

35th Annual Research Days

Thursday, April 9 & Friday, April 10, 2026

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

Thursday Seminar Speaker: Dr. Priya Devarajan
*Guardians of the Airways: The Protective Roles of Specialized CD4 T
Cells in Respiratory Immunity*

Friday Seminar Speaker: Dr. Nandita Garud
Pervasive selective sweeps across human gut microbiomes

Committee Members
Co-Chair: Seth Newsome
Co-Chair: Syed, Mubarak Hussain
Joanne Kuestner
Tayli Lam
Shweta Agarwal, BGSA
Irvin Arroyo-Torres, BGSA



Guardians of the Airways: The Protective Roles of Specialized CD4 T Cells in Respiratory Immunity



Special Thursday
Seminar Speaker

• Dr. Priya Devarajan
Assistant Professor
Stony Brook University

The Devarajan Lab investigates the mechanisms of successful immunity against respiratory infections, focusing on memory T and B cell responses in the nose and lungs. Our research explores how nasal immunity provides a first line of defense to curb transmission of virus and examines the origins of durable lung tissue-resident memory T cells. Additionally, we also study mechanisms of functional immune protection in the aged with a focus on age-associated B cells (ABC). Priya is also passionate about trainee mentorship and in fostering a supportive environment where the next generation of scientists can thrive.

Day: Thursday, April 09
Time: 3:30 PM
Venue: Castetter 100

Pervasive selective sweeps across human gut microbiomes



Keynote Speaker

• Dr. Nandita Garud
Associate Professor
UCLA

The human gut microbiome is composed of a highly diverse consortia of species that are continually evolving within and across hosts. The ability to identify adaptations common to many human gut microbiomes would not only reveal shared selection pressures across hosts, but also key drivers of functions in the microbiome. In this work, we demonstrate that selective sweeps both within and across host microbiomes are a common feature of the human gut microbiome and that targets of selection may be strongly impacted by host lifestyle around the world.

Day: Friday, April 10
Time: 3:30 PM
Venue: SMLC 102

Program Agenda:

Tuesday's schedule (April 7th)

12:30-2:30 p.m.	Poster Printing and Hanging Assistance Hours (Irvin Arroyo-Torres)	CAST Room 040 (Grad Pod)
------------------------	--	---------------------------------

Wednesday's schedule (April 8th)

12:30-2:30 p.m.	Poster Printing and Hanging Assistance Hours (Shweta Agarwal)	CAST Room 040 (Grad Pod)
------------------------	---	---------------------------------

Thursday's schedule (April 9th)

all day	Judges preview posters	
12:30 p.m.	Graduate student lunch with Speakers	CAST Room 1420 (PiBBs)
3:30-4:30 p.m.	SEMINAR - Dr. Priyadharshini Devarajan	CAST Room 100
4:30 p.m.	Flock of Moons Social	111 Harvard Dr SE

Friday's schedule (April 10th)

8:30-9:30 a.m.	SESSION I Talks	Level	CAST Room 100
8:30-8:45 a.m.	Temiloluwa Omotade	GR	
8:45-9:00 a.m.	Miriam Bechtel	UG	
9:00-9:15 a.m.	Hannah Bradley	UG	
9:15-9:30 a.m.	Chris Walker	GR	
9:30-10:30 a.m.	SESSION II Talks		CAST Room 100
9:30-9:45 a.m.	Dale Fastle	GR	
9:45-10:00 a.m.	Emily Schmitt	GR	
10:00-10:15 a.m.	Job Flores	UG	
10:15-10:30 a.m.	Xavier Larason	UG	
10:30-10:45 a.m.	COFFEE BREAK		CAST Greenhouse
10:45 a.m. - 12:00 p.m.	SESSION III Talks		CAST Room 100
10:45-11:00 a.m.	Anejelique Martinez	GR	
11:00-11:15 a.m.	Adam Kranz	GR	
11:15-11:30 a.m.	Savannah Sanchez	GR	

11:30-11:45 a.m.	Zoe Marriner	Postbac	
11:45 a.m. - 12:00 p.m.	Dani Wiley	GR	
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 & Basement
1	Lily Carman	UG	
2	Michael Fragua	GR	
3	Andrea Ibarra	UG	
4	Fatouma Zara Issoufou Kapran	RA	
5	Ana Olivas	UG	
6	William Meija-Garcia	GR	
7	Patricia Sotelo Chavira	GR	
8	Morrigan Vega	GR	
9	Cloe Knutson	GR	
10	Keya Biswas	GR	
11	Miriam Shin	UG	
12	Brooklyn Patterson	UG	
13	Hollis Gray Patton	HS	
14	Ryan Stumbaugh	GR	
15	Cory Henn	GR	
16	Gabrielle Rael	UG	
17	Audrey Vanderhee	UG	
18	Derek Kober	GR	

19	Ashley Willis Mascarenas	GR	
20	Lola Kadlec	HS	
21	Abigail Granath	GR	
22	Rachael Auer	GR	
23	Conner Mertz	GR	
24	Alissa Jones	UG	
2:00-3:00 p.m.	POSTER SESSION II		CAST 1st Floor & Basement
25	Tulaib Azam	GR	
26	Manogya Chandar	GR	
27	Natalia Chavez	GR	
28	Sydney Drummond	UG	
29	Melanie Gonzales	UG	
30	Josiah Lavender	GR	
31	Niko Candia	UG	
32	James Loomis	GR	
33	Esteban Restrepo-Cortes	GR	
34	Emmy Turpin	GR	
35	Lucy Pockman	HS	
36	Ida Rothschild	UG	
37	Benjamin Wellington	Postbac	
38	Christiana Concepcion	UG	
39	Gideon Carver Landau	HS	
40	Isabella King	UG	
41	Serenity Snider	RA	
42	Erika Dunn	GR	
43	Nicholas Ryan	GR	
44	Purbendra Yogi	GR	

45	Tenley Housler	GR	
46	David Traub	UG	
47	Michael Robinson	GR	
3:00-3:30 p.m.	COFFEE BREAK		CAST Greenhouse
3:30-4:30 p.m.	SEMINAR - Dr. Nandita Garud		SMLC 102
4:30-5:30 p.m.	SCHOLARSHIPS + AWARDS CEREMONY		SMLC 102
5:30-6:30 p.m.	RECEPTION		SMLC Lobby
6:30 p.m.	BOSQUE BREWING SOCIAL		106 Girard Blvd SE

Oral Presentations:

Talk 1

Wild African lungfish (*Protopterus aethiopicus*) cocoons have extensive chemical diversity and harbor potential antifungal compounds

Temiloluwa Omotade, Daphne Siciliani, Teckla Angelo, Yasinta Daniel Sylvester, Safari Kinung'hi, Enock Wilbart Mlaponi, Chris T Amemiya, Donald Natvig, Irene Salinas

African lungfish (*Protopterus* spp.) differs from other aquatic vertebrates by their unique ability to live in water and land. In seasons of drought, African lungfish bury themselves in the mud and produce a mucus cocoon that prevents desiccation. Previously, we have showed that the cocoon produced by lungfish during estivation serves as an immunological barrier that protects them from microbial invasion via host cellular immunity. However, whether chemical warfare at the cocoon keeps microbes at bay during estivation is currently unknown. Here we sampled six wild African lungfish (*P. aethiopicus*) from Tanzania four months after the start of the dry season. Notably, only four animals had formed cocoons at the time of sampling. Two mucus cocoons showed high anti-fungal activity against *Mucor* and *Saproglenia* whereas the other two did not. We performed untargeted liquid chromatography-tandem mass spectrometry (LC-MS/MS) metabolomics across five complementary chromatographic and ionization methods to maximize metabolome coverage in the four cocoon samples. A total of two thousand six hundred metabolites were detected across all five acquisition methods, indicating that lungfish cocoons contain broad chemical diversity. Of all the metabolites recovered, approximately 1,700 unique molecular features were detected, including features with predicted functional groups and scaffolds consistent with azole, lactam, peptide, phenyl, and quinone structures. Cocoons with greater antifungal activity were enriched in Azole containing scaffolds. Our results suggest that lungfish cocoon contain chemically diverse metabolome that may underlie their ability to prevent microbial invasion during estivation represents a promising source of natural products with antimicrobial function.

Talk 2

Declining *kdr* Mutant Allele Frequencies in an Emerging *Aedes aegypti* Population in Albuquerque, New Mexico

Miriam A. Bechtel, Sharley A. Wasena, Jessica T. Martin, Jessie L. Smith, Nicholas D. Pederson, Mark A. DiMenna, Kristan Schneider, Douglas J. Perkins, and Ivy Hurwitz

Aedes aegypti is the primary vector of several medically important arboviruses, including dengue, Zika, and chikungunya viruses, that currently lack effective vaccines. Control of *Ae. aegypti* populations rely heavily on pyrethroid and organophosphate chemical adulticides; however, resistance to these compounds is widespread. Pyrethroid resistance in *Ae. aegypti* is associated with single-nucleotide polymorphisms (SNPs) in the voltage-gated sodium channel (VGSC) gene, otherwise referred to as knockdown resistance (*kdr*) mutations. *Ae. aegypti* was first detected in the Albuquerque metropolitan area in 2018 and has since become locally estab-

lished, underscoring the importance of resistance surveillance in this emerging population. In this study, we assessed the longitudinal prevalence of three VGSC kdr mutations, F1534C, V1016I, and V410L, in *Ae. aegypti* collected in Albuquerque, New Mexico, between 2018 and 2024. We isolated genomic DNA from individual *Ae. aegypti* mosquitoes and genotyped using allele-specific quantitative PCR with three-primer assays targeting each SNP locus. Across the study period, mutant alleles at all three loci were initially at or near fixation but subsequently declined. These findings demonstrate temporal reductions in kdr mutant allele frequencies, indicating an increasing susceptibility to pyrethroids. The declined mutant allele frequencies coincide with the introduction of organophosphate-based adulticides, implying a greater selection pressure present among the population. These findings will be used to improve the interpretation of observed kdr allele frequencies and better inform local vector control strategies.

Talk 3

Investigating Molecular Detection Accuracy of Snake Fungal Disease in a Green Anaconda Museum Specimen Under Common Chemical Preservation Techniques

Hannah D. Bradley, Dani L. F. Wiley

Natural history collections are an important resource for current and future wildlife disease research. Historically, preserving morphological traits has been the primary focus of collections, but frequently used chemicals such as Formalin, Ethanol (Ethanol), or Isopropyl alcohol can alter our ability to extract DNA and confirm the presence of certain pathogens. *Ophidiomyces ophiodiicola* (Oo) is a fungal pathogen that causes Snake Fungal Disease (SFD) and is currently spreading across the globe. Museum specimens offer a unique opportunity to historically examine Oo prevalence across wild snake populations, but the impact of preservation chemicals on Oo detection presents a challenge for their utility. In this experiment, we utilized an Oo infected specimen of a recently diseased *Eunectes murinus* (Green Anaconda) and Quantitative Polymerase Chain Reaction (qPCR) and measured how commonly used preservation chemicals influence Oo detection accuracy. The results from this experiment will inform natural history collections on how best to preserve snake specimens for future research and detection of Oo, and add to the growing body of knowledge on the historic, current, and future distribution of Snake Fungal Disease.

Talk 4

Color and size show a neat surprise: Wing chord predicts coloration patterns in female and male Red-winged Blackbirds

Chris J. Walker, Cristina Barros, Fernando Machado-Stredel, Lauryn Benedict

Coloration and body size are important examples of visual communication; as such, male Red-winged Blackbirds (*Agelaius phoeniceus*) have been studied significantly to determine how coloration and body size can reveal underlying dominance structures. Females, on the other hand, have been studied significantly less. In this study, we sought to provide more information on the function behind female Red-winged Blackbird epaulet coloration and how it differs from that of males. In particular, we tested the hypothesis that epaulet coloration honestly

signals body size. While body size and epaulet coloration seem to hold important implications for intrasexual signaling within male Red-winged Blackbirds, it is unknown how true this is for females. From March through July of 2024 and 2025, we collected photographs and measurement data (wing chord, tarsus length) for 34 live males and 23 live females in Greeley, Colorado, United States of America, as well as 15 female study skins from the Denver Museum of Nature and Science. From there, we have analyzed the photographs using ImageJ to determine average epaulet redness and brightness for each bird. We then compared color analysis results to the morphological data. We found no correlation for male redness and brightness and a strong negative correlation for female redness and brightness, suggesting a tradeoff we had not otherwise considered. Additionally, we found strong positive correlations for redness/wing chord in both sexes, a strong negative brightness/wing chord correlation in females, and no correlations for brightness/wing chord in males. Although past studies indicate size and color may both be indicators of male dominance, these two traits appear to have different implications for female Red-winged Blackbirds. Our research provides a new approach for photography-based coloration analysis that can be used for patterned and unpatterned birds, as well as brings to light the differing behavioral factors that may contribute to differences in body size and color traits and their indications related to health, age, or reproductive value.

Talk 5

Biogeographic History and Diversification of Southern Red-Backed Voles (*Myodes gapperi*)

Dale L. Fastle, Danielle J. Parsons, Brian Arbogast, Jason L. Malaney, Joseph A. Cook

Pleistocene glacial cycles repeatedly reshaped North American boreal forests, driving patterns of isolation, expansion, and secondary contact in associated taxa. These dynamics were closely tied to shifting connectivity across the northern continents through Beringia, which alternately functioned as a corridor and barrier for boreal species. The southern red-backed vole (*Myodes gapperi*), a boreal species that is endemic to North American montane forests at mid-latitudes, exhibits pronounced mitochondrial divergence among eastern, central, and western clades based on preliminary mitochondrial (mtDNA) phylogenies. Surprisingly, these clades appear to be paraphyletic, suggesting the possibility of multiple species and multiple independent invasions of North America; however, uneven geographic sampling and limited nuclear sequences have left its evolutionary and biogeographic history unresolved. This study integrates complete mtDNA genomes ($n=72$) and nuclear SNP data generated through double-digest RAD sequencing ($n=30$) to examine genomic structure across the range of this nominal species. Expanded mtDNA phylogenetic analyses will assess whether eastern, central, and western clades form consistently distinct evolutionary groups, while nuclear SNPs will test the validity of mtDNA perspectives and use population genomic approaches to evaluate genome-wide structure, possible admixture, and coalescent-based estimates of relative divergence timing. By comparing mitochondrial and nuclear patterns, this project will test whether observed divergence reflects long-term isolation in multiple refugia, historical movements across Beringia, or more recent postglacial processes such as introgression and range expansion. Special attention will be given to under-sampled southwestern sky island populations that are critical to understanding the history of this nominal species in North America. Together, these genomic perspectives clarify historical intercontinental colonization and diversification of *M. gapperi*,

determine the existence of evolutionarily distinct lineages, and contribute to a broader understanding of how climate fluctuations shaped genetic diversity in North American boreal mammals. Such insights are increasingly relevant for conserving diversity under accelerating environmental change.

Talk 6

Climate Sensitivity of Desert Grasshoppers

Emily Schmitt, David Lightfoot, Jennifer Rudgers, Kenneth Whitney

Thirty years of continuous monitoring has revealed nearly half of all grasshopper populations in the northern Chihuahuan Desert are significantly declining. While research has made substantial progress in modeling species responses to changes in climatic means (e.g., increased temperature, decreased precipitation), we still do not fully understand how more complex changes (e.g., increased variance in the timing and amount of precipitation) will impact populations. My research utilizes non-linear modeling to better understand the relationship between grasshopper population abundance and both the mean and variance of climatic variables (e.g., precipitation, temperature, aridity).

Talk 7

PRDM Paralogues Control Zebrafish Pectoral Fin Development

Job Flores, Dr. Lomeli Shull

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. Using HCR across development (13-somite to 96 hpf), we have created a temporal expression timeline and confirmed fin-bud expression for prdm3 and prdm16 developing buds. 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 quantification.

Loss of prdm16 caused clear defects in pectoral fin development, including abnormal cartilage patterning, disrupted joint formation, and asymmetrical fin morphology, while loss of prdm3 led to subtler phenotypes. In prdm16 mutants also showed significantly longer right-sided coracoid lengths and increased fin fold, endoskeletal disc, and cleithrum lengths compared to wild-type siblings. In prdm3 mutants, the significant changes were decreases in left fin fold length and left SC length, indicating those structures were shorter compared to wild-type siblings. Together, these results play an important role for both prdm3 and prdm16 in pectoral fin development. Our data suggests that these genes are expressed from early fin bud stages through larval fin development, and that loss of either one disrupts normal fin morphology. Moving forward, I plan to test how these changes affect the limb gene regulatory network us-

ing HCR and to evaluate the effects of losing both factors together in double mutants.

Talk 8

Balanced Polymorphism Arising from Temporal Offsets in Temporally Varying Selection

Katerina Johnson, Xavier Larason, Adina Ataran, Davorka Gulisija

Genetic polymorphism plays a crucial role in adaptation to changing environments, yet the mechanisms that maintain polymorphism under temporally varying selection loci remain poorly explored. While previous theoretical models have traditionally assumed synchronous selection across loci or space, natural conditions often impose mismatches in the timing of selection between loci or across space. Here, we examine how timing mismatches in the onset of temporally varying selection across genetic loci and/or space influence the maintenance of genetic variation at one or two selected loci. Using computational simulations and a one or two-locus Wright-Fisher two-deme model, with and without conditions for maintenance of variation, we introduce phase shifts in selection between two loci and between two demes and evaluate their effects on polymorphism persistence across modes (duration and magnitude) of selection and migration rates. Our results show that timing mismatches modulate heterozygosity levels compared to synchronous selection. These findings suggest that varying selection offsets can act as a stabilizing force in varying environments, promoting the long-term maintenance of genetic diversity. This research provides novel insights into the evolutionary dynamics of genetic polymorphism and its implications for adaptation in changing environments.

Talk 9

Gut Instinct: Diet Drives Protein Synthesis in Large Herbivores

Anejelique J. Martinez, Paul L. Koch, Anna K. Behrensmeyer, Seth D. Newsome

Herbivory is the most common foraging strategy among terrestrial mammals, however, these plant-rich diets rich in complex carbohydrates and dietary fiber typically contain low concentrations of nitrogen. Extensive research on wild mammalian herbivores has revealed how their specialized gut microbiomes ferment dietary fiber into short chained fatty acids that the host uses for energy. Less is known about the role of gut microbes in synthesizing amino acids that the host can use for building proteins needed to build and maintain their bodies. Recent field and laboratory studies on small mammals show that symbiotic gut microbes can convert carbon from dietary carbohydrates into essential amino acids (AAESS) that are assimilated by the host to synthesize proteins in red blood cells. Here we assess microbiome contributions to large herbivores body protein by analyzing carbon ($\delta^{13}\text{C}$) isotope values of AAESS in bone or dentin collagen from several species of large terrestrial herbivores (zebra, wildebeest, impala, elephant, black rhinoceros, giraffes) from Amboseli National Park, Kenya. This is a savanna-woodland ecosystem where herbivores have different diets (C_4 grazers, C_3 browsers, and mixed feeders) and digestive physiologies (hindgut versus foregut fermenters). Our goal is to use AAESS $\delta^{13}\text{C}$ to quantify the degree to which host tissues are built from dietary versus microbially derived

AAESS. $\delta^{13}\text{C}$ analysis indicates that grazers consuming C4 grasses characterized by low-protein but high-fiber have more microbially synthesized AAESS, particularly in foregut fermenters, due to their specialized adaptations to promote fermentation and nitrogen recycling. Our findings demonstrate a novel application of compound-specific stable isotope analysis to disentangle dietary versus microbial contributions to host tissue synthesis, highlighting the importance of microbially synthesized protein to nitrogen balance in the large herbivores in diverse terrestrial ecosystems. This integrative approach advances our understanding of how large mammals physiologically meet the ecological challenges of building and maintaining their bodies while subsisting on low-quality (protein-poor) resources.

Talk 10

Acquisition of Three Bacterial Cell-Wall Degrading Genes Enabled Transition To Herbivory In Gall Wasps (Cynipoidea)

Adam Kranz, Jack Hearn, Ellen Martinson

Gall wasps (Hymenoptera: Cynipoidea) originated within a lineage of parasitoid wasps ~200 million years ago. The majority of modern Cynipoids, with the exception of most Figitidae, are plant associates, including gall inquiline and gall inducers. A prominent part of the molecular toolkit Cynipoids use for this lifestyle is a set of enzymes capable of degrading plant cell wall polysaccharides (PCWDE). Cambier et al (2019) first observed that one of these genes, endoglucanase, appeared to be the result of lateral gene transfer from bacteria. This study traces the origin and duplication of three enzymes (endoglucanase, pectin lyase, and rhamnogalacturonan lyase) across 41 representative Cynipoid genomes. Conserved genomic neighborhoods and shared intron placement indicate that each gene was in fact acquired in a lateral gene transfer event from a plant-associated bacterium, and that all three transfers occurred near the origin of the superfamily. Lineages associated with plants retain all three genes, while lineages that have transitioned to entomophagy have lost them. Transcriptomic evidence in Cynipini shows that all three genes are expressed during gall induction, in adult venom gland and larval salivary and gut tissues. Endoglucanase in particular is frequently among the 10 most expressed genes in both larvae and venom glands. Although the precise role of each enzyme remains to be demonstrated, cell walls are a significant barrier to both physical access to plant cell contents and to the digestibility of plant material. We propose that all three PCWDE effectively lower these barriers, and therefore that their acquisition from bacteria facilitated the Cynipoids to transition to plant feeding, a necessary prerequisite to the subsequent evolution of gall induction, one of the most remarkable symbioses in nature.

Talk 11

Autotrophic and Heterotrophic Contributions to Soil CO₂ Fluxes and Variability in a Chihuahuan Desert Grassland

Savannah Sanchez, Marcy Litvak, Megan Rae Devan

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 the ex-

pansion of drylands. The consequences of these shifts are difficult to predict because ecosystem models are largely biased toward mesic systems, which have greater water and nutrient availability, faster decomposition, higher respiration rates, and different microbial communities compared to drylands. The goal of my research is to improve our understanding of carbon cycling in drylands by focusing on one component: soil CO₂ efflux through respiration. Soil CO₂ efflux is a major source of terrestrial CO₂ emissions and, in drylands, is driven primarily by plant root respiration and microbial decomposition of organic matter. I investigate the drivers of soil respiration in the Desert Plains Grassland ecosystem at the Sevilleta National Wildlife Refuge. To achieve this, I measured hourly soil CO₂ fluxes from May to September in 2023 and 2024 in an experimental manipulation with three distinct treatments: bare ground and trenched, bare ground and trenched with litter addition, and *Bouteloua eriopoda* with litter addition. These chamber measurements were paired with meteorological data from the site's eddy covariance tower. Using these data, I fit a generalized additive model (GAM) predicting soil CO₂ efflux from environmental drivers including temperature, soil moisture, and gross primary productivity. The model was then applied to historical tower meteorological data to backcast soil respiration from 2007 to 2024, allowing us to quantify long-term variability and identify the climatic drivers controlling soil CO₂ flux in this dryland ecosystem. Our results show that when scaled by percent cover, soil respiration was generally highest in the *Bouteloua eriopoda* with litter addition treatment, while the bareground and trenched treatment exhibited the greatest variability.

Talk 12

Developmental Code of *Drosophila* Central Complex Stratification

Zoe Marriner, Gabrielle Sanchez, Rahail Ashraf, and Mubarak Hussain Syed

Precisely connected neural circuits are necessary for normal brain function, but the molecular codes that enable their connectivity are not fully understood. The laminar structure of the human brain resembles the layered structure of the fan-shaped body (FB) in the *Drosophila* brain. This neuropil is part of the central complex (CX), a conserved higher-order brain center required for navigation, sleep, and decision-making. How the intricate circuits of the CX assemble during pupal development is not well studied. In particular, the molecular programs that establish layered and columnar connectivity within the FB are largely unknown. Here, we performed a systematic expression screen of candidate cell-adhesion molecules across key stages of pupal development (24, 48, and 72 h after puparium formation) and in the adult. We uncover striking, layer-specific expression of the conserved adhesion molecules Teneurin-A, Teneurin-M, and Beaten Path IV within the FB. Teneurin-A and Teneurin-M are selectively enriched in broad bands of dorsal and ventral layers, respectively. Beaten Path IV marks the intermediate layers early and then expands into the ventral layers. Together, these findings identify a previously unrecognized molecular stratification code of the FB and suggest a molecular framework for establishing laminar organization in this neuropil. Because Teneurins and Beaten Path family members are evolutionarily conserved and have been implicated in human neurodevelopmental disorders, our work provides a foundation for linking developmental wiring programs in insects to general principles of brain circuit formation and disease.

Talk 13

Parallel elevational replacement of hosts and parasites in a highly susceptible songbird genus

Daniele L. F. Wiley, Jessie L. Williamson, Silas E. Fischer, Selina M. Bauernfeind, Henry M. Streby, Kathy Granillo, Christopher C. Witt, Lisa N. Barrow

Elevational replacement distribution patterns underpin montane diversity and reflect the interaction of both biotic and abiotic pressures, but the degree to which parasites exhibit elevational zonation remains unclear. Investigating infection patterns in related host species across elevational gradients can reveal whether parasites and hosts show concordant patterns of elevational turnover, potentially due to shared historical and ecological factors. Here, we assessed patterns of elevational replacement in haemosporidian parasite assemblages that infect three congeneric songbird species: Bell's vireo (*Vireo bellii*), gray vireo (*V. vicinior*), and plumbeous vireo (*V. plumbeus*), each of which breeds across distinct elevations and habitats in the southwestern United States. We screened a total of 248 individuals using cytochrome b PCR and microscopy. We identified 19 haemosporidian haplotypes, including eight novel lineages. We found that each of the three vireo species exhibited high haemosporidian prevalence (55.0–86.2%), with nearly all infections from the genus *Haemoproteus* (subgenus *Parahaemoproteus*). Haemosporidian assemblages varied across elevations; each sampled range of elevations harbored abundant, yet host-specific lineages with different environmental associations. Bell's and plumbeous vireos, but not gray vireos, hosted several phylogenetically distinct, putative generalist lineages, likely reflecting spillover from more diverse local breeding bird communities. Repeated infections in individuals across breeding seasons, together with moderate parasitemia ($\bar{x} \approx 1\%$) suggest that these focal vireo species harbor chronic infections during their respective breeding seasons. These results demonstrate that elevational replacement patterns in avian hosts may be mirrored by their haemosporidian parasites, particularly among host-specialized lineages.

Poster Presentations:

Poster 1

The Effects of PRDM16 Loss on the Development of Craniofacial Muscle Tissue in Zebrafish

Lily Carman, Lomeli Shull, Qoots Denipah-Cook, Bryanna Saxton

PRDM16 is a protein with histone methyltransferase activity belonging to the positive regulatory domain (PRDM) family. PRDM16 is known to play an important role in craniofacial development in humans, zebrafish, and mice. In humans, the loss of PRDM16 is associated with cleft lip and palate, as well as abnormal facial morphology. The loss of PRDM16 in zebrafish and mice is associated with craniofacial defects including irregular cartilage development, impaired bone development, and cleft palate. While the effects of PRDM16 loss on bone and cartilage tissue have been examined in several studies, the effects of PRDM16 loss on craniofacial muscle tissue has not been studied extensively. The proper formation of craniofacial muscle tissue is crucial to development and enables functions such as mastication, jaw movement, eye movement,

and other vital functions. The disruption of craniofacial muscle development can lead to issues such as mandibular and facial deformities. In this study, we utilized a previously generated mutant *prdm16* zebrafish line to analyze the effects of the loss of *prdm16* on craniofacial muscle development. To assess craniofacial muscle organization in *prdm16* mutant zebrafish over developmental time, we collected fish larvae at three, four, and five days post-fertilization and stained them with phalloidin to visualize F-actin muscle fibers. We then analyzed and quantified craniofacial muscle development (including muscle fiber lengths and numbers of fibrils) to identify abnormalities. Future directions include analyzing the role of PRDM16's paralog, PRDM3, in craniofacial muscle development, as well as studying the effects of PRDM3 or PRDM16 loss on the development of craniofacial tendon tissues, which aid in connecting muscles to cartilage and bone structures. Together, these studies will shed light on the roles of these chromatin remodelers in craniofacial muscle and tendon development.

Poster 2

Bulk Stable Isotope Analysis helps reveal Niche Width Breadth and Trophic Position in Small Mammal Communities endemic to Southwestern Sky Islands

M.S. Fragua, P. Manlick, J.A. Cook, S.D. Newsome

Islands are model systems for understanding the evolution and ecology of biological communities. Hypothetically there are functional similarities between oceanic islands and isolated "sky island" mountain ranges in the American Southwest where high elevation biomes are surrounded by desert lowlands. Previous work showed that niche width of some small mammal species expands on oceanic islands with fewer mammalian competitors and predators,

when compared to diverse mainland communities. This study expands that work to examine how competition and predation impact niche width breadth among 5 Southwestern sky islands by comparing bulk stable isotopic (^{13}C and ^{15}N) niche width of species on these simplified (less diverse) communities with conspecific populations from more diverse communities (multiple congeneric species) on nearby mainland (Rocky Mountain) locations. We examine four small mammal species in the sky island system (*Sorex monticola*, *Peromyscus maniculatus*, *Microtus longicaudus* and *Neotoma mexicana*) where each belongs to distinct functional foraging groups. We predict that individual species niches will expand on the simplified sky islands where there are fewer competitors (congeneric species) and predators. We then compare that system to populations on 10 oceanic islands and mainland of the North Pacific Alexander Archipelago. We test whether niche width responds similarly across terrestrial and oceanic archipelagos.

Poster 3

Hyaluronic Acid-Based Dissolving Microneedles for Delivery of Lipid Nanoparticle Vaccines: Fabrication and Characterization

Andrea Ibarra, Peace Ikwuemesi, Olivia Lanier, and Pavan Muttil

Vaccination remains one of the most impactful tools for combating infectious diseases by sig-

nificantly reducing global morbidity and mortality. However, conventional injection-based vaccine delivery methods are often limited by factors such as needle phobia, the need for cold-chain storage, and the risk of accidental needle-stick injuries. Dissolvable microneedles (dMNs) offer a minimally invasive and potentially self-administrable alternative for transdermal vaccine delivery. This study focuses on the fabrication and characterization of hyaluronic acid (HA)-based dMNs designed for lipid nanoparticle (LNP) delivery. LNPs are widely used carriers capable of delivering biologics, including vaccines, by protecting and transporting sensitive cargo for effective administration. HA was selected for its biocompatibility, biodegradability, and favorable safety profile for transdermal applications. Key fabrication parameters, including polymer viscosity and bubble formation, were evaluated to understand their influence on microneedle morphology, structural integrity, and manufacturing reproducibility. HA dMNs were also compared to poly(acrylic acid) (PAA) microneedles, previously developed in our laboratory, to assess differences in fabrication and overall performance. Structural characterization and in vitro penetration studies were conducted to evaluate needle integrity and sharpness, mechanical strength, and insertion capability. In vitro dissolution studies demonstrated that HA microneedles dissolve faster than PAA formulations, suggesting potential advantages for rapid payload release upon insertion. Additionally, LNP loading capacity and distribution within the microneedle matrix were assessed to evaluate the ability of the system to support nanoparticle-based vaccine delivery without compromising structural stability. Collectively, these findings support HA-based dissolvable microneedles as a promising and scalable platform for transdermal LNP delivery. Future studies will include in vivo evaluation of penetration efficiency and dissolution behavior, as well as immunogenicity assessments and long-term stability studies, to further validate their potential for next-generation vaccine applications.

Poster 4

MyD88 influences T cell activation and IFN- γ production in the peritoneal cavity during infection with *Toxoplasma gondii*

Fatouma Z. Issoufou Kapran, Jessica Belmares-Ortega, Eric Y. Denkers

Toxoplasma gondii is an opportunistic parasite that can cause serious and sometimes lethal disease in immunodeficient individuals such as those with acquired immune deficiency syndrome. The parasite can also cross the placenta to infect the developing fetus and is thus a serious congenital infection. Nevertheless, under most conditions, infection with *Toxoplasma* is innocuous, leading to life-long asymptomatic infection. Therefore, understanding the protective mechanisms acting to prevent serious infection is crucial to improve resistance to disease. MyD88 is a key adaptor protein for intracellular signaling involving Toll-like receptors (TLRs) and IL-1 receptors leading to production of proinflammatory cytokines in cells of innate immunity. Using genetically engineered MyD88 knockout mice, we focus here on understanding the influence of this innate adaptor protein on the generation of effector CD4⁺ and CD8⁺ $\alpha\beta$ T cells during chronic infections with *T. gondii*. Our approach was to infect mice with a nonlethal dose of *T. gondii*, then 21 days later challenge with a strain of parasites that is lethal in the absence of acquired immunity. Our survival tests showed a rapid death (within 2 weeks) of knockout mice (KO) whereas wild-type (WT) mice significantly survived longer. Quantification of IFN- γ released by peritoneal exudate cells (PECs) and splenic cells revealed a significant loss of this function in

KO mice upon restimulation with soluble tachyzoite antigen (STAg). FACS data obtained from these cells also displayed differences in CD4⁺ and CD8⁺ $\alpha\beta$ T cell proportions between both strains, specifically a lower detection of T cell activation markers in KO mice and a higher frequency of IFN- γ in WT mice. Overall, these results indicate the role of the adaptor protein in T cell activation and IFN- γ production to promote protection against pathogens such as *T. gondii*.

Poster 5

Investigating the Role of Prdm3 During Pharyngeal Tooth Development in Zebrafish

Ana Olivas, Lomeli C. Shull

PRDMs (Positively Regulatory Domain) are a family of histone methyltransferase proteins that play an important role in gene expression and regulation by modifying chromatin. For proper skull formation, neural crest cells (NCCs) migrate to the head region, where they differentiate and produce the skull. Specifically, two members of the PRDM family, *prdm3* and *prdm16*, regulate the switch of cranial NCCs to craniofacial cartilage. Loss of *prdm3* and *prdm16* in zebrafish results in defects in both the viscerocranium and neurocranium cartilage structures. In zebrafish, a set of pharyngeal teeth is located on the ceratobranchials at the posterior of the viscerocranium. Given the defects in the viscerocranium in *prdm* mutants, we investigated the role of *prdm3* in pharyngeal tooth development. To assess changes in pharyngeal tooth morphology, *prdm3* mutant zebrafish were collected at 6 days postfertilization and stained with Alcian blue and Alizarin red to visualize cartilage and bone, respectively. These whole mount skeletal preparations were dissected and flat mounted, and high magnification images of the pharyngeal teeth were collected. We found that the loss of *prdm3* appears to cause a decrease in mineralization in the pharyngeal teeth, with mutants showing little to no red staining compared to the wild-types, whose teeth exhibited the most staining. Heterozygous fish showed staining from a range of heavily stained teeth to little staining. Future work includes performing quantitative measurements on these structures and analyzing changes in gene expression during early pharyngeal tooth development in *prdm3* mutants. Because tooth development in vertebrates is highly conserved, characterizing the pharyngeal teeth in *prdm3* zebrafish mutants could reveal how *prdm3* influences tooth development.

Poster 6

Heterogeneous Freshwater and Solute Export from a Mountainous Headwater Stream Network

William Meija-Garcia, Manuela Londoño-Gaviria, Alex Webster

Mountainous headwater stream networks are key drivers of freshwater and solute export to downstream waters and exert a strong influence on riverine chemistry due to their high surface-area-to-volume ratios and terrestrial-aquatic connectivity. Varied flow paths across heterogeneous terrestrial subcatchments result in distinct assemblages of geogenic and biogenic solutes delivered to streams, where they may serve as indicators of ecosystem function. Un-

derstanding how landscape characteristics influence freshwater and solute export is particularly important as high-elevation watersheds undergo climate-driven shifts in precipitation patterns and vegetation communities, affecting water resource resilience worldwide. Since 2023, we have conducted monthly catchment-wide synoptic sampling campaigns of stream-flow and water chemistry across gradients of elevation, aridity, vegetation composition, topography, and hydrological connectivity within a major municipal watershed of the southwestern United States. We characterized the magnitude and variability of subcatchment contributions to total watershed export through a residual analysis and inferred stream network function via mass-balance-based ecohydrological metrics. Our residual analysis suggests that high-elevation subcatchments, which receive greater mean annual precipitation, export higher-than-expected and less variable amounts of freshwater, nitrate, phosphate, and dissolved organic carbon (DOC), relative to lower-elevation, drier subcatchments. These patterns reflect hydrological controls on solute export and likely arise from shallower, more dynamic flow paths associated with biogenic solute transport. However, several sites exhibit behavior opposite to that of adjacent subcatchments with similar terrestrial characteristics, suggesting heterogeneous terrestrial nitrate pools, contrasting source types, or localized land disturbance. Furthermore, ecohydrological metrics reveal seasonal DOC enrichment and nitrogen uptake at lower-elevation stream reaches, highlighting differences across the catchment. Through these analyses, we identify subcatchments and stream reaches that disproportionately contribute to catchment-wide export and exert influence on stream network function. These findings provide insights to inform watershed management strategies aimed at maximizing the reliability of freshwater export, improving water quality, and supporting watershed resilience under changing climatic conditions.

Poster 7

Climate Driven Diversification and Connectivity in Southwestern Sky Island Populations of *Sorex monticola*

Patricia G. Sotelo Chavira, Lexi B. Baca, Jason L. Malaney, Danielle J. Parsons, Jesús A. Fernández, Joseph A. Cook

Quaternary (~2.5 Ma-present) climate oscillations influenced evolutionary processes in Southwestern biomes and provide insights into how dynamic climates may shape future genetic structure across species. In the American Southwest, late Pleistocene warming and continued Holocene change have forced forest-associated species upslope, fragmenting formerly connected populations among isolated mountain ranges ("sky islands"). These systems provide natural laboratories for testing how climatic fluctuations structure diversity, demographic history, and evolutionary divergence. The montane shrew (*Sorex monticola*) occupies cool forest habitats across western North America. Recent phylogeographic analyses identified a distinct southern mitochondrial lineage distributed within the Southwestern and Mexican Montane Region (SMMR), including sky islands in Arizona, New Mexico, and northern Mexico. Although geographic isolation among ranges may contribute to population structure, the demographic history of the populations and the extent of historical connectivity among sky islands remain poorly understood. To evaluate alternative hypotheses of population history, complete mitochondrial genome sequencing will be used with nuclear genomic data. Mitogenomes were

generated using Oxford Nanopore MinION sequencing, and nuclear genomic variation will be characterized using double digest restriction-site associated DNA sequencing (ddRADseq) to obtain genome wide single nucleotide polymorphisms. 48 museum specimens representing eight New Mexico sky island regions (Sange de Cristo, Gila, Sacramento, Mogollon, Jemez, San Juan, Manzano, and Mount Taylor) and one adjacent non-sky island locality near the Sevilleta National Wildlife Refuge were analyzed. These samples represent the southern lineage of *S. monticola* and provide a focused framework for testing diversification in the southwestern portion of the species complex. Genomic analyses will infer phylogenetic relationships, quantify population structure, and reconstruct demographic histories to evaluate competing models: cyclic isolation during glacial-interglacial cycles, stochastic colonization followed by long-term isolation, and gradual expansion across montane corridors. Species distribution models will reconstruct potential habitat connectivity under past climatic conditions. The Sacramentos will be further examined where prior mitochondrial data identified an anomalous lineage (*S. neo-mexicanus*); new mitogenomes will test whether this pattern reflects long-term isolation or historical introgression. Together these analyses will clarify how climate driven fragmentation shaped genetic structure across southwestern sky islands and inform expectations for montane persistence under ongoing warming and drought.

Poster 8

Beneath the Wings: Microbial Allies in the Fight Against White-Nose Syndrome

Morrigan Vega

White-nose Syndrome (WNS), caused by the fungus *Pseudogymnoascus destructans*, has decimated bat populations in the United States since its discovery in 2006. The fungus disrupts hibernation, leading to premature arousal and fat depletion, resulting in starvation and death. While WNS has significantly impacted bat species, the role of microbiomes—particularly skin and gut microbiomes—in modulating disease susceptibility remains poorly understood. In humans, microbiomes are known to influence health outcomes, including immune responses and disease susceptibility. Recent studies suggest that bat microbiomes may also play a role in disease resistance. *Myotis lucifugus*, for example, has a less diverse skin microbiome compared to species like *Eptesicus fuscus*. Meanwhile, *Lasionycteris noctivagans* appears resistant to *P. destructans* despite fungal colonization. While there is some coverage of the skin microbiome of bats, the gut microbiome of bats in relation to WNS has not been studied.

This research aims to characterize the gut and skin microbiomes of WNS-susceptible and resistant bat species in the southwestern United States, particularly in New Mexico and Arizona, where WNS is spreading. We hypothesize that differences in microbial diversity and specific microbial metabolites in both skin and gut may contribute to differential responses to WNS among bat species. Understanding these microbiomes could inform conservation strategies as WNS expands into new regions, helping to mitigate its impact on bat populations and the ecosystems they support.

Poster 9

The fourth reason to burrow: triple oxygen isotopes provide insight into how behavior influences water balance

Cloe V. Knutson, Zachary D. Sharp, Seth D. Newsome

Burrowing has been hypothesized for three main reasons: food caching, protection, and temperature regulation. Our study has found a fourth reason animals burrow, water conservation. In arid environments, maintaining water balance can be more critical for survival than obtaining food. As droughts intensify, understanding how desert-dwelling animals manage body water is essential. Triple oxygen isotope analysis provides a novel way to trace water sources in animals, distinguishing contributions from free water (drinking water, food water, and water vapor) and metabolic water (water produced from food-derived oxygen and atmospheric O₂ through respiration). We developed an equilibration method using CO₂-H₂O oxygen exchange to measure $\delta^{18}\text{O}$ and $\Delta^{17}\text{O}$ values via tunable infrared laser direct absorption spectroscopy (TILDAS). Validated against traditional cryogenic distillation methods, this technique enables streamlined analysis of whole blood and plant samples. Applied to desert-dwelling rodents (Heteromyidae), our method revealed seasonal shifts in water use, with free water inputs closely tracking precipitation, due to the humid conditions inside animals' burrows. This humidification of burrows is heightened with warmer temperatures and precipitation events where the air becomes more saturated with water vapor. This water vapor has previously been proposed to rehydrate cached seeds within the burrow, but by modifying existing triple oxygen body water models our study has found that fossorial animals incorporate this water vapor into their body water pool just through breathing and can contribute up to 20% of an animal's body water pool. Leaf water data exposed limitations in existing body water models, underscoring the need for ground truthing ^{17}O -based body water models for paleoclimate reconstruction with modern systems.

Poster 10

Long-term balanced polymorphism at multiple loci under spatial gradients in temporally varying selection

Keya Biswas, Davorka Gullisija

Understanding how genetic diversity persists under fluctuating environmental conditions remains a central challenge in evolutionary biology. While temporally varying selection can maintain balanced polymorphism at single loci under geometric mean overdominance or storage effects, extending this mechanism to multiple independent loci has proven difficult without invoking dominance reversal or physical linkage. Here, we examine whether long-term balanced polymorphism can emerge at many unlinked loci in spatially structured populations experiencing temporally varying selection with a spatial gradient in mean fitness effects, a previously unexplored scenario. Using forward-in-time Wright-Fisher simulations, we compare levels of diversity arising in a structured metapopulation under temporally varying selection, storage effect, directional selection (spatial gradient), and their combinations, under varying migration rates and seasonal durations. Preliminary results show that combining temporal variation with spatial differences in mean selection strength can stabilize polymorphism at a single locus beyond the effects of each mechanism alone, particularly under intermediate migration. The effect appears robust to the introduction of additional selected, unlinked loci. This framework

provides a general explanation for the maintenance of multi-locus diversity without dominance or linkage.

Poster 11

IL-36 γ Induction and MAPK Signaling Activation in Human Intestinal Epithelial and Primary Foreskin Fibroblast Cells During *Toxoplasma gondii* Infection

Miriam Shin, Jessica Belmares Ortega, Fatouma Zara Issoufou Kapran, Eric Denkers

Interleukin-36 γ is a proinflammatory cytokine within the IL-1 cytokine family. The 3 agonist members of this family (IL-36 α , IL-36 β and IL-36 γ) are recognized as crucial signaling proteins involved in recruiting immune cells, as well as signaling for proliferation, activation, or further expression of more inflammatory cytokines within other cells such as epithelial, keratinocytes, dendritic, macrophages, and T cells. IL-36 γ and the closely related proteins IL-36 α and IL-36 β trigger two signal transduction cascades, the mitogen-activated protein kinase (MAPK) pathway and the NF- κ B pathway, which culminate in transcription of pro-inflammatory genes. Despite several studies characterizing IL-36 γ 's function in host immunity, the molecular mechanisms underlying induction and function of IL-36 γ remain enigmatic. Our aim is to gain insight into the functional significance of this cytokine in the immune response to *Toxoplasma gondii*, an invasive protozoan parasite capable of infecting humans, domestic animals, and wildlife. Using the human intestinal epithelial cell line HIEC-6 and primary human foreskin fibroblasts as host cells, I demonstrated that IL-36 γ strongly stimulates MAPK signaling, as revealed by phosphorylation of kinases ERK1/2 and p38. Furthermore, I used semiquantitative real-time PCR to examine the induction of IL-36 γ gene transcription in response to *Toxoplasma* and a panel of recombinant cytokines (IL-22, IL-1 β , and IL-17A). My preliminary data using HIEC-6 cells indicate that *T. gondii* triggers strong upregulation of IL-36 γ gene transcripts. Recombinant cytokines alone induced weaker IL-36 γ transcriptional upregulation. When infected cells were co-stimulated with recombinant cytokines, there was noticeable upregulation of IL-36 γ transcripts. These results together demonstrate that *T. gondii* strongly activates IL-36 γ transcription, and that the unique combination of the three cytokines, IL-17A, IL-22, IL-1 β induces distinctive IL-36 γ expression. Through further research efforts on IL-36 γ and its systemic behavior in the immune response against *T. gondii*, we may be able to better comprehend its role against other pathogens and diseases, as well as its significance in host pathogen interaction.

Poster 12

The Role of VDAC2 in Regulating Mitochondrial Reactive Oxygen Species in Hair cells of *Danio rerio*

Brooklynn Patterson and Andrea McQuate

Hair cells inside the inner ear of all mammals are responsible for converting physical sound vibrations into electrical signals. Because they are highly sensitive sensory receptors, a multitude of things can result in their death. Hair cells do not regenerate in mammals, leading to hearing loss. Hair cells rely on mitochondria because they require a large amount of ATP to function. VDAC2 is a channel on the outer mitochondrial membrane that serves many purposes within

a hair cell, such as cell metabolism, transportation, and inhibiting apoptosis. It is an essential protein for the movement of Ca^{2+} from the ER to the mitochondria. Reactive Oxygen Species (ROS) also play a large role in hair cell functionality. ROS accumulation can lead to oxidative stress, which can cause damage to the hair cell. We hypothesize that VDAC2 is essential for regulating mitochondrial ROS in hair cells. To test this hypothesis, we used zebrafish as our model organism because they have hair cells on the outer surface of their body, making them easier to access. We exposed zebrafish larvae to two fluorescent dyes, MitoTracker and MitoSOX, to visualize hair cell mitochondria and their ROS levels, respectively. We then imaged the hair cells using confocal microscopy. We analyzed the images using IMARIS, with MitoTracker as a mask to measure for MitoSOX. We found that there is no difference in MitoSOX Mean fluorescence between WT and het animals, but a trend towards an increase in ROS in VDAC2 homozygous mutants, though these results require greater statistical power. These data provide new insights into regulators of hair cell ROS, and could provide new information towards mitochondrially-related hearing loss.

Poster 13

Survey and Analysis of the Prevalence of Chronic Wasting Disease in New Mexico Elk and Deer

Hollis Gray Patton

Chronic Wasting Disease (CWD) is a transmissible spongiform encephalopathy that affects elk and deer throughout 36 states. The disease is fatal and incurable, and does not decay in the environment, even without a host. The disease, while low prevalence in New Mexico, has spread quickly and devastatingly through much of the country. This project involves taking lymph node and brain stem samples from Rocky Mountain Elk (*Cervus canadensis nelsoni*) and White Tailed Deer (*Odocoileus virginianus*) at hunter check stations set up in conjunction with the NMDGF wildlife veterinarian. Following the sampling, statistical analysis of the collected data over several years was performed to determine an interval of 99% confidence of the actual prevalence of the disease, accounting for biases. My fieldwork took place from October through December 2025, supporting established NMDGF hunter check stations. Collected samples were sent to the Texas A&M Medical Diagnostic Laboratory to be tested for CWD using an Enzyme Linked Immunosorbent Assay (ELISA) test. Preliminary analysis of data from past years in this area showed a wide estimate of the prevalence, showing a range between 1 and 164 animals infected with CWD, demonstrating a significant need for increased testing to understand how this incredibly dangerous disease is spreading. As such, this project takes an analytical approach to what so far has been a detected/not detected study, estimating prevalence and current spread of CWD in Rocky Mountain Elk and White Tailed Deer in New Mexico.

Poster 14

A Microbial Symphony of Nitrogen Cycling

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 inhabitants shape the environment by conducting redox reactions that contribute to secondary mineral formation, produce 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, the genera of Archaea and Bacteria involved in nitrogen cycling within these systems, and whether they engage in syntrophic relationships, remain poorly characterized. To address this, our study investigates prokaryotic community composition by analysis of the archaeal and bacterial 16S rRNA genes using Illumina MiSeq. Results show bacterial genera associated with nitrogen fixation, nitrite oxidation, and denitrification, alongside archaeal genera linked to ammonia oxidation, together comprising the major steps of the nitrogen cycle. Further investigation using a co-occurrence network analysis revealed strong Spearman correlations between bacterial and archaeal nitrogen-cycling genera, suggesting they engage in syntrophic relationships to support nitrogen cycling. Future work includes bulk isotopic analysis of $\delta^{15}\text{N}$ to trace the environmental sources from which these microbes obtain their nitrogen. These results will provide foundational insight into how microbial communities acquire and cycle nitrogen to establish and sustain growth in lava caves, with broader implications for understanding these ecosystems.

Poster 15

Intestinal Epithelial MHC Class II Expression is Driven by Innate-Derived IFN- During *Toxoplasma gondii* Infection

Cory D. Henn, Jessica Belmares-Ortega, Fatouma Zara Issoufou Kapran, Eric Y. Denkers

Toxoplasma gondii is a widespread intracellular protozoan parasite capable of infecting virtually all warm-blooded animals, including humans. Infection is typically acquired through ingestion of contaminated food or water, making the intestinal epithelium the primary site of parasite invasion. Intestinal epithelial cells (IECs) are known to express major histocompatibility complex class II (MHC II) molecules, which are typically associated with professional antigen-presenting cells of the immune system, but the significance of this observation is not clear. Here, we show that oral *Toxoplasma* infection triggers robust MHC II upregulation on small intestinal IECs, sustained for up to 21 days post-inoculation. To identify the molecular and cellular requirements for this response, we perorally infected a panel of gene-targeted knockout mouse strains, including *Ifn* γ ^{-/-}, *Tcr* β ^{-/-}, *Tcr* γ ^{-/-}, *Myd88*^{-/-}, *Rag1*^{-/-}, and *Rag2/Il2*^{-/-} mice. IFN γ was strictly required for IEC MHC II upregulation, as *Ifn* γ ^{-/-} mice displayed near-zero expression during infection. In contrast, IEC MHC II expression was maintained in the absence of TCR β , TCR γ , *Rag1*, and *MyD88*, indicating that adaptive immune cells and *MyD88*-dependent signaling are dispensable. Importantly, *Rag2/Il2*^{-/-} mice, which lack the innate lymphoid cell compartment showed significantly reduced IEC MHC II expression. Together, our data demonstrate that IFN γ -dependent IEC MHC class II expression during *Toxoplasma* infection requires ILC1 or NK cells of the innate lymphoid compartment.

Poster 16

New Mexico Butterflies Display Variable Responses to Climate Predictors

Gabrielle Rael

Currently, butterflies are experiencing rapid abundance, biodiversity, and biomass declines across North America. Simultaneously, anthropogenic climate change is significantly altering New Mexico's climate, with rising temperatures and more variable precipitation driving an increase in extreme weather events and prolonged drought periods. Butterflies serve as indicators of ecosystem health and environmental change due to their sensitive response to climate and environmental shifts like drought, reduced air quality, or host plant decline. Additionally, they provide crucial, climate susceptible ecosystem services as pollinators, supporting native biodiversity and agriculture. Butterflies are one of the few insect groups that have been adequately monitored to provide accurate long-term data for species and population trends. Although monitoring efforts are quite expansive, analysis of this data is limited and inconclusive. In biodiverse hot spots, like New Mexico, we have yet to fully understand how butterfly biodiversity has shifted with climate. We used data from the New Mexico Butterfly Monitoring Network (NMBMN) to determine changes in butterfly abundance and diversity metrics over time and with climate predictors. Additionally, we assessed species vulnerability based on life history traits and habitat. With these findings, we can better predict how butterfly declines differ in magnitude among regions, local environments, and in association with climate and environmental change to better inform policy, education, and conservation strategies that address biodiversity losses and their consequences.

Poster 17

Genomic Insights into Shrew Diversity and Phylogenetics of *Sorex merriami*

Audrey K. Vanderhee, Danielle M. Land, Danielle J. Parsons, Patricia G. Sotelo Chavira, Jason L. Malaney, John R. Demboski, Joseph A. Cook

Long-tailed shrews (genus *Sorex*) represent one of the most species-rich mammalian clades in the Holarctic, comprising approximately 89 nominal species. As boreal and montane adapted species became fragmented across southwestern "sky islands" during the warming period that followed the Last Glacial Maximum, evolutionary processes related to isolation may have generated geographically structured and potentially cryptic evolutionary lineages. In *Sorex*, morphological characters such as body size, pelage coloration, and cranial measurements often show overlap among taxa, making species boundaries difficult to diagnose and increasing the likelihood of cryptic diversity, which are genetically distinct evolutionary lineages that are not readily distinguishable based on morphology alone. Merriam's shrew is broadly distributed across the southwestern United States, occurring from the southern Rocky Mountains through the Great Basin and Colorado Plateau and into montane systems of Arizona, New Mexico, Utah, Colorado, Nevada, and parts of California. The species has been characterized as associated with relatively cool and moist habitats at moderate to high elevations, including montane forests and subalpine environments. Despite its broad geographic range, *S. merriami* has been largely absent from molecular datasets and, to date, has never been explicitly placed within a compre-

hensive phylogenetic framework for the genus. As a result, its evolutionary relationships and the extent of geographic structure across its range remain poorly understood. In 2020, new records of *S. merriami* from high elevations in the San Mateo Mountains of New Mexico underscored the need for genomic data to confirm species identity and clarify relationships within the genus. To address this gap, we are generating novel genomic resources from both historical and recently collected museum specimens spanning the known geographic distribution of *S. merriami* in western North America. Complete mitochondrial genomes will be targeted for all available samples, including specimens from the Museum of Vertebrate Zoology (UC Berkeley), Denver Museum of Science and Nature, and Museum of Southwestern Biology (UNM). Where DNA quality permits, we also will generate nuclear double-digest restriction-site-associated DNA sequences (ddRADseq) to provide higher-resolution inference of phylogenetic relationships and population structure. Select mitochondrial loci will be validated using Sanger sequencing to confirm next-generation sequencing results. Resolving the genomic diversity and phylogenetic placement of *S. merriami* will clarify patterns of diversification within North American shrews and contribute to broader efforts to document cryptic diversity and evolutionary history in montane systems of the Southwest.

Poster 18

Evaluating Drought Stress in Piñon-Juniper Woodlands Using Thermal Imaging

Derek Kober

Canopy temperature is directly regulated by transpiration and, thus, a potential indicator of plant water status in semi-arid ecosystems. However, little research has been done assessing the reliability of using canopy temperature as a proxy of tree water use, and to assess the optimal temperature for tree function. This project used high frequency thermal infrared imaging to determine: 1) if canopy temperature (at branch, crown, and stand scales) is a good proxy for water use and drought stress in a piñon pine (*Pinus edulis*) and juniper (*Juniperus monosperma*) woodland across seasons and water availability; and 2) if canopy temperature can provide species-specific critical temperature thresholds of tree function in these woodlands. Our overall goal is to improve the ability to quantify water stress remotely at the tree and stand scale in piñon-juniper woodlands. I installed three thermal infrared cameras in 2024 at the New Mexico Elevation Gradient Ameriflux core site US-MPJ: 1 at the top of the flux tower, and 2 at canopy height focused on piñon and juniper clusters. From the thermal images, I identified 12 ROI's (regions of interest), 5 of piñon and 7 of juniper, to generate a time series of the difference between canopy and air temperature ($\Delta T = T_{\text{canopy}} - T_{\text{air}}$). I used high resolution point dendrometers (TOMST) and Granier sap flux probes installed on 2 juniper and 2 pinon trees in view of the cameras to get simultaneous time series of tree water deficit (TWD) and water use. Soil water content (SWC) at 5cm, 10cm, and 30cm, ecosystem-scale evapotranspiration (ET), vapor pressure deficit (VPD), air temperature, and precipitation were also recorded every 30 minutes as part of the US-MPJ flux tower. I found that: 1) ΔT is related to the response of the canopy function, showing that with increased ΔT there is lower ET, lower SWC, and increased VPD; 2) ΔT is a good proxy for species-specific tree water use and TWD in piñon and juniper; and 3) *P. edulis* appears to reach a ΔT threshold at lower SWC levels and earlier in the growing season than *J. monosperma*, reflecting different hydraulic strategies. These findings show that

thermal imaging is a reliable tool to determine water status of semi-arid ecosystems, and that ΔT thresholds can help quantify drought stress of coexisting species from an individual to stand level.

Poster 19

Distribution and Morphology of Rio Grande Sucker in the Upper San Francisco River Basin

Ashley T. Willis Mascarenas, Thomas F. Turner

Little is known about the range the Rio Grande Sucker (*Pantosteus plebeius*) in the upper San Francisco River Basin. In this part of the range, Rio Grande Sucker co-occurs with Desert Sucker (*Pantosteus clarkii*) with evidence of introgressive hybridization at some localities. We are interested in documenting the full extent of the range of Rio Grande Sucker and identifying zones of overlap. We will evaluate morphological and meristic characters that distinguish the two species in allopatry and where they hybridize. To address this, we conducted extensive exploratory sampling throughout the San Francisco headwaters and collected specimens and fin clips for genetic analysis. We then performed geometric morphometric analysis on Desert Sucker and Rio Grande Sucker specimens using tpsDigital for landmarking and the geomorph R package for General Procrustes Analysis, Principle Component Analysis, and Canonical Variate Analysis. We found that species differ significantly in shape but have similar allometric growth trajectories. We will continue this investigation using nextRAD sequencing to document hybridization status and clarify morphological uncertainties associated with introgressive hybridization. Understanding whether morphological characteristics distinguish these species, and how they change with hybridization status, will assist managers in field identification and management of Rio Grande Sucker.

Poster 20

Isotope Analysis of Aquatic Macro Invertebrates in a Northern New Mexico Fishery

Lola Kadlec

As part of a larger project analyzing the diet of North American River Otters (*Lontra canadensis*) in Taos County, NM, through stable isotopes, I looked at macro invertebrate (>5 cm length) that, through scat analysis, were already found to be a substantial part of otter diet. My work looked at freshwater mussels (Family Unionidae) and crayfish (Family Cambaridae) These invertebrates were collected in the summer of 2025 in the Rio Grande Del Norte National Monument by hand and hand net. Samples were frozen, cut up, freeze-dried, weighed, and put into an isotope mass spectrometer at the University of New Mexico Center for Stable Isotopes. We then analyzed the carbon (^{13}C) and nitrogen (^{15}N) signature of each sample. We then compared this isotopic data with existing fish isotopic data to better understand their place in the food web. The main animal we want to compare to the macro invertebrates is the North American River Otter which is a species that was reintroduced into New Mexico in 2008 after being extirpated from New Mexico due to over hunting, pollution, and habitat loss. Collectively this data will help us paint a better picture of otter diet especially as it relates to sport fish which is a concern for some in the fishing community.

Poster 21

Heavy Metal Bioremediation Potential of Fungi Native to the Jackpile Uranium Mine

Abigail Granath, Geisianny Moreira, Jose Cerrato, and Jennifer Rudgers

Fungi play vital roles in metal cycling, offering beneficial applications in both environmental and industrial sectors, including the bioremediation of metals. However, current methods to quantify fungal growth and metal removal efficiency are typically separate, destructive, and labor-intensive, limiting reproducibility and scalability. Here, we developed a high-throughput, microplate-based spectrophotometric assay to monitor filamentous fungal growth in situ with heavy metals. This approach enables non-destructive time series of growth while maintaining compatibility with standard metal quantification techniques, such as inductively coupled plasma-optical emission spectroscopy (ICP-OES). We applied the method to evaluate cadmium and arsenic tolerance and removal efficiency in six fungal species isolated from roots and soils of the Jackpile Mine in New Mexico. Absorbance-based fungal growth curves revealed species-specific responses to cadmium and arsenic exposure. ICP-OES analysis confirmed that cadmium removal efficiency varied among species and was greatest for *Fusarium oxysporum* and *Trichoderma* sp. 1. Together, these results support the utility of microplate-based spectrophotometry for simultaneous assessment of fungal growth and metal removal. This scalable framework can be adapted for diverse, culturable fungal species and metal contaminants in bioremediation studies.

Poster 22

Phenological plasticity could be enabling *Bouteloua eriopoda* to persist at range edge

Rachael Auer, Marcy Litvak, Rae DeVan

Climate change is raising average temperatures, encouraging range shifts and changes in phenology in many plant species. Current ecological theory suggests that at the margins of a species' range, phenology should be more plastic; however, results are mixed and primarily focus on the encroaching edge. Habitat quality often decreases toward range edges, and phenotypic plasticity can be advantageous for dealing with low-quality habitat, providing a competitive advantage. Phenological plasticity may therefore accelerate or slow range shifts at range margins. To investigate the range-edge plasticity hypothesis in a species undergoing a range shift, we studied black grama (*Bouteloua eriopoda*), the dominant grass species in Chihuahuan Desert grasslands. At its leading edge, these grasslands are encroaching into Great Plains grasslands dominated by blue grama (*Bouteloua gracilis*). At the trailing edge, Chihuahuan Desert grasslands are being encroached upon by Desert Shrubland dominated by creosote (*Larrea tridentata*). We used phenocams set up at the Sevilleta LTER in three crucial parts of black grama's range: the leading edge (black grama and blue grama; $n = 3$ years), the trailing edge (black grama and creosote; $n = 10$ years), and the central population (black grama; $n = 10$ years) to measure daily greenness values. Phenometrics (day of year corresponding to Start of Season, Peak, and End of Season) were calculated from the greenness time series, and the mean and variance of phenometrics were then compared across sites. Relative to the central population, black grama at its trailing edge is more phenologically plastic and has a longer growing season.

At its leading edge, however, it did not differ in plasticity or phenology. Our results suggest phenological plasticity could be giving black grama a competitive advantage, allowing it to persist at its range margins at the Sevilleta LTER. However, the lack of plasticity in phenometrics at the leading edge compared to the central population suggests that phenological plasticity may not be facilitating encroachment into Great Plains grassland at the Sevilleta LTER. This research highlights the need to study phenological plasticity across a species' range and suggests that phenological plasticity may be allowing black grama to maintain its current range.

Poster 23

Microbial synthesis of essential amino acids from glycolytic versus TCA cycle derived precursors impacts host protein metabolism

Conner Mertz, Leigh James, Alana Robinson, David Robinson, Christy Mancuso, Cristina Takacs-Vesbach, Seth Newsome

Wild omnivorous and herbivorous mammals consume low-protein, fiber-rich diets and rely on gut microbes for supplementation of essential nutrients. Microbial fermentation of polysaccharides into absorbable energy is well studied, but the contribution of microbially synthesized essential amino acids (EAA) to host protein metabolism remains unclear. Previous work suggests up to 25% of skeletal muscle EAA are microbially derived, but these estimates considered only synthesis from dietary carbohydrates, excluding non-essential amino acid (NEAA) precursors. We fed captive deer mice (*Peromyscus maniculatus*) diets enriched with 2% ¹³C-labeled glutamic acid or alanine. Using stable isotope analysis, 16S rRNA sequencing, and metatranscriptomics, we traced microbial production of EAA and assimilation across host tissues. Mice fed ¹³C-glutamic acid showed enrichment, whereas mice fed ¹³C-alanine did not, indicating microbes preferentially use TCA cycle derived precursors. These findings reveal mechanisms by which gut microbes supply essential nutrients to hosts, shape microbiome ecology, and maintain host protein balance.

Poster 24

Unraveling a comparative landscape of protein-coding genes linked to neuroimmune function during adulthood consequent of prenatal alcohol exposure

Alissa Jones, Ariana Pritha, Ashlynn Aguilar, Andrea Pasmay, Justin Carter, Carlos F Valenzuela, Nikolaos Mellios, Shahani Noor

Prenatal alcohol exposure (PAE) leads to fetal alcohol spectrum disorders (FASD), which are associated with lifelong neurobehavioral deficits. Evidence suggests neuroimmune dysfunction as a key underlying mechanism of FASD-associated adverse central nervous system outcomes. Previous reports have shown evidence of a primed neuroimmune state in adulthood where proinflammatory bias is unmasked following subsequent immune activation in later life. However, PAE-induced region-specific transcriptional changes describing this neuroimmune landscape in adulthood remain poorly defined. We hypothesized that PAE leads to long-term changes in basal mRNA expression, which may involve neuroimmune genes in a brain region-specific manner. Using RNA sequencing, we compared PAE (moderate paradigm) and control brain tissues

generated in female mice. We compared across six regions from adult female PAE offspring: medial prefrontal cortex, anterior cingulate cortex, hypothalamus, hippocampus, midbrain, and medulla. We investigated PAE-induced changes in the brain by mapping dysregulated gene pathways and molecular networks and identifying key transcriptional regulators, focusing on neuroimmune function. Our data identified ≥ 60 differentially expressed genes per brain region. Upregulation of multiple proinflammatory factors and pathways was observed across various regions, suggesting baseline ongoing neuroimmune activation. A comparative analysis of activation states of canonical inflammatory pathways identified multiple upstream transcriptional regulators across multiple brain regions with heterogeneity across immune pathways. These results highlight novel patterns of mRNA dysregulation and reveal region-specific changes in genes linked to glia-immune function in PAE adult females, uncovering potential immune targets to elucidate the mechanisms underlying behavioral dysfunction and provide a framework for future therapeutic interventions for FASD individuals.

Poster 25

Determination of developmental code that defines olfactory navigation system in *Drosophila*.

Tulaib Azam, Jesicka villagrana, Mubarak Hussain Syed, Katherine Nagel.

The brain is a complex organ across vertebrates and invertebrates, that acts as a seat for sensory processing, motor control, and higher-order behaviors. Interestingly, insect brains, like the *Drosophila* also exhibit similar complex behaviors, suggesting that core neural principles are broadly conserved across species. Olfactory navigation is one such complex conserved behavior, seen across arthropods. At the center of these behaviors in *Drosophila* is the central complex (CX), a conserved brain structure essential for sensory integration and motor coordination. All these behaviors arise from precisely assembled neural circuits composed of diverse neuron types, with high developmental precision. Yet the developmental mechanisms that generate this diversity and ensure circuit precision remain poorly understood. Elucidating these processes is critical, as disruptions during brain development can lead to neurological disorders, many of which have unclear origins. Using *Drosophila* as a model system, my research addresses three fundamental questions: (1) How is neuronal diversity generated from neural stem cells (NSCs)? (2) How do distinct neuronal subtypes influence specific behaviors? and (3) How are neural circuits assembled during development? Neurogenesis in *Drosophila* involves tightly regulated spatial and temporal cues. A cascade of temporal transcriptional factors (TTFs) and RNA binding proteins (RBPs) are expressed in a combinatorial fashion, driving the sequential production of distinct neuronal subtypes. This temporal patterning establishes a direct link between genetic programs, circuit formation, and behavior, though many aspects of this process remain unclear. Importantly, many TTFs and RBPs have conserved homologs in vertebrates, where they regulate progenitor maintenance, differentiation, and neuronal subtype specification. This conservation suggests that temporal patterning represents a fundamental strategy for constructing complex neural circuits across species. By dissecting these mechanisms in *Drosophila*, my work aims to define how temporal identity is molecularly encoded during neurodevelopment and how its disruption impacts circuit assembly and behavior, providing a conceptual framework with broad implications for understanding brain development and neurological disorders.

Poster 26

Flowering Synchrony Tracks Precipitation with Consequences for Bee Community Stability

M. Dylan Taylor, Manogya Chandar, Jade McLellan, Emerson Martin, Melanie R. Kazenel, Karen Wright, Terry Griswold, Kenneth D. Whitney, Jennifer A. Rudgers.

“Temporal synchrony in the phenology (life history timing) of species can mediate interactions that influence fitness via survival and reproduction. The phenological synchrony of plants is often determined by environmental cues (e.g., temperature, precipitation) that are expected to shift in the face of global climate change. For animal-pollinated flowering plants, phenological shifts due to climate are particularly concerning, as they threaten the fitness and stability of the pollinators they interact with. In the Southwestern US, the climate has become more arid and variable over the past century. Increases in community-wide flowering synchrony in response to increased aridity may reduce the temporal consistency of floral resources available to pollinators. This is especially harmful to generalist pollinators which rely on multiple plant species across their activity period compared to specialist pollinators which depend only on one to a few plant species. We used 23 years of plant phenology data collected across three dryland ecosystems to measure co-flowering synchrony of the animal-pollinated plant community. We asked how floral synchrony has changed over the past two decades and determined which climate variables best predicted synchrony. We then incorporated 23 years of spatially-paired bee data to ask how abundance stability of the bee community responded to floral synchrony and assessed whether responses varied for diet generalist vs. specialist species. Floral synchrony did not decline over time across all ecosystems, but increased significantly over time in the Desert Grassland. Spring precipitation, driven by Pacific Decadal Oscillation (PDO), was the strongest predictor of floral synchrony across desert ecosystems. A more negative annual PDO decreases total Spring precipitation in the Southwestern US, leading to increases in flowering synchrony. Analysis of bee abundance data revealed a significant decrease in community-level stability with increased flowering synchrony. Declines in stability were greater and more significant for generalist bee species compared to specialists. Overall, our results suggest continued increases in floral synchrony as the desert Southwest climate grows drier and more variable, posing threats to the stability and fitness of flowering plants and their pollinator partners.

Poster 27

Climate-driven changes in light and lake ice thickness alter the balance between primary production and microbial carbon processing in McMurdo Dry Valley lakes

Natalia Chavez, John Priscu, Jade Lawrence, Cristina Takacs-Vesbach

Permanent ice cover regulates light availability and ecosystem dynamics in the lakes of McMurdo Dry Valleys, Antarctica. As such, these lakes are particularly sensitive to climate driven physical changes. Although ice thickness is known to directly influence phytoplankton primary production, the extent to which long-term variation in ice cover thickness alters the coupling between autotrophic and heterotrophic carbon production remains elusive. Here, we evaluate whether multi-decadal variation in ice thickness regulates the strength and coupling of autotrophic and heterotrophic carbon production in permanently ice-covered Antarctic lakes. We

tested the hypothesis that multi-decadal reductions in ice thickness enhance autotrophic production in the photic zone while weakening its coupling to heterotrophic bacterial production integrated across the water column. Using long-term records of ice thickness, phytoplankton primary production (PPR), and thymidine-based bacterial production (TdR), we assess temporal correlations between autotrophic and heterotrophic carbon fluxes and evaluate their vertical and temporal relationships within the lakes. Our data reveal that periods of reduced ice thickness are associated with increased PPR but exhibit weak or inconsistent coupling between PPR and TdR, indicating a spatial and functional decoupling between surface-driven photosynthesis and whole-water-column bacterial carbon processing, supporting our hypothesis. It is clear that physical forcing restructures carbon flow pathways in the McMurdo Dry Valley lakes and provides new information on the sensitivity of Antarctic carbon cycling to ongoing climate variability.

Poster 28

Archaeal and Bacterial community composition and diversity of El Malpais National Monument lava cave microbial mats and secondary mineral deposits

Sydney Drummond, Jennifer Hathaway, Ryan Stumbaugh, Diana Northup

Lava caves are unique aphotic, oligotrophic environments that host microbial life. Chemolithotrophs, microbes that use inorganic chemicals to sustain their life, are ubiquitous in caves, and their unique metabolic strategies can be informative for the study of the origin of life on Earth and on extraterrestrial bodies. Secondary mineral deposits have recently become a focus of microbiological studies of lava caves, and are a good system for studying how small and contained habitats can sustain chemolithotrophic life. However, much of this microbial life and its relationship with the mineral environment is still not well understood. This study used 16S rRNA sequencing of microbial mat and secondary mineral deposit samples from three lava caves within the El Malpais National Monument to determine how microbial composition is similar or different between caves and within the same types of secondary mineral deposits. Bioinformatic tools are being used to analyze microbial community composition, alpha and beta diversity, and co-occurrence between deposit types. These results will be an important addition to the growing study of cave secondary mineral deposits as microbial habitats and in the identification of new bacterial and archaeal diversity in lava caves. They can help inform next steps in studying chemolithotrophic metabolisms in aphotic, oligotrophic environments by indicating what kinds of mineral substrates microbes may be utilizing for energy, and where to sample for further study of these microbes.

Poster 29

Temporal Trends and Climate Predictors of Bee Abundance (*Agapostemon* spp.) in the Chihuahuan desert of New Mexico, United States

Melanie Gonzales, Jennifer Rudgers, Melanie Kazenel

Climate change worldwide is shifting to be more varied with extended periods of hotter and drier conditions. Bee-plant relationships are complex species interactions that require tempo-

rally coincident emergence of bees and floral availability that are being affected by climate change. Bee populations in dry ecosystems are strongly influenced by seasonal changes in weather, and these effects are expected to become more pronounced as the climate continues to change. However, it is still unclear what fine scale windows of weather conditions matter most for bees, and whether weather from earlier months can affect bee populations later in the season. By identifying when and how climate conditions shape bee abundances, this research aims to improve understanding of how bees in semi-arid landscapes respond to changing mean and increasing climate variability. This study aims to gain more understanding on 1) how does the phenology of bee abundance change over time, 2) which climate variables affect bee abundance the most, and 3) is there a lag effect from climate that affects bee abundance?

Poster 30

Raptorial ambition: What prey, if any, is too large?

Josiah S. Lavender, Christopher C. Witt

Prey size distributions provide insight into the ecology and evolution of communities and organismal physiology. Optimal foraging theory suggests predators have an optimal prey size, where the overall energetic benefit is maximized against the energetic cost and risk associated with handling prey. Due to the existence of an optimal prey size, we expect that prey size should be approximately normally distributed for a given predator. Departures from this expectation, such as right- or left-skewed distributions, may reflect aspects of the organism's physiology or the biotic community. Certain anatomical adaptations may also influence prey size distributions: In raptorial birds, for example, hooked beaks for tearing prey mean they are not limited to prey that they can swallow whole, resulting in a large upper limit of prey size. For instance, Golden Eagles (*Aquila haliaetus*; ~9kg) have been known to prey on Mountain Goats (*Oreamnos americanus*; ~60 kg). This seems like an extreme prey size; however, a lack of empirical data on distributions of prey size for raptorial birds makes it impossible to quantify the extremity of prey of varying sizes. Here, we construct prey size distributions for four small owl species known to take relatively large prey, and analyze the shape of these distributions. We use an observation of a Pearl-spotted Owlet (*Glaucidium perlatum*) preying on a Crested Francolin (*Ortygornis sephaena*)—a bird nearly three times the mass of the owl—as a motivating example for our study. We gathered data from the literature on prey of four other *Glaucidium* species and modeled the resulting prey mass distributions using common statistical distributions. For all four species, the empirical distribution was best fit by a Gamma distribution. The right-skewed nature of these distributions indicates that these owl species prefer relatively small prey, possibly due to high availability. Rate and shape parameters of the Gamma distributions showed a significant correlation with predator mass, suggesting that the exact shape of the distributions is influenced by predator mass. We used this relationship to predict the approximate prey mass distribution for *G. perlatum* despite a lack of empirical data on prey of this species.

Poster 31

Auranofin Enhances the Anticancer Activity of Paclitaxel in Cancer Cells

Niko J Candia, Cynthia Tshibangu, Robert J. Lake and Hua-Ying Fan

Background: The Notch signaling pathway regulates cell growth and survival and is often active in many cancers. Auranofin is an FDA-approved drug that has recently been reported to inhibit components of the Notch pathway. However, it is unclear whether inhibiting this pathway can improve the response of cancer cells to chemotherapy.

Objective: In this study, we tested whether auranofin could increase the effectiveness of the chemotherapy drug paclitaxel in cancer cells.

Methods: We treated cancer cells with paclitaxel alone or with paclitaxel plus auranofin. After treatment, we measured cell viability using a crystal violet–based assay.

Results: We found that cells treated with both drugs showed lower viability than cells treated with paclitaxel alone.

Conclusion: Our results suggest that auranofin may increase the sensitivity of cancer cells to paclitaxel and could be useful as part of a combination therapy.

Poster 32

Habitat Heterogeneity Shapes Burrowing Owl Diet in a Conserved Desert Grassland

James N. Loomis

Burrowing Owls (*Athene cunicularia*) are opportunistic predators whose diets reflect local prey availability and habitat structure. We hypothesized that habitat variation within a long-term conserved wildlife refuge in central New Mexico would produce differences in prey community composition among owl pellets. To test this, we analyzed prey remains from approximately 60 burrowing owl pellets collected across three locations within the refuge. Prey items were identified to order and quantified using minimum individual counts. Overall diet composition was strongly arthropod-dominated, with Coleoptera comprising ~34% of total prey items, followed by Solifugae (13.8%), Orthoptera (13.2%), Scorpiones (10.4%), and Hymenoptera (10.1%). Vertebrate prey, including Rodentia and Squamata, represented smaller proportions of total abundance (9.1% and 4.4%, respectively). Multivariate analysis using Bray–Curtis dissimilarity revealed significant differences in prey community composition among collection locations (PERMANOVA, $R^2 = 0.118$, $p = 0.001$), while tests of multivariate dispersion were non-significant. SIMPER analysis indicated that differences among locations were primarily associated with variation in Orthoptera, Scorpiones, and Solifugae, taxa often linked to vegetation structure and substrate characteristics in desert grasslands. In contrast, pellet-level richness (range 1–6 orders) and Shannon diversity did not differ among locations. Levin's standardized niche breadth ($BA = 0.49$) indicated moderate generalist feeding behavior. Together, these results suggest that burrowing owls within this protected refuge maintain consistent dietary breadth while adjusting prey composition in response to habitat-associated differences in arthropod communities. This study highlights the role of habitat heterogeneity in structuring predator diets within protected desert grassland ecosystems.

Poster 33

A tail of two cats: Ecological displacement in sympatric pumas and bobcats

Esteban Restrepo-Cortés, Jonathan S. Keller, Felisa A. Smith

Hypercarnivorous felids exhibit a remarkable suite of morphological, ecological, and behavioral traits that uniquely enhance their ability to capture and process prey. As a result, felids depend on limited prey diversity, making them particularly susceptible to disturbances. In mammalian communities where multiple felid species coexist, their overlapping ecological requirements often lead to niche differentiation or character displacement, processes that facilitate coexistence. These interactions can be especially restrictive for mesocarnivores, as the presence of a larger competitor may impose strong ecological pressures shaping smaller species' behavior, morphology, and/or diet. In this study, we investigate competition between two felids in New Mexico: the mountain lion (*Puma concolor*) and the bobcat (*Lynx rufus*). Specifically, we evaluate whether the presence or absence of an apex predator influences the dietary ecology of the smaller species. We hypothesize that bobcats will show ecological displacement depending on whether they occur in sympatry or allopatry with pumas. To test this hypothesis, we sampled museum specimens from the Museum of Southwestern Biology and analyzed body size, 2D and 3D ecomorphology, and dietary patterns inferred from stable isotope analysis. Comparisons were made between populations where both species occur together ($n = 11$ pumas, $n = 15$ bobcats) and populations where bobcats occur in the absence of pumas ($n = 14$ bobcats). We find evidence of character displacement in bobcats when they co-occur with pumas. On average, bobcats in sympatry have significantly smaller body size, smaller isotopic niches, and lower variation in 3D dental ecomorphology. In allopatry (presumably released from competition with pumas), bobcats have larger body sizes, larger isotopic niches (more diverse diets), broader canines (consistent with larger prey), and greater variation in 3D dental ecomorphology variables related to within-lifetime wear. Our results unite body size proxies and two independent diet measures (stable isotopes and dental ecomorphology), supporting altered bobcat ecology in the presence of pumas. While biotic interactions are often overlooked in interpreting organismal ecology, our findings suggest that sympatry may be responsible for altered ecology among New Mexican bobcat populations. Continuing research will test whether these patterns occur across eight additional sympatric and allopatric felid pairs in North American biomes.

Poster 34

Vectors of bioaccumulation: The impact of microplastics and heavy metals in an ectomycorrhizal interface

Emmy Turpin, Johanna Blake, Kati Seitz, Sara Branco, David Hanson

Microplastics (MPs) are ubiquitous organic pollutants known to co-accumulate with trace metals, posing risks to both environmental integrity and human health. Biological organisms such as fungi and plants produce complex organic constituents that mediate nutrient uptake and drive protective mechanisms in the soil interface. Ectomycorrhizal symbioses, such as the *Suillus tomentosus*–*Pinus contorta* association, represent an exclusionary system that provides

a unique opportunity to study this cycling phenomenon. Although the association between metal constituents and MPs is well established in the literature, limited work has examined the impact of biologically produced organic acids and chelating agents on these interactions and how they may influence metal bioavailability in ectomycorrhizal systems. This study evaluates two components: (1) the impact of biologically derived constituents (malic, citric, and oxalic acids, and hydroxylamine) on the adsorption and desorption of trace metals (Pb and Zn) onto MP surfaces (HDPE and PLA) at relevant soil pH values, and (2) the physiological impacts of metal-loaded plastics on *S. tomentosus* cultures. High-density polyethylene (HDPE) and polylactic acid (PLA) MPs were prepared and loaded into batch reactors containing solutions of 10 mM or 100 mM Pb or Zn with additions of 10 mM malic, citric, or oxalic acid, or hydroxylamine, and allowed to react for 24 hours. Sequential extractions were used to examine bulk chemical adsorption processes. Subsequently, *S. tomentosus* cultures were inoculated with one of the following treatments: plastic alone, metals and plastics, or metal-loaded plastics. Culture growth was monitored over a six-week period. Results demonstrated that the presence of biological acids with greater numbers of carboxyl groups resulted in the greatest increases in both the capacity and rate of metal adsorption onto HDPE and PLA surfaces, with greater adsorption observed for HDPE MPs. Hydroxylamine inhibited the adsorption of metals onto both MP types. Cultures inoculated with metal-loaded HDPE exhibited the greatest reduction in growth, followed by cultures exposed to metals and HDPE, and HDPE alone. The presence of traditionally synthesized plastics (HDPE) shows the greatest risk for amplifying metal uptake in fungal cultures, whereas green plastics (PLA)/metal alone have a less significant impact on organism health.

Poster 35

Coyote Stable Isotope Diet Analysis in Riparian Ecosystem Spring v. Winter

Lucy Pockman and Maya Chynoweth

The coyote (*Canis latrans*) is an important species throughout New Mexico and particularly for the Rio Grande's riverside riparian ecosystem, locally known as the bosque. Coyotes are omnivores. Other studies in different parts of the United States have looked at coyote diets through an isotopic lens in urban landscapes. Building on others' work, we looked at the diet of coyotes who live in a bosque wildland-urban interface to determine whether or not those coyotes are following a similar trend. Across seven months in 2023, we collected coyote hair using 11 hair snares along a fence separating the bosque's floodplain from upland habitat where coyotes and other wildlife regularly cross. Hair snare samples were collected twice monthly. One hair sample from a deceased coyote was included in the analysis. We used carbon (^{13}C) and nitrogen (^{15}N) stable isotope analysis, looking at 10 selected samples of the coyote hair collected. We analyzed the isotopic composition of the coyotes' hair samples. We also did this for both wild and anthropogenic food sources. We then compared the isotopic values of coyotes with their potential food sources to evaluate whether or not anthropogenic food sources are making their way into coyotes' diets. We then compared spring and winter samples to see if anthropogenic food sources were more scarce during the winter months when wild food sources would be more scarce.

Poster 36

Effects of USP30 on Vertebrate Hair Cell Mitochondria

Ida Rothschild, Andrea McQuate

Hair cells are specialized mechanosensory cells found in the mammalian inner ear. These cells convert mechanical signals into chemical ones, relaying the information to the auditory cortex in an energetically demanding process. Loss of mammalian hair cells leads to hearing loss. Hair cells contain high volumes of mitochondria to support the metabolic load. However, mitochondria can produce reactive oxygen species (ROS) during oxidative phosphorylation, especially if they become damaged. To maintain mitochondrial and cellular health, damaged mitochondria undergo mitophagy, where the protein Parkin accumulates on damaged mitochondria to mark them for ubiquitination and removal. USP30 is a deubiquitylase localized to the mitochondrial membrane that negatively regulates Parkin. We hypothesize that USP30 is highly active in hair cells, preventing mitophagy and contributing to the high mitochondrial volumes by allowing damaged mitochondria to remain in the cells. To test this hypothesis, we used CRISPR to knock out USP30 in *Danio rerio* embryos. We assessed mitochondrial health in crisprant hair cells by examining ROS levels using the indicator MitoSox. Preliminary data indicates a lower prevalence of ROS in crisprant fish than in controls. Future methods include repeating ROS analysis in future USP30 $-/-$ fish, calcium imaging analysis, and testing mitochondrial resilience with aminoglycoside. These studies will provide insight into the role of mitophagy regulation in hair cell health, and what role USP30 plays in this process.

Poster 37

Quantifying the Dynamics Between Hair Cell Mitochondria and the Metabolic Enzymes AMP Kinase and SIRT1

Benjamin Wellington, Andrea McQuate

Several forms of human hearing loss are attributed to mitochondrial damage within the sensory hair cells of the cochlea. Hair cells are mechanoreceptors that sense changes in pressure and convert stimuli into electrical impulses. Most notable about these cells are the biological characteristics of their mitochondria, which in some systems display a unique morphology and unusually high volume. Such traits imply a large demand for energy, but also encourage an increased susceptibility to injury. The lateral line organ of zebrafish (*Danio rerio*), our lab's model organism, contains hair cells that serve as experimental analogs to hair cells present within the human auditory system. Previous research has determined that two metabolic enzymes, AMP kinase and SIRT1, are associated with the development and volume of hair cell mitochondria. AMP kinase initiates a variety of energy-saving reactions in periods of low cellular ATP availability, and SIRT1 is involved in a pathway that promotes regulatory mitophagy. Furthermore, these two enzymes are known to interact in a cycle of mutual reinforcement. We hypothesize that AMP kinase and SIRT1 contribute to the unique mitochondrial phenotype found in hair cells. To study this system, we use transgenic zebrafish lines that express fluorescent proteins in their hair cell mitochondria which can be viewed via confocal microscopy. Green fluorescent pro-

teins (GFP) are used to detect mitochondria in fish whose SIRT1 interactive capability has been altered. AMP Kinase Activity Reporter (AMPKAR) proteins are employed to track changes in fish AMP kinase activity under differing cellular energy conditions. Quantification of mitochondrial volume and enzyme characteristics will provide insights into the molecular mechanisms that regulate mitochondrial dynamics within hair cells. Such research could inspire future treatments or preventative measures for mitochondrial disorders in the human auditory system.

Poster 38

SIRT1 Regulates Mitochondrial Calcium Signaling in Hair Cells of *Danio rerio*

Christiana Concepcion, Andrea McQuate

Hearing loss is a significant health problem in America, where 1 in 8 people ages 12 or older have hearing loss in both ears. Hearing loss often results from loss of hair cells, the sensory cells located in the inner ear responsible for converting mechanical vibrations into electrical impulses. Hair cells depend on mitochondria to support the necessary energetic demand. For instance, mitochondrial calcium signaling is fundamental for neurotransmission of the mechanical stimulus. SIRT1 regulates many metabolic processes, including stress responses, DNA repair, and inflammation. SIRT1 activation has been shown to protect hair cells from damage, though the mechanism is unknown. We hypothesize that SIRT1 alters mitochondrial calcium signaling in hair cells. To test this hypothesis, we tested how SIRT1 inhibition affects mitochondrial calcium uptake in response to potassium chloride (KCl). We found that SIRT1 inhibition slightly modified mitochondrial calcium uptake, however a more sensitive assay is needed. To this end, we will create a zebrafish model expressing ChRmine, a redlight-activated ion channel. We first used Gateway cloning to create a zebrafish vector containing ChRmine. Next, we will use microinjection to introduce the vector to single cell embryos. After screening for ChRmine expression and establishing a stable transgenic line, we will repeat our calcium imaging assay with SIRT1 inhibitors and measure the effects on mitochondrial calcium uptake. 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.

Poster 39

2025 Surveys of Amphibian Populations for Chytridiomycosis Disease in Sandoval, Taos, and Rio Arriba Counties, New Mexico

Audrey Hazen, Gideon Carver Landau

The fungal disease Chytridiomycosis (chytrid), caused by the fungus *Batrachochytrium dendrobatidis*, is extremely harmful to amphibians, negatively impacting respiratory and neurological systems. It is the number one cause of amphibian population decline worldwide. Middle and high school students involved in the Bosque School CEBRIN Field and Community Science program, in conjunction with the New Mexico Department of Game and Fish, have been monitoring amphibian populations for the disease since 2012. In 2025, Bosque students collected 25 different presence/absence chytrid samples in select locations in Taos, Sandoval, and Bernalillo Counties in New Mexico. Sampling technique involved catching each amphibian by hand

or with a hand net, then swabbing their ventral side. Swabs were preserved in a 70% ethanol solution, then shipped to Pisces Molecular for PCR lab analysis. Samples included the following species: Woodhouse's Toad (*Anaxyrus woodhousii*), North American Bullfrog (*Rana catesbeiana*), New Mexico Spadefoot (*Spea multiplicata*), Couch's Spadefoot (*Scaphiopus couchii*), Boreal Chorus Frog (*Pseudacris maculata*), and Tiger Salamander (*Ambystoma mavortium*). The data collected go to the New Mexico Department of Game and Fish to help with their amphibian management plans. One of those plans is identifying suitable locations that are unaffected by chytrid so they can be used to reintroduce the New Mexico state listed Boreal Toad (*Anaxyrus boreas boreas*). Additionally, we aggregated our findings since 2012 to look for patterns of chytrid prevalence across time and space in New Mexico.

Poster 40

The sand dollar *Dendraster excentricus*: A New Model to Explore Novelty in Neural Circuits

Isabella King, Eric Edsinger

Decoding how neural circuits function and evolve is a complex challenge but studying how different nervous systems generate similar behaviors may provide valuable insights. Cephalopods possess a complex hierarchical nervous system with a centralized brain connected to decentralized nerve rings, cords, and ganglia within their arms. In contrast, echinoderms lack a centralized brain but possess an independently evolved nerve ring with ganglia and radial nerves. Despite these differences, both groups have multiple specialized appendages arranged along multi-arm axes that serve comparable locomotor and sensory functions. This study explores how *Dendraster excentricus*, the Pacific sand dollar, can serve as a novel model organism for investigating neural circuit evolution. This species is particularly interesting because it exhibits its secondary bilateral symmetry superimposed on the ancestral pentaradial body plan characteristic of echinoderms. To examine its behavior, we used time-lapse videography in both laboratory and field settings to generate behavioral ethograms of *D. excentricus* and applied deep learning tools to analyze locomotion. These datasets, combined with microCT and confocal imaging, allowed us to compare body movements and the coordination of tube feet and spines across individuals. Our results revealed distinct locomotor behaviors in *D. excentricus* that suggest directional control and spatial awareness despite its decentralized neural anatomy. Together, these findings contribute to a broader understanding of how morphological and ecological divergence shape neural circuit function and provide a comparative framework for studying the evolution of nervous systems in marine invertebrates.

Poster 41

Investigating the Genetic Interactions Between *Prdm3* and *Bcl9* in Zebrafish Limb Development

Serenity Snider

Limb development depends on functional gene regulatory networks (GRN) to allow for the development of structures and cells within limbs. The GRN that controls this process are well established. However, the mechanisms of epigenetic regulation controlling the spatiotempo-

ral activation of these GRN's are an active area of investigation. In this study, we investigated the genetic interaction between a chromatin remodeler, *prdm3* and one of its putative downstream target genes, *bcl9* during zebrafish fin development. Bcl9 is a member of the Wnt enhancerosome that regulates expression of Wnt/ β -catenin target genes. Prdm3 is histone methyltransferase and also regulates gene expression through direct DNA binding and chromatin remodeling. Bcl9 is up regulated in *prdm3* mutant neural crest cells. The loss of these genes is associated with cleft palate and limb defects in humans, zebrafish, and mice. Using previously generated mutant zebrafish lines for *bcl9* and *prdm3*, compound heterozygous *bcl9*^{+/-}; *prdm3*^{+/-} animals were generated for this study. These animals were intercrossed and the larvae was collected at 6 days post fertilization. Alcian blue and Alizarin red whole mount skeletal staining was performed to assess cartilage and bone, respectively. To evaluate pectoral fin phenotypes across the allelic series, fins were removed and flat mounted for imaging and analysis. Singular loss of *bcl9* results in significant defects in the coracoid process including abnormal cell stacking in the posterior coracoid compared to control animals. Deviations from the wildtype morphology in the fin fold, endoskeletal disk were quantified and subtle changes were also observed in the cleithrum. Compound loss of *prdm3* and *bcl9* genes and the effect on morphology is under active investigation. Future directions include investigating the developmental expression patterns of *bcl9* and *prdm3* during fin development, as well as changes in the limb's GRN through in situ hybridization chain reaction assays. These studies will help to visualize the spatiotemporal expression of *bcl9* and *prdm3* for proper limb development and shed light on the functional roles for these transcriptional regulators and their genetic interaction during proper development of the limb.

Poster 42

Does rescue risk adaptation ability? A genomics perspective on isolation, translocations, and recovery of the threatened Little Colorado River Spinedace

Erika A. Dunn, Dr. Guilherme Caeiro-Dias, Dr. Megan Osborne, Dr. Thomas Turner

The Little Colorado River Spinedace now persists in three isolated watersheds within the Little Colorado River Basin. This federally threatened minnow faces ongoing pressure from habitat alteration, climatic shifts, and invasion by non-native predators. Over the past two decades, managers have conducted translocations within watersheds to increase abundance and expand habitat occupancy; however, these efforts have not been monitored for potential impacts on genetic diversity of Spinedace. To inform future conservation actions we sequenced the Spinedace genome and analyzed single nucleotide polymorphisms (SNPs) from 475 individuals spanning relict samples from the 1990s and contemporary samples from 2024 and 2025. Our results show that overall genetic diversity has remained relatively stable within watersheds through time. However, levels of genomic divergence among the three watersheds indicates long-term isolation and potential local adaptation to their distinct habitats. Analysis to identify local adaptation are currently ongoing. This study helps address a key management challenge where genetic rescue can benefit declining populations, but mixing could disrupt locally adapted gene pools and lower fitness if local adaptation is confirmed. Our findings provide a genomic framework and baseline to aid in decision making for future translocations as managers maintain and ultimately recover the endemic Little Colorado Spinedace.

Poster 43

Do fermenting mammals have distinct vertebral microstructure?

Nicholas P. Ryan, Jonathan S. Keller, Felisa A. Smith

Mammals consume fibrous plants through chewing and microbial fermentation, but the origin of high-fiber herbivory in early mammal ancestors remains unclear. While tooth morphology is typically used to reconstruct diets, we investigate whether a morphological aspect of the vertebrae could be used to infer feeding ecology. Bone is remodeled throughout an animal's life in response to mechanical demands; the spongy (trabecular) bone architecture of skeletal elements, such as limb bone epiphyses, correlates with ecological traits, especially locomotion. Building on these insights, we hypothesized that mammals relying on microbial fermentation have mechanically stronger lumbar vertebrae than non-herbivores. To test this, we quantified the strength properties of lumbar centrum trabecular bone, including degree of anisotropy, connectivity density, porosity, surface area, mean curvature, and the Euler characteristic. Dietary data were sourced from the MammalBase database; X-ray microCT scans of the third lumbar vertebra were obtained from 40 quadrupedal mammals with varying fiber intakes, and mechanical strength was measured with the ImageJ2 plugins BoneJ2 and StrengthLawExtractor. To account for phylogenetic non-independence we used a mammalian tree from the Open Tree of Life, with analyses controlled for body mass. Bayesian phylogenetic generalized least squares regressions (PGLS), performed using BayesTraits, together with phylogenetic independent contrasts (PIC), were used to test for trait correlations. We find that across species, mechanical strength parameters increased with fiber consumption, indicating that high-fiber herbivores have lumbar bone adapted for greater loading associated with fermentation chambers. Therefore, our results suggest that mammalian diets significantly affect vertebral bone structure and that trabecular bone analysis can provide insights into the ecology of extinct mammals. While we detected a dietary signal, other factors may also influence vertebral bone microarchitecture. Looking ahead, we plan to apply our histomorphometric proxy more broadly to fossil mammals to clarify the evolution of herbivory and improve paleodietary inferences. Achieving this will require advanced segmentation techniques, such as deep learning, for fossil vertebrae with mineral inclusions or taphonomically deformed trabeculae.

Poster 44

How do precipitation mean and variability interact to affect soil microbes

Purbendra Yogi Jennifer Rudgers

Soil microbial communities regulate key ecosystem processes, including primary production and nutrient cycling, yet their resilience to future climate remains uncertain. Climate projections indicate long-term drying in many regions and greater year-to-year variability in precipitation. Drylands, which cover ~40% of Earth's land surface and sustain 35% of the global population, are especially vulnerable to these dual stressors. However, little is known about whether the two aspects of climate change interact to non-additively reduce ecosystem processes. We used the Mean-Variance Experiment (MVE which independently manipulates both the mean (25% reduction) and variance ($\pm 50\%$ redistribution) of annual precipitation—to test how soil

microbes and biocrusts respond to drier and more variable rainfall in three New Mexico ecosystems (Plains grassland, and Chihuahuan Desert grassland and shrub-land). We measured biocrusts chlorophyll pigments and soil enzyme activities Across sites, 28% of responses had significant mean $\times$ variance interactions. Drier and more variable precipitation often produced contrasting outcomes: in some cases, increased variability “rescued” microbial functions suppressed under reduced mean rainfall (e.g., carbon and nitrogen enzymes in shrublands), whereas in others, combined stressors amplified declines (e.g., chlorophyll in desert grassland). Plains grassland microbes were largely insensitive, despite strong plant responses, while shrubland microbes showed the strongest and most interactive responses—opposite to patterns in vegetation. Overall, these results highlight that microbial resilience to climate change depends on the interaction of drying and variability, with consequences that diverge from plant responses. Understanding these dynamics is critical for predicting ecosystem function under increasingly variable future climates.

Poster 45

Characterizing species diversity of chronic wasting disease in the southwestern United States

Tenley N. Housler, Donald O. Natvig, Andrew W. Bartlow, Joseph A. Cook

Transmissible spongiform encephalopathies are neurodegenerative diseases caused by misfolded proteins (prions). No cures exist for these contagious diseases and current treatments only aim to ease the patient’s cognitive decline and death. Five prion diseases are known to infect humans and seven are known to infect animals. Three prion diseases well known to affect mammals and cross species barriers are scrapie in sheep, bovine spongiform encephalopathy (BSE) in cattle, and chronic wasting disease (CWD) in the family Cervidae. Historically, species like mice, hamsters, and primates were experimentally susceptible to BSE infection from being inoculated with scrapie-associated prions. Eventually, BSE caused variant Creutzfeldt-Jakob in humans, and scrapie is hypothesized to have crossed from sheep to cervids to cause CWD. In 1967, CWD was discovered in captive deer (*Odocoileus* spp.) housed in a Colorado wildlife facility that also housed sheep infected with scrapie. CWD affects cervids across 36 states in the U.S. and 6 countries globally but has been only sporadically monitored. Like early-stage BSE research, several rodents (*Peromyscus maniculatus*, *Myodes gapperi*, *Microtus pennsylvanicus*, *Mus musculus*, and *Mus domesticus*), and a primate (*Saimiri* sp.) have been susceptible to CWD when inoculated with CWD prions from infected cervids. In the wild, mammalian species like feral hogs (*Sus scrofa*) and coyotes (*Canis latrans*) have been identified to contract viable CWD prions through environmental transmission, further increasing concerns for spillover to humans. My thesis investigates CWD spillover from cervids to various mammalian species across the southwestern United States. We are collecting ectoparasites and brainstem, lymph node, and colon tissues from feral hog, coyote, and rodent specimens from the Great Basin Desert of Utah, throughout New Mexico, and a private ranch in Texas where CWD was detected in at least 17 captive white-tailed deer (*Odocoileus virginianus*). This study will provide preliminary assessments of potential wild sources for spread of infectious CWD prions. Identifying CWD in wild mammal communities will also contribute to strain diversity analyses as we begin to model the potential role of non-cervid mammal reservoirs and environmental characteristics

in CWD prion circulation.

Poster 46

Soil Respiration Under Piñon and Juniper Trees Following Simulated Piñon Mortality in Piñon-Juniper Woodlands

David Traub, Rae DeVan, Marcy Litvak

Piñon-juniper (PJ) woodlands across the southwestern United States are experiencing widespread piñon pine mortality due to drought and heat stress. While aboveground impacts of this mortality are well documented, the effects of belowground processes are not. Soil respiration is a major pathway of carbon loss from ecosystems, and changes in vegetation composition may alter the magnitude of soil CO₂ efflux and sensitivity to environmental drivers, including soil temperature and moisture. We compared a nine-year time series (2009-2017) of soil respiration rates measured under live piñon (n=3), dead piñon (n=3), live juniper (n=3), and intercanopy areas (n=3), and evaluated CO₂ efflux relationships with environmental drivers in two piñon-juniper woodlands in central New Mexico. In one site, all piñon trees were girdled in 2009, and the second site was untouched and served as a control. We used continuous measurements of soil moisture and temperature measured next to each chamber using in-soil sensors to characterize microclimatic conditions associated with each vegetation type. Soil respiration rates under live piñon trees were: 1) higher in magnitude, 2) less variable and 3) increased more in response to rainfall than soil respiration rates under live juniper trees or in intercanopy spaces. For the first two years, soil respiration rates under girdled piñon were higher, but in the following years, the trend reversed such that respiration rates under live piñon were higher. Compared to live piñon, soil respiration rates under dead piñon were less sensitive to soil water availability and were more variable. Our results indicate soil respiration rates in PJ woodlands are directly influenced by the relative proportion of piñon and juniper. Higher respiration rates under piñon suggest that as live piñon increases in piñon-juniper woodlands, ecosystem respiration should increase. Mortality of piñon caused a short-term increase in soil respiration under dead piñon trees, and although this decreased several years after mortality, higher variability of soil respiration rates under dead trees could contribute to higher variability in total ecosystem respiration rates in these disturbed ecosystems. Overall, this research improves our understanding of how piñon mortality may influence soil carbon dynamics in piñon-juniper woodlands.

Poster 47

Quantifying changes between symbiotic and non-symbiotic yeasts

Michael Robinson, Vince Martinson

In insects, symbiotic microbes are extremely important for nutrition, health, and function of individuals. Most symbionts in insects are bacteria, which are small enough to live in the guts of their insect hosts or sometimes in the cells of their hosts. While the relationships with bacteria and insects are generally mutualistic, bacterial symbionts go through many changes as a consequence of living inside another organism ranging from changes in cell size and shape, to a complete change in genome structure. However, it is unclear if these changes also occur in

eukaryotic symbionts like yeasts. While much more uncommon than bacteria, fungal symbionts provide similar functions to bacteria in the insect and can also live inside the cells of the host. Deathwatch beetles are an example of insects that can have fungal symbionts, which help them survive off of the wood they eat. Fungal symbionts in these beetles come from one of three genera, *Nakazawea*, *Symbiotaphrina*, or *Meyerozyma*. These three genera have species that live as symbionts and are free living, giving us the opportunity to explore if major changes are present between the two types of species. In this work, I explore what the possible differences are, comparing the genome structure, growth rate, cell size, and other characteristics that may have changed between living outside and inside the beetles.

