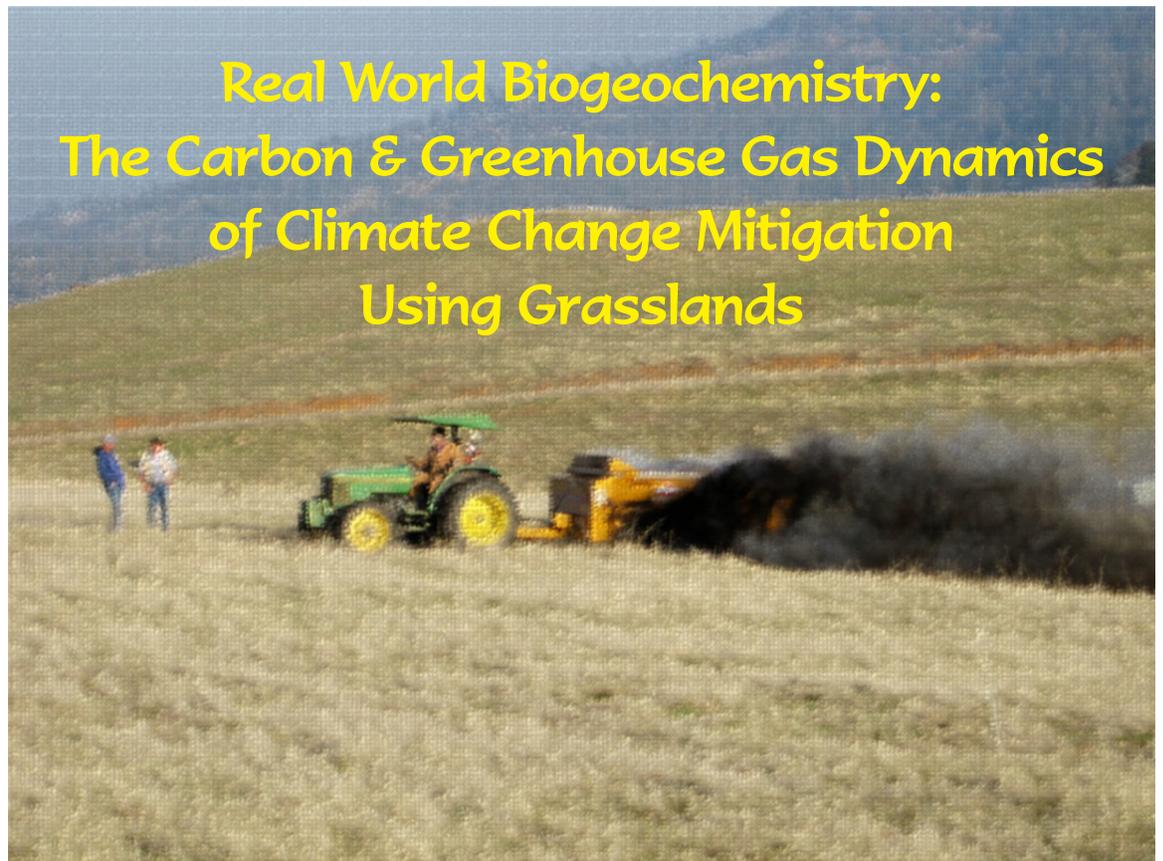


28th ANNUAL RESEARCH DAYS

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

March 28 & 29, 2019



12:30 p.m.,
March 29th,
100 Casterter
Hall

KEYNOTE SPEAKER:

DR. WHENDEE SILVER, Rudy Grah Chair
and Professor of Ecosystem Ecology and Biogeo-
chemistry in the Department of Environmental
Science, Policy, and Management at University of
California–Berkeley

SCHEDULE OF EVENTS

WEDNESDAY, MARCH 27

8:00 a.m.–5:00 p.m. Student Posters displayed in the first-floor hallways of Castetter Hall, judges preview.

THURSDAY, MARCH 28

12:30 p.m. **INVITED LECTURE, Dr. Gerald Smith**, Professor Emeritus and Curator Emeritus, Museum of Paleontology, University of Michigan, *“Interactions among Geologic, Climatic, and Biotic Mechanisms Determine Fish Species Persistence in Western United States,”* Castetter Hall Room 100.

3:30 p.m. **DEPARTMENTAL RESEARCH PRESENTATION, Dr. Eric “Sam” Loker**, Distinguished Professor & Regents’ Professor, Department of Biology, The University of New Mexico, *“The World’s Schistosomes and Their Snail Hosts: My Personal Story, with a Tribute to CETI and the Comparative Approach,”* Castetter Hall Room 100.

4:30 p.m. **SCHOLARSHIP AWARDS**, Castetter Hall Room 100.

4:30–6:30 p.m. Museum of Southwestern Biology (MSB) **OPEN HOUSE AND RECEPTION**, CERIA (Bldg. 83).

FRIDAY, MARCH 29

8:00–9:30 a.m. **CHECK IN** at the Registration Desk, Castetter Hall Foyer.

8:00–9:00 a.m. **BREAKFAST FOR KEYNOTE SPEAKER AND GRADUATE STUDENTS**, Castetter Hall Room 258.

8:00 a.m.–4:30 p.m. **SILENT AUCTION AND BAKE SALE**, Castetter Hall Greenhouse.

8:30–11:00 a.m. **STUDENT ORAL PRESENTATIONS**, 24 talks in two concurrent sessions, 51 & 57 Castetter Hall.

Coffee Break for all attendees, Castetter Hall Greenhouse

11:00 a.m.–12:30 p.m. **LUNCH BUFFET**, Basement and Courtyard of Castetter Hall.

12:30–1:30 p.m. **KEYNOTE LECTURE**, Castetter Hall Room 100:

- **Introduction of the Keynote Speaker** by Dr. William T. Pockman, UNM Professor & Chair of Biology.

- **Keynote Lecture, Dr. Whendee Silver**, *“Real World Biogeochemistry: the Carbon and Greenhouse Gas Dynamics of Climate Change Mitigation Using Grasslands.”*

- **Presentation of a Gift of Appreciation** by Dr. Robert B. Waide, Professor of UNM Biology & Co-Chair of the 2019 Research Day Committee.

1:30–5:00 p.m. **STUDENT POSTER PRESENTATIONS**, First Floor of Castetter West-wing Hallways

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RESEARCH DAY ORGANIZATION

Committee

Chairs: Drs. Robert Waide and Dorothy Scholl

Catherine St. Clair

Dr. Donna George

Dr. Ben Hanelt

Joanne Kuestner

Anne Rice

Melanie Kazenal, BGSA

Aurora Kraus, BGSA

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Department Contributors

The Department of Biology thanks all of its donors.

Your continued support and participation ensures that student research thrives.

The Department of Biology thanks especially Dr. William T. Pockman, Chair and Professor, for his dedicated support. Additional thanks are extended to Catherine St. Clair, the UNM Biology Accounting staff, the Main Office Front Desk student employees, the faculty and students who serves as our judges, and to the many other staff and students who help throughout the day.

KEYNOTE ADDRESS: ABOUT THE SPEAKER

The invited Keynote Speaker for our 27th Annual Biology Research Day is **Dr. Whendee Silver**, who will be speaking on “*Real World Biogeochemistry: The Carbon and Greenhouse Gas Dynamics of Climate Change Mitigation Using Grasslands*” at 12:30 p.m in Castetter Hall Room 100.

Dr. Silver is the Rudy Grah Chair and Professor of Ecosystem Ecology and Biogeochemistry in the Department of Environmental Science, Policy, and Management at the University of California–Berkeley. She received her Ph.D. in Ecosystem Ecology from Yale University.

Professor Silver’s work seeks to determine the biogeochemical effects of climate change and human impacts on the environment, and the potential for mitigating these effects. Currently, the Silver Lab is working on drought and hurricane impacts on tropical forests, climate change mitigation potential of grasslands, and greenhouse gas dynamics of peatlands and wetlands.



Professor Silver is the lead scientist of the Marin Carbon Project, which is determining the potential for land-based climate change mitigation, particularly by composting high-emission organic waste for soil amendments to sequester atmospheric carbon dioxide.

Recently, the Silver Lab was awarded the Innovation Prize by the American Carbon Registry. Professor Silver is a fellow of the Ecological Society of America and was named a University of California Climate Champion for 2016 for outstanding teaching, research and public service in the areas of climate change solutions, action and broad engagement.

Professor Silver’s website is <https://ourenvironment.berkeley.edu/people/whendee-silver>

PAST RESEARCH DAY SPEAKERS

YEAR	SPEAKER	TALK TITLE
2018	Dr. Thomas Swetnam, Regents' Professor of Dendrochronology Emeritus, Laboratory of Tree-Ring Research, University of Arizona, Jemez Mountains Tree-Ring Lab, Jemez Springs, New Mexico	Multi-Century Tree-Ring Perspectives of Human, Climate and Forest Interactions in New Mexico.
2017	Dr. Jonathan T. Overpeck, University of Arizona, Tucson: Director, Institute of the Environment; University Director, Southwest Climate Science Center; Thomas R. Brown Distinguished Professor; and Regents Professor of Geosciences, Hydrology & Atmospheric Sciences	New Perspectives on Future Climate Change Risk and Ecosystem Change.
2016	Dr. Kevin Lafferty, Senior Ecologist, Western Ecological Research Center, U.S. Geological Survey; Principal Investigator, Marine Science Center, University of California–Santa Barbara; and Adjunct Faculty, Ecology, Evolution and Marine Biology, University of California–Santa Barbara.	Parasites and Food Webs.
2015	Dr. Janine Caira, Board of Trustees Distinguished Professor, Ecology & Evolutionary Biology Department, University of Connecticut, Storrs, CT	On the Implications of Going Global for Our Understanding of Biodiversity and Coevolution: The Case of Sharks, Rays and Their Tapeworms.
2014	Dr. Daniel Simberloff, Gore Hunger Professor of Environmental Science, Ecology and Evolutionary Biology, The University of Tennessee–Knoxville	Biological Invasions: What Do They Do, What Can We Do about Them, and Why Are They Controversial?
2013	Dr. Scott Edward, Professor of Biology, Department of Organismic and Evolutionary Biology, and Department of Ornithology, Museum of Comparative Zoology Labs, Harvard University, Cambridge, MA	Genomes, Feathers and Flight: Comparative Genomics of Birds and Other Reptiles.
2012	Dr. Anna-Louise Reysenbach, Prof. Department of Biology, Portland State University, Portland, OR	From Mantle to Microbe: Geological Processes Shape Microbial Communities at Deep-sea Hydrothermal Vents.

YEAR	SPEAKER	TALK TITLE
2011	Dr. Lauren A. Meyers, Associate Prof., Section of Integrative Biology, Institute for Cellular and Molecular Biology, University of Texas–Austin	Modeling Killer Bugs: How Math Helps Us to Track and Control Infectious Diseases.
2010	Dr. Paul L. Koch, Prof. and Dept. Chair, Earth and Planetary Sciences, University of California–Santa Cruz	Conservation Paleobiology: Using the Past to Plan for the Future.
2009	Dr. Suzette A. Priola, Chief, TSE/Prion Molecular Biology Section, Senior Investigator, National Institute of Allergy & Infectious Diseases, National Institutes of Health, Washington DC	Molecular Mechanisms Underlying Prion Disease Pathogenesis.
2008	Dr. Charles Fischer, Prof. of Biology, Pennsylvania State University	Chemoautotrophic Symbioses: Making the Best of a Potentially Toxic Environment.
2007	Dr. Thomas Whitham, Regents' Prof., College of Engineering and Natural Sciences, Northern Arizona University, Flagstaff, AZ	The Genetic Components of Community Structure and Ecosystem Processes, and Their Conservation Implications.
2006	Dr. Deborah Nickerson, Prof. of Genome Sciences and Adjunct Prof. of Bioengineering, University of Washington, Seattle, WA	SNPping in the Human Genome: New insights into Biology and Medicine.
2005	Dr. Nancy Knowlton, Center for Marine Biodiversity & Conservation, Marine Biology Research Division, University of California, San Diego, and Scripps Institution of Oceanography, La Jolla, CA	Marine Biodiversity: From Corals to Microbes.
2004	Dr. Paul W. Ewald, Prof. of Biology, University of Louisville, Louisville, KY	The Startling Scope of Infectious Disease. Or, Why Kissing and Cats are More Scary than SARS.
2003	Dr. Edward F. Long, Monterey Bay Aquarium Research Institute, Monterey, CA	Exploring the Natural Microbial World, from Genomes to Biomes.
2002	Dr. Sandra Postel, Director, Global Water Policy Project, Amherst, MA	Dividing the Waters: Strategies for a Water-scarce Era.

YEAR	SPEAKER	TALK TITLE
2001	Dr. Carlos Martinez del Rio, Dept. of Zoology & Physiology, University of Wyoming, Laramie, WY	Mechanistic Foraging Ecology: Why Animals Eat What They Do and Why It Matters.
2000	Dr. Kenneth H. Nealson, California Institute of Technology & the NASA Jet Propulsion Laboratory	The Search for Life in the Universe: Lessons from the Earth.
1999	Dr. Baldomero Olivera, Dist. Prof. of Biology, University of Utah, Salt Lake City, UT	Neuropeptide Venoms from Cone Snails: 50 Million Years of Drug Development.
1998	Dr. David M. Hillis, Alfred W. Roark Centennial Prof. in Natural Sciences, Dept. of Zoology, University of Texas–Austin	Reconstructing the History of Life.
1997	Dr. Judy A. Stamps, Section of Evolution and Ecology, University of California–Davis	Testing Assumptions about Habitat Selection and Territorial Behavior.
1996	Dr. C.J. Peters, Chief, Special Pathogens Branch, Division of Viral and Rickettsial Diseases, NCID, CDC	Emerging Infections: Filoviruses as an Example.
1995	Dr. Eva Engvall, Prof., Dept. of Developmental Biology, University of Stockholm, & Sr. Staff Scientist, La Jolla Cancer Research Foundation, La Jolla, CA	Laminin: The Beauty and the Beast.
1994	Dr. Jeff Mitton, Prof., Dept. of Environmental, Population and Organismic Biology, the University of Colorado–Boulder	Evolutionary Responses to Environmental Heterogeneity.
1993	Dr. Mimi Koehl, Prof., Dept. of Integrative Biology, The University of California–Berkeley	The Fluid Dynamics of Hairy Little Legs: Feeding, Smelling and Swimming.
1992	Dr. Margo Haywood, Marine Biology Division, Scripps Institution of Oceanography, La Jolla, CA	Bioluminescent Symbioses.

ABSTRACTS: ORAL PRESENTATIONS

8:30–11:00 a.m., Friday, March 29, 2019

Each presentation is 12 minutes long plus 3 minutes for questions.
The bolded author is the presenter.

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

SESSION 1, 51 Castetter Hall

Moderators: [to be named]

- 8:30 1 Plants in Space: Do Lignification Levels and Microgravity Interact to Impact Photosynthesis?
Bianca Serda[†], Maximizing Access to Research Careers (MARC), Department of Biology, UNM; Margaret Turpin, Department of Biology, UNM; Norman Lewis, Institute of Biological Chemistry, Washington State University, Pullman WA; and David T. Hanson, Department of Biology, UNM.
- Plants with the C₃ photosynthetic pathway rely on diffusion of CO₂ from the atmosphere to the chloroplast to capture carbon for growth and development. Leaf anatomy, including cell wall thickness, impacts resistance to CO₂ diffusion and this can be detected using stable isotopes. The heavier stable isotope of CO₂ (¹³CO₂) diffuses more slowly than the light one (¹²CO₂), and the enzyme Rubisco uses ¹²CO₂ faster than ¹³CO₂. The net result of these anatomical and enzymatic effects is that C₃ plants capture more ¹²C when the resistance to diffusion is low, e.g., when cell walls are thin. Lignin is the part of cell walls that gives them rigidity and increases strength for withstanding gravity. Therefore, we selected a C₃ species, *Arabidopsis thaliana*, with modifications to lignin content and photosynthesis, for growth on the International Space Station and Kennedy Space Center, to examine the combined effects of lignification and microgravity on CO₂ diffusion. We hypothesize that the plants grown in space will have thinner cell walls, which will decrease resistance to CO₂ diffusion and decrease the ratio of ¹³C/¹²C in plant tissues, and increase rates of photosynthesis measured using variable chlorophyll fluorescence. Our preliminary data from plants grown on Earth demonstrates that our method for visualizing plant anatomy and lignin content works with frozen tissues, like those we will receive from the ISS, and we do not see differences in ¹³C/¹²C. Measurements of photosynthesis in space and on Earth show a trend of higher rates in space, but no impact of lignification.
- 8:45 2 Aberrant Brain Gray Matter in Murderers.
Ashly Sajous-Turner^{*}, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM; Nathaniel Anderson, Matthew Widdows, Prashanth Nyalakanti, Keith Harenski, Carla Harenski, The Mind Research Network, Albuquerque NM; Michael Koenigs, Department of Psychology, University of Wisconsin–Madison; Jean Decety, Department of Psychology, University of Chicago, Chicago IL; Kent Kiehl, Department of Psychology, UNM and The Mind Research Network, Albuquerque NM.
- Homicide is a significant societal problem with economic costs in the billions of dollars annually and incalculable emotional impact on victims and society. Despite this high burden, we know virtually nothing about the neuroscience of individuals who commit homicide. Here we examine brain gray matter differences in incarcerated adult males (n = 808) who have committed homicide compared to other violent and nonviolent offenders. Homicide offenders' show reduced gray matter in brain areas critical for behavioral control and social cognition compared with other violent and non-violent offenders. This demonstrates, for the first time, that unique brain abnor-

malities may distinguish offenders who kill from other serious violent offenders. (This research project has been reviewed and approved by the MRN Institutional Review Board (IRB) Ethical and Independent Review Services. All investigators have received training in the ethical use and protections of human subjects in research. Study title: Brain, Behavior, and Personality; Protocol #15050.)

9:00 3 Creating a “Smart” Hydrogel for Colonoscopy Preparation.

Darnell L. Cuylear[†], Maximizing Access to Research Careers (MARC), Department of Biology, and Center for Biomedical Engineering, UNM; Phuong A.H. Nguyen, Center for Biomedical Engineering, UNM; and Heather E. Canavan, Center for Biomedical Engineering, and Department of Chemical and Biological Engineering, UNM.

Colorectal cancer (CRC) is the second leading cause of cancer-related deaths in the United States. The most reliable screening method of CRC is a colonoscopy, which requires a four-liter poly(ethylene glycol)-electrolyte lavage solution (PEG-ELS) for preparation. Approximately 34% of all patients who obtain the procedure reported moderate to significant discomfort in association with the preparation. A small percentage of patients (particularly women) experience more severe side effects, including dehydration and reversible kidney failure. PEG has been recognized as a biocompatible polymer since 1950s, but no studies have examined fully the short-term and long-term effects of low and high concentrations of PEG *in vitro*. In this work, we examined the cytotoxicity of this PEG formulation toward cells within the human gastrointestinal tract *in vitro*. Using cell morphology, LIVE/Dead and XTT assays, we found that cell viability is altered with direct exposure to PEG at current dosage, with increasing cytotoxic effects at higher dosages. Therefore, to prevent over-dosage of PEG, and to improve its palatability for patients, we developed a novel hydrogel system to form a stable hydrogel from the PEG-3350. Using ¹H NMR, we confirmed that while the PEG complex is stable at the pH of most liquids, it rapidly releases its cargo at a stomach pH of 1-3. In addition, the PEG complex can release its contents into simulation fasted gastric fluid. These preliminary results show great promise for the creation of a new, more form of colonoscopy prep that could increase the numbers of people undergoing this life-saving screening method.

9:15 4 Bio-3D Printing and Near-Field Electrospinning of Bone-Ligament Tissue Engineering Scaffolds.

Nafisa Elghazali^{*}, Post-Baccalaureate Research and Education Program (PREP), Department of Biology, UNM; Matthew Rush, Center for Biomedical Engineering, and Nanoscience and Microsystems, and Biomedical Engineering, UNM; Emma Garcia, Center for Biomedical Engineering, and Biomedical Engineering, UNM; Chris Buksa, Mechanical Engineering, UNM; Marissa Perez, Ruben Trujillo, Serafina Lopez, Chemical and Biological Engineering, UNM; Lorraine Mottishaw, Center for Biomedical Engineering, and Biomedical Engineering, UNM; and Christina Salas, Center for Biomedical Engineering, and Mechanical Engineering, and Orthopaedics and Rehabilitation, UNM.

Anterior cruciate ligament injury accounts for an estimated 6.68 million cases in the U.S. alone. The current ligament transplantation scheme results in donor-site morbidity while preventing bone-ligament integration and mechanical loading, which can cause inflammation and transplant rejection. Furthermore, synthetic alternatives for ligament repair fail to mimic the intricate, highly defined hierarchical structure of native bone-ligament interface. Three-dimensional (3D) bioprinting is a valuable additive manufacturing technique for patient-specific tissue scaffold reconstruction. By utilizing near-field electrospinning (NFE) and 3D printing to create a synthetic, biocompatible scaffold, the heterogeneous architecture of the bone-ligament interface was emulated to encourage cell growth and proliferation. Highly aligned Poly-Caprolactone (PCL) mats consisting of fibers oriented at 0°, 45°, and 90° degrees were fabricated to mimic native col-

[†] Undergraduate Student, ^{*} Postbaccalaureate Student, [‡] Graduate Student

lagen fibril architecture. Unidirectional PCL fiber layers exhibited an average tensile modulus of 3.09 ± 0.98 MPa with a 0.2% strain offset when composed of 10 layers of individual 18.9 ± 1.84 μm diameter fibers with 164 ± 0.9 μm spacing. While individual PCL scaffolds remained weaker (8.33 ± 3.45 MPa) than native ligament (50-150 MPa), modifications to fiber structure and orientation are being explored to increase mechanical properties. The addition of printed PCL scaffolds with electrospun fibers and poly ethyl glycol diacrylate (PEGDA) hydrogels allowed for a highly aligned structure with cellular integration. Over three days Scaffolds show >80% cell viability and resulted in cellular attachment with aligned growth in PCL scaffolds. Overall, the use of highly oriented load-bearing structures, along with composite scaffolds, offer promising applications for the development of tissue engineered gradients.

- 9:30 5 Experimental Glioblastoma Induces Peripheral Immune Suppression and Thymic Atrophy.
Brynn Cullander[†], Maximizing Access to Research Careers (MARC), Department of Biology, and Department of Biochemistry, UNM; Katayoun Ayasoufi, Department of Immunology, Mayo Clinic, Rochester MN; and Aaron Johnson, Department of Immunology, and Department of Neurology, and Department of Molecular Medicine, Mayo Clinic, Rochester MN.

Human glioblastoma multiform (GBM) is one of the most lethal brain tumors. Categorized as a Grade IV tumor, patients have a median survival rate of approximately fifteen months. There is no cure and available treatments are dangerous with poor success rates. Recently, GBM has been associated with severe immune suppression: GBM lowers T cells, specifically the CD4⁺ population, to levels comparable to HIV/AIDS⁺ individuals. We hypothesized that (1) experimental GBM (GL261 glioma) recapitulates these key peripheral immunosuppressive features, and (2) GL261 glioma causes thymic atrophy and impaired T cell development. Observing immune cell populations at specific time points post-injection in spleens and thymuses of mice intracranially implanted with GL261 glioma and sterile PBS injections, we observed a decline in CD4 and CD8 T cells in the spleens, specifically central memory and naïve CD4 and CD8 T cells. We also observed that B cells did not respond in a tumor specific manner, but rather had a sharp decline after injection and a quick recovery to baseline levels by d14. Additionally, initial brain injury induced thymic atrophy that recovered by d21. By d28 there was a significant decrease in DN3 T cells, and SP CD8 T cells, suggesting this was a tumor-specific response, which interfered with T cell development. Emerging therapies including cancer vaccinations, viral strategies, and immunotherapies depend on an intact immune system to function properly. This demonstrates the importance of understanding the mechanism and nature of GBM-related immunosuppression to improve the success of current and emerging therapies.

- 9:45 Coffee Break, Castetter Hall Botanical Greenhouse.

- 10:00 6 *Boechera depauperata* Recovers Rapidly from Acute Heat Stress.

Marissa Harjoe[†], Joseph Stinziano and David T. Hanson, Department of Biology, UNM.

As global temperatures increase, the ability of organisms to withstand extreme heat events becomes increasingly important. Climate change, and the associated increase in temperature and frequency of extreme heat events, will have distinct impacts on both crop plant productivity and the survival of wild plant species. While considerable efforts have been made to understand thermotolerance in crop species and in the model organism *Arabidopsis thaliana*, few have studied the thermotolerant species, *Boechera depauperata*. It is well documented that *B. depauperata* withstands heat stress at temperatures lethal to its close relative *A. thaliana*, but its survival mechanisms are not understood. Our study aims to assess how photosynthetic capacity recovers after exposure to heat stress. *B. depauperata* was exposed to temperatures of 22°C (no heat stress),

[†] Undergraduate Student, * Postbaccalaureate Student, [‡] Graduate Student

45°C (moderate heat stress) and 50°C (high heat stress) for three hours. We used a thermal imaging camera to take photos hourly throughout the heat stress. Photosynthetic responses to internal CO₂ concentrations, a common method for assessing various parameters associated with photosynthetic capacity, were measured one day prior to stress, immediately after stress, one day post stress and five days post stress. In this way, we were able to capture the range of recovery of photosynthetic capacity from heat stress. Analysis of responses to heat stress showed that *B. depauperata* were able to recover rapidly from acute heat stress.

10:15 7 Spatiotemporal Dynamics of RON and EGFR Crosstalk on the Plasma Membrane.

Justine Keth[†], Maximizing Access to Research Careers (MARC), Department of Biology, UNM; Carolina Franco Nitta, Elton D. Jhamba, Ellen W. Hatch, Mara P. Steinkamp, Bridget S. Wilson and Diane S. Lidke, Department of Pathology and Comprehensive Cancer Center, Health Sciences Center, UNM.

Recepteur d'Origine Nantais (RON) and the Epidermal Growth Factor Receptor (EGFR) are Receptor Tyrosine Kinases, each with important roles in normal and oncogenic signaling. Previous studies have shown that RON and EGFR can undergo crosstalk that alters cellular signaling outcomes, yet the molecular mechanisms facilitating this are unknown. We hypothesized that crosstalk occurs from direct RON/EGFR interactions. We integrated biophysical, biochemical and imaging techniques to define the spatiotemporal details of RON/EGFR interactions. Stable human cell lines containing both EGFR and RON were generated. Our results show that RON is phosphorylated in response to EGFR activation after EGF addition. In contrast, RON activation by its own ligand MSP (Macrophage Stimulating Protein) does not result in EGFR phosphorylation. To further elucidate this crosstalk, we used fluorescence microscopy techniques to determine the location and dynamics of RON/EGFR interplay. High-resolution Single particle tracking (SPT) of quantum dot-labeled RON showed reduced mobility upon EGF stimulation, consistent with EGFR-driven RON activation. Using two color SPT, we observed correlated motion of RON and EGFR in live cells, consistent with the formation of heterodimers. Additionally, RON and EGFR were found colocalized at the plasma membrane by confocal microscopy. As expected, EGF stimulation led to rapid EGFR endocytosis, however, RON was not found in the EGFR-positive endosomes. These results suggest that crosstalk between RON and EGFR is a result of heterodimerization that occurs transiently at the plasma membrane.

10:30 8 Regulation of Long Noncoding RNA During *Toxoplasma gondii* Infection.

Breanne E. Haskins[†], Initiatives to Maximize Student Diversity (IMSD), Department of Biology, and Center for Evolutionary and Theoretical Immunology (CETI), UNM; Kayla L. Menard, Department of Biology, and CETI, UNM; Anthony P. Colombo, Sandia National Laboratories, Albuquerque NM; and Eric Y. Denkers, Department of Biology, and Center CETI, UNM.

In the immune response to infection, the role of long noncoding RNAs (lncRNAs) is emerging, but poorly understood. LncRNAs are >200 nucleotide, non-translated molecules that regulate gene expression either at the transcriptional or post-transcriptional level. We examined lncRNA activity during intracellular infection with *Toxoplasma gondii*, an opportunistic pathogen that is important medically and agriculturally in humans and animals. We isolated RNA from mouse bone marrow-derived macrophages (BMDM), infected with high and low virulence strains of *T. gondii*, and subjected to analysis on a microarray containing probes for 35,923 lncRNAs and 24,881 mRNAs. The microarray results identified more than 1,000 lncRNAs and mRNAs that were up- or down-regulated. We identified categories of lncRNAs associated with immune response genes that were up- or down-regulated after infection, and a subset of these lncRNAs displayed parasite strain-specific regulation. We evaluated a panel of four lncRNAs and their associated mRNAs regulated by *Toxoplasma* by semi-quantitative real-time PCR. Our results

[†] Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

support the preliminary microarray data, thus validating the microarray values and providing a foundation for further study on a subset of highly regulated lncRNAs. Using ROP16 mutant parasite strains, we began functional studies of lncRNAs. ROP16 is a parasite kinase that activates host cell signaling, leading to changes in host gene expression, which we found includes lncRNA expression. Future work will continue to focus on lncRNA molecular function within the cell and the downstream consequences of infection.

10:45 9 Amino Acid for $\delta^{13}\text{C}$ Analysis Quantifies Environmental Change in a Nearshore Ecosystem through the Late Holocene.

Emma A. Elliott Smith[‡], Department of Biology, UNM; Emily L. Whistler, Department of Anthropology, Washington State University, Pullman WA; Todd J. Braje, Department of Anthropology, California Academy of Sciences, San Francisco CA; Paul Szpak, Department of Anthropology, Trent University, Peterborough ON, Canada; Douglas J. Kennett, Department of Anthropology, Pennsylvania State University, State College PA; René L. Vellanoweth, Department of Anthropology, California State University–Los Angeles; Torben C. Rick, Department of Anthropology, Smithsonian Institution, Washington DC; and Seth D. Newsome, Department of Biology, UNM.

Kelp forests are among the most biodiverse and threatened marine ecosystems. For conservation efforts to be effective, it is crucial to develop a thorough understanding of the spatiotemporal dynamics of these systems. Here, we employed $\delta^{13}\text{C}$ analysis of essential amino acids (EAA) from ancient top consumers to evaluate changes in southern California kelp forests across a period of accelerating human impacts (3,500 yBP–present). Because consumers typically route EAA directly into tissues, these molecules are altered minimally through food chains. Moreover, marine producers have highly varied physiologies, causing patterns in their EAA $\delta^{13}\text{C}$ to act as unique “fingerprints” that can be identified in consumers. We analyzed bone collagen extracted from archaeological remains of sea otters (*Enhydra lutris*) and sheephead (*Semicossyphus pulcher*) from two southern California islands. We also characterized EAA $\delta^{13}\text{C}$ profiles for modern marine producer groups as baseline values for comparison. We used linear discriminant analysis and Bayesian isotope mixing models to distinguish between producer groups and to classify consumers according to their reliance on different producers. Our results showed that more than 80% of ancient sea otter and sheephead EAA were derived from kelp, indicating that these consumers were feeding in ecosystems driven by kelp production. In combination with ongoing EAA $\delta^{13}\text{C}$ analysis of modern samples, these findings suggest that kelp forests were more extensive in the late Holocene than they are today at these sites. Our study demonstrates the application of amino acid $\delta^{13}\text{C}$ analysis in integrating historical ecological information and modern conservation biology.

SESSION 2, 57 Castetter Hall

Moderators: [to be named]

8:30 10 Niche Dynamics of the Felid Guild Following the Pleistocene Megafaunal Extinction.

Nicholas Freymueller[‡], Department of Biology, UNM; Corinne Myers, Department of Earth and Planetary Sciences, UNM; and Felisa A. Smith, Department of Biology, UNM.

During the Pleistocene, meso-carnivores such as the cougar (*Puma concolor*) and bobcat (*Lynx rufus*) were potentially outcompeted by larger-bodied felids such as the saber-toothed cats *Homotherium* and *Smilodon*. Extinction of these more massive hyper-carnivores at the terminal Pleistocene likely resulted in unfilled habitat/niche space. I examined if cougars and bobcats began to occupy eco-space vacated by the extinctions of the mega-felids. I employed an ecological niche modeling

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

(ENM) approach using fossil felid occurrences from the Neotoma Paleoecology Database and paleo-climatic reconstructions from the PaleoClim Database. I produced ENMs of felids for the late Pleistocene, mid-Holocene, and modern time periods; I compared ENMs in environmental space between cougars, bobcats, and extinct felids to test for cougar/bobcat niche expansion into those previously occupied megafelid-niches. Preliminary results suggest that cougar and bobcat niches did expand post-megafaunal extinction, but this was mostly due to warmer non-analog climates becoming available. Further, contrary to expectations, I found that neither cougars nor bobcats appeared to fill in the niche space vacated by the mega-felids following their extinction. Finally, while not an initial goal of my analyses, the results suggest that the disappearance of acutely cold non-analog habitats from the Pleistocene likely contributed to the extinction of *Homotherium*, but not *Smilodon*. My findings suggest that felid ecological niches do not appear to have been constricted by interactions with other felids during the Pleistocene. Furthermore, availability of certain habitats appears to be the most crucial factor in determining niche how much of a species' fundamental niche is occupied.

- 8:45 11 Null Models Reveal Fine-scale Parasite Community Turnover in a Diverse Multi-Host, Multi-Parasite System.

Selina M. Bauernfeind^{*}, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM; Lisa N. Barrow, Ohio State University, Columbus OH; Matthew J. Baumann, Serina S. Brady, Museum of Southwestern Biology and Department of Biology, UNM; Andrea N. Chavez, Bureau of Land Management Rio Puerco Field Office, Albuquerque NM; Paxton A. Cruz, John E. Ford, Chauncey R. Gadek, Museum of Southwestern Biology and Department of Biology, UNM; Spencer C. Galen, American Museum of Natural History, New York NY; Andrew B. Johnson, Xena M. Mapel, Rosario A. Marroquin-Flores, Taylor E. Martinez, Jenna M. McCullough, Jade McLaughlin, Daniele L. Wiley, Jessie L. Williamson, and Christopher C. Witt, Museum of Southwestern Biology, and Department of Biology, UNM.

Birds and their haemosporidian parasites comprise a diverse multi-host, multi-parasite system that is uniquely suited for studying evolutionary dynamics of host-parasite relationships. Because of the challenges of surveying entire communities, however, it is difficult to know the extent to which haemosporidian parasite communities vary from place to place. Here we asked whether haemosporidian communities differ among three adjacent mountain ranges in New Mexico that have similar bird communities. To address this question, we conducted community-level surveys of haemosporidians within a narrow elevational zone (2100–2500 m). We screened 776 specimens using PCR and sequencing of an mtDNA 'barcode' (*cytb*). We found 269 infected birds (34.7% of total), of which 50% of infections were *Haemoproteus*, 38.7% were *Leucocytozoon*, and 24.2% were *Plasmodium*. We found 54 unique haemosporidian lineages, of which 56 occurred in one mountain range, 24 occurred in two mountain ranges, and 19 occurred in all three mountain ranges. We developed a null model to test whether the observed pattern differed from the pattern that would be expected if there were no differences among mountains. The null model accounted for uneven sampling and differences in abundance among haemosporidian lineages. The test revealed an excess of lineages occurring in just one of the three mountain ranges, which was consistent when we repeated the null model test using only host species that were sampled in all three ranges. We conclude that haemosporidian species turnover occurs on a relatively small spatial scale, even within the same set of host species and habitats.

- 9:00 12 Impacts of River Modifications on Food Webs—Lessons from Collections in Australia and the American Southwest.

Gregor Hamilton[‡], Department of Biology, UNM, and Thomas F. Turner, Division of Fishes, Museum of Southwestern Biology, and Department of Biology, UNM.

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River flow homogenization caused by dam and weir construction has been correlated with the reduction of community niche breadth, as predicted by food web theory. Stable isotope analysis of natural history collections has been invaluable in gaining these insights. Sufficient collections have allowed for pre-alteration conditions to be established and post-alteration comparisons to be made. Some portion of food web shifts, however, that have been correlated with dam/weir construction may be confounded by other anthropogenic disturbances, particularly effluent from agriculture and human settlements. Advances in stable isotope techniques may make it possible for ecologists to trace baseline shifts in primary production values that would express itself throughout the food web. Here, using collections, we examine food webs from two analog aridland river systems that were heavily modified in the 20th century: the Murray-Darling (Southeast Australia) and the Rio Grande (Southwest U.S.).

- 9:15 13 Characterizing the Gut Microbiome of a Bacterial Cold Water Disease-resistant Line of Rainbow Trout (*O. mykiss*).

Ryan M. Brown^{*}, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM; Gregory Wiens, National Center for Cool and Cold Water Aquaculture, Leetown WV; and Irene Salinas, Department of Biology, UNM.

Commensal microorganisms at mucosal surfaces play a vital role in protecting the host organism from bacterial infection. There are multiple factors that contribute to microbiome selection, including host genetics. *Flavobacterium psychrophilum*, the causative agent of Bacterial Cold Water Disease in salmonids, accounts for acute losses in farmed rainbow trout (*Oncorhynchus mykiss*). The U.S. National Center for Cool and Cold Water Aquaculture has used family-based selective breeding to generate a line of rainbow trout with enhanced resistance to *F. psychrophilum*. The goal of this study is to determine whether selective breeding impacts the gut and gill microbiome of *F. psychrophilum*-resistant compared to a background matched susceptible trout. Mid-gut and gill samples were collected from juvenile fish maintained at high or low stocking densities and microbial diversity assessed by 16S rDNA amplicon sequencing. Results indicate that alpha diversity was significantly higher in the mid-gut of the susceptible line compared to the resistant line, while no significant differences in alpha diversity were observed in the gills. *Mycoplasma* sp. was the dominant taxon in the mid-gut of both groups, although present at a decreased abundance in the susceptible line. We also observed increased abundance of potential opportunistic pathogens in the susceptible line. Within the gills, both lines exhibited similar microbial profiles. Together, these results suggest that selectively bred *F. psychrophilum*-resistant trout may harness a more resilient gut microbiome, attributing to the disease resistant phenotype. Importantly, we observed that environmental factors such as stocking density have a significant impact in shaping trout microbial communities.

- 9:30 14 Amino Acid Isotope Analysis Reveals Species-specific Variation in Diet and Gut Microbial Contribution to Host Protein Metabolism in an Arid Land Small Mammal Community.

Alexi C. Besser[‡], Christina M. Blevins, Emma A. Elliott Smith and Seth D. Newsome, Department of Biology, UNM.

Many mammals consume diets full of recalcitrant carbohydrates, but do not have the enzymes needed to digest these molecules. The role of the mammalian gut microbiome in breaking down carbohydrates and plant toxins has been studied for decades, particularly in hindgut fermenters. The potential role of the gut microbiome in supplementing essential amino acids (AA_{ESS}) to their mammalian hosts has received less attention, despite the fact that herbivores and omnivores are often protein-limited. Desert small mammal communities provide a useful system for studying the potential role of the gut microbiome in supplementing AA_{ESS} to their hosts, because species with different foraging strategies (e.g., granivores vs. omnivores) often co-occur in the same

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habitat, allowing for a comparative approach across diverse diets varying in protein quantity and quality. We used amino acid carbon and nitrogen isotope ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) analysis to examine the potential role of symbiotic gut microbes in the protein metabolism and trophic ecology of five small mammal species, including three granivores (*Dipodomys merriami*, *Dipodomys ordii*, *Dipodomys spectabilis*), an omnivore (*Peromyscus* spp.), and an insectivore (*Onychomys arenicola*) in the northern Chihuahuan Desert (New Mexico, USA). We analyzed the AA_{ESS} $\delta^{13}\text{C}$ values of C_3 and C_4 plants ($n = 45$) and small mammal red blood cells ($n = 50$) collected from a mixed shrubland–grassland habitat that experiences seasonal variation in the relative abundance of C_3 and C_4 primary production. Our analyses indicate two granivorous species, *D. ordii* and *D. spectabilis*, may route some AA_{ESS} from symbiotic gut microbes.

9:45 Coffee Break, Castetter Hall Botanical Greenhouse.

10:00 15 Fitness Differences Between Drug-resistant and Drug-sensitive *Mycobacterium tuberculosis* (*Mtb*) in Varied Host Environments.

Julie Allison Spencer ‡, Department of Biology, UNM; and Helen J. Wearing, Department of Biology, and Department of Mathematics and Statistics, UNM.

Ten million people became infected with tuberculosis (TB) worldwide in 2017; 558,000 of these cases were drug-resistant, while the treatment success rate for drug-resistant TB was only 55%. To understand the epidemic potential of resistant tuberculosis, a key consideration is the effect of fitness on prevalence. Many existing population-level models for transmission of resistant tuberculosis either do not include pathogen fitness or assume that it is fixed. These assumptions obscure the underlying biological reality that pathogen fitness affects the outcome of infections, and that it varies with strain and treatment. A few recently published models of TB transmission have included functions that track distributions of fitness costs; however, multi-scale modeling that explores within-host fitness dynamics within the framework of population-level models is essential. We examined the fitness of *Mtb* in host environments that varied according to the presence or absence of infection with two different *Mtb* strains, and according to the presence or absence of treatment with antibiotics. We developed a mathematical model to assess the effects of a range of fitness values on TB transmission and prevalence, where fitness is defined as a relative cost ($0 < w < 1$) or a relative advantage ($1 < w < 2$). Using this model, we simulated scenarios in which sensitivity or resistance to antibiotics confers costs or advantages. One surprising result of this study is that in some environments, drug-sensitive *Mtb* appears to have an evolutionary advantage over drug-resistant *Mtb*.

10:15 16 Water Source Determination Using Sap Flux and Budyko Analysis.

Devon Fisher-Chavez †, Tomer Duham, Cheng-Wei Huang and Marcy E. Litvak, Department of Biology, UNM.

As climate changes, “hot droughts” or “global change-type droughts” are expected to dramatically affect ecosystems in the Southwestern United States. These areas are already water-limited, making understanding how these global change-type droughts will affect the water balance of semi-arid regions critical. Species able to access groundwater may have a competitive advantage over species that are not able to access groundwater in future global change-type droughts. Little research, however, has been conducted on groundwater usage by plants in semi-arid ecosystems. To determine if a stand of *Pinus ponderosa* (ponderosa pine) are able to utilize groundwater, we observed sap velocity (J_s), soil water content (*SWC*), evapotranspiration (*ET*), micrometeorological methods, and calculated potential evapotranspiration (*PET*). We hypothesized that as *SWC* decreases, ponderosa pine would be more dependent on groundwater sources present, which would be indicated by a weak correlation between J_s and *SWC*. Additionally, a Budyko analysis identified energy-restricted or excessive and water restricted or excessive regimes. A water-balance

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analysis identified if and when water from sources other than precipitation entered the system. The ratio between ET and P (ET/P) was greater than one in some years (i.e., 1.08, 1.127, 1.061, and 1.038 for the years 2012, 2014, 2016, and 2017, respectively), which is a strong indicator of groundwater usage; however, because a non-random correlation between SWC and J_s was observed over the study period (2014–2017), more analysis is required.

10:30 17 Asymmetric Gene Flow in an Understory Fijian Bird.

Ethan F. Gyllenhaal ‡, Xena M. Mapel and Michael J. Andersen, Department of Biology, and Museum of Southwestern Biology, UNM.

Islands have provided a disproportionate amount to the development of allopatric speciation theory, because myriad populations are separated by open-water gaps. Often, these isolated populations are found to be divergent, but little is known about the extent of gene flow between them. The Fiji Bush Warbler *Horornis ruficapilla* is afurtive, understory passerine found on the four largest Fijian islands. These populations are described as subspecies based on slight, but noticeable, vocal and plumage differences. We sequenced thousands of ultraconserved elements to infer population structure and patterns of gene flow within this species. We found that the four island populations formed distinct genetic clusters. Each pair of adjacent islands—Vanua Levu and Taveuni in the north and Viti Levu and Kadavu in the south—were related closely to each other, with deeper divergences between these two pairs. Our demographic analyses, however, inferred low levels of asymmetric gene flow, not just between each member of a given pair, but also between the pairs of northern and southern islands. For each sister pair, the population on the larger island had much higher levels of gene flow into the smaller islands than vice-versa. The discovery of gene flow between non-sister lineages confirms that, despite moderate genetic divergence, these allopatric populations will still interbreed after dispersing over miles of open ocean. Additionally, our finding of uneven gene flow between large and small islands offers a hypothesis to test for inter-island population structure in other Fijian taxa.

10:45 18 Genetic Status of Gila Trout Populations Based on Next-generation RAD Sequencing.

David Camak ‡, Thomas F. Turner and Megan Osborne, Department of Biology, UNM.

Gila Trout (*Oncorhynchus gilae*) is a federally protected species that occurs in headwater streams of the Gila and San Francisco rivers in New Mexico and Arizona. Gila Trout is threatened by introduction of nonnative Rainbow Trout (*O. mykiss*), wildfire, and climate change. It is imperative to understand sources of genetic variation available so as to effectively conserve genetic diversity and existing population structure within Gila Trout. Using a restriction site association DNA (RAD) sequencing approach and the annotated Rainbow Trout genome, we genotyped thousands of single nucleotide polymorphisms (SNPs) for all lineages of Gila Trout and representative lineages of Rainbow Trout that were historically stocked in New Mexico. Results suggest Gila Trout lineages are highly structured with low, yet unique, genetic diversity and low effective population sizes corroborating past results. Previous studies suggested introgression among Iron Creek lineage fish and nonnative Rainbow Trout. Whole genome data, however, showed no indication of hybridization within the Iron Creek lineage. More broadly, our data indicate low genetic diversity within Gila Trout lineages, low genetically effective population sizes, and evidence for local adaptation. We suggest a management strategy focused on increasing genetic diversity among lineages while retaining the unique diversity within each lineage.

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ABSTRACTS: POSTER PRESENTATIONS

1:30–5:00 p.m., Castetter First-floor, West-wing Hallways

The bolded author is the presenter.

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- 19 Native Bees Exhibit Species- and Ecosystem-specific Changes in Abundance with Aridity.

Melanie R. Kazenel‡, Department of Biology, UNM; Karen W. Wright, Department of Entomology, Texas A&M University, College Station TX; Terry L. Griswold, Pollinating Insects Research Unit, USDA-ARS, Utah State University, Logan UT; Julieta Bettinelli, Jennifer A. Rudgers and Kenneth D. Whitney, Department of Biology, UNM.

Despite widespread concern about pollinator declines, evidence of how climate change may influence bee communities is scarce. Bees may be susceptible to changes in both climate mean and variability, including the frequency of extreme weather events such as drought. We studied relationships between native bee abundance and climate at the Sevilleta National Wildlife Refuge (New Mexico, USA), where multiple dryland ecosystem types converge and climate-induced ecosystem state transitions are predicted. We asked: (1) How does native bee abundance vary with aridity (drought) over time? (2) Do bee abundance relationships with aridity differ among three ecosystem types? and (3) Are bee abundances better predicted by present or past year's aridity? We sampled bees in March–October from 2002–2014, aggregated climate data from co-located weather stations, and focused our analyses on five abundant bee species. Bee abundance relationships with increasing aridity ranged from linear (positive and negative) to quadratic and cubic. All species had nonlinear relationships with aridity in one or more ecosystems, suggesting differential susceptibility to changes in climate mean and variance. One species showed consistent abundance optima at average aridity, and thus might respond negatively to climate shifts. The remaining species had differing abundance relationships with aridity among ecosystems; plant communities may thus mediate their climate responses. Lag effects with climate occurred, and the relative importance of present versus prior year's aridity varied among species. Understanding climate change effects on bees will require attention to bee species identity, ecosystem types and transitions, past and present climate conditions, and possible nonlinear responses.

- 20 The Effect of High Amplitude tACS on Visual Working Memory Capacity.

Hope A. Gill*, Post-Baccalaureate Research and Education Program (PREP), Department of Biology, and Department of Psychology, UNM; and Claudia Tesche, Department of Psychology, UNM.

Visual Working Memory (VWM) is a reliable indicator of individual differences and is correlated strongly with broad cognitive function. Transcranial Alternating Current Stimulation (tACS) modulates brain oscillations, which influence cognitive processes. As a result, this study has two main aims: (1) to characterize the effects of tACS on VWM capacity using a high-density electroencephalographic (EEG) array, and (2) to determine if tACS alters VWM capacity and EEG measures differently within high and low working memory capacity groups. Participants will complete three separate sessions that influence the state of the brain through a VWM capacity task known to elicit prominent EEG signals. High Density EEG will be used to monitor and record these prominent Event-Related Potentials (ERP) and oscillatory brain activity before, during, and after verum. tACS will either increase/decrease memory

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capacity, resulting in a change of the amplitude in ERP's. SPSS will be the main software program used for data analyses, while ERP measures will be analyzed through EEGLab. When tACS is applied during the VWM capacity task, the anticipated results are: (1) a decrease/increase in the amplitude of ERP's in high/low working memory capacity individuals, which will correlate with changes in performance accuracy, (2) changes in EEG measures during verum and sham, which will correlate with changes in VWM capacity, and (3) IQ correlates with ERP amplitude across participants. This study could be essential for future stimulation research to help predict the effects individual differences may have on changes in brain dynamics and task performance.

- 21 Long-term Pollinator Monitoring Study in the Chihuahuan Desert at the Sevilleta LTER, New Mexico. **J. McLaughlin**, Department of Biology, UNM; K. Wright, Minnie Bell Heep Center, Department of Entomology, Texas A&M University, College Station TX; J.A. Rudgers, M. Kazenel and J. Bettinelli, Department of Biology, UNM.

A bee monitoring study was created to examine community and population fluctuations in native bees over a long period of time. With its origin in 2001, the study now has accumulated 17 years worth of continuous data, making it one of the longest running bee data sets in the world. Comprised of more than 300 species, this data is an excellent representation of the bee diversity that can be found in the Chihuahuan Desert grass and shrublands. The methodology for this study is fairly simple and requires low maintenance, making it a good candidate for modification and implementation in other ecosystems. Bees are collected in funnel traps at three different sites on the Sevilleta National Wildlife Refuge. Then the collected bees are curated in an arthropod lab at the University of New Mexico, identified to species, and entered into the data set. This data, paired with any multitude of accessible Sevilleta LTER data sets, allow for analyses to address inquiries on a multitude of subjects, including but not limited to: climate sensitivity, community variation, spatial and temporal patterns, phenological relationships, and specialist vs. generalist dynamics. The application of this type of study in other ecosystems, including urban environments, may reveal answers to similar questions.

- 22 Resilience of American Pikas to Wildfire at the Southern Limit of Their Range. **Kelly A. Lizewski**[†], Marie L. Westover, Department of Biology, UNM; Erik A. Beever, Northern Rocky Mountain Science Center, USGS; and Felisa A. Smith, Department of Biology, UNM.

Alpine environments are among those most at risk of climate change due to high rates of endemism in which many cold-adapted species have limited dispersal ability. Among the species that concern conservationists is the American pika (*Ochotona princeps*), a small alpine mammal found in western North America, including the Jemez and Sangre de Cristo Mountains of New Mexico. Within these regions, drought and increased temperatures, coupled with livestock grazing and fire suppression policies, have elevated the probability of severe wildfire occurrences that are proven to alter plant and animal communities. Changes to vegetation following fires have been shown to influence small mammal populations such as woodrats and deer mice, but studies regarding the impact of fire on pikas is constrained to small areas and short time scales. To examine the effects of wildfire on pikas, we surveyed 346 sites of pika habitat in the summers of 2016 through 2018 in the Jemez and Sangre de Cristo Mountains and, using GIS, determined the extent that six fires had on the pika habitat from 1984 to 2016. We found that pikas are resilient to wildfire in New Mexico, whereas other variables, such as elevation, were more influential to their distribution. Identifying pikas' response to fire helps conservationists understand ecological interactions in post fire habitats and contributes to preserving the species.

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- 23 Genetic Monitoring of Population Structure and Effective Population Size in Chihuahua Chub (*Gila nigrescens*).

Brian Fitzgerald[†], **Charisa Bell**[†], Megan Osborne and Thomas F. Turner, Department of Biology, UNM.

Chihuahua Chub *Gila nigrescens* is a freshwater fish native to the Guzman and Bustillos basins in northern Mexico and the Mimbres River in southern New Mexico. Chihuahua Chub has a limited geographic range and persists in small, isolated populations that in recent years have been augmented with hatchery-reared fish. In 1983, Chihuahua Chub was listed as threatened in the United States under the Endangered Species Act. Small population size and hatchery augmentation can impact genetic diversity and it is important to periodically monitor for negative effects. Genetic assessment has not been conducted on this species since 2010, so we sampled Chihuahua Chub at different localities along the Mimbres River in 2018. Interestingly, a previously identified population structure between an upstream locality and downstream localities in the Mimbres River was no longer apparent. Genetic findings are consistent with evidence of dispersal by fishes between localities based on tag-recapture studies. Effective population size has declined since 2010, suggesting that local abundance could be declining, perhaps associated with demographic losses due to wildfire and drought. Conversely, metrics of genetic diversity for hatchery stocks used to augment the population in the wild were stable across time. Based on our data, there is growing concern about the status of Chihuahua Chub in the Mimbres river, yet we are hopeful that recent habitat improvements and periodic hatchery augmentation can improve the status of this species.

- 24 Characterization of Non-specific Mucosal CD8⁺ T Cells in Teleost Fish and Their Candidate Antigen-presenting MHC-I Molecules.

Pankoj Kumar Das[‡], Ryan M. Brown, Elisa Casadei, Aurora Kraus, Ali Sepahi and Irene Salinas, Department of Biology, UNM.

T lymphocytes are known for their vital role in adaptive immune responses of jawed vertebrates; however, non-conventional innate-like T cells also exist and continue to be uncovered in tetrapod species. Previously we identified a population of CD8⁺ T cells that rapidly infiltrates into the olfactory organ (OO) of rainbow trout in response to nasal viral delivery. Given the rapid nature of this response, we hypothesize that these T cells are non-specific. In support, we found that nasal delivery of live and dead bacteria also triggered the infiltration of CD8⁺ T cells in the trout OO. Since pathogen cause selective cell death in olfactory neurons, we hypothesize that these CD8⁺ T cells may be recognizing a self-antigen released by pathogen damage. Lipidomic profiling of the control and viral-treated trout OO identified SM and Ceramide lipids that were upregulated upon viral exposure in the OO, including a ceramide, known to be the antigen of non-conventional T cells in mammals. As a consequence, hydrophobic non-polymorphic MHC-I molecules are the best candidates for the presentation of a lipidic self-antigen. In teleosts, these molecules are L-lineage MHC-I genes. Gene expression analysis of two L-lineage genes LAA and LDA and a non-L-lineage gene, UAA, revealed rapid upregulation of UAA but not the other two. In summary, our results indicate the possible presence of a non-specific CD8⁺ T cell subset in trout mucosal tissues that responds quickly to pathogens and may be activated by self-lipid antigens. Future studies will focus on the functional properties of purified ceramides identified in our lipidomic survey.

- 25 Groundwater Flow Regimes of the Rio Grande Bosque Ecosystem: Impacts of Floodplain Connectivity and Drought.

Katelyn P. Driscoll[‡], Department of Biology, UNM, and Rocky Mountain Research Station, U.S. Forest Service.

Fluctuation in groundwater levels is a major driver of structure, function, and composition of floodplain ecosystems, with the full range of natural variation important for the survival, growth, and reproduction of many riparian species. Annual patterns in water table depth (DWT) are characterized by the timing, frequency, magnitude, duration, and rate of change in groundwater levels. I used long-term well data collected by the Bosque Ecosystem Monitoring Program to characterize the DWT regime of the Middle

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Rio Grande and explore impacts of channelization and drought. Using the Index of Hydrologic Alteration (IHA; Richter et al. 1996), I compared the DWT regimes of sites that do not experience overbank flooding and those where flooding occurs. I also used IHA to compare DWT patterns during drought (Palmer Hydrologic Drought Index; PHDI < -2) and non-drought (PHDI > -2) years. Only some components of the hydrologic regime appear to be influenced by channelization and drought, with timing, rate of change, and duration of high and low groundwater levels appearing resistant to these stressors. Magnitude and frequency of high and low DWT was impacted by the loss of flooding and magnitude during spring months was influenced further by drought. With climate change, less snowmelt runoff, and more frequent dry periods predicted in the future, it is important to understand how the loss of overbank flooding and drought impact groundwater fluctuations. My results can help inform management of the Bosque by identifying areas with relatively intact DWT regimes that have greater potential for restoration success.

26 The Paradox of Polyploidy: Is Variation in Unreduced Gamete Formation the Key Missing Factor?

Benjamin Gerstner[‡], Kenneth D. Whitney and Helen J. Wearing, Department of Biology, UNM.

The primary method for formation of polyploids, in plants, is through the formation and joining of unreduced gametes. Their production is the result of an interplay between genetic and environmental factors that result in variable formation rates of unreduced gametes (FRUG) within populations. Once formed, neo-polyploids (cytotypes) face minority cytotype exclusion (MCE) due to a lack of viable mating opportunities. More than a dozen theoretical models have explored factors that could permit neo-polyploids to overcome MCE. Until now, however, none has explored the variability observed in FRUG and its consequences in overcoming MCE. In this work, we: (1) determine the distribution that best fits available empirical data of FRUG; (2) explore the consequences of using stochastic draws from this distribution for FRUG on an existing model's behavior; and (3) add a component of temporal autocorrelation to draws for FRUG, to evaluate differences in model behavior due to environmental correlates of FRUG. We found that the distribution shape of FRUG is best fit by either a beta or log-normal distribution with a mean of ~2%. Stochastic draws for FRUG decrease the time to overcome MCE and, in some instances, makes overcoming MCE possible when it was not otherwise. Temporal autocorrelation has a small effect in tightening the variability around the generation to switch, further work is necessary to determine appropriate autocorrelation values for FRUG. This work demonstrates that the existing models provide over-estimates for parameter values to overcome MCE and adding variable FRUG will lower those parameter values to overcome MCE.

27 Facultative Hypothermia in Urban Roadrunners.

Tina V. Guo[†], William A. Talbot, Department of Biology, and Museum of Southwestern Biology, UNM; Brian A. Millsap, U.S. Fish and Wildlife Service, Albuquerque NM; Blair O. Wolf, Department of Biology, UNM; and Christopher C. Witt, Department of Biology, and Museum of Southwestern Biology, UNM.

Facultative hypothermia (FH) is an energetic strategy whereby birds or mammals undergo controlled reduction of body temperature and metabolic rate to save energy during periods of inactivity or stress. This strategy is used regularly by bird species in several families to cope with cold nocturnal temperatures, a behavior known as daily torpor. In southern California, Greater Roadrunners (*Geococcyx californianus*) reduce their body temperatures by 5-6°C at night, when ambient temperatures descend to 5-10°C. In this project, we seek to characterize the use of FH by roadrunners living in the colder climate of New Mexico, near the northern and high-altitude limit of the species range. We predict that cold-climate roadrunners will exhibit more pronounced use of FH, reflecting local adaptation to cold ambient temperatures. We captured roadrunners and surgically implanted iButton temperature loggers to monitor core temperature at five-minute intervals over a period of weeks. Simultaneously, we monitored ambient temperatures in the local area. Daily fluctuations in the core temperature allowed us to estimate the

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lower critical body temperature for New Mexico roadrunners. The lower critical body temperature may be a key parameter determining the “cold range limit” of the species. The similarity of lower critical body temperatures between southern California and New Mexico roadrunners indicates evolutionary conservation of FH behaviors. On the other hand, differences between these two populations suggest local adaptation to thermal regimes despite high genetic connectivity. Local adaptation in thermoregulatory behaviors such as FH may be increasingly crucial to persistence of wildlife species in the Anthropocene.

28 Sphagnum Photosynthetic Rates relating to Relative Water Content through Electrical Impedance.

Cassandra Lujan[†], Department of Biology, UNM.

Sphagnum peat moss dominate peatlands, covering 2-3% of the land surface on Earth. Using electrical impedance is a novel way to measure water status, carbon assimilation rates (*A*) of *Sphagnum magellanicum* to relative water content (RWC) through-out drying. Three to four growing tips (capitula) of *S. magellanicum* were placed in a 6800 LiCor gas exchange chamber with controlled light intensity (800 PAR), CO₂ concentration (400 ppm) and incoming air H₂O concentration (18mmol/mol). Opposite phyllids of one capitulum in the chamber were connected to wires, and impedance (*Z*) through tissue was measured with a LCR meter at four different frequencies (0.1 kHz, 1 kHz, 10 kHz, and 100 kHz). One part of *Z*-parameters of impedance (electron flow resistance) was calculated, specifically through-out the plants photosynthetic tissues, and within 1000 seconds into the dry-down process, curves show photosynthetic rates of Sphagnum capitula plateau, most likely due to relative water content (RWC%) decreasing in Hyalocyte cells contributing to chlorocyte photosynthesis decrease, where tissues are experiencing effects of drying. Simultaneously, impedance frequencies 0.1 kHz and 1 kHz quickly diverge, and 10 kHz and 100 kHz frequencies stay in a linear fashion, suggesting that as water begins to decrease within the plants cells, higher wavelengths are able to flow through water with less resistance, then lower intensity wavelengths. This new impedance method is a fundamental way of understanding specifically where drying happens first physiologically. The next step is to determine what the phase shift of electrical impedance tells us about moss structure and function and how this varies throughout latitudinal gradient species.

29 Effects of Simulated Drought on Fungal Community Composition and Root Colonization in North American Grasslands.

Devon Lagueur[†] and Jennifer Rudgers, Department of Biology, UNM.

We investigated the sensitivity of soil fungal community composition and root endophyte colonization to simulated drought and site effects in North American grasslands, because soil and plant-associated fungal communities can ameliorate stress responses in host plants, and these communities are themselves becoming stressed by climate change. Using next generation sequencing techniques, we quantified the response of soil fungal communities to drought and control treatments, compared these results across various sites and species, and microscopically examined relative fungal load by scoring root slides. We found that fungal community composition and root colonization are resilient to drought in grasslands overall, with other factors, such as latitude and soil pH, contributing more to models of diversity and richness than treatment effects. Some plant species/site combinations, however, did experience significant changes in the drought treatment. These patterns indicate that, depending on location and host-plant species, fungal community composition and root colonization in grasslands are affected differentially by climate change. Therefore, as plant and microbial communities are influenced by future climates, some plant species will experience additional effects due to changes in their fungal communities, which is likely to differentially affect plant fitness.

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30 Optimizing the Rapid Photosynthetic CO₂ Response for Complex Leaf Geometry.

Nellie Toliver[†], Joseph Stinziano and David T. Hanson, Department of Biology, UNM.

Leaf-level gas exchange is used to measure photosynthetic performance in plants. During photosynthesis, the enzyme ribulose-1,5-bisphosphate carboxylase oxygenase (Rubisco) catalyzes CO₂ fixation. By measuring the response of photosynthesis (A) to intercellular CO₂ concentration (C_i) (A - C_i curve), we can estimate biochemical limitation on photosynthesis, including the maximum Rubisco carboxylation capacity (V_{cmax}) and electron transport to CO₂ (J), and the CO₂ concentration at which photosynthesis is co-limited by V_{cmax} and J (C_i transition). Using a dynamic method known as rapid A - C_i response (RACiR), we can quickly assess V_{cmax} and J with high data density. This technique was validated in broad, flat-leaf model organisms; however, for leaves with complex geometries, the calculations of C_i can breakdown under dynamic conditions. We hypothesize that diffusional limitations imposed by complex leaf geometries interfere with dynamic CO₂ responses. Measurement cuvette conditions, however, may minimize those effects and allow C_i calculations to be calculated for RACiR. We measured steady state and dynamic (RACiR) A - C_i curves in juniper (*Juniperus horizontalis*) under a range of cuvette conditions that may affect RACiR, including: overpressure, flow rate, and rate of dynamic CO₂ ramp. Our results demonstrate: as overpressure increases, V_{cmax} and J_{max} increase; as ramp rate increases, J_{max} , and C_i transition decrease; and as flow rate increases, C_i transition decreases. Understanding how cuvette conditions affect A - C_i curves in complex leaf structures is essential for accurate estimates of photosynthesis and photosynthetic capacity. Our study provides a framework for optimizing A - C_i curve measurements under steady state and dynamic conditions for complex leaf geometries.

31 Students Get Involved: A Novel Approach to Process Improvement Evaluation in Acute Care.

Eric Schaller, Lexus Salazar, **Sarah Putnam**^{*}, Zachary Potts, John McCready and Danielle Albright, Department of Emergency Medicine, UNM.

Process evaluation is imperative when making changes in a complex environment involving critically ill and injured patients. The Department of Emergency Medicine (EM) at the University of New Mexico uses an iterative approach to evaluate protocol changes in its Emergency Department Resuscitation Unit (EDRU). The collection and analysis of provider-patient encounter data provides department leadership with evidence for assessing protocol changes. As part of a multi-semester course entitled Research in Acute Care, our students collect data on provider-patient encounters in the EDRU. Findings from the data collection are regularly presented to a workgroup of EM clinical faculty for use in guiding protocol decisions. In 2018, our student program collected data on 1,327 provider-patient encounters, including 26 instances of cardiopulmonary resuscitation (CPR), 418 high acuity traumas, 112 strokes, and 164 cases of sepsis. During this same time period, the workgroup met nine times to review findings from this and other data collections. The program has resulted in training, equipment, and protocol recommendations for the EDRU. Our dynamic program is capable of meeting many of the department's process-improvement data-gathering needs. Our program provides experience to future healthcare professionals through both exposure to the clinical environment and experience in quality improvement research. We will continue to adapt our data-collection program as existing protocols are revised and new protocols are implemented. We hope to expand our data collection capabilities through increasing student coverage in the EDRU and possibly expanding to other areas of the hospital.

32 Filovirus Glycoprotein Glycosylation Analysis and Effects on Immunogenicity.

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Filoviruses are hemorrhagic fever viruses that are some of the deadliest pathogens in the world with a fatality rate up to 90%. Symptoms include fever, vomiting, diarrhea, headache and weakness, and can lead to hemorrhaging, multiple organ failure and death. Experimental vaccines use filovirus Surface glycoproteins (GPs) as immunogens to induce protective immune responses. Our laboratory studies the

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glycosylation patterns of different filovirus GPs to develop improved vaccines. Mammalian 293T cells have more complex N-linked glycosylation machinery compared to Sf9 insect cells, but both are capable of O-linked glycosylation. Differences in N- and O-linked glycans on filovirus GPs may induce different immune responses upon vaccination. The glycosylation patterns on the different filovirus GPs, however, have not been elucidated thoroughly. Here, we report purification and glycan analysis of GPs from filoviruses produced in 293T mammalian cells and Sf9 insect cells. Currently, we are assessing effects of different glycosylation of the understudied Lloviu virus GP on immunogenicity in mice.

33 Microbes Masquerading as Minerals: Implications for Life Detection on Other Planets.

Joseph Medley[†], Department of Biology, UNM; Michael Spilde, Institute of Meteoritics, UNM; and Diana Northup, Department of Biology, UNM.

In the search for evidence of extraterrestrial life, one of our strongest candidates remains Mars. Evidence of water on Mars, its location within the circumstellar habitability zone, and the existence of lava caves within the Martian sub-surface make it especially appealing. Martian lava caves are important as they are similar to those found on Earth and provide protection from the inhospitable environment at the Martian surface. Until now, the study of lava-cave microbiology has been limited to microbial mats; however, such caves also contain many common, macroscopically identifiable, secondary-mineral growths which preliminary investigations demonstrate harbor microorganisms. We sampled each type of secondary mineral morphology from three different lava caves at El Malpais National Monument in New Mexico as analogues for those on Mars due to the semi-arid climate and limited vegetation above them. Secondary minerals are fitting targets in the search for extraterrestrial life as their morphologies can be described, quantified, and differentiated from other deposits lacking microbes. Bulk chemical analysis, scanning electron microscopy, energy dispersive X-ray spectroscopy, and genetic sequencing were used to analyze each secondary mineral deposit and to create a continuum of our various deposits, ranging from low-microbial content to high-microbial content. These results will provide scientists at NASA with information necessary to identify and analyze secondary mineral deposits. This has important implications for life detection on extraterrestrial bodies as such deposits are likely to possess evidence of life should we ever have the opportunity to study them.

34 Effect of Photo-Oxidation on A β 40 Aggregation.

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Extracellular plaques composed of β -sheet rich amyloid-beta (A β) fibrils are believed to cause neurodegeneration and cognitive decline in Alzheimer's disease. Fibrils can form through a primary nucleation-dependent aggregation pathway or secondary nucleation mechanism in which preformed fibrils cause A β monomers to misfold and aggregate into amyloid fibrils. As A β aggregation is believed to occur during the prolonged asymptomatic stage before neurodegeneration, it is important to gain insights into the aggregation process. Photodynamic therapy utilizes photosensitizing molecules to produce reactive oxygen species, which in turn can oxidize an array of biomolecules including proteins. Recently, we have shown that a novel A β fibril sensor, the anionic phenylene ethynylene oligomer OPE1-, exhibits controllable photosensitizing activity. When bound to A β fibrils, OPE1- becomes highly fluorescent, sensitizes the production of singlet oxygen, and induces fibril oxidation upon irradiation. As the singlet oxygen species is short-lived, the controlled photosensitization lowers off-target oxidation. In this study, we evaluated the effects of OPE1- induced A β 40 fibril oxidation on its seeding potency. Morphologies of the fibrils produced by both seeding conditions were imaged by transmission electron microscopy and fibril secondary structures were analyzed by circular dichroism spectroscopy. Thus far, our results show that oxidation of the fibril seeds does not alter A β 40 aggregation or its secondary structure after three days of

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incubation. We plan to investigate further the effect of oxidation on fibril cell toxicity. The results from this study contribute to a better understanding of amyloid aggregation via secondary nucleation pathway, which is important in understanding Alzheimer's disease process.

- 35 Increased Chemo-sensitivity to DNA-damaging Agents Conferred by the Exercise Myokine, Irisin in Breast Cancer Cells.

Shania Vel Sanchez †, Maximizing Access to Research Careers (MARC), Department of Biology, and Department of Cell Biology and Physiology, UNM; Rachel Earley and Helen Hathaway, Department of Cell Biology and Physiology, UNM.

Breast cancer is a disease that affects one in eight women. Epidemiological studies have shown that exercise is associated with a decreased risk of developing cancer, and improving prognosis of many cancer types, including breast cancer. Our studies demonstrate that irisin, a myokine produced by muscle cells upon exercise, increases the sensitivity of malignant p53 mutant MDA-MB231 breast cancer cells to the chemotherapeutic doxorubicin (dox) by more than 90 fold. Irisin did not alter the dox sensitivity of malignant, p53 wild-type MCF7 breast cancer cells, or normal non-malignant MCF10A breast epithelial cells. Our studies will investigate the molecular mechanisms through which irisin sensitizes selected breast tumor cells to DNA damaging agents. Based on our data demonstrating that irisin induces chemo-sensitization only in the p53 mutant cells tested, we hypothesize that irisin sensitizes p53 mutant cells to DNA damaging chemotherapeutics by inhibiting cell cycle checkpoint genes, suggesting that irisin co-treatment may improve the effectiveness of current breast cancer therapeutics. Developing a dox/irisin combination therapy to achieve a significantly lower dox dosage would minimize the toxicities and side effects associated with DNA damaging chemotherapeutics. To identify the mechanism through which irisin is sensitizing cells, we are measuring proliferation, cytotoxicity, and apoptosis in the high throughput IncuCyte imaging system, in addition to metabolic endpoint assays. We will assess also the role of p53 mutations and downstream signaling pathways using knockdown and overexpression approaches. Our studies suggest that irisin may offer therapeutic benefits for breast cancer prevention and treatment.

- 36 Evaluating the Cytotoxicity of Commercial Poly(N-Isopropyl acrylamide).

Diego Trujillo †, Maximizing Access to Research Careers (MARC), Department of Biology, UNM; Heather Canavan and Phuong Nguyen, Department of Chemical and Biomedical Engineering, UNM.

Poly(N-Isopropyl acrylamide) (pNIPAM) is a thermo-responsive (“smart”) polymer that responds to changes in thermal energy near physiologically relevant temperatures, changing its relative hydrophobicity. Mammalian cells attach to pNIPAM at 37°C and confluent cell sheets detach spontaneously when the temperature is shifted below its lower critical solution temperature (LCST, ~32°C). Although pNIPAM is recognized for its ability to aid in the creation of cell sheets, and most techniques used to polymerize NIPAM yield biocompatible films, some formulations from commercially available (cpNIPAM) may be toxic due to the presence of short chain polymers and/or the NIPAM monomer itself. A previous study showed that cpNIPAM films generated from one commercial provider are, in fact, cytotoxic. In this study, we explore the anomalous response of mammalian cells to commercially available NIPAM, including evaluating several sources of cpNIPAM. We hypothesize that—rather than the inclusion of some unknown cytotoxin commonly used by different vendors—commercially available pNIPAM contains lower chains of low molecular weight oligomers due to incomplete polymerization. Our preliminary finding supports this hypothesis: monomeric NIPAM is a known cytotoxin, while higher MW commercial forms of pNIPAM are shown generally to be biocompatible. We find that cpNIPAM is more cytotoxic to cell lines than previously outlined in scientific studies, regardless of its source (manufacturer). Cytotoxicity has been observed to increase at higher concentrations of cpNIPAM, as well as longer exposure times. These results indicate that, prior to use, all individuals should purify further their source of pre-polymerized NIPAM.

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- 37 Development of a Fluorescently Activated Cell Sorting Technique to Identify Gut Microbiota Important in Host Protein Metabolism.

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Gut microbiota contribute to the health and fitness of animals. Within a single host, hundreds or even thousands of different microbial species form tight symbiotic communities influenced by many factors, including host diet. These communities often metabolize and synthesize compounds that their host species cannot and supply essential compounds needed to maintain host homeostasis and reproduce. These processes are likely important for hosts that consume low-quality diets and experience seasonal or persistent protein limitation. To date, the role gut microbiota play in host protein metabolism has not been systematically explored. We hypothesize that taxonomic and functional differences in gut microbiota correlate with diet and that microorganisms are largely responsible for supplying essential amino acids (AA_{ESS}) to hosts with protein-poor diets. This project combines amino acid carbon isotope ($\delta^{13}\text{C}$) analysis with fluorescently activated cell sorting (FACS) to quantify the relative contribution of key microbial taxa to the production of AA_{ESS} used to synthesize host tissues. Currently, pilot data are being analyzed to identify the most abundant species of Bacteroidetes and Firmicutes in gut contents to develop nucleotide-specific probes. Mouse gut microbiota will be hybridized with phylum-specific probes, using a fixation-free protocol, and individual populations from gut contents will be sorted and their amino acid $\delta^{13}\text{C}$ values will be measured to quantify the proportion synthesized by gut microbiota from non-protein macromolecules (e.g., carbohydrates) in the host's diet. This approach enables us to directly link AA_{ESS} production to specific gut microbiota taxa and determine the relative importance of different populations to the host.

- 38 Effects of Geomorphology on Light Attenuation in the Rio Grande.

Mollie Hanttula[†] and Rebecca Bixby, Department of Biology, UNM.

Light penetration in aridland rivers, like the Rio Grande, is restricted by parameters including turbidity, depth, and flow. Understanding the relationships among these parameters and light penetration will help provide a better understanding of habitat limitations for primary producers, which are dependent on light for photosynthesis. The light attenuation within the water column decreases light availability with increasing depth, in turn regulating the depth and distribution of present primary producers (Krause-Jensen and Sand-Jensen 1998). The purpose of this research is to examine the role of geomorphology of an aridland river in understanding the relationships among depth, turbidity, and light attenuation to better understand the abiotic factors and to develop a standardized method that can predict how the producer communities are distributed throughout differing aridland river turbidity gradients. Two sites were chosen along the Rio Grande in the Albuquerque reach along a gradient of turbidity. Velocity (m/s), depth (cm), light intensity (μmol), and turbidity (NTU) were collected in vertical transects through the water column that were >25 cm in depth. Preliminary results show that changes in both turbidity and water depth were statistically significant ($p < 0.05$) when predicting light penetration intensity, with light availability decreasing exponentially at greater water depths along the vertical column transect, causing a bathtub ring of macrophytes along the shoreline. By understanding the controls of light penetration in turbid waters, future studies can better delineate the limited environments for primary producers often constrained by geomorphology of aridland rivers.

- 39 Who Will be Dead After We Save the Bats?

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Monument, Tulelake CA; Rickard Toomey, Mammoth Cave National Park, Mammoth Cave, KY; Jason Walz, Oregon Caves National Monument and Preserve, Cave Junction OR; and Diana E. Northup, Department of Biology, UNM.

White-nose syndrome (WNS) is a devastating disease to the bat population in the United States. The fungus *Pseudogymnoascus destructans* causes bats to come out of torpor early in the winter, expending crucial energy stores and resulting in the death of up to 99% of a given bat hibernaculum. A new method of UV-C treatment has been shown to be effective in killing *Pseudogymnoascus destructans*; however, caves are home to a wide range of microbial communities, which may be harmed by UV-C. The aim of this experiment is to investigate if this treatment will have potential collateral damage on native cave bacterial species. Samples are being taken from caves across three national parks, cultured in the lab, and the resulting isolates will be exposed to UV-C treatment. Initial cultures from Lava Beds National Monument and Oregon Caves National Monument have resulted in 1,068 subcultures that currently are under investigation. Cultures for Mammoth Cave National Park will be collected in the spring of 2019. Sequencing of the 16S rDNA gene will be used to identify a maximum of 100 unique bacterial cultures per National Park for UV-C testing. Understanding the potential negative implications of UV-C on native microbial cave ecosystems is crucial before this treatment can be considered for wider implementation.

40 Describing the Microbiota of Lava Tube Formations.

William Briggs[†] and Diana Northup, Department of Biology, UNM.

A broad range of shapes, textures, and colors exist in lava caves beneath the ground. Some of these are evidently sites of high microbial activity, while others appear to be no more than exposed rock. Forty-seven samples were taken from a broad range of structures in three lava caves in northern California. The 16s rRNA genes of the organisms present in these samples was amplified using PCR and sequenced using high throughput Illumina MiSeq technology. In this project, we have analyzed the data produced in this way, to begin an understanding of the microbiota of these subterranean structures. The sequences were divided into all of the individual variants present in each sample. Then these were assigned a taxonomic classification using the SILVA 132 database. Exploratory and illustrative graphics were produced in R to visualize and aid in understanding. Using these methods, we have gained an appreciation of the microbiota of these geomicrobiological environments. We found that none of these samples is without significant diversity in bacteria and archaea. All samples have many phyla present from both domains. Some have a few genera that account for a majority of the sequences present. Others are characterized by having a large number of genera present in small abundances. In this paper, we use data analysis methods to describe the differences and similarities in these microbiota, and create a system of describing these subterranean morphologies based on the bacteria and archaea which inhabit them.

41 Dismantling Dogma by Modeling Mastitis: the Impact of Asymptomatic Infections.

O. Liota Weinbaum[‡], Department of Biology, UNM; and Helen J. Wearing, Department of Biology, and Department of Mathematics and Statistics, UNM.

Despite widespread compliance with control recommendations, chronic infectious disease remains problematic in animal agriculture. Efforts to disrupt transmission target symptomatic individuals, but disease persists at the population level. *Staphylococcus aureus* mastitis in dairy cows is a painful inflammation of the udder that reduces milk volume and quality. The only considered transmission mechanism is contact between the milk of symptomatic cows and the udders of susceptible cows via milking equipment. One control practice is to milk symptomatic cows last, known as the Milk Last Intervention (MLI); however, asymptomatic cows are also infectious, and we suspect that they play an important role in maintaining the disease in a herd. In this study, we develop a mathematical model parameterized from the literature, as well as from USDA industry surveys, to address the following question: could MLI significantly reduce infectious or symptomatic cow-days per lactation? We classify cows according to infection stage and implement the model in a stochastic discrete time framework. We also investigate how different charac-

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teristics of the asymptomatic infectious class influence our model predictions. When accounting for the contribution of asymptomatic cows to transmission, our study predicts that MLI is not effective, because they are milked in any order relative to susceptible cows. Our results indicate that quantifying the infectivity level and the duration of the asymptomatic stage should be the foci of future work. A broader understanding of *S. aureus* infection is needed urgently to inspire new non-pharmaceutical interventions, as antibiotic resistant strains like MRSA confound traditional attempts at control.

- 42 *Drosophila melanogaster* Gene CG13196 for Heart Development and Function.

Alahana Jakeway[†] and Tyanna Lovato, Department of Biology, UNM.

Drosophila melanogaster is a useful genetic model to study heart development and function due to its short reproductive cycle, lifespan and genetic similarities to the vertebrate heart. I am specifically studying the gene CG13196, which is an uncharacterized gene expressed in the inflow tracts of the *Drosophila* heart. Using CRISPR technology, our lab has generated two mutant lines of CG13196, and currently, I am analyzing the heart beat function and structure using SOHA (semi-automated optical heart beat analysis) and antibody staining. I also have generated a GFP-Flag tagged transgenic line, and am attempting to generate an enhancer-*lacZ* reporter line to determine the regulation of CG13196. Understanding the function and regulation of genes like CG13196 will provide insight into the complex systems that promote optimal functioning of the heart.

- 43 Assessing the Feasibility of Hepatitis C Virus Elimination in New Mexico.

Helen J. Wearing, Department of Biology, and Department of Mathematics and Statistics, UNM; and **Paul Henderson**[†], Department of Mathematics and Statistics, UNM.

An estimated 3.5 million Americans are infected with hepatitis C virus (HCV), although the majority of new infections occur in populations of people who inject drugs (PWID). With the emergence of novel and more effective treatments that target HCV, understanding the dynamics of infection within such populations is of growing importance for the planning required for large-scale treatment and prevention of the disease. Here, we expand upon a previous model investigating treatment scale up in populations of PWID (Martin *et al.*) by allowing the tracking of treatment and reinfection. The compartmental-based differential equation model accounts for varying classes of infection, risk (based on whether individuals are on or off opiate substitution therapy) and treatment. The model projects the effects that varied (re)infection and (re)treatment may have upon the dynamics of HCV prevalence within a local/closed population of intravenous drug users. In particular, we characterize the transient dynamics and the time to new equilibrium levels of infection. Based on our model projections, local elimination of HCV appears possible, with the range of parameters that permit elimination corresponding to feasible treatment strategies.

- 44 CG7777 Expression in the *Drosophila* Dorsal Vessel.

Ashlynn Bennett[†], Department of Biology, UNM.

The heart is a complex organ that undergoes various stages of development and subsequent remodeling with age. *Drosophila melanogaster* serves as an excellent model organism for studies involving heart structure and its relationship to gene expression due to its similarities to vertebrates in early heart development and a high degree of genetic functional conservation as compared to human disease states. CG7777 is a *Drosophila* gene that is known to code for aquaporins, a vital heart structure. Expression of this gene has been documented in the formation of the dorsal vessel, a structural element of the *Drosophila* heart, in late stages of embryonic development. When failing, the adult heart has been observed to re-activate fetal gene expression patterns. To determine if CG7777 expression is reactivated, knockout lines and fluorescently tagged lines were created using the CRISPR/ Cas-9 system and studied using heart beat analysis. Ongoing research is being performed to determine the outcome of these modifications on the expression pattern of CG7777 in adult *Drosophila*.

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- 45 Ectoparasites of the Beringian Coevolution Project: Curation of the Eckerlin Flea Collection at the Museum of Southwestern Biology.

Lizon A. Cenac †, Laurel A. Cenac, Mariel L. Campbell, Museum of Southwestern Biology, UNM; Ralph P. Eckerlin and Joseph A. Cook, Museum of Southwestern Biology, and Department of Biology, UNM.

Parasitic arthropods are responsible for transmission of human and animal pathogens, and their ability to act as disease vectors appears to be accelerating as climates and ecosystems change. Museum collections contain valuable temporal and spatial information about the diversity of these arthropod vectors, yet those data have largely remained invisible due to lack of identification, curation, and digitization. Over the last two decades, expeditions by the Museum of Southwestern Biology across high-latitude regions of North America and Asia through the Beringian Coevolution Project (BCP) have produced >20,000 lots of endo- and ectoparasites. Fleas collected during the BCP expedition were mounted on slides, partially identified, and now are being digitized, curated, archived, and matched with their mammalian host records. This project will complete an inventory of the more than 1,800 slides in the collection and create a workflow for specimen identification, object tracking, and databasing to make these specimens publicly available for research. Preliminary results show 1,093 inventoried slides represent at least 31 flea species and four families in the Order Siphonaptera. These fleas were collected from 849 mammal hosts, representing 52 species, nine families, and four orders (Carnivora, Lagomorpha, Rodentia, Eulipotyphla) from Canada, Russia, and the United States. Once curated, this collection will provide an invaluable resource for the study of host-parasite distribution patterns and potential for pathogen transmission at high latitudes.

- 46 Preparation and Description of Several Skull Elements of *Gomphotherium productum* from the Late Barstovian of Española Basin of Northern New Mexico.

Timothy A. James †, Department of Anthropology, UNM; and Gary S. Morgan, Curator of Biology, New Mexico Museum of Natural History and Science, Albuquerque NM.

Excavations at the Chamita and Tesuque Formations from Española basin in northern New Mexico yield exceptionally preserved fossil elephants. While most mammal genera geologic lifespans are ~2 million years, the New Mexican Miocene elephant *Gomphotherium productum* occurred for more than seven million years (~7–14 Ma) despite shifting paleoenvironmental conditions. Thus, *G. productum* may possess unique ecological adaptations that allowed it to persist or *G. productum* may represent multiple species. To test these hypotheses, I prepared *G. productum* fossils using microscribes and dental picks at the New Mexico Museum of Natural History (NMMNH), and I described their anatomy and measured them using a flexible measuring tape. These fossils represent the oldest, best-preserved record of late Barstovian proboscideans. I compared several ontogenetic stages for several *G. productum* crania and partial mandibles from the Chamita and Tesuque Formations. I examined and measured a juvenile maxilla and mandible (NMMNH P-25280); an abnormally small, adult cranium (P-19204) with a fragmentary tooth row; a young adult (P-28972) with associated mandibles and complete tooth row; and a complete adult crania (P-63875) possessing an intact zygomatic arch, maxillary tooth row, and right tusk with an associated mandible yet in the field. My preliminary results include quantitative comparative measurements and qualitative visual comparisons of these specimens to assess whether they represent multiple species or possess unique ecomorphological adaptations such as mandible procumbency.

- 47 Using Micromammal Teeth to Evaluate Megafaunal Extinction Ecology.

Jonathan S. Keller ‡, Department of Biology, UNM; Thomas W. Stafford Jr., Stafford Research Laboratories, Lafayette CO; Sara K. Lyons, Department of Biology, University of Nebraska, Lincoln NE; Seth D. Newsome and Felisa A. Smith, Department of Biology, UNM.

During the terminal Pleistocene extinction (TPE) 10–14 ka, human invasion of the New World drove 100+ genera of megafauna extinct. Here, we examine the ecological consequences of the TPE with

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respect to changes in the small mammal community. We use a multi-proxy approach, exceptionally preserved fossils, and a fine-grained age model of Hall's cave in Texas to study effects of the TPE on body size and isotopic dietary niche of several taxa with an emphasis on the grasshopper mouse, *Onychomys*. We measured bone collagen carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) values to estimate isotopic niche widths over time using Bayesian-based spatial metrics. We also constructed a dichotomous key to identify specimens, which revealed some previously sampled "*Onychomys*" were actually granivorous/insectivorous *Reithrodontomys* and omnivorous *Peromyscus*. *Onychomys* ranged from -12.4‰ to -19.4‰ $\delta^{13}\text{C}$ and 7.4 to 12.5‰ $\delta^{15}\text{N}$. We found the greatest average $\delta^{15}\text{N}$ values (12.0‰) in the oldest strata ~ 11.5 ka, declining $\sim 2\text{‰}$ by ~ 7 ka, which closely matches contemporaneous declines in other co-occurring small mammal taxa. We suspect this drop reflects a baseline shift in vegetation nitrogen due to changing climate. Post-baseline shift *Onychomys* are larger than the largest modern individuals, and bone collagen $\delta^{15}\text{N}$ values positively correlate with proxies of body size. This may indicate ancient *Onychomys* fed at a higher trophic level. Our ongoing work couples isotope data with novel ecomorphological measures to more finely characterize ecological shifts in *Onychomys*, *Reithrodontomys*, *Peromyscus*, and other small mammal taxa after the TPE.

48 Disentangling Natural Dispersal Versus Human-mediated Introduction of the Longfin Dace Across the Trans-continental Divide.

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A long-standing objective of biogeography is to relate patterns of genetic diversity to historical and contemporary processes that influence the distribution of populations across a landscape. For some taxa, the role of human-mediated dispersal can confound the signal from natural processes and obscure our understanding of a species' evolutionary history. The longfin dace (*Agosia chrysogaster*) is a small-bodied minnow native to the Upper Gila River basin in New Mexico. Accounts as early as the 1950s proposed that the longfin dace was introduced recently into tributaries of the Mimbres River and the Rio Grande. Human-mediated dispersal was hypothesized as a mechanism for crossing the trans-continental divide, but recent molecular evidence suggests that headwater capture events may have mediated the east to west movement of other fish taxa (e.g., *Pantosteus plebeius*). Therefore, it is plausible that populations of the longfin dace found east of the trans-continental divide were established via a similar headwater capture event as *P. plebeius* as opposed to human-mediated dispersal. We sequenced 294 individuals collected across Arizona and New Mexico to determine range-wide patterns of historic genetic structure. Additionally, we assayed a panel of nine microsatellite loci for 165 individuals collected in New Mexico to infer the mechanism of colonization across the trans-continental divide.

49 Comparison of Community Dynamics of Flowering Plants Across Three Aridland Ecosystems.

Alesia Hallmark[‡], Jade McLaughlin and Jennifer Rudgers, Department of Biology, UNM.

Plant phenology, the timing of important life events such as leaf growth or reproduction, can be cued by many abiotic factors. In aridlands, plant growth and reproduction may be controlled by photoperiod, stochastic rain events, or temperature. Variation in these environmental variables may lead some species to "boom" in good years or fail to grow or reproduce in extreme seasons or years, especially in aridlands. Here, we leverage plant phenology and biomass datasets to study the intra- and interannual variation in flowering communities at three semi-arid biomes. We relate indices such as diversity, abundance, and synchronicity to site-specific meteorology spanning two decades in order to answer the following questions: (1) Is community structure of all plants directly comparable to flowering community structure? (2) Do flowering communities vary more across space than through time? (3) For each species, do flowering dates change over time, with increasing aridity, or according to seasonal precipitation?

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50 Metabolic Consequences of Point Mutations in the Human NPC1 Protein.

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The NPC1 protein is a cholesterol transporter responsible for facilitating the movement of cholesterol from the late endosome/lysosomal system into the cytoplasm, where it is subsequently processed and stored. There is strong evidence suggesting that variations in the NPC1 gene are involved in the development of obesity, but causality has not been established yet. A recent population genetics study with a cohort of 150,000 individuals has strongly implicated a methionine to isoleucine substitution at position 642 as causal, either alone or linked to multiple other variants. In this novel project, we will be establishing whether mutations in the NPC1 gene are directly causal through cholesterol accumulation and through Seahorse assays designed to measure the effects of these mutations on cell-wide metabolism. By transfecting human fibroblasts lacking NPC1 activity with plasmids containing the mutant variant, we will expect to see metabolic effects such as cholesterol accumulation in the endosome, as well as increased glycolytic flux, decreased oxidative metabolism, and increased lipogenesis consistent with obesity. Establishing NPC1 variants as causal factors for obesity will represent one of the only obesity or diabetes candidate genes of high effect based on ethnicity in non-Hispanic white and Hispanic populations, respectively.

51 Tracking Physiological Functions During Drying with Phase Shifts.

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Gas exchange measurements are an essential tool in the tracking of physiological functions of plant cells, especially in relation to photosynthesis and carbon balance. Pairing gas exchange data with electrical measurements, including impedance and phase shift for an alternating current through plant tissue, can be used to characterize the environment inside and outside cells and track its changes along gradients of interest, such as water content. This analysis can reveal physiologically relevant features of the cellular environment, including ion density and membrane presence or thickness; however, we still lack a biochemical interpretation of some electrical markers. Here, we aim to establish the significance of phase shift as a marker for physiological function. We examined the relationship between simultaneously recorded respiration rates, impedance, and phase shift values in Sphagnum moss (*S. magellanicus*) capitula as they dried. Measurements included four distinct frequencies of alternating current, and were made for both light and dark conditions, using three populations from different longitudes. We analyzed the paired trends in respiration, impedance, and phase shift and found insightful parallels. In particular, we were able to relate inflection points between these characters as moss dried, and we identified a reaction in the phase shift curve correlated to a change from negative to positive carbon balance in cells. More research incorporating measurements of the chemical compositions of the microenvironments around cells could reveal phase shift to be a valuable marker of physiological activity in plants.

52 Expansion of a High Elevation Rodent (*Neotoma mexicana*) in the American Southwest.

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The geographic distribution of species is dependent on numerous biotic and abiotic factors that comprise a species' fundamental niche. Elevation can dictate where species live and move, as it is associated with hypoxia and temperature differentials. The negative relationship between temperature and elevation creates ecological separation along elevational gradients. Since the Last Glacial Maximum, North American species have expanded north or to higher elevation areas as the climate warms, and these trends are expected to continue. The American Southwest is a region with tremendous topographical relief, resulting in the convergence of many biomes (e.g., deserts, mixed conifer and alpine forests). The Mexican

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Woodrat (*Neotoma mexicana*) is a rodent found in the coniferous forests of the Southwest at high elevations relative to the distantly related, but sympatric White-Throated Woodrat (*N. albigula*). The area of syntopy is narrow, suggesting these species may have distinct ecological niches. Species range expansion and contraction across a landscape can be inferred using molecular genetics. In this study, we compare the evolutionary histories of two *Neotoma* species to determine the direction and extent of post-glacial population expansion in the Southwest. Using museum specimens, we sequence the mitochondrial gene cytochrome *b* to identify individuals to species. With these genetic sequences, we test whether *N. mexicana* conforms to post-glacial expansion expectations.

53 Evaluation of Antimicrobial Activity of Alzheimer's Amyloid- β Peptide.

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Alzheimer's Disease (AD) affects more than five million Americans. A primary pathological hallmark of the disease is plaques composed of amyloid- β (A β) fibrils. The cause of AD is unknown, yet observations of abnormal microbiota and the co-localization of viral DNA and inflammation with AD pathology have led to a novel hypothesis that A β expression and deposition may be central to its function as an antimicrobial peptide (AMP). Our research seeks to determine how A β functions as an AMP by investigating the peptide's toxicity toward bacteria using a live/dead assay via flow cytometry, a metabolic assay of cell viability, and a cell plating assay to quantify the effects of A β on bacterial growth and viability. Flow cytometry has shown a deleterious effect of monomeric A β on the membrane integrity of *E. coli* bacteria in the stationary phase of growth, where coinubation with concentrations of 50 $\mu\text{g/ml}$ and 100 $\mu\text{g/ml}$ for three hours has shown increases in significant membrane permeation by 700% and 1,000%, respectively. Studies of A β 's effect on cell viability in the exponential phase of growth; however, have so far been inconclusive. Future work will include transmission electron microscopy to visualize the effects of membrane permeabilization and studying the insertion of A β into bacterial and control lipid membrane models using a Langmuir-Blodgett trough. The role that infection plays in AD is an exciting new approach to investigate the cause of the disease, with the potential to lead to better detection and treatments for a wide array of neurodegenerative diseases.

54 Seasonal and Geographical Variation in Cricetid Thermoregulation of Southern California

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Many climate models predict higher average global temperatures as well as increased magnitude and frequency of extreme heat events. Nocturnal rodents will increasingly be subject to warmer conditions, which will directly impact activity periods and ability to balance water and energy budgets. To examine thermoregulatory capacity of species exposed to extreme temperature variation, we measured the thermoregulatory function of four *Cricetid* species (*N. albigula*, *N. lepida*, *P. eremicus*, *P. crinitus*) at three sites in the Mojave Desert. Additionally, we conducted winter versus summer measurements for two of the sites. We used flow-through respirometry to measure resting metabolic rate, evaporative water loss and body temperature. We continuously measured these parameters through temperature treatments from 15°C to 43°C. To examine the potential effects of warming and extreme events on relative animal function, we compared performance as a function of body size, site and season. The results demonstrate little difference in the thermal neutral zone of each species independent of site or season; however, the onset of increased evaporative water loss initiates at lower ambient temperatures in the winter, which may explain an increase in the maximum temperature tolerated during the winter. These desert species face extreme climate pressures, and their distribution largely depends on physiological tolerance to extreme temperature variations and limited water availability. Understanding physiological performance under these pressures will be a good predictor of species distribution under increasing climate variability.

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DEPARTMENT OF BIOLOGY

The Department of Biology at the University of New Mexico offers excellent opportunities for education and research in many areas of modern biology: botany, cell biology, computational biology, evolution, genetics, ecology, microbiology, molecular biology, phylogeny, and zoology. The department is one of the largest academic units on the UNM campus, with more than 45 full-time faculty members, more than 1,700 undergraduates, and 125 graduate students.

Outstanding facilities for undergraduate and graduate research are available on and off campus. The department is housed in three buildings: Castetter Hall, Marron Hall, and The Museum of Southwestern Biology, providing support for a range of research activities. A full range of computer facilities is available for all students, faculty and staff. The Molecular Biology Facility provides faculty, students and staff with state-of-the-art equipment for sequencing DNA and genomic analysis. Cell biology and microscopy facilities allow sophisticated imaging investigations to be conducted. The Sevilleta Field Station at the Sevilleta National Wildlife Refuge 80 km south of Albuquerque includes housing during field studies as well as laboratory and computer facilities. The Museum of Southwestern Biology has an excellent collection of birds, fish, amphibians, reptiles, mammals, parasites, and plants. Students and faculty also conduct research at field sites throughout the Southwest and Rocky Mountain Region, and in the Gulf of California. Field projects are often undertaken even further afield, in Latin America, Australia, Africa, and the Antarctic.

Undergraduate Research Programs

We encourage undergraduates to participate in research, and nearly half of B.S. students in biology become involved in some kind of research project. The possibilities range from volunteer work, work-study, and non-work-study jobs, to independent research projects leading to graduation with honors. Students can arrange research projects with individual faculty members or they may participate in one of several research programs, many of which are striving to attract minorities and women in an effort to benefit students of all ethnic backgrounds and under-represented groups. Independent research through any of these programs may be integrated with our departmental honors program.

Graduate Programs in Biology

Master's and doctoral degrees are offered at the Department of Biology at UNM with emphases in the areas of arid-land ecology, behavioral ecology, botany, comparative immunology, cellular and molecular biology, community ecology, ecosystem ecology, evolutionary biology, freshwater sciences, genetics, invertebrate zoology, microbiology, parasitology, population biology, and vertebrate zoology. The department offers excellent opportunities for graduate education and research in many areas of modern biology. The research degree is the heart of the graduate program. The department offers Ph.D., M.S. (I), and M.S. (II) degrees. M.S. (I) is a research degree with the same philosophy as the Ph.D. It is not a prerequisite of the Ph.D., but may lead to work on that degree. The M.S. (II) is not a research degree and normally does not lead to work in the doctoral program; it is intended primarily for individuals who wish to supplement their baccalaureate programs with additional course work.

Students considering study toward an advanced degree should obtain information about required preparation and tests as soon as possible. Biology Graduate Program applications are due in early January for admission the following Fall. Further information about all Biology programs can be obtained from the departmental website (<http://biology.unm.edu>) or the Graduate Program Coordinator (biograd@unm.edu).

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