Energy in Terrestrial Foodwebs

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Sky islands are isolated mountain ranges characterized by high elevation, complex topography, and rich biodiversity surrounded by lowland deserts. In New Mexico, sky islands vary in altitude, size, and primary productivity, influencing resource availability for endemic consumers. These areas provide a naturally replicated study system to test the longstanding but poorly resolved hypothesis for the mechanisms driving food chain length and could provide a compelling example of how microbes (brown energy) influence aboveground food web structure. Our study focuses on four small mammal species with diverse dietary strategies—insectivorous montane shrew (Sorex monticola), omnivorous deer mouse (Peromyscus maniculatus), folivorous long-tailed vole (Microtus longicaudus), and generalist mexican woodrat (Neotoma mexicana) —found across five New Mexico sky islands that vary in ecosystem size (i.e., primary productivity). We are using bulk tissue (bone collagen) carbon (d13C) and nitrogen (d15N) isotope analysis to quantify dietary variation at the population level. We are also measuring the d13C composition of individual amino acids in bone collagen to quantify the assimilation of green (plant) versus brown (bacteria/fungi) energy. Patterns in d13C values of essential amino acids are distinct among plants, bacteria, and fungi, reflected in small mammal tissues with minimal isotopic alteration because eukaryotic consumers cannot synthesize these compounds. Additionally, we will use amino acid d15N analysis to estimate trophic level, allowing us to examine the relationship between brown energy integration, trophic position, and overall food chain length.

The Influence of Culture, Religion, and Ecology on Death in Tanna Vanuatu

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Death and dying evoke significantly different beliefs and practices across cultures. This study investigates interactions between social and physical ecologies in the context of mortuary practices in Tanna, Vanuatu – a context where climate change and an influx of Christian faiths may contribute to changing norms and institutions surrounding death. We conducted interviews with ni-Vanuatu people to understand the intersections between death, spirituality, and nature in ni-Vanuatu belief and practice. We describe evidence of religious syncretism in death practices and speculate about how climate change will impact landscapes of death for ni-Vanuatu people.

Hummingbirds Regulate Fat Reserves Using Nocturnal Torpor

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Hummingbirds are small and have high metabolic rates; therefore, they must budget their energy within strict limits. Because they fast at night and during migratory flights, energy reserves (fat), are especially vital during these periods. During migrations, hummingbirds rely on stopover sites along their routes, where they rest for several days and replenish fat. They can also use nocturnal torpor, which is a state of reduced metabolism, lasting several hours. Torpor is effective in conserving fat and compensating for shortfalls, but it comes with risks, so its frequency and duration vary. We measured fat content, metabolic rates, and torpor use in two species of migrating hummingbirds, Calliope (Selasphorus calliope) and Rufous (Selasphors rufus), at a stopover site in Southwestern New Mexico. From this data, we constructed a mass-balance model to predict fat thresholds for torpor entry, torpor durations, and minimum morning fat reserves. Hummingbirds entered torpor if their fat contents were below a distinct threshold. Torpor duration increased as initial fat content decreased, and birds that entered torpor had relatively constant morning fat reserves. We hypothesize that hummingbirds will vary their torpor duration and frequency to meet a minimum morning fat goal. Our model serves as an indicator of energetic health in migrating hummingbirds, as climate and land-use change alter timing and abundance of food resources along their migratory paths. The model can also be applied to other animals by adjusting its parameters.

Metabolic Adaptations of Microbial Communities in Jemez Hot Springs: Linking Lipid Biosynthesis to Biogeochemical Cycling

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Microbial communities in extreme environments, such as the hydrothermal springs found in Jemez, New Mexico, employ unique metabolic strategies to survive extreme conditions of pH, salinity, and temperature. These metabolic adaptations, shaped by evolutionary pressures, optimize resource utilization, particularly in lipid biosynthesis and modification. To investigate these pathways, I will integrate molecular techniques, including 16S rRNA gene sequencing and metagenomic shotgun sequencing. These approaches will reveal microbial community composition, functional genes, and gene expression patterns, providing insights into metabolic responses to environmental pressures. Metagenomic data will enable genome reconstruction and prediction of key metabolic functions, including lipid metabolism, carbon fixation, and stress responses. A critical component of this research is stable isotope analysis, specifically compound-specific isotope analysis (CSIA) of fatty acids using GC-IRMS. Measuring carbon and hydrogen isotope ratios in microbial lipids will trace organic matter sources, assimilation, and transformation. Additionally, carbon and nitrogen isotope analysis of amino acids will assess how microbes balance nutrient sources in lipid biosynthesis. By integrating genomic data with stable isotope analysis, this study will clarify how microbes allocate resources, utilize substrates, and modify lipid biosynthesis across environmental gradients. This framework advances our understanding of microbial ecology in geothermal systems while informing broader questions related to climate change resilience, astrobiology, and ecosystem function.

Genomic Evidence for Speciation and Hybridization in Sympatric Orientallactaga Species: The Role of Climate in Central Asia’s Gobi Desert

Lexi B. Baca, Joseph A. Cook, Jason L. Malaney, Department of Biology, UNM

The three putative species of genus Orientallactaga (five-toed jerboas), O. balikunica (Balikun jerboa), O. bullata (Gobi jerboa), and O. sibirica (Siberian jerboa) are syntopic rodents distributed across Central Asia's Gobi Desert. This shared distribution provides an opportunity to investigate the region’s historical biogeography and speciation mechanisms, particularly the interplay between allopatric and sympatric divergence, including potential speciation with gene flow. To unravel the evolutionary history of these species, we conducted genomic analysis using mitochondrial and nuclear genomes (ddRADseq). We reconstructed phylogenies and employed coalescent modeling to assess divergence times, incomplete lineage sorting, introgression, and ancestral variation retention. Additionally, we applied coalescent-based demographic expansion modeling to explore spatial and temporal population dynamics. Admixture analysis quantified allele sharing in sympatric populations, allowing tests for post-allopatric secondary contact. We also integrated niche modeling to assess historical and contemporary distributions and the role of climate in shaping the evolutionary history of Orientallactaga. Our findings suggest that climatic oscillations facilitated divergence through isolation, while secondary contact during historical and contemporary warming periods led to genomic introgression across species. The observed incomplete lineage sorting underscores the complex evolutionary processes in the Gobi Desert. We highlight how historical isolation and gene flow have shaped diversification in this genus and discuss the potential influence of contemporary climate warming on its evolutionary trajectory.

North American Porcupine Home Ranges and Use of Recent Fire Landscapes in New Mexico Through GPS Collaring

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The North American Porcupine's (*Erethizon dorsatum*) range extends from Canada to the northern tip of Mexico, meaning New Mexico is approaching the southernmost end of its range. As a species, they are greatly understudied in the southwest region of the United States. Aiming to fill some of these natural history gaps, this project looks at porcupine space use trends, focusing in a ~40-hectare section of an urban riparian cottonwood forest in central New Mexico (colloquially known as the *bosque*). This has been carried out through radio telemetry and GPS collaring. A fire burned intensely across approximately 25% of the studied area in May of 2022, raising questions about how porcupines use recent fire landscapes. This project aims to uncover home ranges of these animals, how they vary between sexes and across seasons, and space use trends within this recent wildfire site. Further, this study incorporates collaboration with local elementary schools, providing youth with hands-on field experiences to teach the importance of conservation and field science.

Stable Isotope Tracing Reveals Gut Microbial Synthesis of Essential Amino Acids from Non-Essential Precursors

Conner Mertz, Leigh James, Alana Robinson, Christy Mancuso, Cristina Takacs-Vesbach, Seth Newsome, Department of Biology, UNM

Wild mammals frequently consume protein-deficient diets and likely depend on their gut microbiome to supplement essential nutrients, such as essential amino acids (AAESS). Research has focused on the gut microbiome's role in carbohydrate metabolism but its ability to help maintain host protein balance is underexplored. Recent evidence suggests gut microbes can provide AAESS to their host through de-novo synthesis using dietary carbohydrate precursors. However, previous estimates of the microbial contribution of AAESS to host protein are likely conservative because microbes can synthesize AAESS from a diverse pool of metabolite precursors, including non-essential amino acids (non-AAESS). The extent mammals assimilate microbially synthesized AAESS from dietary non-AAESS precursors is unknown. We performed a feeding experiment on deer mice (Peromyscus maniculatus) fed low (2.5%) to medium (5%) protein diets enriched with a 2% carbon-labeled non-AAESS (13-C glutamic acid or 13-C alanine). Genetic and compound specific stable isotope analyses were performed to (1) quantify the microbial transformation of dietary non-AAESS to AAESS by evaluating isotopic enrichment in mice tissues and (2) identify microbial communities responsible for this exchange. We found significant isotopic enrichment of certain AAESS in mice fed 13-C glutamic acid, but minimal enrichment in mice fed 13-C alanine, suggesting only certain non-AAESS are readily used as a substrate by the gut microbiome for AAESS synthesis. The gut microbiome responds to its nutritional environment by producing and exchanging metabolites that ultimately impact the host. Our study reveals how gut microbes provide essential nutrients to their host to compensate for dietary resource limitations.

FimH Protein from E.coli as a Potential Vaccine Target to Prevent Urinary Tract Infections

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Urinary tract infections (UTIs) are among the most common bacterial infections, affecting millions of individuals annually worldwide. The FimH protein of E.coli plays a crucial role in the bacterial attachment to uroepithelial cells in the majority of urinary tract infections. We aimed to develop a durable, immunogenic nanoparticle (NP) based vaccine that targets this bacterial binding protein to prevent UTIs. A unique conjugate vaccine was constructed and tested in a mice model. Utilizing SpyTag/SpyCatcher technology, the lectin domain of FimH was conjugated to a Mi3 Nanoparticle via spontaneous amidation to display an array of FimH peptides on its surface and be used for vaccination. We hypothesized that the vaccine would result in efficient antibodies that could successfully recognize and bind to the native FimH protein in-vitro, as it consisted of the full domain of the bacterial protein. Immunization is currently underway, and antibodies will be collected during the peak immune response and tested for binding ability to FimH. The results of this study would allow us to further pursue this project and investigate whether the antibody binding can inhibit the attachment of FimH to host cells, and eventually challenge mice with an E.coli infection to determine whether or not the induced antibodies have significant effect on the prevention of a urinary tract infection.

Comparative Analysis of Mosquito Species Diversity and Abundance in Urban, Suburban, and Rural Settings of Bernalillo County, New Mexico

Maia M. Hizny, Kenwyn R. Cradock, Jacob A. Greenberg, Department of Biology, UNM

This project aims to investigate mosquito species diversity and distribution across urban, suburban, and rural settings in Bernalillo County, New Mexico. Using innovative 3-D printed mosquito traps, we are collecting specimens from various habitats to compare species abundance and presence across different environments. Our study focuses on identifying key mosquito species, including Aedes vexans, Aedes albopictus, Aedes aegypti, Culex quinquefasciatus, and Culex tarsalis, which are anticipated to be the most abundant in these settings. Preliminary data has highlighted the emergence of Aedes albopictus in the region, a species not previously dominant, raising concerns about potential shifts in mosquito populations and disease vectors. In the next phase of the project, we will analyze blooded mosquitoes to identify their bloodmeal hosts, which will provide insight into host preference and potential disease transmission patterns. This research will contribute to a better understanding of the ecological dynamics of mosquito populations in varying environments and may inform public health strategies for mosquito-borne disease prevention in Bernalillo County and similar regions.

Fungal Cooperation or Death?

Raul Salas, Abigail Granath, Department of Biology, UNM

Fungi and plants may cooperate to speed up the cleaning process of heavy metals. However, there is not much information regarding symbiosis between plants and Ascomycota fungi in heavy metal bioremediation. I expect the sunflowers may die from the fungi growing around them but I am not against successful symbiosis. In this experiment, I will use sunflowers, which can absorb heavy metals, to test if fungi and sunflowers can work in unison to remove these materials. First, I grew wild sunflowers with three different species of fungi to see if symbiosis is possible or if they will be killed by the fungi. I used a set of nine sunflower seeds growing around three different fungi samples (three seeds per sample) in clamshell containers and waited for germination to occur. Then, I observed if the sunflower seed survived and successfully grew with the fungi or if it was killed. If fungi and sunflowers can work together, then they can be used as candidates to aid in heavy metal bioremediation. The first species outright killed the sunflower seedlings, absorbing the seeds completely. The second species had a higher rate of success, having 5 out of 18 seeds sprouting healthily. The third and final species had 3 seeds sprouted, however, they appeared thin and frail. In the end, a mix occurred, where some sunflower seeds showed signs of symbiosis, while others were consumed by the fungi sample. Ongoing work will test other species and confirm the identities of the fungi tested so far.

Impact of Desiccation on Fungi and their Ability to Remediate Arsenic

Ethan Lombardi, Annabella Beck, Abigail Granath, Department of Biology, UNM

After heavy metals have been mined, the resulting wastes can pollute surrounding environments. The pollutants can be carried by the wind or be washed downstream, with potentially harmful impacts to humans and native wildlife. Fungi have been found to potentially help remove these heavy metals from environments. However, to find fungi useful for remediation they have to survive harsh environments, such as drought. Melanated fungi in particular are known to be more resilient to drought compared to non-melanated fungi. In this experiment, we subjected both melanated and non-melanated fungi to drought conditions to measure the impact on their growth and their remediation potential. We hypothesize that melanated fungi will be most likely to survive desiccation and be more effective at removing metals. After desiccating the fungi, we prepared the specimens and ground them into a powder. We dispersed this powder over soil treated with arsenic. Then, we poured distilled water over the soil to simulate rain. The desiccated melanated fungi species were found to absorb the highest levels of arsenic compared to non-melanated species.

Poster Presentation 16

Kian Hill

As our climate continues to change at a concerning rate with increasing environmental stressors, the living creatures that inhabit this world will start an even more intense battle for their dwindling resources. To help mitigate this change, it is advantageous to know how organisms will behave in a limited resource environment. Our focus is fungi because they have historically been under-looked and might offer insight into how soil communities will be affected by climate change. We investigated how fungi will compete differently in a limited resource environment in a controlled laboratory, which will help us understand how fungi work in the natural environment. We wanted to understand the strategies fungi will implement to gain more resources while limiting the availability of resources to competitors. These strategies that fungi develop will help them compete in their environment. In this march madness style bracket, we pit each fungal species against each other and predict the one with the best competitive traits will outgrow their competitors, becoming the winner. For this bracket, 4 different fungal species were pitted against each other, two to a single Petri plate, while keeping all other variables consistent and monitoring growth and pigmentation. Initial results suggest that species A and B have the highest success rates for dominating a Petri plate, however, when pitted against each other, culture B was the winner. This research helps us understand how fungal communities will develop when environmental factors limit the resources and habitat in landscapes of the future.

How can fungi be used to our advantage in order to alleviate heavy metals from the environment?

Sunnie Repka, Department of Biology, UNM

Fungi are important to our environment because they can absorb heavy metals that pollute waters and soils and reduce human health. However, due to how many species of fungi there are, and how little we know about fungal ecology, there is little research on how well fungi absorb these metals. The objective of this experiment is to test (1) how different species of fungi interact with arsenic, and (2) how the arsenic affects their growth. I will test four different species of fungi and separate them into groups; one with arsenic introduced, and one without. I replicate each combination three times for a total of twenty-four cultures. I will randomize my groups to make my results as robust as possible. I hypothesize that some of the fungi will completely absorb the arsenic, while others will have their growth inhibited. This research is important to see how different species of soil fungi will intake harmful heavy metals, like arsenic, and how we can use that to reduce pollution in the environment.

Isolation and Quantification of Micro(nano)plastics in Human Cerebrospinal Fluid: Insights into Disorders Related to Brain Waste Clearance

Sakshi Patil, Margaret Park, **Josiah Kingston**, Marcus Garcia, Risa Smith, Rui Lui, Tamara Howard, Jessica Gross, Shahani Noor, Bill Shuttleworth, Chad Cole, Matthew Campen, Andrew Carlson, Eliane El Hayek

Our team has made a significant breakthrough by developing a novel approach to isolating and quantifying micro(nano)plastics (MNPs) from human tissues using analytical chemistry and advanced spectrometry. Our initial findings show that these particles accumulate more in the human brain than in the liver and kidney, raising concerns about brain waste management and potential toxic effects. Here, we assess the quantity and physicochemical properties of MNPs in human cerebrospinal Fluid (CSF). A KOH (10%) digestion was completed with a benzene wash. The initial quantitative measurement using pyrolysis-gas chromatography-mass spectrometry (Py-GC-MS) was conducted on CSF samples (n=14), which detected polymer concentrations ranging between 13.3 and 82.8 µg/ml, with a mean of 22 µg/ml for the summed polymer concentrations. These elevated concentrations observed in CSF are higher than those reported in other biological fluids. Transmission electron microscopy images detected the occurrence of heterogeneous aggregates containing particulates in sub-micron and nanometric sizes with crystalline structures. Further research will determine whether plastics contribute to neurodegeneration by investigating their association with metal clearance dysfunction in CSF and glymphatic system biomarkers. This study establishes advanced methods to isolate and quantify purified MNPs from human CSF to implement accurate correlation studies with brain waste clearance and CNS pathologies.

History Provides Clues to Future Persistence of Montane Shrews in the Southwest

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Climate cycling during the Quaternary (last ~2.5 million years) influenced evolutionary processes in Southwestern biomes and provides insights into how dynamic climates may shape future genetic structure across species. The transition to a warmer climate at the terminus of the Pleistocene (~12k years ago) forced forested-associated species to retreat to higher elevations in the Southwest and yields an opportunity to evaluate how gene flow disruption contributed to diversification. We focus on montane shrews (Sorex moniticola and Sorex neomexicanus); sky island mammals of the Southwestern and Mexican Montane Regions (SMMR). Geographic isolation hypothetically influenced genetic diversity and population structure. We use single nucleotide polymorphisms double digest, restriction-site associated DNA sequencing (ddRAD seq) of mitogenomes derived from museum specimens to evaluate alternative hypotheses of population history. We create Species Distribution Models to reconstruct the historical distributions of these montane shrews during past climate shifts (e.g., glacial cycles) and then model demographic history to test for shared patterns of spatial and temporal divergence among shrews. We also predict how future climate may impact montane species on sky islands in the SMMR. In sum, this research aims to integrate insights into how historical glaciation shaped species distributions, structured sky island communities, and influenced evolutionary divergence. These historical insights provide a foundation for predicting future biodiversity trends in these ecosystems, including identifying at-risk populations and potential source populations for translocation to aid in management of vulnerable species.

Polyamines and Inflammation in Hypoxic Pulmonary Hypertension

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Chronic Hypoxia (CH) is a common cause of pulmonary hypertension (PH). Although the pathogenesis of CH-induced PH has yet to be fully elucidated, current evidence suggests that immune dysregulation plays a major role in disease progression. Th17 cells, a subset of CD4+ T cells, are pro-inflammatory and are normally suppressed by regulatory T cells (Tregs) to maintain immune homeostasis. Using a Treg lineage fluorescence reporter mouse model, we have demonstrated that CH decreases Tregs while promoting the expression of Th17-associated markers in former Tregs (exTreg-Th17) in the spleen. This immune imbalance fosters autoreactive inflammation, raising questions about T-cell differentiation mechanisms and whether immune cells accumulate in the lungs, shaping PH progression.

Polyamine metabolism has been implicated in both PH development and Th17 cell pathogenicity. However, the impact of CH on polyamine metabolism remains poorly understood and may explain immune dysregulation. Our lab showed that CH increases the polyamine, putrescine, in lungs. We hypothesize that CH increases exTreg-Th17 cells and decreases Tregs in the lungs and elevates putrescine in the spleen. To test this, we quantified these cells in the lungs using flow cytometry and assessed polyamines concentrations in spleens from CH-exposed mice using gas chromatography/mass spectroscopy. These analyses provide insight into the mechanisms driving T cell differentiation and their impact on PH pathogenesis.

Hypertension-Induced Kidney Damage: Role of ASIC1a in Structural and Functional Changes

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In the U.S., nearly half of adults have systemic hypertension (≥130/80 mmHg), a major risk factor for heart disease and stroke. The kidneys regulate blood pressure, and hypertension often worsens kidney disease. We found that deleting acid-sensing ion channel 1a (ASIC1a) induces age-related hypertension in male but not female mice. We hypothesize that hypertension is associated with structural and functional damage in the kidneys. To assess structural changes, we analyzed glomerular cross-sectional area (CSA), number, and renal fibrosis in young (~6 mo.) and aged (18 mo.) wild-type (Asic1a$^{+/+}$) and knockout (Asic1a$^{-/-}$) mice. Aged male Asic1a$^{-/-}$ mice had increased glomerular CSA ($p = 0.0014$), fibrosis ($p < 0.0001$), and reduced glomerular number ($p = 0.0009$). Aged female Asic1a$^{-/-}$ mice had elevated blood pressure and fewer glomeruli ($p = 0.0080$), but no genotype-related differences in CSA or fibrosis. To assess function, we measured urine protein, osmolality, and blood urea nitrogen (BUN). Male Asic1a$^{-/-}$ mice had lower urine osmolality in both young ($p < 0.0001$) and aged ($p = 0.0024$) groups. While urine protein was elevated with age ($p = 0.0001$), neither urine protein nor BUN differed by genotype. Despite glomerular structural changes being linked to hypertension, they do not cause overt kidney dysfunction. However, lower urine osmolality in male Asic1a$^{-/-}$mice suggests early kidney dysfunction independent of hypertension, warranting further study.

Genetic and Morphological Divergence in the Five-Toed Jerboas (Orientallactaga): Insights into Intraspecific Variation and Niche Overlap in the Gobi Desert

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The three putative species of Orientallactaga (five-toed jerboas), O. balikunica (Balikun jerboa), O. bullata (Gobi jerboa), and O. sibirica (Siberian jerboa) are syntopic rodents distributed across Central Asia's Gobi Desert. While prior genetic analyses identified these sister species as distinct, significant infraspecific genetic structure suggests a complex history of diversification and coalescence. To refine our understanding of their evolutionary history and inform the historical biogeography of the Gobi Desert, we sequenced the complete mitochondrial cytochrome b gene (1140 bp) for 75 specimens across Mongolia, an underrepresented region in prior studies. These sequences, combined with 321 GenBank records, were used to construct Maximum Likelihood and Bayesian phylogenetic trees, revealing three new clades and illuminating processes likely responsible for their complex genetic structure, Additionally, 2D geometric morphometric analyses of 60 specimens uncovered significant morphological variation within O. sibirica, which corresponds with geographic genetic variation and may reflect adaptative responses to the broad environmental range of this species. In contrast, the syntopic O. balikunica and O. bullata exhibited low interspecific morphological variation. To investigate niche diversification further, we compiled occurrence data from GBIF (624 individuals, we georeferenced 349 samples) to generate Species Distribution Models and conduct niche identity tests. Combined, these analyses provide new insights into the ecological and evolutionary dynamics of Orientallactaga in the Gobi Desert.

Histomorphological changes in the lymphatic system of African lungfish during water-land-water transitions.

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The African lungfish, Protopterus annectens estivates every dry season, creating a protective mucus cocoon. When water returns, the cocoon dissolves, and the lungfish re-enters a free-swimming phase through a process known as arousal. Previous work has shown that granulocytes migrate from the gut, kidney and gonads to the skin of African lungfish during estivation. Furthermore, lymphatic micropumps may play a role in estivation, although the specific changes in the structure and function of the African lungfish lymphatic system remain unexplored. The goal of this study is to investigate the histomorphological remodeling of the lymphatic micropumps happening in African lungfish gut across different physiological states: free-swimming, estivated, and 24 hours post-arousal. We found that the number of gut lymphatic micropumps per area unit significantly increased in estivated fish compared to free-swimming controls, with numbers recovering 24 hours after arousal. Additionally, the lymphatic micropumps displayed morphological changes along the water-land-water cycles. Specifically, in estivated fish, we observed a trend towards a larger diameter of the micropumps, along with a change in shape, more elongated and irregular. On the other hand, 24 hours after arousal, the lymphatic micropumps begin to recover the morphology we observed in free-swimming fish, showing a slightly smaller diameter and a rounder shape. Our results indicate that water-land-water transitions in African lungfish are associated with significant remodeling of the intestinal lymphatic system, perhaps reflecting the lungfish's metabolic and immunological needs in each environmental condition. These findings provide insights into the functional plasticity of lymphatic systems in vertebrate animals and their role in the African lungfish ability to endure fluctuating aquatic environments.

Exploring the mechanism behind uranium induced transcriptional changes on the gut

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Background: There are over 500 Abandoned Uranium Mines scattered across the Southwest, which co-occur with greater incidences of metabolic and digestive diseases in Indigenous

and Hispanic populations. There is a need to understand the effects of particulate heavy metals on the digestive system. Previously, our group demonstrated organoids to be a relevant model for investigating the physiological impact of environmental toxicants on the intestinal tract.

Objective & Hypothesis: Our objective is to understand the effects of non fissile uranium bearing particulate dust (UBD) on the colon, specifically looking at the function of various cell types. We hypothesize that UBD exposure induces proliferative qualities in differentiated cells rather than increasing proliferative cells.

Results: Upon exposure, enteroendocrine cells (EEC) expanded four fold, while proliferative cell types decreased. Additionally, the number of cells undergoing replication was decreased. Downstream analysis found that groups of microRNAs were more spread apart in the UBD treated condition, while the control showed more connections between groups. Additionally, several genes involved in the microRNA biogenesis pathway showed an upward trend in the UBD treated condition.

Conclusions: These results suggest that acute uranium dust exposure induces changes in the ratio of proliferative and differentiated cell types, and may affect their primary functions through microRNAs.

Landscape’s impact on the genomic structure of the Great Plains Toad in New Mexico

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The Great Plains Toad (Anaxyrus cognatus) is distributed across diverse landscapes, including deserts, shrubland, chaparral, and grassland habitats. Their range extends from southern Canada to central Mexico; New Mexico represents a unique part of this the range due to the high variability of habitats. We aim to identify whether different landscapes play a role in facilitating or inhibiting genetic connectivity of the Great Plains Toad in New Mexico. We predict that urban development such as roads inhibit genetic connectivity, while agricultural land would increase genetic connectivity by facilitating movement of the species. Museum samples (n=29) were collected from 1999-2023 and obtained via loan. We used double digest restriction-site associated DNA sequencing (ddRAD-seq) to obtain 20029 loci and assessed population structure using PCA and DAPC analysis with the adegenet package in R. Bioclimatic variables (aspects of temperature and precipitation) were obtained from the Worldclim 2 database and used to model species distribution with the biomod2 package in R. Preliminary results suggest the New Mexico population contains two sub-populations, one eastern subgroup and one western subgroup, separated by the Rio Grande. Future work includes using an Estimated Effective Migration Surface (EEMS) to visualize and model population connectivity based on the genetic data. We will also obtain rasters for landscape features such as roads, land cover, elevation, and watersheds and compare models to elucidate drivers of genetic differentiation in this species. These results will be useful for assessing areas of high genetic connectivity and for developing conservation and management strategies for this species.

Survey of Fungal Species in Sandhill Crane (Antigone canadensis subsp.) Winter Grounds in New Mexico

I. Gurney, S. Shrum Davis, D. Natvig, Department of Biology, UNM

Migratory birds present a unique set of exposure conditions as they transport microorganisms across their migration routes. Sandhill Cranes (Antigone canadensis subsp.) spend their summers in the arctic and winters in southern Texas and New Mexico. Sandhill cranes are hunted in rural New Mexico for their breast meat, creating a direct contact interface between cranes and humans. A yet unpublished 2023 survey of Sandhill Crane mycobiomes at the Bernardo Waterfowl Area near Socorro, NM, yielded several different Candida species, including C. albicans and C. glabrata. These fungal species are among the group that causes over 95% of the cases of candidiasis, a serious fungal infection. Relatively little is known about the ecology of Candida species and their natural habitats outside of clinical settings, but current evidence suggests complexity with respect to species distributions and ecological roles. To investigate the possible natural reservoirs of these fungi, environmental samples were collected from the same Sandhill Crane winter grounds as the previous survey. Samples included water and vegetation from the fallow cornfields where the cranes graze. Fungal isolates were identified by sequencing the ribosomal internal transcribed spacer (ITS) region. Sequencing results revealed the presence of C. lusitaniae in both water and on vegetation, but it is yet unclear whether this species naturally occurs there or if it was introduced via crane droppings.

Exploring the Therapeutic Potential of Dexpramipexole in Neuropathic Pain and Inflammatory Cytokine Modulation

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Introduction: Dexpramipexole (DPX), an investigational drug approved for clinical trials to treat inflammatory conditions, has demonstrated effectiveness in pain alleviation, possibly through anti-inflammatory properties. However, it remains unknown whether DPX, acting within the central nervous system (CNS), can reduce neuro-immune proinflammatory actions induced by peripheral sciatic nerve chronic-constriction-injury (CCI) in a mouse model. CCI leads to pathological sensitivity to light touch, referred to allodynia. The current study evaluated the spinal action of DPX on CCI-induced allodynia in mice to determine whether DPX acts by suppressing spinal proinflammatory actions. The spleen produces pro- and anti-inflammatory cytokines; thus, splenic cytokine levels were analyzed. Hypothesis: spinal DPX controls CCI-induced allodynia via spinal anti-inflammatory actions leaving peripheral cytokine expression levels intact.

Methods: The von Frey fiber test was applied to assess light touch sensitivity of the hindpaws before and after CCI or SHAM surgery in female C57BL/6 mice. On day 14 post-surgery, mice received intrathecal vehicle (saline; 10ul) or DPX (500ng/10ul) followed by hindpaw reassessment 1hr later. CNS (spinal cord, brain) and spleen were collected. Splenic mRNA gene expression of IL-10 (anti-inflammatory), IL-1B and TNF-a (pro-inflammatory) were assessed.

Results: Vehicle-treated CCI mice remained fully allodynic at 1-hr after injection. Mice with CCI given DPX exhibited full allodynia reversal 1hr later. Splenic-cytokine mRNA expression did not differ between treatment groups. Analyses of cytokine protein levels in CNS tissues are underway. Results suggest that intrathecal DPX reverses neuropathic pain by acting in the spinal cord, while leaving peripheral splenic cytokine expression intact.

SIRT1's Impact on Mitochondrial Calcium Signaling in Hair Cells of Danio rerio

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Hearing loss is a significant health problem in America where 1 in 8 people ages 12 or older has hearing loss in both ears. Hearing loss often results from the loss of hair cells, sensory receptors located in the inner ear responsible for converting mechanical vibrations into electrical impulses the brain processes for hearing and balance. Mitochondrial calcium signals are implicated in this process. SIRT1 is a protein crucial for cellular processes such as regulating metabolism, responding to stress, supporting DNA repair, and modulating inflammation. We hypothesize that modulating SIRT1 alters mitochondrial calcium signaling in hair cells. To test this hypothesis, we use the zebrafish model with multisite gateway cloning and tol2 transgenesis to produce zebrafish expressing ChRmine, a red-light activated ion channel. We will use the calcium indicator mitoGCaMP3 to measure calcium signals after ChRmine activation. We will first create a transgenic line expressing ChRmine. Next, we will treat the fish with SIRT1 inhibitors. We will measure changes in mitochondrial calcium levels in hair cells using widefield calcium imaging. Currently, this project is in its early stages. This project will provide a deeper understanding of SIRT1 and its role in hair cell function with mitochondrial calcium signaling. In the future, this work may pave the way for interventions that slow down age-related hearing and potentially develop drugs that modulate SIRT1 activity to protect hair cells from damage.

Heat and desiccation resistance of biological soil crust fungi in semi-arid grasslands of the southwestern USA

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Across the southwestern USA, climate has become both warmer and drier in association with anthropogenic climate change. Such changes may have negative impacts on biological soil crusts (biocrusts), which are consortia of surface soil microbes, algae, lichens, and bryophytes that support soil health in arid and semi-arid ecosystems. Fungi are understudied members of biological soil crust communities that may have large contributions to their tolerance of heat and desiccation because of their drought resistance traits, particularly relative to bacteria. We isolated fungal species found in the biocrusts of semi-arid grasslands of the Sevilleta National Wildlife Refuge in central New Mexico, USA. Fungi were isolated during spring and fall biocrust collection campaigns in 2024 from a long-term (11 year) biocrust disturbance experiment consisting of 10 replicates each of soil disturbance and control plots (6 m x 6 m) Petri plates of fungal growth media in the laboratory, we subjected a subset of isolates to both hotter (25, 30, 35, 40) and drier (thin agar to speed desiccation) conditions. We tracked individual fungal growth for a one week period. We discovered strong variation among fungal species in the sensitivity of growth to heat and desiccation, as well as variable traits including exopolysaccharide and melanin production.

Learning Morphometrics

John Korbin, Department of Biology, UNM

My work aims to streamline the study of animal form by enabling and applying automated, efficient, and precise comparisons across large datasets, advancing the field of morphometrics. and providing new insights into evolutionary biology. Specifically, I am developing a novel approach to simplify morphometric analysis by combining machine learning (ML) with high-resolution 3D X-ray CT imaging. I am currently working on a machine learning pipeline that can automatically determine an object's embedding in a morphometric latent space, represented by a user-defined 1D vector of finite length. Allowing the ML model to determine the best embedding method trades "explainability" for "data density" - meaning that the latent space will not provide a direct, intuitive interpretation for each component of the 1D vector. However, by requiring this vector to reproduce the original 3D geometry after being decoded by a second ML model, this embedding will preserve the object's original geometry - including internal features. Thus, the latent space vector will still capture the same morphological information which is traditionally collected manually with calipers or through photographic methods along with other currently ignored features. I will test this new approach against traditional 2D approaches on three classically “difficult” mammalian systems (Chiroptera: Genus Myotis; Rodentia; Genera Ctenomys and Dicrostonyx). In addition, I have created a SketchFab site (sketchfab.com/Biodiversity) to enable educators, the public, and other scientists to access images I have generated from Museum of Southwestern Biology specimens.

Neurodevelopment; linking neural circuit development and associated behavior.

Tulaib Azam, Dr. Syed Mubarak Hussain, Department of Biology, UNM

The brain is a complex organ at the center of the nervous system in all vertebrates and many invertebrates, that acts as a seat of sensory motor functions and behaviors. Olfactory navigation is one such complex conserved behavior, seen across arthropods. The central complex (CX) in Drosophila is a conserved brain structure involved in complex behaviors and functions. All these Complex behaviors result from neural circuits developed of diverse neuron classes, with high developmental precision. Diversity arises over time from type II NSCs as they express temporal transcriptional factors (TTF's) and RNA binding proteins (RBPs). There seems a sound relationship between genetic programs, neural circuit development, and behavior. Yet, poorly understood.

Here, we focus on the development of essential components of olfactory navigation circuit vFBs, H delta K, and vPFNs. We use Edu based methods to show the developmental time points and assembly of the olfactory navigation circuit components. We show, how an early transcriptional factor – seven up (Svp) regulates the development of the circuit and an ectopic increase in neural population of vFBs and H delta K classes upon loss of Svp. We also show CRISPR based knockout of Svp results in loss of vPFN neurons, thus specifying (directly or indirectly) this class of neurons. Svp knockout impart navigational behavior changes in flies. Thus, the findings suggest that TTF's can control complex behaviors by regulating the development of individual components of the circuit.

Evolution of the genetic architecture of plastic regulation

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Phenotypic plasticity is the ability of organisms (genotypes) to rapidly adjust their phenotypes in response to environmental changes, making it a key mechanism for persistence in the face of drastic environmental shifts. Plasticity itself can be genetically controlled. For instance, a transcription factor locus may regulate the expression of a structural trait locus, producing different phenotypes—an architecture known as epistatic plasticity. Alternatively, the trait locus may self-regulate, expressing different phenotypes directly in response to environmental cues—termed environmentally sensitive loci. While both models are empirically supported, the evolutionary forces shaping these competing architectures remain unclear. Here, we use a population genetic model that separates the molecular basis of trait expectation in the absence of plasticity from that of plasticity modulation to explore how selection drives the coupling or decoupling of these components. We examine a broad range of factors, including the rate of environmental change and the costs and benefits of plasticity, in Wright-Fisher populations evolving in silico forward in time. We find that epistatic plasticity is favored in rapidly changing environments when plasticity is costly for adaptive genotypes. Conversely, environmentally sensitive loci evolve more readily when environmental changes occur more gradually. This research sheds light on the evolution of the genetic architecture of phenotypic plasticity in dynamic environments, offering insights into how organisms rapidly adjust to environmental shifts.

Keywords: phenotypic plasticity, molecular regulation of plasticity, epistatic plasticity, environmentally sensitive loci, genetic architecture, varying environments.

Hybridization dynamics and range expansion across environmental variables in spadefoots

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Environmental and climatic change has been a constant throughout biological history, but the rate and extent of these changes has accelerated because of anthropogenic influences. As plant and animal ranges inevitably shift in response to these changes, questions emerge about hybridization dynamics between closely-related species that may be differentially adapted to their environments. Plains spadefoot toad females (Spea bombifrons) have been known to choose desert-adapted New Mexico spadefoot toad (S. multiplicata) males as mates under hot and dry conditions. Past studies using mtDNA and nuclear microsatellites have suggested that heterospecific S. multiplicata loci persist in the S. bombifrons genome after several generations. Additionally, the stepping-stone model has been posited for S. bombifrons' range expansion into the desert after the Last Glacial Maximum. In tandem, these hypotheses suggest that there is an adaptive advantage to hybridization between the two species that may facilitate range shifts of S. bombifrons. We aim to use genome-wide nuclear data (i.e., thousands of loci), which provides insight into ancestry inherited from both parents with higher resolution, to address the following research goals: 1) identify specific geographic regions where introgressed individuals occur and 2) identify environmental conditions driving hybrid introgression and heterospecific retention of potentially adaptive alleles. The results from this research will illuminate the role of hybridization in response to changing environmental conditions and species distributions as these factors continue to change because of human impacts.

Groundwater variation drives respiration in Middle Rio Grande riparian floodplain ecosystems

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Little is known about carbon flux, or ecosystem metabolism, in river floodplains, particularly of dryland ecosystems, despite their potentially large and changing contributions to carbon storage and loss. We hypothesized that the region of intermittent saturation (ROIS), which is the subsurface interface between terrestrial and aquatic ecosystems, is a biogeochemical ‘hotspot’ for ecosystem respiration and carbon transformation. Groundwater mean depth and variability in the ROIS facilitate aquatic and terrestrial interaction and are in need of further study for the role they play in carbon fluxes. We have developed a novel method utilizing high-frequency sensors in groundwater wells to capture potentially quick and sporadic biogeochemical ‘hot moments’ of ecosystem respiration in the ROIS in the riparian floodplain of the Rio Grande in northern New Mexico. We deployed four EXO1 sondes, fitted with floats to maintain them within the top 1 meter of groundwater, across two floodplain sites for one year to capture biogeochemical activity in the ROIS. Each sonde is equipped with sensors to record data on temperature, conductivity, groundwater depth, turbidity, fluorescent dissolved organic matter, and dissolved oxygen (DO) in 15-minute intervals. We quantified the size of each respiration event using DO as a proxy for ecosystem respiration. We found evidence that the coefficient of variance of groundwater depth drives the size of respiration events, where higher variation in the two days preceding a respiration event significantly correlated with larger respiration events across wells and sites. Our work demonstrates the effectiveness of collecting continuous in-situ data from the ROIS and suggests that groundwater variation is a key driver in floodplain ecosystem respiration.

The Impact of Isolation and Habitat Size on Genetic Structure: A study of Myodes gapperi across New Mexico's Sky Islands

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My master's thesis leverages the sky island topography of various mountain ranges in New Mexico to explore how isolation over the past 10,000 years has impacted evolutionary divergence across montane species. Using the red-backed vole (Myodes gapperi) as a model, we will examine the effects of habitat size, connectivity, and climate history on the genetic structure of populations over five mountain ranges (i.e., sky islands). Mitogenome sequencing will be used to construct maximum likelihood trees of M. gapperi to show how infraspecific variation is structured among populations by comparison to interspecific divergence values of M. gapperi and sister taxa (e.g., M. californicus). We predict that (1) Genetic variation will scale with sky islands size (2) Populations from closer mountain ranges will show less genetic structure than more distant populations. (3) populations from sky islands isolated by dramatic elevational relief (i.e., intervening deserts) will show greater structure than those separated by less dramatic lowlands. (4) Populations in the Gila and San Mateo mountains, the southernmost region of the species' range, will exhibit distinctive variation. (5) All populations will show signals associated with demographic contraction. Genetic variation can reflect high/low adaptive potential, so that conservation efforts/resources can be focused. Using M. gapperi as a species representative of high elevation communities, we begin to illuminate best policies for effective conservation.

Assessing the ecological drivers and consequences of partial migration in Hudson River striped bass over multiple decades

Caitlin Zimmer, Oliver Shipley, Yong Chen, Seth Newsome, Department of Biology, UNM

Climate change and shifts in human land use can strongly influence connectivity, structure, and resilience of aquatic populations. Partial migration (PM), where only some individuals from a population migrate while the rest remain resident, can mitigate population-level responses to environmental stressors as it creates diverse subpopulations that rely on a range of habitat and energetic resources. However, little is known of the underlying mechanisms promoting PM and whether these shift over time. In the Hudson River Estuary (HRE), striped bass (Morone saxatilis) are known to exhibit anadromous PM behavior and are a recreationally important, sentinel species. Here, we measure carbon isotopes (δ13C) of essential amino acids (AAESS) in striped bass scales to determine variation in contingent diversity over three decades (1989-2017). By combining δ13C values of AAESS with historical records of in-situ water quality data, we will identify the abiotic drivers of contingent structure, looking at factors like freshwater discharge, temperature, and dissolved oxygen. To determine how contingent structure affects striped bass population-level stability, we will calculate population stability as the degree of variation in annual striped bass young of year abundances over the study period. Results from this study will be applicable to management decisions as they will provide insight into the importance of life history diversity to population stability and will highlight which contingents are the most affected by changing environmental conditions.

Resilience Solutions Incubators: A New Model for Community-Engaged, Transdisciplinary Learning Experiences

Abigail Granath, Jennifer Rudgers, Jose Cerrato, Department of Biology, UNM

The Resilience Solutions Incubator (RSI) at the University of New Mexico (UNM) is a new, hands-on course model designed to engage undergraduate students in climate resilience research through transdisciplinary collaboration and community partnership. Our pilot course focuses on the intersection of fungal biology and heavy metal remediation to empower early-stage students to address real-world challenges in pollution and ecosystem health. Students gain practical research skills while working alongside local stakeholders, including microbiology techniques, data visualization, and effective science communication. The RSI model prioritizes ethical research practices, integrates Indigenous knowledge, and fosters “brain gain” by connecting students with meaningful regional problems to solve. Preliminary results show increased student engagement, confidence in STEM skills, and meaningful community impact. This poster presents the structure, pedagogy, and early successes of the RSI course, demonstrating how innovative education models can simultaneously cultivate climate resilience and enrich undergraduate learning experiences.

Testing mitochondrial DNA adaptation to climate by modeling a rare case of partial introgression

Josiah S. Lavender, Kyana N. Montoya, David P. L. Toews, Christopher C. Witt, Department of Biology, UNM

Adaptation of mtDNA to the external environment is poorly understood in endotherms. In Homo sapiens, and in some songbird species, patterns of mtDNA allele frequency variation along climatic gradients suggest climate adaptation, but underlying evolutionary processes are difficult to infer. Introgression of mtDNA between divergent nuclear DNA lineages offers a unique demonstration of differential fitness of mtDNA genotypes. Partial introgression of mtDNA genotypes may suggest that relative fitness of the two genotypes is dependent on environment (spatially variable selection); alternatively, introgression may be recent, ongoing, and incomplete (spatially uniform selection). We use a spatiotemporal model of a partial introgression event to distinguish between these two possibilities. Previous work on Audubon's Warblers (Setophaga coronata auduboni) showed that two ~4% divergent mtDNA haploclades systematically replace each other across a ~500-km latitudinal gradient in the southwestern U.S. One haplotype apparently introgressed southward from a nuDNA contact zone in southwestern Canada between Audubon's and Myrtle Warblers (S. c. coronata). Preliminary model results and data on current haplotype frequency suggest that, following hybridization between the two S. coronata lineages, selection on mtDNA initially caused rapid, southward introgression; however, the width and shape of the current mtDNA contact zone suggest stability governed by spatially varying selection. This evolutionary scenario suggests that the two functionally divergent mtDNA lineages, when paired with Audubon's Warbler nuDNA, are differentially adapted to climate.

Pleistocene climate fluctuations, not sea level change, shaped the near-simultaneous ecological and biogeographic diversification of an avian species complex along the Thai-Malay Peninsula

David J.X. Tan, Paisin Lekcharoen, Jacky S.M. Soh, Robert Teo, Yip Jen Wei, Ariel Wee, Frank E. Rheindt, Philip D. Round, Michael J. Andersen, Department of Biology, UNM

The Thai-Malay Peninsula is one of the most interesting biogeographical transition zones in the world since it forms the boundary between the highly biodiverse Indochinese and Sundaic zoogeographic regions. However, it is unclear if faunal turnover along this peninsula was driven by climate fluctuations or sea level change. To investigate this question, we combined phylogeographic and phylogenomic analyses with paleogeographical models to reconstruct the biogeography of the Mangrove and Blue-winged Pittas (Pitta megarhyncha and P. moluccensis), a species complex that likely speciated along the Thai-Malay Peninsula. Our results revealed a surprisingly recent Pleistocene divergence between the two pitta species, as well as a near-simultaneous cryptic divergence between migratory and non-migratory populations of the Blue-winged Pitta. Our paleogeographical models suggested that these divergences occurred independently of sea level change and were instead linked to the formation of allopatric forest refugia during glacial cycles of the middle to late Pleistocene. Our results suggest that faunal diversification during this time was mostly driven by climatic fluctuations, not sea level change.

Untangling the drivers of rodent foraging in a stochastic desert ecosystem

Joshua M. Cortez, Philip J. Manlick, Seth D. Newsome, Department of Biology, UNM

Foraging is a fundamental aspect of animal ecology with direct consequences for body condition and survival. However, the proximate mechanisms linking foraging to fitness remain largely unknown. We hypothesized that precipitation, resource availability, and competition interact to dictate the body fat of rodents, which in turn affects individual survival. Specifically, we predicted that high precipitation would increase abundance of higher quality resources. Further, we predicted that individual rodents who consume high quality resources will have an increase in their body condition and apparent survival. We combined data on precipitation and net primary production with data on rodent diet variation (carbon isotope values) and body condition (percent body fat) collected from the Sevilleta LTER and developed a series of structural equation models to understand the pathway by which resource use influences body condition. We then constructed a Cormack-Jolly-Seber survival model using body fat as an individual covariate to test the effect of body condition on apparent survival. In agreement with our predictions, results show that the consumption of higher quality resources yielded a higher percentage of body fat within individuals, which in turn yielded higher apparent monthly survival. Results of our study fill in crucial gaps in our understanding of how environmentally mediated resource availability is linked to individual fitness. This is critical as consumers in arid dryland ecosystems will likely face shifting resource landscapes due to global climate change.

Documenting Ord’s Kangaroo Rat Habitat Use Within a Wildland Urban Interface

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Within Albuquerque (NM) the Ord’s Kangaroo Rat (Dipodomys ordii) habitat is growing smaller and smaller due to the urban development around it. My research aims to find out how this species’ population in this area is impacted because of this fragmentation. Alongside my work with the kangaroo rats, I want to know what other species are prevailing within that studied area, establish a baseline population estimate, and diet analysis. I have been live trapping small mammals using Sherman box traps and collecting hair and fecal samples, along with ear tagging them for mark capture recapture studies. Samples have been processed at the University of New Mexico, Center for Stable Isotopes. I have compared my data with that from the University of New Mexico team researching kangaroo rats at the Sevilleta National Wildlife Refuge (Socorro County, NM).

Detection and Diet Analysis of Collared Peccary in Valencia County (NM)

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Building upon Myers and Bosque School’s 2023 documentation of collared peccary (Pecari tajacu) in Bernalillo County (NM) we work to document the species in adjacent Valencia County (NM). The species’ now known extent in Bernalillo (NM), Torrance (NM), and Socorro (NM) Counties left a hole in their known range as the species expands northward. Our work attempts to fill in the knowledge “donut hole.” Employing detection methods including observation, camera traps, track detection, crowd-sourced community (citizen) science reporting, and hair snares, we have worked to document the species' emerging presence in Valencia County. Using a novel hair snare method involving a wood frame, stakes, and wire brushes we collected hair from collared peccary along the Rio Grande’s riparian cottonwood (Populus deltoides) dominated forest. The collection of hair allows us to employ stable isotope analysis (specifically $\delta^{13}C$ and $\delta^{15}N$ measurements) to further understand their diet in the area they are expanding into and how those values compare to those of collared peccary in surrounding New Mexico Counties.

Stable Isotope Diet Analysis of Northern River Otter in Rio Grande del Norte National Monument (NM) and Albuquerque Biopark (NM)

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The Northern River Otter (Lontra canadensis) was reintroduced to New Mexico between 2008-2010. They were extirpated from New Mexico by the 1930s due to over harvesting, habitat degradation including water pollution, and urbanization. These factors led to not only extirpation in New Mexico, but close extinction of the Northern River Otter across North America in the 20th century. One major concern about the reintroduction of these otters is that they will compete with anglers for sport fish. Therefore, I am looking at the diet of the Northern River Otter in a primary reintroduction area within the Rio Grande del Norte National Monument, Taos County (NM) to see if they are eating more sport or non-sport fish. I am doing this through stable isotope analysis on collected river otter hair. In order to collect their hair, I set up multiple non-invasive, non-barb wire, hair snares near areas with high otter activity. Initial hair snare success has been low, and therefore I am modifying our hair capture technique. In the meantime, I have determined reference stable isotope values from captive northern river otter from the Albuquerque (NM) Biopark.

Using stable isotope analysis to track migratory patterns of warbler species from 2019-2022

Alto Bridges, Bosque School Researcher at the Center for Stable Isotopes

There are various species of warblers in the Parulidae family that travel through New Mexico as migrants. Recently, a number of warbler species are showing range changes. I specifically looked at Lucy's Warbler (Vermivora luciae), Yellow-rumped Warbler (Dendroica coronata) and MacGillvray's Warbler (Oporonis tolmiei). Through federally and state permitted bird banding activities, Bosque School and its partner bird banders, have kept a library of bird feathers from mist net captured birds including from these warbler species. Gathering more information on the migration of these species' crossing through New Mexico, and where these migratory birds are coming from is becoming increasingly important for understanding future conservation efforts. Because of this, my project focuses on using this collected data and processing it at the University of New Mexico's Center for Stable Isotopes using hydrogen stable isotopes signatures within bird feathers to track their migration and gather more information on the changes these warblers have made over the past few years regarding where they molt. Comparing the differences in their migration may give us a better understanding of how these species may affect each other.

EFFECTS OF CHANNEL STRUCTURE AND SUSPENDED SEDIMENTS IN LIGHT PENETRATION IN THE RIO GRANDE

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Light penetration in aridland rivers, like the Rio Grande, is restricted by high suspended sediment loads. In turn, limited light availability can limit algae that depend on light for photosynthesis. This research investigates associations among crucial parameters (light penetration, water depth, stream velocity, and turbidity) to better understand habitat limitations for primary producers that depend on light for photosynthesis. The goal is to predict where suitable algal habitat is located in the river, given abiotic conditions. Velocity (m/s), depth (cm), light intensity (µmol) in the water column, and turbidity (NTU) were collected at four sites along the Middle Rio Grande to analyze how these parameters change in relationship to each other. All parameters were measured in increments of 5 centimeters from the water surface to the riverbed. Preliminary results showed that turbidity levels increased from upstream to downstream sites and highlighted depth and turbidity as key drivers of light availability ($p>0.05$). A predictive relationship between algal biomass and environmental variables will help assess suitable algal habitat with different turbidity scenarios under drought conditions brought on by climate change. Droughts are hypothesized to increase turbidity levels because normal sediment loads will mix with lower surface water levels. This impact on primary producer dynamics has importance for aridland rivers, like the Rio Grande, in terms of implications to the structure and function of ecosystems.

How Will Native New Mexican Fungi Handle Climate Change?

Julianna Ford, Christina Moya, Abigail Granath, Department of Biology, UNM

Fungi are important organisms in dryland ecosystems, and their abilities can be widely applied to solve real-world problems. The fungi that we are focusing on came from an abandoned uranium mine and have the potential to remediate heavy metals. Like many other organisms on the planet, fungi are bound to be affected by the issue of climate change. However, it is unknown how most fungi will tolerate climate warming. Fungi that produce the pigment melanin are proposed to improve fungal heat tolerance. We investigated how fungi will handle climate warming, while maintaining their ability to improve the health of our ecosystem. We tested the effects of warming on fungi by growing them in an incubator that includes temperatures seven degrees hotter than the current average temperature range. We exposed cultures of 4 species of fungi to increased temperatures (19.5°C - 36°C) in the laboratory (two melanin producing and two non-melanin producing). We also grew fungi in a similar temperature range to what they are experiencing now (15.5°C - 32°C). We allowed fungi cultures to grow for 14 days. We expected more significant growth under heat stress from the melanin-producing fungal species than the non-melanin producing species when they were exposed to higher temperatures. The melanin-producing fungi exhibit more tolerance to heat stress. This, in-turn, illustrates the ability of melanin-producing fungi to withstand increasing temperatures due to climate warming. Fungi that can withstand increases in temperature are more likely to be able to grow effectively as well as potentially bioremediate heavy metals in future increased temperature ranges.

Development of cultures of fungi to measure the interaction between fungi and metals.

Joshua Abraham, Abigail Granath, Department of Biology, UNM

There are a lot of toxic, heavy metals like uranium and lead naturally in New Mexico and as a product of mining. Bioremediation is the treatment of pollutants or waste by the use of microorganisms that break down the undesirable substances, including heavy metals. We hypothesize that metals affect fungal growth and the impacts differ among species. Here, we tested whether lead affected 3 species of fungi grown in solid culture media (malt extract agar) during 2 weeks. We compared their growth and morphology and tested whether fungi reduced lead concentration in the media. After 2 weeks of culture, one species of fungi (V13A) had a big différence in color pigment and growth between the media with and without lead. One species of fungi (AG18B) did not differ in color or growth, and the final species (M35RF) had little difference. At the end of the experiment, we expect to see large differences among several species with lead. Bioremediation methods like these can help to improve our ability to clean up mining legacies in New Mexico and elsewhere.

Plant species interactions influence temporal stability

Kamren Decker, Lana Bolin, Jennifer Rudgers, Department of Biology, UNM

Some species are highly stable, changing little after perturbation, while other species are unstable, suffering from perturbation but often recovering quickly afterward. However, the drivers of temporal stability in plants remain unresolved. One possible contributor to plant stability is a lack of reliance on other species, such as pollinators, seed dispersers, and belowground microbial mutualists, for fitness. For example, if a plant species relies on animal pollinators to reproduce, and the ecosystem is disturbed in a way that reduces pollinator abundance, then the fitness of this plant species also may be negatively impacted even if the plant itself is unaffected by the disturbance. Thus, the temporal stability of the plant is not a function merely of its own tolerances, but also of the tolerances of the species it interacts with. To test if species that rely on other species for fitness are less temporally stable than species that do not, we leveraged long-term species-level biomass data collected over 24 years at the Sevilleta National Wildlife Refuge, combined with new species interaction data on these species. We found that animal-pollinated plant species are less temporally stable than wind-pollinated species, as predicted. However, there was no relationship between seed dispersal mode (animal- vs. wind-dispersed) or reliance of microbial mutualists (legumes interact with N-fixing bacteria, while other plant species do not). These results suggest that plant reliance on some species interactions, but not all, can reduce plant temporal stability.

Astemizole induced necrosis induced by lysosomal dysfunction mechanisms

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Among them, the second-generation antihistamine astemizole has been shown to be cytotoxic though its mechanism of cytotoxicity is unknown. Our research seeks to comprehend the mechanism behind astemizole's cytotoxic effects. Our research investigates the mechanism behind astemizole's cytotoxic effects using three different cell lines including A549 human lung cancer cells, PC3 human prostate cancer cells, and THP-1 human monocytic cancer cells. To determine whether astemizole caused a dose-response that could affect viability/proliferation, we performed MTT assays and observed a decrease in cell viability. Furthermore, we assessed biomarkers of autophagy, including LC3-II, SQSTSM 1 (p62), PARP 1, and Galectin-3, using Western Blots. Immunoblot analyses exhibited high intensities of LC3-II and SQSTSM 1, suggesting upregulation and inhibition of autophagy. Moreover, fluorescent microscopy analysis demonstrated production of autophagic vesicles in A549 cells stably expressing GFP-tagged LC3, indicating the alterations in autophagy. Galectin-3, a biomarker for lysosomal disruption, at high intensities indicated that astemizole is inducing lysosomal damage inside the cells. In conclusion, our findings suggest that the primary cytotoxicity of astemizole arises from lysosomal dysfunction, pushing cells towards a path of necrosis.

The Future of Vaccination: The Power of Needle-Free Microneedles

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Vaccination is one of the most effective methods for preventing infectious diseases; however, traditional injection methods face challenges such as needle phobia, cold-chain requirement for vaccine storage, and risk of accidental needle-stick injuries. Microneedle-based vaccine delivery offers a promising advancement in immunization strategies. Using mouse models, our research demonstrated poly(acrylic acid) (PAA)-based dissolvable microneedles (dMNs) to be an efficacious delivery method. This research explores hyaluronic acid (HA) as a versatile polymer for developing dMNs and compares its efficacy with PAA-based dMNs. The biocompatibility, biodegradability, and minimal toxicity of HA ensure safe polymer interaction with tissue under the skin, reduce adverse reactions, and increase patient acceptance and compliance. These characteristics make HA an ideal candidate for transdermal vaccine delivery. The dMNs are fabricated via micro-molding techniques to allow precise control over needle dimensions, sharpness, and mechanical strength. We evaluate these parameters using characterization studies for optimization. We intend to incorporate vaccines such as Virus-Like Particles (VLPs) into HA-dMNs and compare vaccine-containing dMNs with conventional injections to assess immune response in preclinical models. Furthermore, we assess whether HA-dMNs can withstand extreme storage and transportation conditions. If successful, dMNs will enhance global public health by advancing immunization and revolutionizing vaccine delivery in remote regions by overcoming cold chain limitations and simplifying logistics.

Latent Profile Analysis of Psychopathy Subtypes

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Psychopathy is a highly malignant and complex detriment to society at both individual and collective levels. Seminal literature distinguishes between two subgroups of individuals scoring high on psychopathy. Primary psychopathy (considered “true psychopathy”) is characterized by emotional deficits and genetic inheritance, whereas secondary psychopathy (“environmentally acquired psychopathy”) is characterized by heightened anxiety, reactivity, and impulsivity (Karpman, 1948). Anxiety level has historically been used as the main determinant between primary and secondary psychopathy subtypes. More recently, however, it has been speculated that other factors (e.g. impulsivity or empathy) play a potential role in distinguishing between these subgroups. Despite decades of research, refinement in identifying subtypes of psychopathy is required to better design more efficacious treatment approaches and to more robustly predict antisocial outcomes, including recidivism. Here, we first performed a latent profile analysis (LPA) in a sample of n = 365 incarcerated adult men who scored high on the Psychopathy Checklist-Revised (PCL-R). Our results reveal three distinct subgroups: manipulative, aggressive, and externalizing. We then investigated the extent to which empathy, measured via the Interpersonal Reactivity Index (IRI), and anxiety, measured via the State-Trait Anxiety Questionnaire (STAI), play a role in differentiating between these new latent groupings. This three-factor models suggests that variants of psychopathy may be more nuanced than the original two-subtype model posits, and LPA may play a pivotal role in further elucidating the differences between these subgroups.

Genetic Variation and Phylogenetic Relationships of Neotoma mexicana in New Mexico Sky Islands

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Climate shifts likely shaped the distribution and evolution of montane populations in the Southwest. Neotoma mexicana (Mexican woodrat) occurs across geographically isolated sky islands of New Mexico and offers an excellent opportunity to explore the impact of Pleistocene glacial and interglacial cycles on the geographic structure of Southwest montane communities. However, the taxonomy of the N. mexicana complex is unresolved and likely reflects a complex history of diversification. A series of taxonomic revisions and the discovery of cryptic species raises questions about systematics and the monophyly of this complex. We aim to assess genetic variation and the phylogenetic relationships in N. mexicana populations from four geographically isolated sky islands: Jemez Mountains, Sacramento Complex, Mogollon Rim, and Mount Taylor. We will use mitochondrial and nuclear genomes (ddRAD-seq) to investigate how historical climate events influenced isolation, gene flow, and divergence among these populations. The dynamic history of these high-elevation populations will further resolve the taxonomic uncertainties within the complex and provide insights into evolutionary processes shaping the assembly of montane sky island communities, ultimately informing our understanding of past and future responses to climate change in forested habitats.

The Effects of Cadmium on Adipogenesis and Breast Cancer Metastasis in the Bone Niche

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Cadmium, a heavy metal whose use has surged since the 20th century, is prevalent in battery production, electroplating, paints, and metal alloys due to its physical properties. Cadmium is also a known toxicant under investigation for its carcinogenic and obesogenic potential. Although it is known that cadmium is involved in carcinogenesis and enhanced cancer metastasis, the exact mechanisms by which this occurs are not well known. Our research group has identified that exposure to a similar metal, tungsten, drives adipogenesis in the bone niche, propagating breast cancer metastasis to this area. Given that cadmium also accumulates in the bone and has carcinogenic and obesogenic properties, our study aims to investigate if cadmium can also enhance adipogenesis and breast cancer metastasis in the bone. If we can model a similar interaction as previous studies, it may be possible to extrapolate our findings to other heavy metals that accumulate in the bone. We will employ both in vitro and in vivo models to examine this relationship. These models will be used to investigate if cadmium drives bone marrow adipogenesis and uncover the underlying molecular mechanisms behind it. These models will allow us to determine the extent of cadmium's impact on adipocyte differentiation, allowing us to determine its subsequent effects on breast cancer metastasis to the bone.

Enhancing Cognitive Performance and Stress Resilience During Sleep

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Memory loss poses a severe risk to a person’s quality of life and their well-being. Different approaches have been proposed to enhance and improve mental and cognitive abilities, but none have been proven effective. Deep sleep or Slow-Wave Sleep (SWS) is known to play an essential role in memory consolidation and memory retention over time. SWS is characterized by slow, high-amplitude EEG oscillations, or slow oscillations (SOs), that drive memory consolidation, especially of hippocampal-dependent declarative memory. The main objective of this project is to enhance learning and memory using closed-loop auditory stimulation during sleep, evaluate the effects of active vs. sham stimulation through the discovery learning tasks, and examine the effects of this closed-loop auditory stimulation on markers of stress and anxiety. Understanding the effectiveness of closed-loop auditory stimulation to enhance memory and cognitive performance will contribute to preventing and treating the rising problem of memory loss.

Effects of USP30 on Vertebrate Hair Cell Mitochondria

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Hair cells are specialized sensory cells found in the inner ear of mammals. These cells convert mechanical signals into chemical ones and relay the information to the auditory cortex in the brain via individual neurons. Hair cells require a lot of energy to function properly, which is supplied by high volumes of mitochondria.

Damaged mitochondria can synthesize cytotoxic reactive oxygen species (ROS), creating a risk to the cell. In order to maintain mitochondrial and cellular health, old and damaged mitochondria undergo mitophagy, where they are engulfed and digested by the lysosome. Several genes are involved in the regulation of mitophagy. For example, Parkin accumulates on damaged mitochondria. This accumulation leads to ubiquitination and, eventually, mitophagy.

USP30 is a deubiquitylase localized to the mitochondrial membrane. USP30 hydrolyzes ubiquitin chains, removing signals from parkin that mitochondria are targets for mitophagy. We hypothesize that USP30 is highly active in hair cells, preventing mitochondrial removal.

To test this hypothesis, we will use CRISPR to silence USP30 in Danio rerio embryos. We will assess mitochondrial health in hair cells by examining superoxide levels and calcium uptake, two indicators of mitochondrial health. We will also apply aminoglycoside, an antibiotic that damages mitochondria, to test the mitochondrial resilience. Because mammalian hair cells are not capable of regenerating, the loss of hair cells leads to hearing loss. Understanding the role that USP30 plays in mitochondrial regulation provides insight into hearing loss prevention.

PRDM Paralogues Control Zebrafish Pectoral Fin Development

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Proper limb development requires precise temporal and spatial activation and repression of gene regulatory networks. Epigenetic regulators and chromatin remodelers, including the family of histone methyltransferases, add hierarchical control to the proper activation of developmental GRNs. In this study, we investigated the function of two histone methyltransferases, Prdm3 and Prdm16, in zebrafish pectoral fin development—the homologous structures to mammalian forearms.

Both Prdm3 and Prdm16 are strongly expressed in the pectoral fin bud at 24 hours post-fertilization, as shown by hybridization chain reaction experiments. To assess pectoral fin phenotypes, PRDM3 and PRDM16 mutant zebrafish larvae were collected at 6 days post-fertilization and stained with Alcian Blue and Alizarin Red to visualize cartilage and bone, respectively. Pectoral fins were dissected and flat mounted for imaging and analysis.

Loss of either PRDM3 or PRDM16 resulted in significant defects in fin development, including abnormal cartilage patterning, disrupted joint formation, and asymmetrical fin morphology. Prdm16 mutants exhibit longer right-sided coracoid lengths, as well as increased fin fold, endoskeleton disk, and cleithrum lengths compared to wild-type variants. Together, these results demonstrate a necessary role for Prdm3 and Prdm16 in controlling pectoral fin development. Future directions include assessing changes in the limb gene regulatory network through hybridization chain reaction experiments. These studies will allow us to further dissect the molecular mechanisms of PRDM histone methyltransferases in facilitating limb development

Hispid Cotton Rat Stable Isotope Diet Analysis in a Cottonwood-Dominated Riparian Forest Before and After Wildfire, Flooding, and Restoration Using Goats

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The Hispid Cotton Rat (Sigmodon hispidus) is a newly discovered species in Bernalillo County (NM). Across four years (2021, 2022, 2023, 2024), we conducted small mammal trapping in a cottonwood-dominated riparian forest along the Rio Grande focusing on S. hispidus. In 2022, an eight-hectare wildfire burned parts of our study area, which has since experienced a period of regrowth. Hautau (2022) used stable isotope analysis of S. hispidus hair samples and noted a shift in the diet of S. hispidus pre- and post-fire. During April-July, 2023, the site was flooded by high runoff. In 2024, vegetation restoration involving goats took place in the area. Here, we used carbon (delta^{13}C) and nitrogen (delta^{15}N) stable isotope analysis to characterize the diet and ecology of S. hispidus within this changing environment. We analyzed the isotopic composition of S. hispidus hair samples and potential food sources including local C 3 and C 4 plants and invertebrates. Our pre-fire, post-fire, post-fire post-flooding, and post-goat samples were collected from both the burn site and a control site. After capturing S. hispidus using Sherman box traps, we took standard field measurements, a hair sample, and then released each animal. We compared the isotopic values of S. hispidus with their potential food sources. We further evaluated how their diet reflects the fluctuating environment and how it has changed over the four-year time scale of our sampling, including the two years evaluated by Hautau.

Unraveling the Circular RNA Landscape of Prenatal Alcohol Exposure in Adulthood and Its Potential Interactions with Neuroimmune-Linked Protein-Coding Genes

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Prenatal alcohol exposure (PAE) can lead to fetal alcohol spectrum disorders (FASD), with confirmed long-term neuroimmune genetic dysregulation linked to PAE-associated neurobehavioral deficits. However, gene dysregulation in adulthood remains poorly understood. Circular RNAs (circRNAs), novel non-coding RNAs, play key roles in gene regulation. We hypothesize that PAE alters mRNA and circRNA expression in neuroimmune pathways with brain region-specific effects. Using bulk RNA sequencing, we analyzed mRNA and circRNAs comparing PAE and control conditions in six mouse brain regions: anterior cingulate cortex (ACC), hypothalamus, hippocampus, midbrain, medulla, and frontal cortex. Data were processed using DESeq2 (mRNA) and Limma (circRNA), applying adaptive shrinkage for conservative log fold change estimates. Significant differential expression was defined as $\log2FC > 0.5$ and $p\text{-value} < 0.05$. Pathway analysis identified dysregulated pathways and potential disease associations. At least 9 circRNAs and 134 mRNAs were differentially regulated in various brain regions. Notably, several circRNAs including circRims1 and circRims2, were significantly upregulated in the ACC, suggesting potential contribution to proinflammatory pathways. RNY1 was consistently upregulated, implicating PAE-induced neuroimmune sensitization. Interestingly, circHIPK3, linked to proinflammatory immune function, was found upregulated in the ACC, medulla, hippocampus, and midbrain. These findings reveal novel circRNAs and mRNAs linked to neuronal and neuronal-glial interactions, offering insight to new pathways underlying neurobehavior and neuroimmune dysfunction in individuals with FASD.

Evaluating the Impact of the Implementation of the POTTER Risk Calculator on Emergency General Surgery Colectomy Outcomes

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Emergency General Surgery (EGS) patients undergoing colectomy experience higher morbidity and mortality rates than elective cases. The Predictive OpTimal Trees in Emergency Surgery Risk (POTTER) calculator is an artificial intelligence–based tool validated for predicting mortality and complication rates in EGS patients. We hypothesized that implementing the POTTER risk calculator reduces unfavorable outcomes in EGS colectomy patients.

We performed a retrospective chart review at a single academic institution for patients ≥18 years undergoing colectomy by the EGS service. Two cohorts were defined: pre-implementation of the POTTER risk calculator in the pre-operative setting (March 1- August 31, 2024) and post-implementation (September 1, 2024- February 28, 2025). In-hospital mortality, overall complications, length of stay, and discharge disposition were compared between the two cohorts. P-values <0.05 were considered statistically significant.

We identified 52 patients undergoing colectomy, 25 were in the post-implementation cohort (48.1%). In-hospital mortality for EGS colectomy patients was 22.2% pre-implementation and 16.0% post-implementation (p=0.828). We found no significant difference in the average length of stay (18.0 ± 17.6 versus 15.9 ± 12.4 days, p=0.621), discharge disposition (50.0% versus 56.0% discharged home, p=0.818), or complication rates (63.0% versus 36.0%, p=0.096).

Implementation of the POTTER risk calculator in surgical decision-making did not yield significant differences between the two cohorts. Although modest improvements in all outcomes were observed with use of pre-operative POTTER scoring in surgical decision-making, statistical significance was limited by the sample size. Future investigations are warranted to better characterize the impact of POTTER score on EGS care.

Conserved progenitor transcription factors are required for the proper development of fan shaped body neurons

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Olfactory navigation and sleep are complex behaviors- mediated by an evolutionarily conserved insect brain region, the central complex. Recent connectome studies of the central complex have described about 3000 neurons of about 250 different types. What genetic and developmental programs regulate the formation of the CX cell types is poorly understood. Previous work has identified that ventral fan-shaped body (vFB) neurons, which are odor-encoding neurons, and dorsally projecting fan-shaped body (dFB) neurons, which are sleep-regulating neurons, are generated from the same neural stem cell (NSC), the Dorsolateral II (DL1) Type 2 NSC. Generation of distinct neural types requires the combination of temporal transcription factor (TTF) cascades in both Type II NSCs and Intermediate Neural Progenitors (INPs), which are generated by asymmetric divisions of the DL1 NSC. We want to show how INP TTFs regulate these complex behaviors by regulating the differentiation and specification of dFB and vFB neurons. Our preliminary work has demonstrated that knockdown of conserved genes; Opa, Eyeless, and TFAP2 led to a loss of vFB neurons, and Opa knockdown led to a gain of dFB neurons. This suggests that temporal transcription factors play different roles in the differentiation of these two neurons and may in part account for differences in their functions.

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