DEPARTMENT OF BIOLOGY

32nd Annual Research Days

April 6-7th, 2023

Castetter Hall

Ecology, evolution, and conservation of wildlife in a fiery world

Special Thursday Seminar Speaker

Dr. Gavin Jones, PhD
United States Forest Service

Fire is an important ecosystem process, but bigger and hotter fires are affecting large areas of the Western US. What do these fires mean for our ecosystems and the wildlife that depend on them?

Jones Lab uses empirical field data, ecological theory, and quantitative approaches to figure out how to more effectively conserve wildlife and their ecosystems. Jones lab research advances understanding of how to conserve species and biodiversity in a rapidly changing world, with changing human needs and pressures.

Day: Thursday, April 06
Time: 3:30 PM
Venue: Castetter 100

Plasticity underlying escalation of alcohol use

Keynote Speaker

Dr. Karla R. Kaun, PhD
Associate Professor, Department of Neuroscience, Brown University

Investigating how drugs of abuse affect molecular mechanisms within reward memory circuits is key to understanding how cravings are acquired and expressed. Using the fruit fly, we can parse out how alcohol alters the dynamic molecular landscape of memory circuits, influencing alcohol preference and use.

The Kaun Lab uses a curiosity-driven approach that combines collaborative and diverse scientific and life experiences to understand the fundamental principles of addiction. We appreciate the freedom and beauty of failing because it creates growth and knowledge.

Day: Friday, April 07
Time: 3:30 PM
Venue: SMLC 102

32nd Annual Research Days
Thursday, April 6 &
Friday, April 7, 2023

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

Keynote Speaker: Dr. Karla R. Kaun
Seminar Title: Plasticity underlying escalation of alcohol use

Special Thursday Seminar: Dr. Gavin Jones
Seminar Title: Ecology, evolution, and conservation of wildlife in a fiery world

Committee Members
Co-Chair: Seth Newsome
Co-Chair: Syed, Mubarak Hussain
Tom Turner
Joanne Kuestner
Domonique Ramirez
Donna George
Maya Shamsid-Deen, BGSA
Jonathan Keller, BGSA

Univerity of New Mexico Biology Department
32nd Annual Research Days
Thursday April 6th - Friday April 7th, 2023

Thursday, April 6, 2023 12:30 PM - 5:30 PM

12:30 PM	Graduate Student Lunch with Keynote Speaker	PIBBS
1:30 - 3:30 PM	Poster Printing and Hanging Assistance Hours (BGSA reps)	CAST 1st Floor
3:30 - 4:30 PM	Special Seminar: Dr. Garvin Jones, US Forest Service	CAST 100
4:30 - Until	Hausammann Brewhaus Social	

Friday, April 7, 2023 8:30 AM - 6:00 PM

10:00am - 2:45 PM	BGSA Bake Sale and Silent Auction	Greenhouse
8:30 - 9:30 AM	**Session 1 Cell and Molecular Biology Talks (4 talks)**	**CAST 100**
8:30 - 8:45 AM	Adil Wani	
8:45 - 9:00 AM	Brendan Sanders	
9:00 - 9:15 AM	Claire Doherty	
9:15 - 9:30 AM	Benjamin Garcia	
9:30 - 10:45 AM	**Session 2 Plants, Fungi, & Algae Talks (5 talks)**	**CAST 100**
9:30 - 9:45 AM	Carolina Valderrama Hincapie	
9:45 - 10:00 AM	Simon Doneski	
10:00 - 10:15 AM	Kayley You Mak	
10:15 - 10:30 AM	Louis Hight	
10:30 - 10:45 AM	Jeremiah Westerman	
10:45 - 11:00 AM	Break	
11:00 AM - Noon	**Session 3 Ecology and EvolutionTalks (4 talks)**	**CAST 100**
11:00 - 11:15 AM	Eve Rowland	
11:15- 11:30 AM	Oona Takano	
11:30 - 11:45 AM	Ryan Ozatalar	
11:45 - Noon	Katey Driscoll	
Noon - 1:00 PM	Buffet Lunch	
1:30 - 3:30 PM	Open Laboratory Visits	

1:00 - 2:00 PM — **Session 1 Posters** — **CAST 1st Floor**

1. Adina Abudushalamu	2. Adriana Fuentes	3. Amir Mani	
5. Ariadna Torres	6. Austin Hendricks	7. Branden White	8. Brandi Hess
9. Brenda L Ramos Villanueva	10. Cassandra Miller	11. Diego DeMmon	12. Dylan Marti
13. Ellie Larence	14. Helena Mieras	15. Irvin Arroyo-Torres	16. Xanthe Mille
	17. Sarah Maestrejuan	18. Simon Doneski	

2:00 - 3:00 PM — **Session 2 Posters** — **CAST 1st Floor**

19. Alexa Gonzalez	20. Alexis Reyes	21. Ethan Gyllenhaal	22. Grant Forbri
23. Helena Mieras	24. Julian Rojo	25. Kevin McQuirk	26. Khadijah Burk
27. Kyana Montoya	28. Leigh James	29. Lucy Liang	30. Marelessis Palomin
31. Maya Shamsid-Deen	32. Nicholas Ryan	33. Nolan Perryman	34. Paige Patterson
	35. Raquel Mendoza	36. Yago Santos	

3:00 - 3:15 PM	Break	
3:30 - 4:30 PM	Keynote Seminar: Dr. Karla R. Kaun, Brown University	SMLC 102
4:30 - 5:30 PM	Student Scholarships & Awards Ceremony	SMLC 102
5:30 - 6:30 PM	Reception	SMLC 102
6:30 - Until	Bosque Brewing Social	

A skeletal correlate for herbivory?

Nicholas P. Ryan, Department of Biology, UNM
Jonathan S. Keller, Department of Biology, UNM
Felisa A. Smith, Department of Biology, UNM

The consumption of fibrous plant materials by mammals typically involves extensive chewing and symbiotic microbial fermentation in the gut. However, it is unclear when high-fiber herbivory originated in mammaliaforms and early true mammals and, further, whether it began with the evolution of systems of fermentation or mastication. Here, we seek to develop a skeletal correlate for fermentation to decipher the evolution of mammalian herbivory. The density of trabeculae in trabecular bone (spongy or cancellous bone) is associated with vascularity because intraosseous blood vessels travel through foramina and intertrabecular spaces. We hypothesize that the trabecular bone in lumbar vertebrae adjacent to the highly vascularized fermentation chamber of hindgut fermenting mammals will be more vascularized than those of non-fermenting mammals. To test this, we obtained cross-sectional images (transverse slices) of x-ray computed tomography (XRCT) scans of first and second lumbar vertebrae for five pairs of closely related fermenting and non-fermenting extant mammals. We compared their trabecular densities quantitatively by binarizing images of centrum spongy bone in BoneJ, an ImageJ plugin-in. Preliminary results suggest herbivores have more dense networks of trabeculae in the lumbar centra than non-herbivores. Future research will analyze trabecular bone microanatomy for other elements of the axial skeleton, including the more posterior lumbar vertebrae (L3-L7), sections of the more posterior ribs, and the pelvic rim. With further testing, we plan to apply this new histomorphological skeletal proxy for fermentation to the fossil record to untangle the evolution of herbivory across Mammalia.

The E93 Connection: Linking Steroid Hormones, Neural Stem Cells, and Sleep Promoting dFB neurons in Drosophila.

Adil R. Wani, Department of Biology, UNM
Budha Chowdhury, Advanced Science Research Center, CUNY
Jenny Luong, Department of Psychiatry, UPen
Gonzalo M. Chaya, Department of Biology, UNM
Hannah Deutsch, Department of Psychiatry, UPen
Krishna Patel, Department of Biology, UNM
Orie Shafer, Advanced Science Research Center, CUNY
Matthew Kayser, Department of Psychiatry, UPen
Mubarak H. Syed, Department of Biology, UNM

Molecular mechanisms regulating the formation and function of neural cell types are not fully understood. Studying the developmental programs by which neuronal types are specified and connected to form unique functional circuits regulating discrete behaviors is an important area of neuroscience. We are investigating this long-standing question using the recently identified and conserved Drosophila sleep-wake circuit, which is composed of dorsal fan-shaped body (dFB) neurons, helicon cells, and ring neurons. We utilized novel lineage filtering tools to show that sleep-promoting dFB neurons are born from DL1 and DM1 late-Type II neural stem cells (NSCs) expressing ecdysone-induced protein Eip93(E93). We also found that loss of E93 and EcR in Type II NBs leads to defects in dFB neuron number indicating that E93 and upstream EcR specifies the identity of sleep-promoting dFB neurons Interestingly, the knockdown of E93 in type II NSCs affects adult sleep behavior. Our data show that we have identified steroid hormone-mediated NSC-specific developmental programs that regulate the formation and function of the sleep-wake circuit.

Investigating the costs and benefits of a nutritional fungal endosymbiont

Nolan L Perryman, Austin A. Hendricks, Jeffrey Booker and Dr. Vince Martinson
Department of Biology, University of New Mexico

Research on insect symbiosis is dominated by insect–bacteria models, however, the role of fungal symbionts in developing insect hosts is poorly understood. Fungi are de novo synthesizers of essential nutrients, such as B vitamins, sterols, and amino acids, therefore, reciprocal pairing between a host and its microbial symbionts can permit it to thrive on diets devoid of essential nutrients. Here, we address the progression of fungal symbiosis using a system of beetle–fungal symbiosis: the cigarette beetle (Lasioderma serricorne) with its symbiont Symbiotaphrina kochii. The beetle fungal–symbiosis model provides a powerful means to investigate insect–fungal relationships for the following reasons: the symbiont is both intracellular and extracellular, beetles can be reared without their symbionts, and the beetles can be reinfected to create controlled symbiotic pairings. Here, we addressed the following questions: 1) Is the conferred fitness benefit of S. kochii to the cigarette beetle only present in low-quality diets, 2) what is the relationship between the beetle's developmental stage and the number of viable symbionts, and 3) when reared on a low-quality diet, does the beetle increase the number of viable symbionts to compensate for a heightened nutritional demand? Preliminary findings reveal no cost to hosting a symbiont when the diet quality is high. Next, we find differences in the number of viable symbionts in larvae, pupae, and adults; however, symbiont growth is not different between beetles reared on low-quality versus high-quality diets.

THE EFFECTS OF EPISTASIS ON MULTI-LOCUS BALANCED POLYMORPHISM IN TEMPORALLY CHANGING ENVIRONMENTS

Adina Abudushalamu, Department of Biology, University of New Mexico
Eve Rowland, Department of Biology, University of New Mexico
Davorka Gulisija, Department of Biology, University of New Mexico

Evolution can occur rapidly, at contemporary time scales, whereby we observe notable genetic changes in populations within generations. In temporally changing environments, it is assumed that this rapid evolution occurs readily by natural selection on existing gene variants, particularly balanced polymorphism. However, known mechanisms of multi-locus balanced polymorphism in temporally varying environments are restrictive and typically require gene linkage. We use a multi-locus population-genetic model of Wright–Fisher subdivided populations and forward-in-time computer simulation to examine conditions for multi-locus balanced polymorphism at unlinked loci in temporally varying environments under the conditions of the spatial storage effect (a plausible natural mechanism) with different types of interactions between loci (epistasis). The spatial storage effect cannot maintain balanced polymorphism at the unlined loci but has never been examined in combination with different types of epistasis. Preliminary simulations show that sign epistasis increases diversity compared to the absence of epistasis between two loci, under the storage effect and population subdivision. On the other hand, positive and negative epistasis typically decrease diversity at unlinked loci compared to the absence of epistasis, under the storage effect when there is a population subdivision. We are currently examining the maintenance of multi-locus polymorphisms under the spatial storage effect and epistasis in the absence of subdivision. Overall, we show that higher levels of balanced polymorphism are possible with epistasis under the spatial storage effect, expanding our understanding of multi-locus balanced polymorphism. This research helps elucidate the basis for rapid adaptation in temporally varying environments.

TEMPORAL VARIATION IN BODY SIZE, DIET, AND ENDOPARASITES IN WESTERN DIAMOND-BACKED RATTLESNAKES (CROTALUS ATROX)

Irvin Arroyo-Torres, Museum of Southwestern Biology, Department of Biology, UNM
Sara V. Brant, Museum of Southwestern Biology, Department of Biology, UNM
J. Tomasz Giermakowski, Museum of Southwestern Biology, Department of Biology, UNM
Samantha Armijo, Museum of Southwestern Biology, Department of Biology, UNM
Lisa N. Barrow, Museum of Southwestern Biology, Department of Biology, UNM

The period between 1970 and 2020 experienced a global mean surface temperature increase higher than any other 50-year period over the last 2,000 years with associated increases in precipitation variability. If the climate continues to change in this way, we can expect changes to communities of primary producers, primary consumers, and higher trophic levels. Crotalus atrox (Western Diamond-Backed Rattlesnake), just as other predators, is likely to be affected by changes to its prey communities. Diet changes, temperature increases, and droughts could affect the size, age of sexual maturity, parasitic infection rates and composition, and fitness levels of C. atrox populations. We hypothesize that the C. atrox in New Mexico have experienced measurable changes to their body size, diet composition, and endoparasite communities. We examined C. atrox specimens from three time periods: 1940-1960 (n=34), 1980-1990 (n=53), and 2011-2021 (n=57). We dissected C. atrox museum specimens and recorded body measurements, sex, age class (juvenile or adult), prey items from gut contents, and endoparasite prevalence. Differences in body size, diet, and endoparasite prevalence were investigated between sexes and time periods. Adult male tail length has increased between the 1940-1960 and 2011-2021 snakes, suggesting an increase in hemipene size. There is no significant difference in diet of C. atrox between the three time periods. Through the three time periods, body size and diet composition have remained stable. Endoparasite communities were significantly different between 1940-1960 and 2011-2021 snakes. This shows that endoparasite communities of C. atrox are dynamic and change through time.

DOES CURRENT BOTANICAL COLLECTION COVERAGE REFLECT THE TRUE DIVERSITY OF THE SEVILLETA?

Khadijah Burke, UNM Herbarium, Museum of Southwestern Biology, Department of Biology

The Sevilleta is a botanically significant research area that spans across 3,600 square kilometers in mid-New Mexico. It belongs to a network of Long Term Ecological Research (LTER) programs, which aim to synthesize ecological data over time across an array of ecosystems. Despite the magnitude of work and research done at this site, botanical collection coverage is incomplete. This project aims to create a basic synthesis of Sevilleta collections, which can then be used to determine biases and gaps within herbaria. Complete datasets of all collections originating in the Sevilleta will be downloaded from the Global Biodiversity Information Facility (GBIF) and the Southwest Environmental Information Network (SEINet). The data will be analyzed to determine patterns in where specimens were collected, when they were collected, and which taxonomic groups may be numerically misrepresented. Some anticipated biases include more collections being made near roads or nearby facilities, and more frequent collections during biological spring and summer. Rare, less charismatic species will likely be under-collected, whereas abundant, showy species will be over-collected. All of this will reveal the areas that are the most lacking in Sevilleta collections, and therefore, the areas that can be improved upon the most. Museum collections are an extremely valuable tool when it comes to long term research, which is the main focus of the Sevilleta as an LTER program. What better way to preserve long term ecological data than placing it in a museum to be held and used for research, education, and conservation efforts indefinitely?

Characterization of the T cell Receptor Repertoire in Protopterus dolloi

Diego DeMmon, Department of Biology, UNM
Irene Salinas, Department of Biology, UNM

T cell receptors (TCRs) are an essential element of adaptive immunity in all jawed vertebrates. Two subsets of T cells can be distinguished by the receptor on their cell surface, classified as either αβ or γδ T cells. αβ T cells have diverse repertoires so that they can recognize the vast diversity of antigens they encounter. In contrast, γδ T cells exhibit reduced diversity in their TCR repertoire and have been described in mammals and teleost fish as being more abundant in epithelial tissues such as the skin. In addition, these unique T cells have been observed to play innate-like roles in tissue homeostasis and repair. It is unknown when this dichotomy between T cells and the restricted diversity of γδ TCRs in peripheral tissues first appeared during jawed vertebrate evolution. Here we characterize the spleen (central) and skin (peripheral) TCR α, β, γ and δ repertoire in the sarcopterygian fish the African lungfish (Protopterus sp.), the earliest extant relative to all tetrapods. Using colony PCR in two different individuals we observed that that P. dolloi skin has a less diverse TCRγ and TCRδ repertoire characterized by a longer CDR3 region (9-19 Amino Acids) compared to skin TCRα and TCRβ, as well TCRγ and TCRδ in the spleen (8-17 Amino Acids). These results indicate that specialization of γδ T cells with innate-like functions in the skin predates the origin of tetrapods.

A novel population of IL-12 and MyD88-independent T cells are required for resistance to a uracil auxotrophic strain of Toxoplasma gondii

Claire M. Doherty, Paige R. Patterson, and Eric Y. Denkers
Center for Evolutionary and Theoretical Immunology and Department of Biology, University of New Mexico, Albuquerque, New Mexico, United States of America

Current views of the immune response to Toxoplasma gondii place TLR/MyD88-dependent IL-12p70, IFN-γ and activated inflammatory monocytes as central mediators of host defense against this microbial pathogen in mouse models of infection. Here, we used the engineered uracil auxotroph strain OMP as a tool to untangle early immune responses elicited by T. gondii. Unexpectedly, we found that Rag1-deficient mice lacking T and B lymphocytes succumb to OMP infection within 14-21 days post i. p. inoculation coincident with fulminant parasitemia at the site of inoculation. In wild-type mice that resist OMP, we observed an influx of B2 B cells, CD4+ and CD8+ T lymphocytes into the peritoneal cavity peaking 6-8 days post-infection. Both CD4 and CD8 T cell populations were composed predominantly of effector/memory CD44+C-D62L- cells. Subsequent experiments with μMT and Tcrb-/- mice pinpointed αβTCR+ T lympho-cytes as the critical cell population required for resistance. Use of MHC-deficient deficient mice, anti-CD4+ and anti-CD8+ mAb depletion in WT mice, and adoptive transfer into Tcrb-/- ani-mals each revealed contributions of both CD4 and CD8 T cells to resistance. Protection in the OMP model occurred independently of MyD88 and, interestingly, IL-12p40. The cytokine IFN-γ, widely regarded as the major mediator of resistance to Toxoplasma, was only partly needed to survive OMP infection. Cell elicited by OMP were capable of selectively lysing infected target macrophages. Together our studies provide insight into a novel and rapidly arising T lympho-cyte-dependent protective response to T. gondii which operates independently of MyD88 and IL-12, and only partially requires IFN-γ.

RARE AND ENDANGERED ARTHROPOD-PLANT SYMBIOSES IN NEW MEXICO – MAPPING TRENDS AND BIASES

Simon Doneski, UNM Herbarium, Museum of Southwestern Biology, Department of Biology

Arthropods and their plant-host interactions in New Mexico have vastly been understudied due to lacking data and collections of both plants and arthropods in the state. In this project we seek to examine several known arthropod-plant host symbioses. We will focus on four rare species of arthropods: the Sacramento Mountains Checkerspot butterfly (Euphydryas anicia cloudcrofti), the Glorious Scarab Beetle (Chrysina gloriosa), Wood's Jewel Scarab (Chrysina woodi), and LeConte's Chrysina (Chrysina lecontei). We further will investigate these arthropod's respective host plants: New Mexico Beardtoungue (Penstemon neomexicanus), Ponderosa Pine (Pinus ponderosa), Juniperus spp, Arizona Sycamore (Platanus wrightii) and Texas Black Walnut (Juglans nigra). Utilizing data from the Global Biodiversity Information Facility (GBIF), the Southwest Environmental Information Network (SEINET) and Symbiota Collections of Arthropods Network (SCAN) we will conduct a collection analysis of these species pairs. We will map the overlap and distributions of both species for each pair, then separately examine the museum and herbarium collections of these specimens and interpret the gaps and biases within both organisms' collections. This data will show trends in collection and range shift, as well as biases in our collection and point towards where future effort is needed in collections and in sampling. This collection analysis of symbiotic taxa between plants and arthropods will also serve to amplify the conservation stories of these understudied organisms in New Mexico.

RHIZOBIAL BIOPRIMING OF LUPINUS PERENNIS FOR CONSERVATION AND RESTORATION IN THE CONCORD PINE BUSH

Simon M. Doneski, Department of Biology, UNM
Donald L. Taylor, Department of Biology, UNM

Lupinus perennis is a rare perennial flower, native to New Hampshire, it also the host plant for the federally listed Karner Blue Butterfly (Lycaeides melissa samuelis) and the Frosted Elfin butterfly (Callophrys irus) which is currently under review for federal listing. One of the conservation issues that has driven these two species nearly to extinction is the disappearance of Lupinus perennis. Lupines have a highly evolved symbiosis with nitrogen fixing bacteria and, in this study, we investigate whether the inoculation of plants with bacterial symbionts cultured from the roots of Lupinus perennis can be used to improve lupine seedling establishment and survival. However, nothing is currently known about the specific rhizobia which is associated with Lupinus perennis. We are also assessing the biodiversity of these rhizobial strains by amplifying and sequencing the ribosomal 16s gene from the root cultures that we collected across three different sites in the Concord Pine Barrens in New Hampshire. We additionally sought to test the hypothesis that larger nodules indicate more fit strains of nitrogen fixing bacteria by separately culturing and inoculating plants with strains from small or large nodules. Plants were given an injection of the inoculum as seedlings and then monitored for 90 days where data related to growth and finally biomass was recorded.

PROCESS-BASED STREAM RESTORATION EFFECTIVELY ALTERS RIPARIAN PLANT COMMUNITY STRUCTURE AND FUNCTION

Katelyn P. Driscoll, Department of Biology, UNM & USFS Rocky Mountain Research Station
Laurel F. Martinez, Department of Biology, UNM
Dr. Thomas F. Turner, Department of Biology, UNM

Ecological restoration has long attempted to recover populations, communities, or ecosystems using structural interventions. These treatments often fail to achieve desired outcomes and for two decades scientists have pushed for a shift to process-based restoration. In streams, process-based treatments attempt to reestablish natural hydrogeomorphic conditions by raising water tables, retaining sediment and runoff, and increasing overbank flooding. If successful, process-based treatments in streams will alter the dominant environmental filters through which streamside communities assemble: water availability and fluvial disturbance. Recently, process-based treatments including beaver dam analogs (BDAs) and plug and ponds (P&Ps) have been applied across many landscapes; however, implementation has outpaced field verification and little is known regarding their effectiveness. We used a before-after-control-impact study and Bayesian analysis to determine the probability that BDAs and P&Ps affected riparian plant functional diversity or functional traits related to water availability and fluvial disturbance. We found high probability that BDAs and P&Ps altered functional richness, evenness, and dispersion, and shifted the streamside plant community to one that is more riparian in nature. Changes in abundance of traits such as anaerobic tolerance, moisture use, and rooting depth suggest treatments likely raised water tables and increased overbank flooding. These results indicate BDAs and P&Ps can effectively recover hydrogeomorphic processes and alter the streamside plant community in a short timeframe. Process-based stream restoration may rapidly shift abiotic filters in valley bottoms and could be an effective tool for achieving management goals related to restoring degraded streams and reestablishing lost or extensively altered riparian ecosystems.

How much do we know about the Bosque flora right in our backyard?

Grant Forbrig, Department of Biology, UNM
Harpo Faust, Museum of Southwestern Biology, UNM

The Bosque is the riparian environment that skirts the Rio Grande River located in central New Mexico and its land is diminishing currently. This ecoregion is considered unique with its Cottonwood trees and permanence of a ground water supply, a rare sight to see in the arid southwest U.S. Despite proximity to a major city, Albuquerque, the area contains incomplete collection data and public knowledge of the flora that inhabits it. Compiling when collections occurred and where, will allow for gaps in our understanding of the region to be filled. These gaps can then be looked at as potential research points for the future. To get these results, database platforms collection repositories like Global Biodiversity Information Facility and Southwest Environmental Information Network will be used to synthesize all known plant collections in the area. This information will additionally help determine common and rare taxa in the region, as well as when collection efforts were focused at. This data can then be synthesized into charts detailing collection histories. The expectation is to find collections occurring in species that have colorful flowers and are more enduring than plain flora. There should also be a noticeable decrease in water loving plant collections as the natural river environment disappeared after Cochiti dam was constructed. This data will allow scientists to concentrate on underrepresented taxa in the future and let it be the focus of collection efforts. Highlighting commons species will be helpful to others as potential guides on the area's flora as well.

IMPEDANCE EFFECTS ON SUNFLOWERS

Adriana Fuentes, Department of Biology, UNM
Dave Hanson, Department of Biology, UNM
& Laura Green, Department of Biology, UNM

The water dynamics in sunflowers are analyzed by recording how the difference in day and night affects the behavior of the sunflower. Alongside this, droughted and watered sunflower dynamics are measured to compare the reactions of the sunflowers under watered conditions to drying conditions. To accomplish this, we took multipip impedance measurements at 100000 frequency of 3 separate sunflowers spanning over a duration of 2-3 days with 2 watered and 2 droughted sunflowers being measured over the same period of days. The results showed a higher lamina impedance over a vein impedance and a nosier impedance at night compared to day. While the droughted sunflowers showed impedance being nosier at day instead of night.

Nasal viral exposure activates neurons and induces expression of an antiviral neurotransmitter in the brains of adult zebrafish

Aurora Kraus1, Ben Garcia1, Jie Ma2, Kristian Herrera3, Hanna Zwaka3, Ryan Wong4, Florian Engert3, Irene Salinas1

1 Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico, Albuquerque, NM 87131, USA.
2 Department of Fish & Wildlife Sciences, University of Idaho, P.O. Box 441136, Moscow, ID 83844-1136, USA.
3 Department of Molecular and Cellular Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA.
4 Department of Biology, University of Nebraska Omaha, 222 University Dr E, Omaha, NE 68182

Olfactory sensory neurons (OSNs) that allow us to smell are in constant contact with the environment and extend directly into the olfactory bulb (OB) of the brain. This anatomical location means that OSNs are constantly exposed to pathogens like viruses, yet pathogens rarely infect the brain via the olfactory route. We used a zebrafish model to study the ways that neurons are involved in protecting the brain from a model neurotropic viral pathogen. We found that virus is directly sensed by neurons in the OO, which transmit these neuronal signals to the OB in the brain. One day following viral exposure, we observe changes in behavior in adult zebrafish. By single-cell RNA sequencing, we found that following viral exposure there is am expansion of immature neurons in the OB expressing the gene adcyap1, which encodes for the neuropeptide PACAP-38. This neurotransmitter is evolutionarily conserved, and is known to play key role in causing migraines, a neuroimmune disease associated with chronic nasal viral infection. To further understand the role of PACAP-38 in our model, we performed immunohistochemical staining against PACAP-38 and found that it was upregulated in the OB 1d after intranasal IHNV exposure. We also performed assays to determine whether PACAP-38 is antiviral, and found it to have antiviral activity at biologically relevant concentrations. Our work reveals how encounters with viruses in the olfactory periphery shape the vertebrate brain by inducing antimicrobial programs in neurons and altering host behavior.

Conserved transcription factors Eyeless and Scarecrow regulate the specification of olfactory navigation input neurons

Alexa Gonzalez, Department of Biology, University of New Mexico
Aisha Hamid, Department of Biology, University of New Mexico

Mubarak Hussain Syed, Department of Biology, University of New Mexico

The molecular mechanisms responsible for the generation of diverse neural types populating the brain are not completely understood. The proper production of diverse neural types in Drosophila is essential for the formation of unique circuits that mediate various essential behaviors, including olfactory navigation. One neural stem cell type in Drosophila's central brain, denoted as type II neural stem cells (type II NSCs), divide asymmetrically to generate intermediate neural progenitors (INPs) that amplify and diversify most of the neural types populating the adult Drosophila brain. The temporally expressed genes in type II NSCs and INPs are thought to regulate the production of diverse neural types. However, how type II NSCs and INPs together generate distinct neural types in the central complex is currently unknown. This study focuses on the INP specific transcription factors and their role in the specification of a unique neural type called ventral fan-shaped body (vFB) neurons, which are the tangential input neurons of the olfactory navigation circuit. Our preliminary data shows that INP specific knockdown of Eyeless results in a complete loss of vFB neurons. We also found that late factor Scarecrow is essential for the proper specification of the vFBs, thus suggesting a developmental role of late INP factors to produce vFB neurons properly. Altogether, our results suggest that temporally expressed transcription factors in INPs, Eyeless and Scarecrow regulate the specification of olfactory navigation input neurons. In the future, we will test if Eyeless and Scarecrow regulate the olfactory navigation behavior.

Reexamining repeated waves of colonization in a Pacific bird species complex

Ethan F. Gyllenhaal, Department of Biology and Museum of Southwestern Biology, UNM
Serina S. Brady, Carnegie Museum of Natural History
Alivereti Naikatini, South Pacific Regional Herbarium, Institute of Applied Sciences, University of the South Pacific
Paul M. Hime, Biodiversity Institute and Department of Ecology and Evolutionary Biology, University of Kansas
Joseph D. Manthey, Department of Biological Sciences, Texas Tech University
John Kelly, Department of Ecology and Evolutionary Biology, University of Kansas
Robert G. Moyle, Biodiversity Institute and Department of Ecology and Evolutionary Biology, University of Kansas
Michael J. Andersen, Department of Biology and Museum of Southwestern Biology, UNM

Islands have long been a model for understanding how phenotypes change in diverging populations in the absence of ecological differences and geographic contact. The lack of geographic isolation between island taxa means their reproductive barriers, and potentially long-term viability as distinct lineages, cannot be tested like in continental taxa. There are rare exceptions to this rule of isolation, including in the whistlers of Fiji. This lineage makes for an excellent study system to explore the phenomenon of secondary contact on islands, and it proved influential to Ernst Mayr's contributions to the Modern Evolutionary Synthesis. He hypothesized the confluence of an "old" and "young" lineage coming into contact for the first time. We revisit this system with a genomic dataset (RADseq) to analyze population structure, phylogeny, and gene flow in the Pachycephala vitiensis species complex. We find support for Mayr's hypothesized lack of reproductive isolation in these once isolated island taxa, but not for his hypothesis of colonization pattern. For reproductive isolation, we demonstrate two clear instances of secondary contact, resulting in extensive hybridization on a larger island and a hybrid population on a smaller island. We also identified one region associated with major plumage differences between the actively hybridizing taxa. Our hypothesized biogeographic story emphasizes two waves of colonization with rapid plumage evolution over a story of "old" and "young" lineages.

Altered Neuronal Firing Following a Spreading Depolarization: an *in vivo* Study

Brandi R. Hess, Department of Neurosciences, UNM HSC
Natalie J Pinkowski, Department of Neurosciences, UNM HSC
Carissa J. Mehos, Center for Brain Recovery and Repair, UNM
Betty Fish, Center for Brain Recovery and Repair, UNM
Russel A. Morton, Department of Neurosciences, UNM HSC

Spreading Depolarizations (SD) are slowly propagating waves of tissue depolarization that result in the suppression of neuronal firing for multiple minutes. SD's are known to occur in rodents suffering from moderate or severe traumatic brain injuries and are also associated with visual auras that often preceeded migraines in humans. Our previous work establishes that SD's initiate in a closed skull concussion-like model in mice. The presence of SD's in our injury model is tightly associated with acute behavioral deficits that last hours. The behavioral deficits are attributed to neurological impairment, but a mechanistic understanding of that impairment remains unclear. We hypothesize that there is a period of altered neuronal firing that is associated with the period of acute behavioral symptoms of a concussion. Using two-photon microscopy we will investigate individual neuronal function with genetically encoded calcium indicators (GCaMP). The purpose is to measure the firing rate of an individual neuron prior to, immediately after, and during the acute recovery to assess baseline firing and recovery of individual neurons following an SD. In our preliminary data we have confirmed the complete suppression of neuronal firing immediately following the SD. We aim to determine the amount of time until neuronal firing returns to baseline rates following an SD.

SUPPORTIVE FUNGI IN SPACE: PLANT-FUNGAL ASSOCIATIONS MAY IMPROVE PLANT YIELD AND SOIL DEVELOPMENT IN EXTRATERRIESTRIAL REGOLITH

Louis Hight, Department of Biology, UNM
David Hanson, Department of Biology, UNM

For long-term missions to the moon and Mars, the ability to effectively grow plants for food, medicines, and construction materials in situ would improve safety and sustainability. However, delivery of large quantities of soil or water for hydroponic systems would be cost prohibitive. Supplemented regolith could provide an abundant source of growing media, especially if it could be biologically conditioned to be more favorable for plant growth. Plant-fungal associations improve plant productivity in many environments, so we are exploring how the inclusion of symbiotic fungi would affect plant growth and soil development in lunar and Martian regolith. We grew Helianthus annuus (Sunflower) in simulated lunar and Martian regolith with viable Glomeromycota fungal spores and with heat deactivated spores, and measured growth rate and biomass accumulation after three weeks to assess the potential for future work.

IMPROVING BACTERIAL BIOMASS ESTIMATES: ADJUSTING rRNA DATA IN GUT MICROBIOME STUDIES FOR TAXA WITH MULTIPLE GENE COPIES

Leigh James, Department of Biology, UNM
Conner Mertz, Department of Biology, UNM
Emily Reynebeau, Department of Biology, UNM
Seth Newsome, Department of Biology, UNM
Cristina Vesbach, Department of Biology, UNM

Wild herbivorous and omnivorous small mammals often consume diets deficient in the amount of protein required for growth and homeostasis. Recent evidence suggests that gut microbiota may supply the missing essential amino acids to their mammalian hosts. However, the extent to which intestinal-bacterial biomass is influenced by the quantity and quality of protein is unclear. Quantitative Polymerase Chain Reaction (qPCR) has been regularly used to quantify bacterial biomass by targeting the 16S rRNA gene. However, this technique fails to account for bacterial taxa with multiple copies of the gene and can overestimate bacterial biomass. We used qPCR with bacterial specific primers to determine (1) whether raw 16S rRNA gene abundance can be corrected using taxonomic information to more accurately quantify bacterial biomass and (2) if diet impacts intestinal bacterial abundance. We found that the relationship between the adjusted 16S rRNA gene abundance and the raw 16S rRNA gene abundance was positive and linear (R2 =1). Biomass increased longitudinally along the intestinal tract but varied by the quality and quantity of protein in the diet. The adjusted means for the 16S rRNA gene copies per gram in the small intestine (duodenum and ileum) were 3.75 x 109 and 1.01 x 1010 respectfully, while the large intestine (cecum) was 1.23 x 1011. Together our results demonstrate that adjusting qPCR results for gene copy of the taxa can reduce biomass estimates significantly, but that this method is sensitive enough to determine spatial and dietary differences of the gut microbiome.

A COMPUTATIONAL MODEL OF SARS-COV-2 INFECTION

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

The ability to accurately predict clinical outcomes following SARS-CoV-2 infection is a key objective in COVID-19 research. Currently, a critical line of inquiry meriting additional investigation is the impact of age and waning vaccine protection on immune defenses. However, the spatial-temporal dynamics of viral progression and host immune response are challenging to study in-vivo. Spatial Immune Model of CoronaVirus (SIMCoV), a scalable computational model that simulates hundreds of millions of cells, was developed to address these challenges, providing insight into key features of SARS-CoV-2 disease progression. SIMCoV has previously provided parsimonious explanations for diverse viral load trajectories and clinical outcomes, replicating observed viral growth dynamics by modeling virions, inflammatory signals, lung epithelial cells, and CD8+ T cells. To improve SIMCoV's accuracy and address currently salient questions, additional functionality designed to evaluate the vaccine and age-related impacts on the immune system and viral response will be added to create SIMCoV- Upper Respiratory Tract (SIMCoV-URT). In SIMCoV-URT, innate immune defenses will expand through the precise inclusion of antibody response, alpha interferon, and natural killer cells. Additionally, SIMCoV-URT will shift to modeling the upper respiratory tract, a highly studied and clinically significant region in COVID-19. By developing SIMCoV-URT, we hope to elucidate the course of COVID-19 within the framework of conventional conditions - aged immune systems and temporally diminished vaccine defenses. Findings will provide a more thorough understanding of the viral and immunological dynamics consequential to patient outcomes, illustrating the utility of spatially explicit computational models in studying within-host dynamics of SARS-CoV-2 infection.

POPULATION GENETIUCS OF SAND SHINERS (NOTROPIS STRAMIEUS) ACROSS THE GREAT PLAINS.

Lucy Liang, Department of Biology, UNM
Megan Osborne, Department of Biology, UNM
Guilherme Caeiro-Dias, Department of Biology, UNM

The sand shiner, Notropis stramineus, is a small body fish that inhabits a variety of environments including sandy-bottomed streams and rivers. Sand shiners are distributed across the Great Plains to the eastern United States. On the basis of morphology two subspecies are recognized. However, genetic analysis using microsatellites and a mitochondrial gene identified five clades within sand shiner suggesting at least five cryptic species that were not associated with previously described subspecies. Here we used microsatellite data from 7 loci to investigate the distribution of genetic diversity within three of these groups (clades A, M and R) represented by 29 localities and 866 samples. Preliminary analysis showed that all populations sampled encompass relatively high levels of genetic diversity with the highest gene diversity in the most widely distributed M clade (Upper Mississippi River), followed by the A clade (Arkansas, Canadian) and the R clade (Red River). Allelic diversity was lowest in the Red River group. We found that a significant proportion of genetic variance was explained by differences between previously identified genetic clades (A, M and R) and between localities within clades. Results provide insights into the evolutionary history of the group.

This research project has been reviewed and approved by the UNM Institutional Animal Care and Use Committee (IACUC). All investigators/assistants in this study have attained animal-use certification regarding the ethical treatment of animals (D16-00565 A4023-01).

Botanical Collection Analysis of the New Mexico Bootheel

Sarah Maestrejuan, Department of Biology Undergraduate

The bootheel region of New Mexico is a unique ecological area that fosters an incredible amount of diversity. This region is bounded by the Arizona border on the west, the Texas border on the east, and the Mexico border in the south. It houses 3 of the 5 ecoregions of the state; alpine conifers, juniper scrub, and desert basin. It is also home to the sky island region which is known for endemic species. This area accounts for 1.2% of the area in the state, but accounts for 40.7% of known plant species in the state. The purpose of this research is to summarize known efforts and biases that have caused gaps. Over 126 years, there have only been 7,600 collections. This project will analyze and summarize the number of taxa, rare species, collection density, and botanists of interest. It is expected that a vast majority of the bootheel region is under collected and there are major biases present due to minimal collections and collectors. The collections in the UNM Herbarium as well as the data collected from databases will likely show significant plant diversity relative to region size. The importance of this project lies in the area itself. The bootheel region of New Mexico is ecologically significant due to the presence of sky islands and the meeting point of 3 ecoregions. Further investigations into this area will likely reveal a significant need for continued collections.

Inside the brain of a rainbow trout: How translocated gut commensal bacteria cause sickness behavior and regional CNS immunity via polyamine shifts

Mani, A.1; Salinas, I.1
1Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, University of New Mexico, Albuquerque, NM 87131, USA.

The gut-brain axis is a vital communication pathway that regulates organismal physiology across various species, including teleost fish. This communication is mediated by microbiota and their metabolites, and their dysregulation can have deleterious effects on the host. In this study, we investigated whether translocated gut commensal bacteria induce immune responses in different regions of the brain and alter behavior using rainbow trout as a model. We found that the olfactory bulb is a more immune effector part of the brain under normal conditions. To simulate acute bacterial translocation in vivo, live commensal bacteria obtained from healthy trout gut were injected into animals intravenously. The bacteria entered the telencephalon inducing acute inflammatory responses 4 hours after injection, and the TL bacterial loads returned to baseline within 24 hours. Microbiome sequencing revealed a selective entry of anaerobic Gammaproteobacteria into the TL, which were predicted to function in polyamine synthesis and catecholamine degradation. We measured polyamine levels in the OB and TL at 4 and 24 hours post injection and found that while putrescine and spermidine levels remained unchanged, spermine levels were significantly lower in the TL but not the OB of bacteria-injected trout. Injection of gut-derived microbiota induced lethargy but not behavioral fever. These findings suggest that translocated gut bacteria into the blood result in a transient and selective translocation of bacteria into the TL, dysregulating brain polyamine metabolism and lethargy decoupled from behavioral fever. However, it remains to be investigated whether bacterial penetration into the brain directly mediates these responses.

CREATING PROTOCOL FOR FUNGI COLLECTION IN NEW MEXICO WITH THE UNM HERBARIUM

Dylan W. Martin, Senior BAEPD Student, UNM
UNM Herbarium

Fungi play numerous ecological roles in ecosystems—as saprotrophic nutrient cyclers, mutualistic symbionts, and pathogens—making an impact on all ecosystems (Andrew, 2018). An enormous body of knowledge has been amassed through the construction and refinement of intricate taxonomic keys dedicated to distinguishing fungi based primarily on morphology (Lofgren, 2021). Considering the importance of herbaria and citizen science in the collections of specimens for future research, it is expected that fungi are under-curated or neglected. This project attempts to address the lack of attention to fungi in our own backyard. The purpose is to create the protocols that allow fungi to get from the field into the UNM Herbarium. The current holdings of macro-fungi at UNM are 358 specimens, which is a low number of the known diversity in the state. The average species count for the New Mexico Mycological Association's annual foray is approximately 100 species that are collected and identified over one weekend, most of which are held at other institutions due to the lack of process protocols. The desire of this project is to grow the interest in proper cryptogamic vouchering, starting with macro-fungi, and train others in the field and the lab to carry on this work. This unique research is being assisted by the Sam Mitchel Herbarium of Fungi at the Denver Botanical Gardens. This is significant for an R1 University like UNM in preserving local biodiversity as the climate changes and affects the various eco-regions of New Mexico overall.

Enchanting Species of Rare or Threatened Plants in New Mexico

Raquel Mendoza, Department of Biology, UNM

Vouchered plant collection representation of the botanical diversity of the state of New Mexico is far from complete. There are several species of significance gathered into a special list arranged by their individual distribution and risk of becoming extinct. Of these, a smaller group consists of plants endemic to New Mexico, or exclusively found in the state. This list is determined by various organizations like the U.S. Forest Service, Navajo Nation, New Mexico Rare Plant Technical Council, and a few more. It is important that we understand which species are in danger and collect enough data to preserve the information these plants have for as long as possible. If we do not collect and preserve this knowledge before the plants are gone, we may never be able to get them back again. This work can be used for genomic data, medicinal properties, and simply historical accounts of our land at this place and time. It is likely that the species at higher risk of extinction will be found in more populated, urbanized counties. The more population dense areas are more developed and polluted. Threatened species are often not able to acclimate as fast as they are being forced into new boundaries. The data for this research comes from the Southwest Environmental Information Network (SEINet) database, Global Biodiversity Information Facility (GBIF) and statistics from the U.S. Census Bureau to determine a possible correlation between the most populated counties and where most threatened species exist.

MANAGEMENT SHORT-TERM IMPLICATIONS ON LUPINUS PERENNIS, DUFF AND SUPPORTING VEGETATION IN THE CONCORD PINE BUSH

Helena Mieras, Department of Biology, UNM
Cooper Kimball-Rhines, New Hampshire Fish and Game
Heidi Holman, New Hampshire Fish and Game
Jennifer A. Rudgers, Department of Biology, UNM

As anthropogenic effects impact the globe in adverse ways, the importance of protecting threatened and endangered species increases. Among the greatest threats to biodiversity are habitat loss and fragmentation. To mitigate these impacts, restoration and habitat management have come to the conservation forefront. This is especially true for the Concord Pine Bush habitat in Concord, New Hampshire, which is characterized by low-growth pine trees and exposed sandy soil. This unique habitat is home to a number of threatened and endangered species, including the endangered Karner blue butterfly (Lycaeides melissa samuelis). The Karner blue butterfly is in an obligate symbiotic relationship with wild blue lupine (Lupinus perennis), on which they lay their eggs and are the sole larval food. This project examines the impacts of management practices (burning, herbicide, and mowing) on the health of lupine and habitat suitability. We ask (1) how does management affect lupine health metrics (e.g. number of stems) and (2) do important lupine habitat properties such as duff depth, supporting vegetation, and ground cover change under different management treatments? Using linear mixed effect models, we tested the combined impacts of these management practices on lupine, duff accumulation, and supporting vegetation. Duff accumulation was significantly greater under a combination herbicide and burning management practice. This in turn negatively impacts the suitable germination habitat for lupine. The results of these analyses demonstrate the relationships and interactions present in the Concord Pine Bush that impact lupine health and therefore, the health of the Karner Blue butterfly.

PRINCIPAL DEVELOPMENT OF HERBARIA-BASED LEARNING AT THE SEVILLETA NATIONAL WILDLIFE REFUGE

Helena Mieras, UNM Herbarium, Museum of Southwestern Biology, Department of Biology

With climate change gaining ever more public attention, an emphasis on scientific education is necessary. It has been shown that a "student's initial encounter with the fascinating patterns of organismal diversity in taxon-oriented courses (mammalogy, entomology, botany, etc.) often leads to a life-long interest in research and education in systematics, natural history, or evolutionary ecology." In the State of New Mexico, ranking 4th in native species richness in the US, there is a clear need for a curriculum focused around herbaria-based learning to catalog the diversity of our state, serve as a research or educational resource, and cultivate herbarium advocates. A particular need is seen at the Sevilleta National Wildlife Refuge (SEV), which rests at an especially diverse region of ecotones in New Mexico and houses a National Science Foundation long-term ecological research site. At a confluence of scientific and public engagement, the Sevilleta hosts both experiments and people alike. The aim of this project is to design a herbaria-based curriculum for the SEV to be used into perpetuity. As part of this, an abbreviated version of this curriculum will be implemented in instructing underrepresented youth participating in the "PearlZ in the Wild" program. Emphasis will be placed on hands on activities; taking students through the Herbaria work-flow – from the field to the collection itself. This initiative will provide comprehensive herbarium curriculum to be used at the SEV and perhaps adapted for other herbaria throughout the state. In addition this project will provide hands-on, long-lasting experience for the participating students.

New Mexico Lichen: The Cryptic Fates of Cryptogams: Biases, Gaps and Trends in Herbarium Collections

Xanthe Miller, University of New Mexico
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Comprising more than 20,000 species and covering as much as eight percent of the Earth's surface, lichens have historically been understudied by botanists as well as mycologists. Consistent with this pattern, New Mexico lichens lack a comprehensive lichen flora. This project focuses on Ascomycota, which comprise the fungal component of the majority of lichens. It explores the holdings of New Mexico lichens in herbarium collections, major collection regions, the taxa best represented, and significant collectors. It uses national and international databases, including the Lichen Portal of the Consortium of North American Lichen Herbaria. The project hypothesizes that New Mexico lichen are underrepresented in herbarium collections compared with vascular plants and non-symbiont fungi, and that collections are disproportionately from cooler, moister ecoregions in New Mexico as well as areas more accessible to population centers and roads. A recent North American study finds the most rare lichen taxa are those on bark or leaf substrates. As southwestern forests decrease in area and biodiversity, and New Mexico's own forests come under increased pressure from climate warming, fire and other factors, those lichen may be lost, making their study all the more urgent. The goal of this research is to identify gaps, biases and trends in New Mexico lichen collections, to better suggest directions for future efforts.

Matching mitochondrial cline and environment in Audubon's Warblers

Kyana N. Montoya (1)
C. Jonathan Schmitt (2)
Andrew B. Johnson (1)
David L. Toews (3)
Christopher C. Witt (1)

1. University of New Mexico & The Museum of Southwestern Biology, Albuquerque, NM
2. Harvard University & Harvard Museum of Natural History, Cambridge, MA
3. Pennsylvania State University, State College, PA

Audubon's Warblers (Setophaga coronata auduboni) possess two mitochondrial haplotypes: a more northerly haplotype introgressed from the Myrtle Warbler (Setophaga coronata coronata) and a more southerly ancestral haplotype. Compared to the Audubon's Warbler, the Myrtle Warbler is a more migratory bird living at higher latitudes, so their mitochondria should be adapted to tolerate higher thermal and oxidative stress. Therefore, we hypothesized Audubon's Warblers having the northern mitochondrial haplotype should also be found in areas with higher latitudes and lower temperatures, and Audubon's Warblers having the southern haplotype should be associated with lower latitudes and higher temperatures. Using 565 haplotyped and georeferenced Audubon's Warblers throughout the Southwest, we mapped the mitochondrial haplotype cline across the landscape. We plotted the distance from the cline center of individuals with haplotypes mismatched to the cline against environmental variables. Consistent with previous studies, we found the cline tracks a southwest to northeast route increasing in northern mitochondrial haplotype with increasing latitude. Deviations from the cline were informative about the underlying environmental drivers of the cline position.

The Biogeochemical Role of Microbes in Lava Tube Caves

Ryan D. Ozatalar, Department of Biology, UNM
Diana Northup, Department of Biology, UNM
Jennifer Hathway, Department of Biology, UNM

Silicon is the second most common element in the Earth's crust, typically in the form, silica (SIO2). Silica is used by a variety of eukaryotic organisms, from diatoms to plants to make their skeletal structures. While eukaryotic silica uptake is well researched, prokaryotic uptake is poorly understood, with few research papers exploring prokaryotic uptake, precipitation and/or solubilization (making a usable form) of silica. Lava caves present a unique opportunity to study these processes, as the cave walls have numerous secondary silica formations on the cave walls. These deposits contain and protect evidence of microbial influence and DNA allowing for possible detection of life on other planets/moons by looking into these formations. Understanding secondary silica formation will discern if prokaryotes actively make or are simply trapped during the secondary silica formation. We obtained samples from silica rich deposits in lava caves at Lava Beds National Monument in California. We sequenced 100+ cultured bacteria and are running 51 isolates through a silicate test kit to test for silica uptake from the environment as well as using a color changing media testing for silica solubilization from an unusable silica form to a usable form. This work is adding fundamental knowledge in establishing a prokaryotic role in silica formation. These newly established mechanisms will add to the sparse literature and refine the Earth analogue for extraterrestrial detection of life in subsurface environments on other planets/moons.

Mast cell receptor FcεRI and integrin VLA-4 crosstalk downstream of antigen-induced activation

Marelessis Palomino, Department of Pathology, UNM
Derek A. Rinaldi, Department of Pathology, UNM
William Kanagy, Department of Pathology, UNM
Rachel Grattan, Department of Pathology, UNM
Alessandra Cambi, Cell Biology RIMLS 283, Radboudumc, Nijmegen, Netherlands Diane S. Lidke, Department of Pathology, UNM

Mast cells are known as sentinels of the immune system that experience a range of mechanical stimuli from shear stress in lymph to topographical cues in tissue. Mast cells also play a role in the progression of asthma and chronic airway inflammation, where the remodeling of a healthy airway into a fibrotic one changes the Young's Modulus of the tissue from ~2 kPa to ~16-18 kPa in fibrotic tissue. Others have shown that integrin mechanosensing enhances FcεRI-mediated signaling, but the role of integrin signaling in this process is poorly understood. Because mast cells express the integrin VLA-4 (α4β1), which binds to fibronectin that is markedly increased on fibrotic ECM, we hypothesize that the stiffness of the substrate influences the strength of mast cell outcomes. We combined biochemical, single-cell ratiometric calcium imaging, confocal and TIRF microscopy techniques with hydrogel-coated culture plates of varying stiffness to understand the mechanosensing capability of mast cells. Here, we demonstrate that RBL-2H3 cells display altered morphology, reduced FcεRI-mediated secretion capability and altered calcium signaling that is correlated with a reduction in substrate stiffness. VLA-4 outside-in signaling is propagated by the small G-protein, Gα13. The reduction in outcomes on substrates can be recapitulated on tissue culture plastic with treatment of myristoylated-FEEERA (mp6), an integrin-β1 specific inhibitor of Gα13- mediated outside-in signaling. Mp6 also altered calcium release and cytokine secretion, while FcεRI surface expression and Syk recruitment to receptor clusters are unaffected. These results provide evidence of downstream crosstalk between FcεRI

What the HIEC?1 IL-36gamma Production in Human Intestinal Epithelial Cells During Toxoplasma gondii Infection

Paige R. Patterson, Department of Biology, UNM
Claire M. Doherty, Department of Biology, UNM
Eric Y. Denkers, Department of Biology, UNM

The third leading cause of human food-borne death in the United States, the protozoan pathogen Toxoplasma gondii first establishes infection within the epithelial cells of the small intestine. The immune responses at this critical site have been little studied in the context of Toxoplasma even though epithelial cells are known to produce cytokines and chemokines capable of controlling the outcome of infection. Recent work by our lab has established IL-36gamma as a cytokine of interest during mouse infection. The role of this cytokine during infection of other species, including humans, is unknown. Here, we investigated the role of this newly described cytokine using the human-derived small intestinal epithelial cell line HIEC-6. Using both the highly virulent Toxoplasma strain RH and the less virulent cyst-forming strain PTG, we successfully established infection in HIEC-6 cells, as determined by immunofluorescence microscopy. We then investigated whether T. gondii infection triggered IL-36gamma expression in these cells. Employing quantitative PCR, we determined infection-induced changes in transcript levels of IL-36gamma in HIEC-6 cells compared to human foreskin fibroblasts (HFF). We found that Toxoplasma triggered elevated levels of IL-36gamma in HIEC-6 cells relative to HFF despite similar levels of infection. Our results establish that human epithelial cells, like those of the mouse, respond to infection through high level expression of IL-36gamma. Future work will determine whether other IL-36gamma-related cytokines are also triggered by Toxoplasma infection of HIEC-6 cells, and whether any such mediators impact the ability of the parasite to survive and proliferate in these human epithelial cells.

Causes and consequences of avian malaria in the tropical Andes.

Brenda Ramos Villanueva, Department of Biology and Museum of Southwestern Biology, UNM
Daniele L. Wiley, Department of Biology and Museum of Southwestern Biology, UNM
Jessie L. Williamson, Cornell Lab of Ornithology; Department of Biology and Museum of Southwestern Biology, UNM
Christopher C. Witt, Department of Biology and Museum of Southwestern Biology, UNM

Avian malaria is a general term for a group of vector-born, Haemosporidian parasites of birds. Infection by these parasites is known to influence bird longevity, behavior, and fecundity. Over the last two decades, PCR-based screening has revealed that avian malaria occurs worldwide and is very diverse. Two outstanding questions about avian malaria will require diverse approaches: (1) How do climate and host species influence occurrence and intensity of infections? And (2) How does infection affect host condition and performance? Here we add two new layers of data to an existing dataset of PCR-screened museum specimens that were collected across Andean elevational gradients. First, we stained and screened blood smears for avian malaria parasites using microscopy, and we quantified the intensity of infection (parasitemia) for each individual. Second, we collected data on blood characteristics of the same individuals that were screened. Blood characteristics included hemoglobin concentration, hematocrit, and cellular hemoglobin concentration, sensitive indicators of erythropoietic activity, which is known to be suppressed during human malaria infections. We found that microscopy surveys recapitulated biogeographic patterns from PCR-based results, showing a striking peak in prevalence at intermediate elevations. Further, parasitemia was higher in areas in which infections were more prevalent. Blood characteristics revealed a distinct signature of malaria infection, suggesting compensatory erythropoiesis is part of avian immune defense. In summary, adding additional datasets that overlap with existing studies helps us learn more about levels of parasite infection and what they tell us about connections among biogeographic, phylogenetic, and climate patterns.

PREVALENCE OF SYMBIOTAPHRINA FUNGI IN PTINID BEETLES

Austin A. Hendricks, Department of Biology, UNM
T. Keith Phillips, Department of Biology, Western Kentucky University
Tobias Engl, Max Planck Institute for Chemical Ecology
Rüdiger Plarre, Bundesanstalt für Materialforschung und -prüfung
Vincent G. Martinson, Department of Biology, UNM

Many insects thrive due to powerful microbial symbioses that allow them to fill unique niches. Ptinid beetles are major pests that target diverse food sources, ranging from stored food products to books in historical libraries. The best documented ptinids are Lasioderma serricorne and Stegobium paniceum which feed on flour and tobacco. Both of these species contain fungal endosymbionts in the genus Symbiotaphrina that are critical to their development and may serve as potential targets for pesticides. Despite similar life histories and nearly identical symbionts, these two species of beetles are separated by 8 million years, which indicates that other ptinid beetles may have similar symbiont relationships. Despite the economic threat that the 2,200 species of Ptinidae beetles pose, fewer than 50 have been checked for microbial symbionts, and only a handful have been screened using contemporary genomic methods. Here, we used ITS rRNA gene amplicon data to identify possible fungal symbionts in 70 species of Ptinidae beetles collected from 9 countries and 4 continents. We found that 20 species of beetles from 6 of the ptinid subfamilies had sequences that aligned to Symbiotaphrina. Phylogenetic analyses of these Symbiotaphrina sequences show that, despite the wide geographic range of the individuals surveyed, only three species of Symbiotaphrina were detected. Some individuals surveyed had multiple species of Symbiotaphrina, and individuals taken from different L. serricorne colonies had completely different symbiont communities, indicating that different species of beetles may be exchanging different species of symbionts in the wild.

The ontogeny of organized nasopharynx-associated lymphoid tissue in Rainbow Trout: Implications for vaccinations

Eliza Casadei1, Alexis Reyes1, Benjamin Garcia1, Fen Dong2, Irene Salinas1
1Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico.
2Department of Aquatic Animal Medicine, College of Fisheries, Huazhong Agricultural University, China.

Effective vaccination regimes must be timed to the development of the adaptive immune system, which is made up of B cells and T cells that provide long term memory against antigens. Previous studies have demonstrated that the development of lymphoid organs correlates well with responses to vaccination. Properly timing vaccines is especially important in aquaculture settings, where vaccination at the earliest effective time can have major impacts on fish mortality. To establish ideal time points for vaccination of farmed rainbow trout (Oncorhynchus mykiss), we sampled trout during development to determine the ontogeny of the organized nasopharynx-associated lymphoid tissue (O-NALT), a nasal lymphoid tissue that we believe acts as a localized mucosal site for adaptive immunity to vaccines. We found that CD8+ T cells first seed the nasal cavity by 715 degree days (DD) of age, while IgM+ B cells are present in the nasal cavity by 998 DD. By 1400 DD the characteristic bulging structure of the O-NALT is present in trout. Our findings indicate key time points when intranasal vaccination will be an effective strategy for inducing long term immunity in farmed trout, and provide a framework for further studies on early life vaccination in aquaculture settings.

USING TOTAL INTERNAL REFLECTION FLUORESCENCE MICROSCOPY TO ELUCIDATE THE SIGNALING DYNAMICS OF PD-1, CD28, AND THE TCR COMPLEX

Julian A. Rojo, Department of Chemical Engineering, UNM
Elizabeth M. Bailey, Department of Pathology, UNM SOM
Diane S. Lidke, Department of Pathology, UNM SOM

T-cell receptor (TCR) signaling is an essential part of the adaptive immune response. The strength of TCR signaling is modulated by signals sent by coreceptors, preventing both hypersensitivity and immunodeficiency. Programmed cell death protein 1 (PD-1) is a coinhibitory receptor that dampens T-cell activation and is a prevalent target for cancer immunotherapies. These therapies prevent interactions between PD-1 and its ligand, enabling the T-cell to remain active and detect malignant cells. However, the signaling mechanisms of PD-1 and how they integrate with those of stimulatory receptors like the TCR and CD28 are incompletely understood. PD-1 is thought to inhibit signaling by forming a complex with the phosphatases SHP-1 and SHP-2, leading to the dephosphorylation of nearby positive signaling proteins. However, these phosphatases also serve as transient positive modulators in other pathways. We hypothesize that PD-1 can mediate positive and negative signaling depending on its proximity to inhibitory tyrosine residues and stimulatory receptors. To test this, we are using supported lipid bilayers that allow us to selectively activate PD-1, CD28, and the TCR complex. These samples are interrogated using total internal reflection fluorescence microscopy (TIRFM), allowing us to visualize the cell-bilayer interaction. Ultimately, this project aims to better understand how PD-1/TCR/CD28 interact and how these interactions impact T-cell activation. Understanding these signaling mechanisms will give us better insight into immunotherapies and why they may not work, allowing researchers to improve the prognosis of patients.

STORAGE EFFECT TO THE EVOLUTIONARY RESCUE: PERSISTENCE IN VARIABLE HABITATS

Eve N. Rowland, Department of Biology, UNM
& Davorka Gulisija, Department of Biology, UNM

Predicting how populations will respond to environmental changes is the key to understanding the long-term effects of global climate change. Natural populations that experience environmental perturbations are forced to adapt, migrate outside of their range, or become extinct. An evolutionary mechanism, known as "storage effect" (SE) may enable populations to rapidly adapt to changing environments and persist. Natural selection can use stored genetic polymorphism to rapidly adapt to environmental changes instead of having to rely on novel mutations, thus increasing the probability of persistence. The importance of SE to adaptation, however, has only been examined in theoretical models that assume large populations with a constant size. Therefore, these predictions likely do not apply to critically endangered natural populations that have a small population size. Here, we develop a novel ecological-evolutionary model that tracks persistence under SE while allowing for changes in population size or extinction in a small population, subject to genetic drift. We model habitats under various evolutionary pressures (mutation, migration, selection under logistic size control, and genetic drift) to mimic natural scenarios and examine its properties across a wide range of parameters using forward-in-time computer simulations. We find that the SE can be established under a wide variety of habitats, where it allows for persistence in populations that otherwise would have gone extinct. A model of SE has multiple applications for wildlife management and conservation research and broadens our understanding of persistence in the face of environmental change.

THE EFFECT OF ACUTE HEAT STRESS ON ANTIMICROBIAL PEPTIDE EXPRESSION IN THE RAINBOW TROUT SKIN

Yago Santos, Department of Biology, UNM
Irene Salinas, Department of Biology, UNM
Elisa Casadei, Department of Biology, UNM

Intensive aquaculture exposes fish to several anthropogenic stressors which can compromise fish health making them more susceptible to disease. Acute stress is a reversible phase characterized by physiological changes that starts with the release of hormones including cortisol. In fish, skin is the first line of defense against danger signals and can promptly sensing and responding to maintain homeostasis; yet skin can be also damage by stressors. To avoid harm, the skin produces a thick mucus layer that covers the whole fish body, which is rich in antibodies and small molecules, e.g., antimicrobial peptides (AMPs) that can directly interact and kill pathogens. Among AMPs, beta-defensins are present in many organisms, including fish where they are highly expressed in the skin shaping the microbiota and contributing to fish health. Our aim is to study the effects of heat-stress on the expression of beta-defensins (omDB) in trout skin. Trout were sampled at 16◦ C (Control) and at 25◦ C (stressed). Skin and plasma samples were collected to evaluate changes in the omDB gene expression, tissue morphology and physiological markers. Our results show that stressed fish have higher levels of cortisol and glucose, followed by a higher density of mucus cells in the skin. Heat-stress caused a differential modulation of omDB genes; namely, omDB-1a and -4 were upregulated, while omDB-1b and -5 were downregulated. These results suggest that beta-defensins are involved in the early response to heat-stress in trout skin. However, we still need to investigate the mechanism modulating these molecules during stress.

ELUCIDATING HOST-MICROBE SYMBIOSIS IMPACTS ON HOST GENETIC DIVERSITY THROUGH A LONG-TERM STUDY

Maya L. Shamsid-Deen, Department of Biology, UNM
Joshua C. Fowler, Department of BioSciences, Rice University
Tom E. X. Miller, Department of BioSciences, Rice University
Jennifer A. Rudgers, Department of Biology, UNM
& Kenneth D. Whitney, Department of Biology, UNM

Plant-microbe interactions have shaped the evolutionary pathways of both taxa, and hold promise for allowing these lineages to persist in the future. Microbes may function as a benefit to plants during harsh climatic years, which may allow more individuals to persist and reproduce under climate change. Through this buffering effect, we hypothesize that symbiosis may lead to more genetic diversity in plant populations. Currently, there are no studies assessing how microbial symbiosis impacts host genetic diversity. Using genotype-by-sequencing (GBS) data we quantified genetic diversity in paired endophyte-present and -absent plots of six native North American grasses from a ten-year long-term study. We calculated plot level allelic diversity through averaging the allelic richness across all loci, and used a type II ANOVA to test if endophyte status was a significant predictor of allelic diversity. Allelic diversity was higher in endophyte present plots, supporting our hypothesis. Further, our demographic data indicate that fungal symbionts reduce demographic variability in seed production and support higher seed production in stochastic environments. Through broadening our understanding of the impact host-microbe context-dependent interactions have on genetic diversity, we are better equipped to make predictions about maintenance of biodiversity under anthropogenic climate change.

Body size shifts in North American birds since the Late Pleistocene

Oona M. Takano, Department of Biology & Museum of Southwestern Biology, UNM

Recent studies suggest that modern birds are decreasing in body size by up to 1.8% per decade, in conjunction with climate change. The Late Pleistocene (126,000–12,000 years ago) was a time of climatic fluctuations tracking glacial-interglacial cycles. As the climate warmed at the end of the Late Pleistocene, large-bodied birds and mammals in North America experienced elevated extinction rates. Body size is an important trait that determines metabolic rate, diet, and species interactions. I examined body size changes across multiple bird orders from the Late Pleistocene to today using fossils from Rancho La Brea in California to understand whether climate or competition is driving body size shifts. I quantified size changes for 22 bird species from the Late Pleistocene (20,000–35,000 years old) to today by measuring large wing and leg skeletal elements as body size proxies. I used t-tests to analyze average size differences in each species between time periods. Preliminary results indicate no evidence for consistent body size decrease across bird orders since the Late Pleistocene, which would imply climate-driven change. Rather, the direction of size change differs between species and skeletal elements measured, suggesting complex effects potentially related to changes in diet and competitive pressure. Studying the effects of past climate change and faunal extinction on surviving species will provide better predictive power for understanding how modern birds will respond to climate change and lower species diversity.

The secrets of snail success, differential fitness at the expression level.

Kevin A. McQuirk, Department of Biology, UNM

The snail Physella acuta has achieved global distribution, extending far beyond the native range (North America). The invasive P. acuta represent a subpopulation within the species that has a mitohaplotype A with ~10% sequence difference from mitohaplotype B, present in the native range. To study the underlying biology, field collected (NM) P. acuta were genetically characterized to initiate lab-populations with haplotypes A and B. The population fitness (growth rate, age to maturity, reproductive output, survival) was compared for A and B snails maintained under constant (lab-)conditions. Additionally, a rewilding approach was employed; exposing lab-reared snails in cages to variable environmental conditions at field sites and comparing fitness with lab-maintained snails over 1- or 2-weeks. The parasite fauna (digenetic trematodes) of P. acuta was surveyed to develop a PCR screening assay to exclude field-exposed snails that incurred infections. The fitness of populations A and B did not differ for lab-maintained P. acuta (7 experiments). With rewilding, however, population A had greater fitness than population B in 3/7 experiments. For a 1-week experiment (fitness A>B), RNAseq was performed for differential expression (DE) analyses comparing A and B snails, lab maintained and rewilded. Trinity de novo assembly yielded a A+B reference transcriptome (377492 transcripts > 500nt, N50 1074, BUSCO 99%). Ongoing DE analyses showed modest changes in transcriptional profiles of B snails between lab and field; P. acuta A snails displayed greater transcriptional diversity, involving several biological processes. Such patterns may provide a fingerprint for differential population success within P. acuta.

Comparing Amphibian Pathogen Detection Dynamics Using Museum Frozen Collections

Ariadna S. Torres, Department of Biology, UNM
Dani L. Wiley, Department of Biology, UNM
Kadie Omlor, Department of Biology, UNM
Celina M. Eberle, Department of Biology, UNM
Lisa N. Barrow, Department of Biology, UNM

Wild populations of amphibians have recently suffered declines linked to emerging pathogens including Batrachochytrium dendrobatidis (Bd), Ranavirus (Rv), and Perkinsea (Pk). Pathogen screening protocols require high-quality tissue or skin swab samples to detect infections, however research has shown that infection prevalence and intensity are not equally reported between all tissue types and pathogens. Museum frozen tissue collections offer unique insight that can be used to inform conservation practices and retroactively determine pathogen emergence in wild populations. Using tissue collections from the Museum of Southwestern Biology, we aim to determine whether there are differences in infection detection rates and reported intensities of infection between sampled tissue and between different pathogens. We also aim to investigate pathogen dynamics across host distributions with varying climatic conditions. We screened toe and liver DNA extractions collected from two common North American water frogs (Rana catesbeiana n=60 and Rana clamitans n=85) across their ranges in the eastern U.S. using established qPCR protocols. First, we determined whether toe and liver samples from the same individual frog were consistent in their assessment of infection. Then, averaging the pathogen DNA detected from replicate qPCR analyses, we assessed infection load between tissue types and infected individuals. Our results will aid in establishing better protocols for using museum tissues to screen populations for important pathogens, as well as inform collection techniques for future host-pathogen research. Our results will also shed light onto how pathogen detection may differ across geographic space and climate variation.

Drought legacy impacts plant and plant-soil interactions to improve Bouteloua gracilis biomass recovery post drought in a desert grassland ecosystem

Cassandra Maria Luz Miller, Department of Biology, UNM & Sevilleta LTER
Scott L. Collins, Department of Biology, UNM & Sevilleta LTER
& Jennifer A. Rudgers, Department of Biology, UNM & Sevilleta LTER

Climate projections predict a future of increasing aridity and precipitation variability, with consequences being most acute in drylands. Plant-soil-feedbacks (PSF) may be utilized to promote ecosystem recovery from extreme drought. Altered precipitation regimes can be a strong selective filter of plant allele frequencies, complicating our current understanding of field-based PSF. Accounting for plant-genotype specific PSF is necessary to contextualize contemporary evolutionary change. Here we asked: Does drought disrupt PSF to alter the pace of ecological recovery? We designed a greenhouse PSF experiment with two novel variations: 1) Soil inoculum was collected from field plots with a drought legacy and their paired ambient control plots. 2) We added a novel plant genotype treatment for a full-factorial manipulation of plant genotype (drought/control), soil microbial inoculum origin (blue/black grama rhizosphere), drought history (drought/control plots), and microbe manipulation (live/sterile).

Preliminary results indicate that blue grama control genotypes biomass significantly increased (~20%) with the addition of live inoculum from black grama that did not have drought legacy (P= 0.0140). Additionally, blue grama drought genotypes root biomass increased significantly (~15%) with the addition of live inoculum from black grama that did not a drought legacy (P = 0.0222). This suggests that plant genotype interacts with drought history of the soil microbial communities and confirms the consistency of negative PSF interactions with blue grama and positive interactions with its competitor, black grama. Our work emphasizes the importantance of considering localized plant genotype-specific soil interactions and how climate legacies may disrupt these interactions.

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

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

Aging is an inevitable process that affects nearly one hundred percent of organisms and is the greatest risk factor for diseases like cancer, cardiovascular disease, and neurodegenerative disease. Despite this irrefutable fact, aging is not well understood. Previous research, such as genetic single gene deletion studies in model organisms such as S. cerevisiae and C. elegans show the potential ability to alter the aging phenotype. McCormick et al. showed that many yeast single gene deletions extend replicative lifespan (RLS), with some of the most extended strains having genes deleted in the Spt-Ada-Gcn5-acetyltransferase (SAGA) complex. SAGA complex genes also have human orthologs, making them an important area of aging research. For example, Sgf73, whose deletion extends yeast RLS by a staggering 55.1%, has a human ortholog that plays a significant role in the neurodegenerative disease Spinocerebellar ataxia type 7. Although the SAGA complex has multiple functions, one such function tied to extended lifespan by gene deletion is the removal of ubiquitin from the H2B histone. We hypothesize that changes in gene expression are responsible for the changes in lifespan. My research aims to explore the differential expression caused by the SAGA complex deletions to answer why these SAGA deletions extend lifespan in yeast. By understanding the role SAGA plays in the aging of yeast, we can apply these findings in more complex model organisms with the eventual goal of applying our findings to the human genome and resultant aging phenotype.

Analyzing Metabolic Pathways in Five Different Species of Fungi From the Genus Symbiotaphrina

Carolina Valderrama Hincapie, Department of Biology, UNM
Vincent G. Martinson, Department of Biology, UNM

Two different species of fungi Symbiotaphrina kochii and S. buchneri are mutualistic symbionts of the beetles Lasioderma serricorne and Stegobium paniceum, respectively. They can be found intracellularly in a midgut organ of the adult and larval beetle called the mycetome, and extracellularly in the adult female accessory glands, near the ovipositor. Studying and understanding the relationship between gut microbiome-host interactions helps us identify factors that have coevolved as well as the key contributors to each other's development, to acknowledge the outcomes that could result from the separation of the host from its gut microbiota and vice versa. Moreover, the genus Symbiotaphrina includes another three species: S. sanguinea, S. microtheca, and S. lignicola, that are being cultured and studied in the laboratory. These three species of Symbiotaphrina did not develop a mutualistic symbiosis with the beetles, which provides the opportunity to directly compare the consequences of a symbiotic lifestyle in these fungi. Additionally, while the non-symbiont species present hyphal growth and the two symbionts present yeast-like growth, S. sanguinea has both types of growth simultaneously. To identify one of the differences between the free-living and the symbionts, we performed a series of experiments with the purpose of analyzing their metabolism. In this presentation, I will present the analysis of the differences that were found between the metabolism of the free-living vs the symbiotic species.

Effects of Pollination Syndromes on Alpine Plant Communities

Jeremiah Westerman, Department of Biology, UNM
Hannah Marx, Department of Biology, UNM
Joseph Kleinkopf, Department of Biology, UNM

The floral traits of flowering plants in alpine ecosystems are incredibly diverse and the drivers of this diversity are currently understudied. Both biotic and abiotic modes of pollination have the potential to be major drivers of plant evolution as they are essential for plant reproduction. Different combinations of floral traits increase the effectiveness of specific methods of pollination. In this study, we assigned pollination syndromes to each species collected from eight alpine peaks in the southern Rocky mountains given unique floral trait combinations previously described in the literature. Multiple correspondence analysis (MCA) analysis was performed to assess the significance of assigned pollination syndrome categories as discriminant factors. We then mapped pollination syndromes assigned to each species onto a phylogeny representing their evolutionary relationships and used multiple metrics to quantify the phylogenetic structure of pollination syndrome traits. By mapping the pollination syndromes to their respective species on the alpine plant phylogeny this study will determine the impacts of pollination syndromes (and potential pollinators) on the diversity of flower color and species richness of the alpine plant community as a whole and on a peak by peak basis.

ANALYSIS OF WING PATTERNS TO BETTER CHARACTERIZE DIFFERENCES BETWEEN SPECIES WITHIN THE SAME GENUS

Branden White, Department of Biology, UNM
Quinlyn Baine, Department of Biology, UNM
Ellen Martinson, Department of Biology, UNM
Vince Martinson, Department of Biology, UNM

A myriad of gall-forming fruit fly species within the genus Aciurina (Diptera: Tephritidae) populate the intermountain West of North America. Genus range is constrained by the host plant Ericameria nauseosa. Each fly species is characterized by a unique wing pattern and gall morphology (A. bigeloviae induces cotton covered galls, A. trixa to smooth galls, etc). However, Aciurinia is currently understudied and may be a source of undiscovered biodiversity. Two previously described species, A. bigeloviae and A. trixa may actually represent additional undescribed species that are specialized to host plant variety. To test this, I developed a series of measurements and categorizations of wing patterns from 91 female Aciurina specimens collected from fifteen different sites between 2021-2022. Four wing patterns that were consistent yet visually distinct from each species were measured and compared to the general size of the wing. Two wing patterns that were either present or absent for each species were categorized then analyzed using Chi square tests. We found statistically significant data via wing morphometric trait distinctions that, when combined with known gall morphology, A. bigeloviae can be split into two distinct host races.

COMMUNITY-LEVEL BACTERIAL EVOLUTION FOR THE BIOREMEDIATION OF BIOFUEL N-BUTANOL

Kayley T. You Mak, Department of Biology, UNM, Genomics and Bioanalytics Group, Los Alamos National Laboratory
Erik R. Hanschen, Genomics and Bioanalytics Group, Los Alamos National Laboratory
& Blake T. Hovde, Genomics and Bioanalytics Group, Los Alamos National Laboratory

n-butanol is a strong biofuel candidate since it is more energy dense and less volatile than ethanol; additionally, butanol can utilize existing pipelines and infrastructure. The bottleneck for industrial production of n-butanol is the high toxicity. Most microbes cannot survive above 1.5% v/v, although some genetically engineered microbial strains have been improved to tolerate 2% v/v. Due to the high toxicity, a biofuel spill of n-butanol could be devastating. We propose to develop bioremediation capability along with the biofuel capacity in order to mitigate future spills of n-butanol. To acclimatize and adapt bacteria to metabolize toxic n-butanol, we used high throughput tolerance assays, community-level ecological competition and evolutionary experiments with various selection pressures, and phenotypic and genomic characterizations. Communities were tested in a range of butanol concentrations in carbon and nutrient rich media. Bacterial communities that could grow in the 1-2% v/v concentrations of n-butanol were successively passaged to adapt to the stressful environment. The bacterial community composition was assessed over time and strains were isolated. The bacterial communities tolerant to n-butanol were then transitioned into a less carbon-rich media to look for breakdown of the butanol. Nuclear magnetic resonance (NMR) was used to quantify how much butanol remained in the cultures and identify breakdown products. The tolerable concentration of n-butanol was found to be lower than 2% v/v for most communities tested, with growth mainly at 1% v/v. In the ecological experiment, bacterial community dynamics were heavily influenced by n-but nol concentration. Two bacterial strains were found and further tested.