

33rd Annual Research Days

Thursday, April 4 & Friday, April 5, 2024

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

Thursday Seminar Speaker: Dr. Aparna Bhaduri
Understanding Cell Types in Human Cortical Development

Friday Seminar Speaker: Dr. Nancy Johnson
Mycorrhizae in Agriculture: Past, Present and Future

Committee Members

Co-Chair: Seth Newsome

Co-Chair: Syed, Mubarak Hussain

Joanne Kuestner

Donna George

Adil Wani, BGSA

Rachel Seddon, BGSA



Understanding Cell Types in Human Cortical Development

Thursday Speaker



Dr. Aparna Bhaduri,
Assistant Professor,
Department of Biological
Chemistry,
University of California
Los Angeles

The Bhaduri Lab studies human brain development and brain cancer. Our main questions are to ask what signals within a cell are drivers of how it generates the diverse cell types we observe in the human brain, and also which signals from other brain regions or cell types are required to develop or refine these identities. In parallel, we explore how these cues are hijacked in brain cancer. To execute these studies, we leverage single-cell analyses and stem cell derived models of the human brain.

Day: Thursday, April 04

Time: 3:30 PM

Venue: Castetter 100

Mycorrhizae in Agriculture: Past, Present and Future

Friday Speaker



Dr. Nancy Johnson,
Regents' Professor,
Department of Biological,
Sciences,
Northern Arizona
University

Arbuscular mycorrhizae are ancient symbioses that predate the evolution of roots. These plant-fungus associations can enhance plant nutrition and increase plant resistance to disease, drought, and salinity. Furthermore, arbuscular mycorrhizal fungi (AMF) form enormous (but invisible) networks of hyphae that generate soil structure and increase nutrient retention in ecosystems. Agriculture does NOT eliminate mycorrhizae, but it DOES change them. Current farming practices may inadvertently select for AMF that convey little or no benefit to crops. Tillage reduces the diversity of AMF and selects for a few genera that thrive in agroecosystems. Also, fertilizers can shift the balance of costs and benefits such that AMF are no longer mutualistic. Future agricultural management practices that aim to harness the potential benefits of mycorrhizae must account for the ecological and evolutionary mechanisms underlying this ancient symbiosis.

Day: Friday, April 05

Time: 3:30 PM

Venue: SMLC 102

Thursday's schedule

12:30 p.m.	Graduate student lunch with the speaker	CAST Room 1420 (PiBBs)
1:30-3:30 p.m.	Poster Printing and Hanging Assistance Hours (BGSA reps)	CAST 1st Floor
3:30-4:30 p.m.	SEMINAR: "Understanding Cell Types in Human Cortical Development"	CAST Room 100
4:30 p.m.	Hausammann Brewhaus Social	2004 Central Ave SE

Friday's schedule

8:30-9:30 a.m.	Ecology + Evolution I (Session 1)	Stage	CAST Room 100
8:30-8:45 a.m.	Jeremiah Westerman	UG	
8:45-9:00 a.m.	Ryan Stumbaugh	GR	
9:00-9:15 a.m.	O. Liota Gongora Weinbaum	GR	
9:15-9:30 a.m.	Shayne Halter	GR	
9:30-10:30 a.m.	Cell + Molecular (Session 2)		CAST Room 100
9:30-9:45 a.m.	Benjamin Garcia	GR	
9:45-10:00 a.m.	Brendan Sanders	UG	
10:00-10:15 a.m.	Marelessis Palomino	UG	
10:15-10:30 a.m.	Alexa Gonzalez	UG	

10:30-10:45 a.m.	COFFEE BREAK		
10:45 a.m. - 12:00 p.m.	Ecology + Evolution II (Session 3)		CAST Room 100
10:45-11:00 a.m.	Lisa Garcia	GR	
11:00-11:15 a.m.	David Robinson	GR	
11:15-11:30 a.m.	Jian Xiong David Tan	GR	
11:30-11:45 a.m.	Ellie Larence	UG	
11:45 a.m. - 12:00 p.m.	Tatyana Falkowsky	UG	
12:00-1:00 p.m.	LUNCH (Buen Provecho)		CAST Basement
1:30 - 3:30 p.m.	Open Laboratory Visits		
	Center for Stable Isotopes		PAIS 1315
	Neural Diversity Lab		Cast 207
	Salinas Lab		CETI 2564
	Vesbach Lab		CET 3517
1:00–2:00 p.m.	POSTER SESSION I		CAST 1st Floor
	Savannah Sanchez (1)	GR	
	Josh Lopez-Binder (2)	GR	
	Danielle Land (3)	GR	
	Ali Abouismail (4)	GR	
	Ethan Wilson (5)	GR	
	Janna Martinez (6)	UG	
	Leigh James (7)	UG	
	Marina Seheon (8)	UG	

	Brenda Ramos Villanueva (9)	UG	
	Bernadette Holberg (10)	UG	
	Zera Adame (11)	UG	
	Roxanne Marquez (12)	UG	
2:00-3:00 p.m.	POSTER SESSION II		CAST 1st Floor
	Kyana Montoya (13)	GR	
	Elizabeth Walker (14)	GR	
	Esteban Restrepo Cortés (15)	GR	
	Kayley You Mak (16)	GR	
	Celina Eberle (17)	UG	
	Alan Ibarra (18)	UG	
	Huachan Liang (19)	UG	
	Mikayla Ranspot (20)	UG	
	Maria Nava Martinez (21)	UG	
	Spencer Moezzi (22)	UG	
	Caleb Keener (23)	UG	
	Ariadna Torres (24)	UG	
	Renae Simonson (25)	UG	
	Adina Abudushalamu (26)	UG	
3:00-3:30 p.m.	COFFEE BREAK		
3:30-4:30 p.m.	SEMINAR: <i>Mycorrhizae in Agriculture: Past, Present and Future</i>		SMLC 102
4:30-5:30 p.m.	SCHOLARSHIPS + AWARDS CEREMONY		SMLC 102
5:30-6:30 p.m.	RECEPTION		SMLC 102
6:30 p.m.	BOSQUE BREWING SOCIAL		106 Girard Blvd SE

Oral Presentations:

Effects of Pollination Syndromes on Alpine Plant Communities

Jeremiah Westerman, Department of Biology, UNM

Hannah Marx, Department of Biology, UNM

Joseph Kleinkopf, Department of Biology, UNM

The alpine plant community can be surprisingly diverse; however, the drivers of this diversity remain understudied. In this study, the floral morphology of alpine plants was used to determine their pollination syndromes and identify their major pollinator groups. Given the pollination syndromes and a phylogeny containing the members of the alpine plant community, a phylogenetic community analysis was used to assess patterns of overdispersion or clustering in the alpine plant communities of eight mountain summits across the southern Rocky Mountains. Across all summits bee pollination was the most common assigned syndrome for sampled species, followed by a combination of fly and wind. For all of the summits, there was no significant pattern of overdispersion or clustering in the phylogenetic community structure with respect to pollination syndromes. Therefore, it is likely that the major pollinator groups, identified using pollination syndromes, are not driving the diversity of alpine plants across the sampled summits. To better understand all possible factors contributing to the diversity of alpine plants in the southern Rocky Mountains, future studies should consider the effects of a wider range of ecological and environmental factors on the alpine plant community, the geologic and glacial history of the region, and should perform direct observation of floral visitors to remove the possible ambiguity inherent to pollination syndromes.

A MICROBIAL SYMPHONY OF NITROGEN CYCLING: SYNTROPHIC RELATIONSHIPS BETWEEN ARCHAEAL AND BACTERIAL SPECIES WITHIN LAVA CAVE ENVIRONMENTS

Ryan E. Stumbaugh, Department of Biology, UNM

Diana E. Northup, Department of Biology, UNM

Cristina Takacs-Vesbach, Department of Biology, UNM

Lava cave systems are a valuable reservoir of prokaryotic life, housing hundreds of species of Archaea and Bacteria. These microbial deposits shape the environment by conducting redox reactions that contribute to secondary mineral formation, contain novel antibiotic compounds, and are considered analog systems for astrobiology research. Further, within these environments, prokaryotes are the foundational organisms responsible for cycling growth-limiting elements, such as nitrogen, to sustain the microbial ecosystem. However, questions remain: what genera of Archaea and Bacteria associated with nitrogen cycling roles are present, and do they engage in syntrophic relationships to accomplish their nitrogen cycling goals? To address this, our study investigates prokaryotic community composition by analysis of the 16S rRNA gene using Illumina MiSeq. Initial results show multiple nitrogen cycling associated genera, with higher abundance from the archaeal domain, specifically *Nitrososphaera* and *Nitrosopumilus*. Further analysis will allow us to examine bacterial and archaeal species co-occurrence to identify potential syntrophic relationships to explore. Future work includes investigating basaltic wall rock composition to identify possible nitrogen sources for microbial communities, examining metagenomic data to identify viral genes and potential families contributing to nitrogen cycling, and gene screening of bacterial and archaeal genes encoding nitrification enzymes. These results will provide foundational insight into how these communities acquire and retain nitrogen to establish and perpetuate their community's growth in lava caves, a small piece of a complex puzzle necessary to entirely understand how to approach the study and comprehension of these microbial ecosystems.

IMPACTS OF INNATE IMMUNITY ON VIRAL REASSORTMENT RISK DURING RIFT VALLEY FEVER EPIZOOTICS

O. Liota Weinbaum, Department of Biology, UNM

Quincy D. Harris, Department of Biology, UNM

Rebecca C. Christofferson, Pathobiological Sciences, Louisiana State University, Baton Rouge, LA

Helen J. Wearing, Department of Biology and Department of Mathematics & Statistics, UNM

The mosquito-borne Rift Valley Fever Virus (RVFV) is emerging across the African continent and into neighboring regions. RVFV causes significant mortality in livestock and contributes to food insecurity. Minimizing RVFV livestock infections would reduce dangerous human infections. However, the World Health Organization recommended against RVFV live attenuated vaccine (LAV) use during epizootics to reduce the risk of reassortment between wildtype and vaccine strains of the virus. As coinfection is a prerequisite for reassortment, we assess how much coinfection would result from various vaccination strategies using a compartmental model of RVFV epizootic transmission. We developed a framework of differential equations that describes the interactions between adult cattle, *Culex* sp. mosquitoes, wildtype strain, and LAV strain. We evaluated total coinfection, total wildtype infection, and total excess host mortality. We calculated global sensitivity indices and investigated imperfect vaccination and vector population dynamics. We explore how within-host, inter-virus competitive inhibition via innate immunity impacts coinfection. Near epizootic onset, the goals of reducing total excess mortality and avoiding coinfection align. Until cases have plateaued, vaccination efforts could shorten the outbreak by reducing total wildtype infections. Reduced wildtype infection would also reduce the opportunity for RVFV hybridization with other enzootic viruses. These results imply that prioritizing prevention of RVFV wildtype and vaccine strain interaction leads to greater mortality, more infection, and longer outbreaks. Surveillance systems are needed to detect outbreaks as early as possible, and capacity-building is needed for rapid deployment. A One Health approach of strategic cattle vaccination could stabilize food systems and prevent zoonosis.

ENERGY MANAGEMENT OF MIGRATING HUMMINGBIRDS IN THE AMERICAN SOUTHWEST

Shayne R. Halter, Department of Biology, UNM

Blair O. Wolf, Department of Biology, UNM

Christopher C. Witt, Department of Biology, UNM

Andrew E. McKechnie, Department of Zoology, University of Pretoria, South Africa

Carlos Martinez del Rio, Professor Emeritus, Department of Zoology and Physiology, University of Wyoming

Hummingbirds are the smallest of all birds, with the highest mass-specific metabolic rates of any vertebrate. They get almost all their energy from floral nectar, consuming it directly as carbohydrates during the day, and synthesizing it as fat to use at night while they are inactive. Migrating hummingbirds also store fat to fuel flights between breeding and wintering grounds. Our research investigates how hummingbirds maintain energy balance, given the interplay between costs of their daily existence, nectar availability, and fat loads needed for successful migrations. Hummingbirds sometimes enter torpor at night to conserve fat when they are energy deficient. During autumn 2022, we captured 1,306 hummingbirds at a migration stopover site along the Mimbres River in New Mexico. We used Quantitative Magnetic Resonance technology to measure fat and lean masses of each bird. We performed metabolic trials on 117 of these birds to measure torpor use. We collected a feather from each bird to determine natal and molting origins, using hydrogen stable isotope ratios. Preliminary analysis indicates that hummingbirds with less body fat are more likely to use torpor. Furthermore, they enter torpor at specific fat thresholds and emerge in the mornings with consistent minimum fat levels. Data from feather hydrogen measurements indicates that hummingbirds arriving at our study site later originated from higher-latitude breeding grounds and may be making longer journeys. Further analysis of our data will provide an understanding of how migrating hummingbirds balance their energy in a changing environment with increasingly unpredictable food supplies.

How fish make antibody responses without lymph nodes: the development and structure of the organized nasopharynx associated lymphoid tissue in rainbow trout

Benjamin J Garcia, University of New Mexico Department of Biology

Alexis Reyes, University of New Mexico Department of Biology

Ali Abouismail, University of New Mexico Department of Biology

Chrysler Martinez, Chief Manuelito Middle School

Yago Serra dos Santos, Oklahoma State University

& Irene Salinas, University of New Mexico

Despite the absence of lymph nodes and germinal center (GC) structures known to be essential for the induction of antibody responses in mammals, teleost fish can produce robust cellular and humoral immune responses. Long-held dogma indicated that these responses developed in a “diffuse” manner, but our recent work has found structures analogous to GCs in the organized nasopharynx-associated lymphoid tissue of teleost fish. The O-NALT contains IgM⁺ B and CD4⁺ T cells consistently polarized in a manner reminiscent of highly organized mammalian structures. Expression of major MHCII was also polarized, with high expression near the basement membrane and along the epithelial barrier in direct contact with the environment. Besides B cells, we have observed 3 types of APCs: dendritic cells, macrophages, granulocytes. In-vivo staining of phagocytes with dextran indicated both resident populations which remained in the O-NALT, as well as populations exiting the tissue and entering the vasculature. The O-NALT develops in a manner closely analogous to mammalian NALT, with CD8⁺ T cells seeding the tissue early on, followed by IgM⁺ B cells and CD4⁺ T cells approximately 20 days later. This transition from putative effector to inductive immune function is in line with previous work and further solidifies the evidence that the O-NALT share both structure and function with similar mammalian tissues. This is the first detailed histological characterization of GC structures in teleost fish and offers insights into the structural organization and function of the O-NALT as an immune inductive site.

DIFFERENTIAL GENE EXPRESSION IN THE SPT-ADA-GCN5-ACETYLTRANSFERASE COMPLEX IN EXTENSION OF THE REPLICATIVE LIFESPAN OF *S. CEREVISIAE*

Brendan M. Sanders, Department of Biochemistry and Molecular Biology, UNM

Blaise L. Mariner, Department of Biochemistry and Molecular Biology, UNM

Mark A. McCormick, Department of Biochemistry and Molecular Biology, UNM

Aging is an inevitable process that affects one hundred percent of organisms and is the greatest risk factor for much of disease. It is a significant risk factor for in diseases like cancer, cardiovascular disease, and neurodegenerative disease. Despite this irrefutable fact, aging is not well understood. Previous research performed in the McCormick lab has shown that single-gene deletions in model organisms like *S. cerevisiae* and *C. elegans* have shown marked increases in lifespan. Several lifespan-extending gene deletions that have previously been found in my lab encode proteins in the Spt-Ada-Gcn5-acetyltransferase (SAGA complex), a chromatin remodeling complex with acetyltransferase and deubiquitylation modules. For example, the yeast gene *SGF73* is an important component of the deubiquitylation module (DUBm) of the SAGA complex. When specific genes encoding components of SAGA are deleted, yeast replicative lifespan has been shown to be extended significantly. My research aims to determine the role *sgf73* Δ and other single-gene deletions play in the extension of yeast replicative lifespan by RNA sequencing these mutant strains. The strains of interest include *sgf73* Δ and *ubp8* Δ , important components of the DUBm (deubiquitinase module) of SAGA, which removes ubiquitin from lysine 123 of histone H2B. Understanding the role these particular genes and the SAGA complex play in downstream transcriptional regulation through RNA sequencing and chromatin immunoprecipitation (ChIP) sequencing will further clarify the histone remodeling performed by the SAGA complex, and how this might regulate transcription of specific gene sequences and further uncover undiscovered genes and mechanisms involved in aging.

Understanding Podosome Formation in Mast Cells

Marelessis Palomino¹, Rachel M. Grattan¹, Diane S. Lidke¹

¹Department of Pathology, University of New Mexico, Albuquerque, NM, USA

Mast cells, through a receptor called FcεRI, initiate allergic responses. This receptor binds to Immunoglobulin E (IgE), an antibody that circulates in our body. When an allergen that IgE recognizes enters our body, it binds IgE and crosslinks the IgE-bound receptors, starting a signaling cascade. Actin polymerization is immediately involved in this signaling process, which helps in the release of inflammatory mediators and causes changes in cell morphology such as cell membrane ruffling. Podosomes are actin-rich structures that play a crucial role in cell migration and adhesion. Mast cells migrate through different tissues in our body that vary in degrees of stiffness, making it essential to understand the structure and function of podosomes in inflammatory response. However, podosome function in mast cells, and what regulates their formation, is not understood. We hypothesize that podosomes form at sites of crosslinked IgE-FcεRI. To test this hypothesis, we are using confocal microscopy and immunostaining for the cytoskeleton proteins, actin and Vinculin, to confirm the presence of podosomes in resting and activated states. We also use fluorescently-labeled IgE to determine the spatial relationship between podosomes and FcεRI. Our current results show that crosslinked FcεRI often colocalizes with podosomes. We are currently working to determine the dynamics of podosome formation and the signaling pathways involved.

Conserved transcription factors in intermediate neural progenitors regulate the specification of olfactory navigation input neurons.

Alexa Gonzalez, Department of Biology, University of New Mexico

Aisha Hamid, Department of Biology, University of New Mexico

Mubarak H. Syed, Department of Biology, University of New Mexico

The molecular mechanisms responsible for the generation of diverse neural types in the brain are not completely understood. The proper specification of neurons is essential for the formation of unique circuits that mediate essential behaviors. In *Drosophila melanogaster*, Type II neural stem cells (T2NSCs) give rise to transit-amplifying progenitor cells known as intermediate neural progenitors (INPs), which divide to give rise to ganglion mother cells that divide to produce neurons of different types. Previous findings have found that both T2NSCs and INPs express time-dependent transcription factors (TFs) during larval development. Our hypothesis suggests that the molecular programming of TFs in NSCs and INPs determines neuron specificity. In this study we look at a neural type called ventral fan-shaped body (vFB) neurons, the tangential input neurons of the olfactory navigation circuit. Two INP TFs are the late-expressed Eyeless (*ey*) and Scarecrow (*scro*) factors, that work in a negative-feedback loop of regulation. Both are known to play a role in the neural upbringings of sensory development. We employ genetic tools including Gal-4 genetic driver lines, overexpression inserts and RNAi silencing gene mechanisms. These are essential to manipulate the expression of individual factors and observe the spatial, functional, and morphological contribution of these molecules in vFB specificity. Our study suggests that INP factors contribute to neural specificity of olfactory navigation input neurons, and therefore promote neural diversity. Understanding the factors linked to neural development offers an insight to human brain development and propels the advancements in treatment for neurodevelopmental disorders.

CAN CARBON AND NITROGEN STABLE ISOTOPES FROM JUNIPER IN NEOTOMA PALEOMIDDENS BE USED TO RECONSTRUCT CLIMATE OVER THE PAST 34,000 YEARS?

Lisa S. García, Department of Biology, UNM
Felisa A. Smith, Department of Biology, UNM
Scott L. Collins, Department of Biology, UNM

Paleomiddens are debris piles created by woodrats (*Neotoma* sp.), which under the right conditions can persist for many tens of thousands of years. The contents within these middens provide unique historical ecological records, giving us a window into past ecological dynamics. But can they be used to infer climate? Using woodrat paleomiddens collected from Titus Canyon in Death Valley National Park California, we examined the stable isotope composition of juniper (*Juniperus* sp.) from 34,000 to 5,000 years ago using two stable isotopes ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$). Carbon ($\delta^{13}\text{C}$) reflects photosynthetic efficiency and may be influenced by aridity and temperature; carbon dioxide (CO_2) concentrations between 34,000 and 5,000 years ago varied by about 75ppmv, with a considerable difference in temperature ($>8\text{-}10^\circ\text{C}$). Nitrogen ($\delta^{15}\text{N}$) may also reflect aridity because the less precipitation, the higher the nitrogen in the soil. Preliminary results reveal that carbon stayed remarkably consistent, with the isotopic values during the last glacial maximum close to the values during the Holocene despite the changes in CO_2 and temperature. Nitrogen significantly increased from the past to the present, which might reflect shifts in aridity. Further analyses of stable isotopes in modern juniper leaves from the locations of the analyzed paleomiddens will help relate nitrogen values to temperature and/or aridity. Our data highlight physiological changes in juniper over tens of thousands of years, and possibly their environment.

Antarctic Lake Viromes reveal potential virus associated influences on nutrient cycling in ice-covered lakes

David Robinson^{1*}, Rachael M. Morgan-Kiss², Zhong Wang³, Cristina Takacs-Vesbach¹

The McMurdo Dry Valleys (MDVs) of Antarctica are a mosaic of extreme habitats which are dominated by microbial life. The MDVs include glacial melt holes, streams, lakes, and soils, which are interconnected through the transfer of energy and flux of inorganic and organic material via wind and hydrology. For the first time, we provide new data on the viral community structure and function in the MDVs through metagenomics of the planktonic and benthic mat communities of Lakes Bonney and Fryxell. Viral taxonomic diversity was compared across lakes and ecological function was investigated by characterizing auxiliary metabolic genes (AMGs) and predicting viral hosts. Our data suggest that viral communities differed between the lakes and among sites and that these differences were connected to microbial host communities. AMGs were associated with the potential augmentation of multiple biogeochemical processes in host but most notably with phosphorus acquisition, organic nitrogen acquisition, sulfur oxidation, and photosynthesis. Viral genome abundances containing AMGs differed between the lakes and microbial mats, indicating site specialization and we identified significant coupling between viral and bacterial communities ($p=0.001$). Finally, host predictions indicate viral host preference among the assembled viromes. Collectively, our data show that: (i) viruses are uniquely distributed through the McMurdo Dry Valley lakes, (ii) their AMGs can contribute to overcoming host nutrient limitation and, (iii) viral and bacterial communities are tightly coupled.

The impact of Blue-winged Pitta (*Pitta moluccensis*) range expansion on the conservation of the Mangrove Pitta (*Pitta megarhyncha*) in Singapore

David J.X. Tan, Department of Biology, University of New Mexico, USA

Jacky Soh, National Parks Board, Singapore

Frank E. Rheindt, Department of Biological Sciences, National University of Singapore, Singapore

Philip D. Round, Department of Biology, Mahidol University, Thailand

& Michael J. Andersen, Department of Biology, University of New Mexico, USA

The Mangrove Pitta is a globally near-threatened bird species that inhabits mangrove swamps in South and Southeast Asia. Because of the widespread regional destruction of mangrove forests for aquaculture and coastal developments, Mangrove Pitta populations have declined rapidly in recent decades. In the city-state of Singapore, where 8.9% of the nation's original mangroves remain, only 10–20 Mangrove Pittas are thought to persist, which places the population at risk of inbreeding and local extirpation. The recent range expansion of the closely related Blue-winged Pitta into Singapore further threatens the long-term viability of the Mangrove Pitta population due to the possibility of increased interspecific competition and hybridisation. Understanding the population health of the Mangrove Pitta is thus essential to assessing the species' capacity for long term recovery and developing conservation strategies. To assess the genetic diversity, inbreeding coefficient, and effective population size of the Mangrove Pitta, we used reduced-representation sequencing to subsample the genomes of 10 Mangrove Pittas from Singapore for single-nucleotide polymorphisms. We also sequenced six Blue-winged Pittas from the newly established population in Singapore to test for evidence of hybridisation and introgressive gene flow between the two species. Our results show that the Mangrove Pitta population exhibits low genetic diversity but does not appear to be inbred. We also found no evidence of hybridisation or introgression between the two species. Our results suggest that mangrove restoration is urgently needed, and that the Blue-winged Pitta range expansion is unlikely to have a negative impact on the Mangrove Pitta in Singapore.

COMPUTATIONAL MODELING OF INTERFERON IN SARS-COV-2 INFECTION

Ellie J. Larence, Department of Computer Science, UNM.

Melanie E. Moses, 1. Department of Computer Science, UNM. 2. Santa Fe Institute, Santa Fe, New Mexico.

As of January 2024, COVID-19 has been officially recorded as causing over 7 million deaths globally. While risk factors such as age and sex have been identified, it remains challenging to understand the mechanisms that cause dramatic variation in patient outcomes following SARS-CoV-2 infection. However, growing evidence has linked severe COVID-19 with a dysregulated host interferon (IFN) response. IFNs serve as an innate signaling molecule in host defense, locally upregulating interferon-stimulated genes (ISGs) upon recognition of viral material and thereby inducing an antiviral state in neighboring cells. However, the spatial-temporal dynamics of viral progression and host IFN response are challenging to study *in vivo*. Agent-based models (ABMs) explicitly represent pathogens and host cells in a spatially aware system, making them an ideal technique to simulate the structurally limited and temporally localized effects of IFN. In this work, we expand the Spatial Immune Model of CoronaVirus (SIMCoV), an ABM of SARS-CoV-2 infection in the lungs, to incorporate IFN by replicating the localized antiviral state induced by ISGs in grid points neighboring infected cells. By extending SIMCoV's focus to the innate immune response, we aim to quantify the within-host spread of SARS-CoV-2, evaluate relative impacts of innate and adaptive immunity, compare agent-based to ordinary differential equation modeling approaches, and simulate infection under high-risk conditions - aged immune systems with correspondingly diminished IFN response. These results provide a more thorough understanding of the viral and immunological dynamics consequential to patient outcomes following SARS-CoV-2 infection.

MULTIDISCIPLINARY DEVELOPMENT OF AUTONOMOUS PLANT GROWTH SYSTEMS FOR USE ON THE INTERNATIONAL SPACE STATION AND BEYOND (PART OF THE NASA MINDS COMPETITION)

Louis Hight, Department of Biology, UNM

Tatyana Falkowsky, Department of Biochemistry, UNM

Pascale Allred, Department of Biochemistry, UNM

CHILIHOUSE is a multidisciplinary team of undergraduate students with the goal to develop technologies for crop production during space travel, on the moon, and on Mars. Each year, we compete in the NASA MINDS competition (part of MUREP) and have previously worked on systems to develop growth methods for plants on the surface of Mars. This year, we are developing a remote robotics system to assist in monitoring plant growth. Currently, plant growth and research on the International Space Station (ISS) is labor intensive, requiring astronauts to manually collect data. This results in a low capacity for plant research and further crop growth on the ISS, and this will be mirrored in long-term space flight. Our system is designed to address the issue of efficiency and increase capacity for plant research in space by autonomously interacting with plants and reporting data via LiDAR and a robotic arm. Our modular design is compatible with existing infrastructure on the ISS, making it deployable for current space missions as well as future endeavors on the moon and Mars. To accomplish this, our team brings together robotics, computer science, and biology to create a usable and cohesive system with real-world applications.

Poster Presentations:

Poster 1

PLANT AND MICROBIAL CONTRIBUTIONS TO SOIL CO₂ EFFLUX IN A CHIHUAHUAN DESERT GRASSLAND

Savannah Sanchez, Department of Biology, UNM

Marcy Litvak, Department of Biology, UNM

Jennifer Rudgers, Department of Biology, UNM

Megan Rae Devan, 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 2023 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.

Poster 2

Investigating the Relative Importance of the Two Major Types of Drought on Dominant New Mexican Tree Species' Water-Uptake and Carbon Sequestration Rates

Josh Lopez-Binder, Department of Biology, UNM

Will Pockman, Department of Biology, UNM

Marcy Litvak, Department of Biology, UNM

Climate change is increasing ambient temperature across ecosystems in New Mexico. This results in both higher atmospheric drought (increased vapor pressure deficit, VPD) and soil drought (decreased soil water content, SWC). Developing a mechanistic understanding of how plants respond to increased VPD and fluctuations in plant soil water availability is crucial to predicting future ecosystem water status and tree mortality. I am quantifying the relative influence of VPD and SWC on tree water use in trees from four ecosystems in the New Mexico Elevation gradient: juniper savanna (US-Wjs), piñon-juniper (US-Mpj and US-Mpg), ponderosa pine (US-Vcp) and mixed conifer (US-Vcs). Here, I report on my findings for Ponderosa pine only. I used long-term timeseries of 30 minute tree water use (sap flow) and bole-water storage measured in five trees (using Granier probes) of ponderosa pine at US-Vcp, and ecosystem meteorological and soil data that simultaneously measure VPD and SWC. I used multivariate linear models to account for temporal autocorrelation and find the relative effect size of VPD, SWC and VPDx-SWC interaction terms, and identify a critical SWC threshold. These trees are more sensitive to VPD when SWC was high (this occurred more in the spring, and in the summer when monsoons were large). Sap flux in larger trees was relatively more sensitive than smaller trees to VPD, indicating they may access deeper, wetter soil. I also found that a significant proportion of spring transpiration in these trees relies on tree water reserves, which get depleted as the soil dries.

Poster 3

Evolutionary and demographic history of high-latitude shrews (Genus *Sorex*; Eulipotyphla; Soricidae)

Danielle M. Land*, Stephen E. Greiman, Batsaikhan Nyamsuren, Satoru Arai, Niccolett V. Ochoa, Jason L. Malaney, Andrew G. Hope, Joseph A. Cook

Danielle M. Land, Department of Biology, University of New Mexico
Stephen E. Greiman, Department of Biology, Georgia Southern University
Batsaikhan Nyamsuren, Department of Biology, National University of Mongolia
Satoru Arai, National Institute of Infectious Diseases
Niccolett V. Ochoa, Department of Biology, University of New Mexico
Jason L. Malaney, New Mexico Museum of Natural History and Science
Andrew G. Hope, Division of Biology, Kansas State University
Joseph A. Cook, Department of Biology, University of New Mexico

Shrews (genus *Sorex*) are an evolutionarily diverse clade with 89 nominal species and a Holarctic distribution. However, species limits, diversification history, and phylogeographic relationships for many taxa and major clades remain unexplored. In this study, we developed phylogenetic hypotheses to test the validity of the *Sorex* 'caecutiens' and 'minutus' species groups and incorporated additional species to reconcile relationships within subgenus *Sorex*. We sequenced or obtained (GenBank) mitochondrial cytochrome b sequences for over 1,000 shrews to generate a time-calibrated phylogenetic tree. Some nominal species have expansive Palearctic or Holarctic ranges, while others inhabit limited regions such as montane areas or islands. Most nominal species are composed of multiple lineages, which suggests undescribed or cryptic variation. Pulses of deeper diversification corresponded to climate oscillations during the Pleistocene, revealing complex community assembly. Much of Asia remained ice-free during this period, contributing to minimal genetic structure within widespread continental species. There is an exception for Eurasian montane regions and Pacific Coastal archipelagos, where populations reflect ancestral separation. We used expansion statistics for individual clades to refine the spatial and temporal context of colonization across this broad region. Comparative approaches encompassing multiple closely related species provide preliminary perspectives to questions surrounding episodic, recurrent processes of expansion and isolation for mammals and associated communities across Eurasia. Our next steps will add nuclear insights to test the generality of the mitochondrial results.

Poster 4

Determining optimal booster interval times for intranasal vaccines in rainbow trout

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Aquaculture, a rapidly growing industry in the United States and Europe, faces significant challenges from infectious diseases. Vaccination plays a crucial role in disease prevention and improving fish health. However, the effectiveness of vaccination wanes over time and boosters are needed to prolong protection, which is currently unknown. This study investigates the optimal timing for a booster dose of an intranasal vaccine against infectious hematopoietic necrosis virus IHNV, a major fish viral pathogen.

One hundred and sixty rainbow trout (*Oncorhynchus mykiss*) were divided into eight experimental groups (10/group) and intranasally vaccinated with live attenuated IHNV vaccine. We tested two interval booster regimes, one at 4 weeks and another at 6 weeks. Serum, nasal cavity, and spleen samples were collected for both intervals. Serum-neutralizing antibody titers indicate a trend towards higher levels in the 6-week compared to the 4-week boosted group, albeit this difference was not statistically significant ($P=0.07$). Currently, the same experiment is being repeated to measure the binding affinity of specific IHNV antibodies using surface plasmon resonance. Additionally, we will quantify the expression of *aicda*. By identifying the most effective timing for booster vaccines, this research will contribute to the development of more robust and efficient vaccination strategies, ultimately promoting the health and sustainability of the aquaculture industry.

Poster 5

MOLECULAR MECHANISM REGULATING THE FATE AND FUNCTION OF THE DROSOPHILA SLEEP-WAKE CIRCUIT

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Behaviors that are conserved across species rely on neural circuits comprising diverse cell types. How neural stem cells produce diverse neural cell types is an open question in neurobiology. We use the *Drosophila* central complex as a model to investigate the neural stem cell-specific genetic, and developmental programs that specify diverse cell types and circuits. Currently, my work focuses on the development of a sleep-wake circuit, which includes sleep-promoting dorsal fan-shaped body neurons that inhibit downstream helicon cells to promote sleep. Using inherited RNAi genetic knockdown we induced type-II specific neuroblasts expression from a LexA-LexAOP Gal4 driver lines with different Imp RNAi constructs. Previous results from our lab have identified unique Type II neural stem cells that generate the dFB neurons and these Type II neural stem cells express IGF2 mRNA-binding protein (Imp). Additional data/behavioral assays are necessary to further solidify Imp interactions with the circadian rhythm circuitry and its effects on sleep behavior. This research was supported by the National Science Foundation, the Sloan Foundation, and the Brain & Behavior Research Foundation

Poster 6

EFFECTS OF GROUNDWATER LEVELS ON THE ABUNDANCE AND DIVERSITY OF TERRESTRIAL ARTHROPODS IN THE SAN ANTONIO OXBOW REGION OF THE RIO GRANDE

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Terrestrial arthropods play important roles in ecosystems as detritivores, herbivores, pollinators, and prey for other organisms. The importance of these roles can be seen in the isolated wetland habitat of the San Antonio Oxbow region of the Rio Grande which supports a diverse variety of plant and animal species. This diversity relies on higher groundwater levels because if water access decreases, competition between species may intensify. Increased drought and isolation from the Rio Grande have caused changes in the health of this Oxbow ecosystem. One way to assess environmental changes is by monitoring arthropod populations. The purpose of this research was to analyze terrestrial arthropod populations in the Oxbow to evaluate groundwater availability within the wetland. Arthropods were collected monthly from pitfall traps (n=5) from April-October (2022) and March-September (2023); at the same time, groundwater levels were measured with a water level meter. After removal from the pitfall traps, the arthropods were frozen, separated from detritus and identified to the lowest taxonomic level in the lab. The overall species abundance from 2022 at 412 individuals was greater than the abundance in 2023 at 303 individuals; additionally, 2022 had higher average groundwater levels at 147.3 cm per month. With changes in water flow in the Oxbow, the growth of native vegetation is decreasing, and this leads to a decrease in arthropods as well. This provides an opportunity to understand the significance of groundwater levels in the Oxbow and insight into the terrestrial arthropod communities within the Bosque ecosystems.

Poster 7

Does the Gut Microbiome Use Carbon Derived from Non-Essential Amino Acids to Synthesize Essential Amino Acids?

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Due to resource limitation, wild small mammals often consume diets deficient in the amount of protein required for their growth and homeostasis. To date, most research has focused on the role of the gut microbiome in carbohydrate metabolism, however its role in host protein metabolism is just beginning to be explored. Recent evidence suggests gut microbes perform de-novo synthesis of AAESS using dietary carbohydrate precursors that are subsequently utilized by the host to build its structural tissues (e.g., skeletal muscle). However, microbes can synthesize AAESS from other metabolite precursors, including non-essential amino acids. Here, we assessed if deer mice (*Peromyscus maniculatus*) incorporate microbially derived AAESS from non-essential amino acids into their skeletal muscle. Mice were fed semi-natural low (2.5%) to medium (5%) protein diets containing ¹³C-labeled alanine or glutamic acid, two non-essential amino acids synthesized from intermediaries in glycolysis and the tricarboxylic acid cycle respectively. Amino acid stable isotope analysis was performed on host muscle to quantify isotopic enrichment and assess the origin of the AAESS integrated into host muscle. We then used 16S rRNA gene sequencing to describe microbial diversity throughout the intestinal tract. We found that all AAESS in mice muscle were enriched in the ¹³C-glutamic acid treatment, showing that the gut microbiome readily uses this non-essential amino acid as a substrate for AAESS synthesis. In contrast, we found minimal evidence of AAESS synthesis from ¹³C-alanine. Our results contribute to a greater understanding of the complex interactions between gut microbes and their mammalian hosts.

Poster 8

Molecular Insights and Evolutionary Implications for Protein Interaction within the Class II Aldolase Domain of *Drosophila* Adducin

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Protein domains function like individual parts of a machine within proteins and when combined allow proteins to perform complex tasks. These domains often serve as protein interaction platforms. One such protein is Adducin, which connects to the actin cytoskeleton, thus aiding in cell structure. Adducin comprises a head domain with a protein fold conserved in Aldolase enzymes that function in glycolysis, a middle neck region, and a flexible tail. Although the Aldolase domain head of Adducin evolved from the eponymous glycolytic enzyme, it does not have enzymatic activity, and its precise function remains to be fully elucidated. We have discovered that the Aldolase domain of Hts, the fly homolog of Adducin, can bind directly to Mud, a critical cytoskeletal protein involved in cell division. We have explored this binding in detail using computational structural modeling and protein interaction experiments. We find, unexpectedly, that essential Mud-contacting amino acids in Hts are conserved with many aldolase enzymes, where they likely participate in forming a tetrameric enzyme. Interestingly, when we removed the C-terminal tail from the Aldolase enzyme, it bound Mud similarly to the Hts domain. Chimeric Hts and aldolase enzyme proteins suggest how an ancient enzyme fold might have evolved into a protein interaction domain. Lastly, our search through protein databases indicates that the family of Adducin proteins first emerged in very simple multicellular organisms. In summary, our study shows how the Aldolase domain in the Adducin family binds a key protein partner and how such function may have evolved.

Poster 9

DOES LIFE HISTORY EVOLUTION AFFECT PARASITE SUSCEPTIBILITY IN CRANES?

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Haemosporidian parasites are a diverse group of apicomplexan protozoans that include the causative agents of avian malaria and infect a wide range of bird species. Bird species vary strikingly in susceptibility to haemosporidians, but the causes of this variation are poorly known. One possibility is that evolutionary transitions in host life histories affect coevolutionary dynamics, with implications for parasite loads and parasite diversification. The cranes (Aves: Gruiformes) have been underrepresented in parasite sampling efforts, but the existing data suggest that they have coevolved with a specialized group of haemosporidians that are currently grouped under the species name *Haemoproteus antigonis*. Here, we aim to elucidate the effects of host life history evolution on parasite communities by comparing haemosporidians across a sample of 400 hunter-killed sandhill cranes from New Mexico. Our samples included the greater sandhill crane (*Antigone canadensis tabida*), a large-bodied (~6 kg), short-distance migrant that nests in the Rocky Mountains, and the lesser sandhill crane (*A. c. canadensis*), a small-bodied (~3 kg), long-distance migrant that nests in Alaska and Siberia. The evolutionary divergence of these two host taxa likely occurred during the Pleistocene, and was followed by divergence in body size, migration distance, tracheal morphology, and sexual selection intensity. Our preliminary data shows that these host sister taxa differ in haemosporidian prevalence in ways that vary by haemosporidian genus. These results indicate that divergence in host life history characteristics can lead to rapid evolutionary shifts in parasite susceptibility.

Poster 10

OPTIMIZING MICROBIAL ENUMERATION TECHNIQUES IN LAKES OF ANTARTICA'S MCMURDO DRY VALLEYS, A COMPARATIVE ANALYSIS OF TRADITIONAL MICROSCOPY AND FLOW CYTOMETRY

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The Long-Term Ecological Research (LTER) project in the McMurdo Dry Valleys (MDV), Antarctica, represents a collaborative effort to monitor ecological changes in one of Earth's most extreme environments. One component of this project involves the study of microbial populations in several MDV lakes, which contain unique aquatic ecosystems characterized by minimal nutrient availability, high salinity, and low biomass. Water samples are collected biannually from specific depths beneath lakes covered in permanent ice, aiming to track microbial dynamics over time. Historically, our protocol for bacterial enumeration has employed direct counting or computer-assisted enumeration with ImageJ, facilitated by fluorescence microscopy. However, these methodologies are labor-intensive and difficult to apply to microbial populations with low abundance and varying degrees of species diversity. This project provides a comparative analysis between the traditional, microscopy-based techniques and flow cytometry, a more automated technique known for its precision in cell enumeration. Furthermore, flow cytometry offers additional insights into properties such as cell size and morphology that are imprecise with direct count methods. By examining discrepancies and correlations between the two sets of results, this project intends to identify the most efficient but accurate method for bacterial enumeration in these extreme environments.

Poster 11

Biocrust microbial community recovery following fire in the northern Chihuahuan Desert, USA

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Biological soil crusts (biocrusts) fulfill important ecological roles in dryland ecosystems but are threatened by increasing climate-change-induced disturbances, such as more frequent and intense fires, that could affect their abundance and function. Biocrusts stabilize soils, influence dryland ecohydrology, increase soil fertility and plant productivity, and contain microbes that can fix atmospheric carbon and nitrogen. As fire disturbance increases it is necessary to understand the dynamics of recovery of cyanobacteria dominated biocrusts. Biocrusts are commonly overlooked in fire recovery research, and the interactions between bacteria and fungi in the recovery process are unknown. This study aims to understand how the community compositions of biocrust fungi and bacteria change in the event of fire, and if there are interspecies interactions between bacteria and fungi during recovery. Using metagenomics of biocrusts from different burn sites at Sevilleta LTER, we determined that bacterial diversity significantly increased over time since fire. There was no significance in species richness or evenness within the bacteria. Fungal analyses are underway. Though it is predicted to take years for a full recovery, restoration of biocrusts post fire is possible post fire.

Poster 12

Soil Degradation: How Can We Restore the Skin of the Earth?

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Soil degradation affects one-third of global land area and drylands are vulnerable to increased soil degradation, involving a loss in crucial ecosystem services such as carbon sequestration, nutrient and water retention, and soil stabilization. An important pillar to soil health is microbial communities and how they respond to climate change. Drylands house unique topsoil microbial communities called biological soil crusts -- biocrusts -- which make up the top 2 cm of the soil and are comprised of cyanobacteria, fungi, lichens, and mosses. It's imperative that we understand how dryland topsoil communities respond to intensifying environmental stressors, and discover ways to facilitate resistance to these disruptions. This project addresses how enriching biocrusts with native microbes can promote resistance and recovery from disturbance such as trampling and heat. Biocrusts with a legacy of either trampling disturbance or no disturbance were harvested from the field and subjected to either 25 °C or 35 °C. Other than controls, biocrusts were inoculated with one of 12 combinations of cyanobacteria and fungi species. Chlorophyll concentration (chl a), scytonemin concentration, and soil stability were measured to determine soil health and cyanobacteria abundance. Biocrusts that were not enriched with microbial addition were remarkably susceptible to high heat and legacy effects of trampling, with lower chl a concentrations and lower soil stability class. While biocrusts that were inoculated with culture showed no significant decrease in chl a or soil stability class under heat and trampling disturbances.

Poster 13

Exploring nesting phenology and divergent mitochondria along an elevational gradient

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Elevational gradients are useful systems to study variation in breeding phenology because they allow observation of a single species facing a range of environmental factors over a close geographic area. Temperature decreases with increasing elevation, but factors affected by temperature including snow cover depth and duration and plant bud emergence must also be considered in the timing of breeding to ensure synchrony between hatch date and peak resource abundance. However, because montane regions typically possess tough terrain, strong seasonality, and are difficult to access, our understanding of breeding phenology in these environments is poor. Gonad development, nest initiation, and egg-lay date occur later with increasing elevation, but temperature was not the sole predictor. Variables directly influencing egg-lay date vary with elevation. We are interested in determining if these factors play similar roles in Audubon's Warbler breeding phenology, and if there are any differences between the two divergent mtDNA observed in Audubon's Warblers. We collected Audubon's Warbler nestlings along an elevational gradient spanning 1000m of the Sandia Mountains throughout the breeding season in 2023 and aged them to determine nest initiation date. We then tested if there was an association between nest initiation, elevation, and mitochondrial haplotype. Understanding how Audubon's Warbler populations time their breeding along an elevational gradient can help us predict their current breeding phenology and how it will shift in the face of a changing climate.

Poster 14

Microbial Diversity in Great Basin National Park and Humboldt-Toiyabe National Forest Caves

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The Humboldt-Toiyabe National Forest and Great Basin National Park, located in eastern Nevada, contain a wealth of caves whose microbial diversity has only been explored to a limited degree. The caves are located in the desert formed millions of years ago through sulfuric acid speleogenesis. Previous research has delved into gypsum and carbonate-associated sulfate as well as elemental water quality in nearby cave springs. Additionally, lamppnflora, microbial biofilm communities, have been studied in the area, revealing highly diverse organisms between caves. The first goal of the project is to characterize the diversity of archaea, fungi, and bacteria between and within the caves using 16S rRNA gene sequencing and scanning electron microscopy. The second goal of the project is to understand how microorganisms are contributing to nutrient cycling within the cave by looking for evidence of chemoheterotrophy, chemoautotrophy, and chemolithoautotrophy. We will also look for evidence of microbial mining of the rock walls and/or precipitation of different deposits of rock. Bulk geochemistry analysis will determine nutrient sources. Initial sample collection will be performed through March 2024. 16S rDNA samples will be collected and stored in sucrose lysis buffer and stored at 80 C until DNA extraction. DNA will be extracted using the DNeasy PowerSoil Kit (Qiagen). By studying the biogeochemical cycles within the cave and the microbial diversity, we can understand how specific microorganisms may metabolize nutrients in an oligotrophic environment. This research will have implications in other fields, such as searching for life on other planets and other subterranean microbial ecosystems.

Poster 15

PREY CHOICE BY PUMA (PUMA CONCOLOR) IN A HUMAN-MODIFIED HIGH ANDEAN ECOSYSTEM

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Puma conservation is often motivated by their influence of ecosystem processes through “top-down” control of diverse prey species. Suitable habitat and sufficient prey populations determine whether pumas can maintain a population. To understand how northern, high-Andean pumas persist in a highly human-disturbed region, we performed scat analyses to characterize dietary ecology. We opportunistically collected, dissected, and analyzed 47 scats. Across all scats, nine-banded armadillos (*Dasypus novemcinctus*) and stump-tailed porcupines (*Conepatus rufescens*) represented the most frequent prey and comprised 47.84% and 26.25% of overall biomass consumed, respectively. We also reported Colombian puma predation of the red-tailed squirrel (*Syntheosciurus granatensis*) and a small sigmodontine rodent for the first time. Uniquely, we only documented northern high-Andean Colombian pumas preying on animals <10 kg and specializing on armadillos (Levins’ standardized niche breadth $B_{sta} = 0.42$). These findings are consistent with prior predictions that pumas consume smaller prey in lower latitudes, more tropical ecosystems, and more human-disturbed landscapes. We suggest that puma diets in the northern high Andes are most similar to those of the Coffee Region ($J=0.69$) because they are both highly human-disturbed and ungulate depleted, not only due to geographic proximity. Our results contribute to biogeographic patterns of puma prey preference, elucidate local dietary ecology of a Colombian puma population, and corroborate calls to conserve pumas in highly human-disturbed ecosystems.

Poster 16

INCREASING BACTERIAL TOLERANCE AND METABOLISM OF THE BIOFUEL, N-BUTANOL USING COMMUNITY-LEVEL EVOLUTION AND FUNCTIONAL GENOMICS

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n-butanol is a strong biofuel candidate since it is more energy dense and less volatile than ethanol. The bottleneck for industrial production of biobutanol is the toxicity; most microbes cannot survive about 1.5% v/v. We propose to develop bioremediation capability along with the biofuel technology to mitigate future spills and their consequences. Two main approaches were used: community-level screening and functional genomics, both followed by directed evolution to increase biodegradation. For the first approach, a bacterial library from historic bioremediation projects was re-isolated and re-characterized, then mixed into artificial communities of ~20 strains ("master mixes"). These master mixes were screened for tolerance to butanol, and continuously exposed to increase tolerance. Promising communities were then tested for growth with butanol as the sole carbon source. Secondly, we looked for bacteria with alcohol dehydrogenase enzymes and looked to increase butanol metabolism. We found that the tolerance for n-butanol may be improved with repeated exposure, but it was difficult to switch from tolerance to metabolism. Bacterial community dynamics may be influenced by n-butanol concentration, and there was putative butanol metabolism found with both research approaches.

Poster 17

Invasion genetics of introduced bullfrogs (*Rana catesbeiana*) in New Mexico

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The American bullfrog, *Rana catesbeiana*, is an extremely successful invader that was originally introduced to ecosystems for a variety of purposes such as pest control or human consumption. Now listed in the IUCN's Top 100 Most-Invasive Species, the bullfrog has been linked to species' declines across the globe related to disease spread, direct predation, and competition for resources with native species. With the introduction of the bullfrog to the Southwestern United-States, many native species may be substantially affected given the high environmental stress they already experience in arid desert conditions.

Bullfrogs are interesting as an invasive species because they have consistently been shown to have low genetic variation among invasive populations, even with genetic backcrossing and re-introduction. Although bullfrogs are relatively well-studied, little is known about their invasion history in New Mexico. The goal of this study is to investigate the population genetics of bullfrogs across their introduced range in New Mexico. We sequenced the mitochondrial locus, cytochrome b (*cytb*), of 85 individuals from multiple sites across New Mexico including the West and Middle Fork of the Gila River, the Middle Rio Grande Basin, and the Mora River.

We expect to find low genetic diversity within introduced bullfrogs with high similarity to their associated source populations, signifying genetic bottlenecks. We also expect to find evidence that source populations are from numerous sites across their native eastern range with multiple introduction events. Our study provides an initial picture of the invasion history and genetic variation of bullfrogs in New Mexico.

Poster 18

Astemizole induced necrosis induced by lysosomal dysfunction mechanisms

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Functional inhibitors of acid sphingomyelinase are known to induce toxicity in cells, potentially leading to cell death. Among them, the second-generation antihistamine astemizole has been shown to be cytotoxic though its mechanism of cytotoxicity is still unknown. Our research seeks to comprehend the mechanism behind astemizole's cytotoxic effects. Various cell lines, including A549 human lung cancer cells, PC3 human prostate cancer cells, and THP-1 human monocytic cancer cells were used. MTT assays were performed in 96-well plates to determine whether astemizole caused a dose-response that could affect viability/proliferation. A decrease in cell viability was observed in which an LD50 between 10 to 20 μM was obtained, depending on the cell line. Western blots assessed protein levels of LC3-II, SQSTSM 1 (p62), PARP 1, and Galectin-3. After the immunoblot analyses for both LC3-II and SQSTSM 1, both being biomarkers of autophagy, high intensities were observed in both proteins, suggesting both upregulation and inhibition of autophagy. In addition, production of autophagic vesicles was determined in A549 cells stably expressing GFP-tagged LC3 using fluorescent microscopy. Increased autophagic vesicle production was found, indicating the alterations in autophagy. Cleavage of PARP 1, a biomarker of apoptosis, was not observed in the immunoblot analysis, which failed to demonstrate a possibility for an apoptotic mode of cell death. Galectin-3, a biomarker for lysosomal disruption, 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.

Poster 19

Genetic analysis indicates a large introduction of predatory, nonnative Smallmouth Bass in the Grand Canyon

Huachan Liang, Thomas Turner, Megan Osborne

Smallmouth bass (*Micropterus dolomieu*) is a species of centrarchid (sunfishes) that are native to much of the eastern United States. Over the past several years, smallmouth bass have been periodically detected below Glen Canyon Dam on the Colorado River, where they are not native. On June 30th 2022, juvenile smallmouth bass were also detected implying that there was reproduction. Smallmouth bass are predators and their presence in the Colorado River will most certainly negatively affect imperiled native fishes. In this study, we used microsatellite data from a sample of juvenile smallmouth bass to estimate effective population size of the parental generation. We also used sibship analysis to determine how many families the sample of juveniles represented. Estimates of effective population size based on the linkage disequilibrium method was $LD Ne=106$ (95% CI=86-133). The results of sibship analysis were generally consistent with a monogamous mating system. One hundred full-sibling pairs were detected with high probability (>95%). The large effective population size of the parental generation and presence of multiple familial lines among the juveniles is concerning, as it suggests a growing population downstream of Glen Canyon Dam.

Poster 20

Using carbon and nitrogen isotope analysis of baleen to examine nutritional stress in gray whales (*Eschrichtius robustus*) in the northeast Pacific Ocean

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Gray whales (*Eschrichtius robustus*) in the northeast Pacific exhibited an unusual mortality event in 2019-2022 that resulted in the death of at least 502 individuals. Strandings included all demographic groups, and recent analysis show that this population declined by 24% since 2016. The goal of this study is to validate an isotope-based method to assess nitrogen balance in whales as a proxy for nutritional stress. We are measuring carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope values of baleen, a metabolically inert tissue that can be subsampled to provide a multi-month eco-physiological record at the individual level. This approach will enable us to identify periods of metabolic homeostasis versus nutritional stress during the ~1-1.5 years of each whale's life prior to death. The development of new methods to assess physiological conditions of free-ranging individuals provides us with valuable information on this species' vulnerability to environmental changes. Our preliminary results show that $\delta^{15}\text{N}$ values increased in most whales before death. The observed increase is similar in magnitude to increases in nitrogen isotope values observed in other mammalian species experiencing nutritional stress. In contrast, $\delta^{13}\text{C}$ values do not show consistent patterns in the months prior to death but do show oscillations that potentially reflect individual migratory strategies. We anticipate this study will produce a novel method to identify nutritional stress in gray whales, as well as characterize age- and sex-specific variation in foraging ecology of this elusive species.

Poster 21

Population genomics of four co-distributed frog species in a barrier island system

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In nature, small populations are often of concern because of limited genetic diversity, which underlies adaptive potential in the face of environmental change. Assessing patterns of genetic variation within co-distributed species sampled across varied landscapes can therefore illuminate their capacity to persist over time. We sequenced new genome-wide sequence data (double digest restriction site-associated DNA sequencing) for four frog species (*Anaxyrus terrestris*, *Hyla cinerea*, *H. squirella* and *Rana sphenoccephala*) sampled from two barrier islands and the adjacent mainland of northern Florida. We calculated genomic diversity metrics and analyzed spatial patterns of genomic variation for each species. We found higher genomic diversity within mainland individuals compared to island individuals for all species, suggesting a consistent effect of small island area on diversity across species. Three species (all but *A. terrestris*) showed significant signatures of isolation-by-distance, and some clustering analyses indicated separation of island and mainland individuals within species. We identified subtle differences in the strength of these patterns among species, with the strongest genetic differentiation observed in *R. sphenoccephala*. Finally, we found evidence of recent migration between island and mainland populations for all species, which likely explains the limited genetic structure observed and contributes to the persistence of these small populations.

Poster 22

A Hybrid Technique for Syndesmotic Fixation: A Review of the Literature

Dr. Richey, Andy Moezzi and Spencer Moezzi

With approximately 187 ankle fractures per 100,000 people each year 10% of ankle fractures are accompanied by a syndesmotic rupture. Addressing the syndesmotic rupture is important because if ignored it can prolong the patient's recovery by two-fold increasing the risk of chronic instability, persistent pain, and arthritis. The goal of surgery when presented with a syndesmotic rupture is to provide anatomic reduction and increased rotational stability to the joint. Today's surgeons are faced with two options which include a trans-syndesmotic screw or using the suture button technique, in this literature review we will be exploring a third option which is a hybrid between the two.

Poster 23

TOMB RAIDING BEETLES: DIETARY SHIFTS IN LASIODERMA SERRICORNE AFTER NEW WORLD COLONIZATION

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The cigarette beetle, *L. serricorne* is infamous for being a major pest in the United States and abroad. For more than 500 years, the cigarette beetle has been known for its voracious appetite for tobacco, and its diet has thus been primarily associated with tobacco. However, during the uncovering of King Tut's tomb, the cigarette beetle was found to be embedded in resin, and it's hypothesized to have been feeding off of chamomile within the tomb. This raises the question of if the diet of *L. serricorne* has shifted from being chamomile based in the past, to tobacco based in the present. To explore this, *L. serricorne* were housed and grown in vials containing dietary mixtures of varying amounts of wheat flour (contemporary lab diet), dietary yeast, two types of tobacco, and chamomile. To determine the efficacy of the diets, date of first emergence and overall beetle emergence were measured. Results suggest that diets of wheat flour resulted in the earliest and highest emergence rates of beetles, with chamomile being the next best diet, and both types of tobacco having late, as well as low emergences. In regards to the results, it would appear that the proposed ancient diet chamomile for *L. serricorne* functions better for the species than the contemporary diet of tobacco. These results indicate the stability of dietary efficiency for *L. serricorne*, while also prompting further questions regarding dietary preferences for the beetle.

Poster 24

Dynamics of Amphibian Pathogen Detection Using Extended Museum Specimens

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Natural history collections have long served as the foundation for understanding our planet's biodiversity, yet they remain a largely untapped resource for wildlife disease studies. Extended specimens include multiple data types and specimen preparations that capture the phenotype and genotype of an organism and its symbionts—but preserved tissues may not always be optimized for downstream detection of various pathogens. Frogs are infected by an array of pathogens including *Batrachochytrium dendrobatidis* (Bd), Ranavirus (Rv), and Amphibian Perkinsea (Pr), which provides the opportunity to study differences in detection dynamics across tissue types. Here, we used qPCR protocols to screen two tissue types commonly deposited in museum collections, toe clips and liver, from two closely related host species, *Rana catesbeiana* and *Rana clamitans*. We compared Bd, Rv, and Pr infection prevalence and intensity between species and tissue types and found no significant difference in prevalence between species, but Bd intensity was higher in *R. clamitans* than *R. catesbeiana*. Additionally, toe tissue exhibited significantly higher Bd infection loads and was more effective for detecting Bd infections. In contrast, Rv was detected from more liver than toe tissue, but the difference was not statistically significant. Our results support the use of extended specimen collections in amphibian disease studies and demonstrate that broader tissue sampling at the time of specimen preparation can maximize their utility for downstream multi-pathogen detection.

Key words: Amphibian Perkinsea, amphibians, *Batrachochytrium dendrobatidis*, Chytridiomycosis, frogs, holistic specimen, natural history collections, Ranavirus

Poster 25

Glial cells coordinate inter lineage developmental timing

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One interesting question that the neuroscience community has asked is, how do different cell lineages communicate during development? To help answer this question, 2 specific type II neuroblasts located in the *Drosophila* brain, called DL1 are used as a model. These neuroblasts indirectly create migrating glia cells that start from the central brain and end up in the eye region starting in late L3 larvae. While these cells are moving, they may be using attractive or repulsive signals to help guide their journey. Immunohistochemistry is used to prepare *Drosophila* brains for imaging. The GAL4/UAS and LexA/LexAop systems are used to knock down gene expression for this project.

Poster 26

EPISTASIS MODULATES LEVELS OF BALANCED POLYMORPHISM IN CHANGING ENVIRONMENTS

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In temporally changing environments, evolution can occur rapidly by natural selection on balanced polymorphism, allowing population persistence. This makes the maintenance of balanced polymorphism a central issue in population biology. However, known balancing mechanisms at multiple loci in varying environments are restrictive. While sign epistasis could promote balanced polymorphism at two loci, the effects of such genetic interactions need to be sizable to protect polymorphism in the face of stochastic perturbations in finite populations. Therefore, it is unclear if and to what degree epistasis can foster balanced polymorphism in nature. We use forward-in-time computer simulations under the Wright-Fisher model to explore the effects of different levels and types of epistasis on balanced polymorphism between two selected loci in finite populations inhabiting uniform and spatially heterogeneous temporally changing environments. We show that epistasis is unlikely to promote polymorphism in the absence of spatial heterogeneity: weak epistasis cannot maintain variation on its own. However, in combination with the balancing effect of spatial heterogeneity under the spatial storage effect, weak epistasis notably modulates levels of balanced polymorphism. Diminishing epistasis typically decreases balanced polymorphism at both loci, while reinforcing epistasis typically increases balanced polymorphism at the loci, compared to the absence of epistasis. While sign epistasis increases polymorphism, its effects are relatively weaker than those of reinforcing epistasis. Overall, we show that genetic interactions, particularly reinforcing epistasis, can promote higher levels of balanced polymorphism in finite populations, expanding our understanding of the basis of rapid adaptation in the face of environmental change.



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