The University of New Mexico Department of Biology

# 27th ANNUAL RESEARCH DAYS

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

March 22 & 23, 2018

## *KEYNOTE LECTURE*

**4:00 p.m., March 23rd,**
**Ballroom B, Student Union Building**

# SCHEDULE OF EVENTS

## WEDNESDAY, MARCH 21

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

## THURSDAY, MARCH 22

3:30–4:20 p.m. **Department Research Presentation:** *"Of Mosquitoes and Men: Modeling the Ecology of Dengue and Zika Viruses,"* by **Dr. Helen Wearing**, Associate Professor, UNM Department of Biology, 100 Castetter Hall.

4:30 p.m. **Scholarship Awards**, by **Dr. William Pockman**, Chair and Professor of UNM Department of Biology.

4:30–6:30 p.m. **Museum of Southwestern Biology (MSB) Open House**, CERIA (Bldg. 83).

## FRIDAY, MARCH 23

8:30–9:30 a.m. **Check In** at the Registration Desk, foyer, Castetter Hall.

9:00–10:45 a.m. **Student Oral Presentations, Sessions 1 & 2**, 51 & 57 Castetter Hall.

11:00 a.m.–12:30 p.m. **Student Poster Presentations, Session 1**, first floor of the west wing of Castetter Hall.

12:30–1:30 p.m.
- **Lunch** provided in the Basement & Courtyard of Castetter Hall.
- **BGSA Lunch** with the Keynote Speaker, 107 Castetter Hall.

1:30–3:00 p.m. **Student Poster Presentations, Session 2**, first floor of the west wing of Castetter Hall.

4:00–5:00 p.m. **Keynote Lecture**, Ballroom B, Student Union Building:
- **Introduction of the Keynote Speaker** by **Dr. William T. Pockman**, Professor & Chair of UNM Department of Biology.
- **Keynote Lecture.**

5:00–8:00 p.m. **Reception for our Keynote Speaker and a Silent Auction**, Ballroom C, Student Union Building:
- **Reception and Silent Auction**.
- 7:00 p.m., **Last Call for Bids on Silent Auction Items**.
- 7:30 p.m., **Silent Auction Ends**.

## TABLE OF CONTENTS



# RESEARCH DAY ORGANIZATION

### Committee

Chairs: Drs. Robert Waide and Dorothy Scholl

Catherine St. Clair
Dr. Donna George
Dr. Ben Hanelt
Joanne Kuestner
Anne Rice
Aurora Kraus, BGSA
Diana Macias, BGSA

### Sponsor

The University of New Mexico Department of Biology,

### 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 has yet to be determined.

# PAST RESEARCH DAY SPEAKERS

| YEAR | SPEAKER | TALK TITLE |
|---|---|---|
| 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 Investigatior, Marine Science Center, UniversKeity 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, Porland, OR | From Mantle to Microbe: Geological Processes Shape Microbial Communities at Deep-sea Hydrothermal Vents. |
| 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. |

| YEAR | SPEAKER | TALK TITLE |
|---|---|---|
| 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 | SNPing 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. |
| 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. |

| YEAR | SPEAKER | TALK TITLE |
|---|---|---|
| 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

## SESSION 1, 9:00–10:45 a.m., 51 Castetter Hall

**The bolded author is the presenter.**

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

9:00 1 Identifying Substrates of Circadian Clock Regulated CRY1 or CRY2 Dependent SCF-FBXL3 Mediated Degradation.

**Valerie Perea** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, and Department of Chemical Biology, UNM; Stephanie J. Papp and Katja A. Lamia, The Scripps Research Institute, La Jolla CA.

The circadian clock endogenously regulates rhythms that prepare organisms for environmental and physical changes. The disruption of clock rhythms has been associated with an increased risk of metabolic disease and cancer. Transcription factors CLOCK and BMAL1 regulate expression of clock-controlled genes, including cryptochromes CRY1 and CRY2. CRY1 and CRY2 heterodimerize with PER proteins, then bind to CLOCK and BMAL1 to repress their own transcription in a negative feedback loop. Mammalian CRY1 and CRY2 are targeted for degradation by ubiquitination by the E3 ligase SCF-FBXL3. In previous work, SCF-FBXL3 has been shown to promote degradation of critical oncoprotein c-MYC with CRY2 acting as a cofactor, thus establishing a novel mechanism of clock regulation in mammals. Additional substrates will be identified utilizing the BioID approach. This system, based on *E. coli* enzyme BirA, fuses BirA to the protein of interest. BirA then biotinylates proximal, interacting proteins. Biotinylated proteins then may be immunoprecipitated using streptavidin beads, with the candidate interacting proteins identified by mass spectrometry. We made fusions of BirA with CRY1 or CRY2 and co-expressed each of them with an SCF-FBXL3 mutant blocking degradation of candidate proteins. This approach will enable us to identify additional substrates of this mechanism and further our understanding of how the circadian clock protects against disease.

9:15 2 Interactions between *Toxoplasma gondii* and Retinoic Acid-differentiated Neuro-2A Neuroblastoma Cells.

**Alicia Romero** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; and Eric Y. Denkers, Center for Evolutionary and Theoretical Immunology, Department of Biology, UNM.

The intracellular parasitic protist *Toxoplasma gondii* infects a large percentage of the human population. In most cases, infection is asymptomatic, but in immunodeficiency the parasite can cause devastating disease. During acute infection, parasites widely disseminate as rapidly dividing tachyzoites. After approximately two weeks, tachyzoites differentiate into the slow-growing bradyzoite stage, and they initiate encystation in tissues of the central nervous system. Recent evidence indicates that neurons are targeted preferentially for infection and stage-transition, but the cellular and biochemical basis for this phenomenon is little understood. We hypothesize that neuronal cell-*Toxoplasma* encounter may lead to unique interactions central to cyst formation and long-term parasite persistence. Here, we employed the mouse neuroblastoma cell line Neuro-2A (N2A) as an *in vitro* model to study the crosstalk between *T. gondii* and neuronal cells. Infection of undifferentiated and retinoic acid differentiated N2A cells revealed that cyst formation was significantly more prevalent in differentiated neurons, as demonstrated by parasite specific immunofluorescence microscopy. Interestingly, when we activated N2A signaling through the cell surface co-stimulatory molecule CD40, we found that cyst generation was inhibited. Current

experiments seek to characterize variations in life-cycle specific genes upon stimulation with anti-CD40. The importance of understanding control of bradyzoite differentiation and persistence is that, currently, encysted parasites in the brain are resistant to elimination. Knowledge of key interactions between *Toxoplasma* and host neuronal cells may open the way for clinical strategies to eliminate the parasite.

9:30 3 Comparison of External Bacterial Diversity of New Mexican *Myotis velifer* Bats in New Mexico Gypsum and Carbonate Caves.

**Ally M. Weidner †**, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; Ara S. Winter, Department of Biology, UNM; Debbie C. Buecher, Buecher Biological Consulting, Tucson AZ; Edwards W. Strach, Patrick L. Lewis and Diana E. Northup, Department of Biology, UNM.

The integument is the largest organ of the body; it is comprised of diverse communities of microorganisms that serve as the first line of defense between hosts and their environment. Despite the important role it plays in host immunity, few studies have been conducted on external integument microbiomes. Over the last decade, the fungal disease white-nose syndrome (WNS) has emerged and spread rapidly across North America. This epidemic has killed more than 6.7 million bats, a major impact for species that play a pivotal role in ecosystems and agriculture. Little research has documented the ecology of their external microbiome. The aim of our project is to determine which host factors influence the external bacterial makeup and compare the bacterial diversity present on individuals inhabiting different cave environments. We collected 29 *Myotis velifer* bat swab samples from one carbonate and two gypsum caves in New Mexico. We used 16S rRNA gene analysis to assess bacterial diversity. Swab samples were used for genomic DNA extractions and Illumina MiSeq sequencing assays. All data were normalized using QIIME 1.9 and analyzed with python scripts. Microbiota have been shown to play vital roles in host health and immunity. Because little is known about the bat skin microbiome, it is impossible to infer its impact on invasive pathogens. By studying the nature of external microbiota we can identify drivers that influence its makeup—a possible factor in the infection of WNS on bats. This will provide insight into which bat species are most vulnerable to WNS.

9:45 4 Computational Costs of Fitting Tomogram Tiltseries of Flexible Molecules with Gaussian Mixture Models.

**Elena Delgado †**, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; Kasra Manavi and Lydia Tapia, Department of Computer Science, UNM.

Each year ~1,500 people in the United States die from anaphylactic shock. Experimental studies have shown that the spatial organization of antibody-allergen assemblies (IgE-fcεRI complexes) plays a key role in initiating these reactions. Thus, imaging and identification of the underlying structures of these molecular assemblies is crucial to the understanding of allergic mechanisms. One technique to image assemblies in their natural physiological environments is electron microscopy (EM). In EM, levels of particle emission from a sample irradiated with an electron beam are measured and used to produce a tomogram, a 2D projection of the 3D sample where the intensity of the image pixel is proportional to the density of the sample. This study introduces a novel method for modeling and fitting molecular structures into low-resolution (20–40 Å) EM datasets using Gaussian Mixture Models (GMMs). First, GMMs are created to represent the all-atom structures. Next, parameters of the GMMs are refined to best represent the dataset. Finally, the refined GMMS are used to perform conformation fitting. This method iterates 330 times during each fitting with an average computational cost of 1045 seconds per iteration, resulting in a runtime of ~4 days. We hypothesize that the conversion of tomograms from pixels to binary values for quality evaluation takes up the largest percentage of the time per iteration. To test this, we will take timing measurements during binary conversion, parameter refinement, and conformation fitting. This data will determine which parts of the method are candidates for further op-

timization to reduce method runtime. (Supported by NSF CAREER IIS-1528047, IIS-1553266, and CCF-1518861, NIH NM STMC P50GM085273, and UNM IMSD R25 GM060201.)

10:00 5 Moderate Prenatal Alcohol Exposure Produces Deficits in the Extinction of Contextually Conditioned Fear Learning in Adult Female Rat Offspring.

**A.H. Moezzi †**, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; J.L. Wagner, N.S. Graham, K.H. Christensen, D.R. Barto, S. Davies, D.A. Hamilton and D.D. Savage, Department of Neurosciences, Health Sciences Center, UNM.

We have shown functional deficits in frontal cerebral cortex due to moderate prenatal alcohol exposure (PAE). As frontal cortical circuitry is responsible for higher cognitive function, we modeled this construct using extinction learning. We compared the extinction of contextual fear learning after maximal freezing was obtained in our PAE rats. Throughout pregnancy, the experimental group consumed 5% ethanol, whereas the control group consumed saccharin for four hours per day. The mean peak maternal serum ethanol concentration was 60.8 mg/dL. Neither maternal weight gain nor pup birth weights were affected by this level of drinking during pregnancy. Female offspring were weaned on PD24. Eight- to nine-month-old offspring were subjected to two consecutive days of contextual fear conditioning, followed by eight consecutive days of extinction. Both conditioning days consisted of two five-minute sessions, separated by two hours. Each conditioning trial started with a 3½ minute period to allow the rat to explore the context followed by a 30-second tone, which co-terminated with a two-second 0.5 mA foot-shock. Freezing behavior during each five-minute session was monitored throughout all conditioning and extinction trials. All offspring acquired the task, with no differences in freezing on the first day of extinction. Differences in freezing began to appear in subsequent extinction trials and were most prominent during the fourth minute of each extinction session. Our conclusion is that there are behavioral deficits in moderate PAE rat offspring that may be attributable to functional damage in the frontal cortex. (Supported by NIAAA R01-AA019884.)

10:15 6 Novel Sensors for Detecting Alzheimer's Disease Related Tau Protein Aggregates.

**Salomon L. Alires †**, Initiative for Maximizing Student Development (IMSD), and Department of Biology, UNM; Florencia Monge, Biomedical Engineering Graduate Program, and Center for Biomedical Engineering, UNM; David G. Whitten and Eva Y. Chi, Center for Biomedical Engineering, and Department of Chemical and Biological Engineering, UNM.

The pathological hallmarks of Alzheimer's Disease are extracellular amyloid plaques composed of amyloid-beta fibrils and intracellular neurofibrillary tangles composed of tau filaments. Currently, there is no reliable method to detect these plaques and tangles *in vivo*. Robust detection of tau filaments is especially lacking. We have recently shown that a new class of synthetic sensors based on an oligo phenylene-ethynylene scaffold (OPEs) selectively detected the fibrillar conformation of model proteins. Upon binding, the OPEs become highly fluorescent for optical detection. In this study, we tested OPE sensing capability of a synthetically derived six amino acid tau peptide VQIVYK (PHF6). This sequence is found in the third repeat microtubule-binding domain of the tau protein and its hyperphosphorylation is noted to be critical in the formation of neurofibrillary tangles. PHF6 was synthesized and purified; three sensors, an anionic OPE1-, cationic OPE2+, and the mostly commonly used dye Thioflavin T were tested. Incubation of PHF6 in water at 70˚C and 2 mg/mL reproducibly resulted in fibril formation, as confirmed by transmission electron microscopy and circular dichroism. Whereas Thioflavin T did not detect PHF6 fibrils, the anionic OPE1- selectively detected the PHF6 fibrils over unincubated PHF6 and displayed a higher affinity for the fibril conformer compared to the cationic OPE2+. Thus, our results show that OPE1- is an effective and selective sensor for PHF6 fibrils, potentially providing a new imaging modality for studying and tracking tau filaments in neurodegenerative disorders such as Alzheimer's disease.

10:30 7 Activation of the Signaling Intermediates β-catenin by the Intracellular Protozoan Parasite *Toxoplasma gondii*.

**Hoang V. Bui** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; Cameron H. Ranken and Eric Y. Denkers, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM.

*Toxoplasma gondii* is a globally distributed parasite that infects humans and other warm-blooded animals. While infection is usually asymptomatic, *Toxoplasma* causes a life-threatening disease in individuals with weakened immune systems. In normal individuals, *Toxoplasma* elicits a strong protective immune response facilitating host survival. Simultaneously, the parasite avoids immune elimination to enable establishment of latent infection. The balance between activation and evasion of immunity is likely reflected in interactions of *Toxoplasma* with host intracellular signaling cascades involved in defense. The Wnt/β-catenin pathway has an emerging function in the immune system. We hypothesize the Wnt/β-catenin signaling affects the host cell response to *Toxoplasma*. We infected cells *in vitro* with *Toxoplasma* tachyzoites and employed Western blotting to assess activation or suppression of β-catenin. In experiments employing mouse bone marrow-derived dendritic cells (DC) and human fibroblasts, up-regulation of β-catenin was detected after direct infection. To test whether β-catenin up-regulation involves active invasion or release of soluble mediators by extracellular parasites, we performed transwell experiments, in which parasites were separated from their host cells by a semi-permeable membrane. Under these conditions, there was no upregulation of β-catenin. To further confirm a requirement for entry into the host cell, parasites were pre-treated with the actin inhibitor mycalolide B, a drug known to block tachyoite invasion. DC exposed to *T. gondii* under these conditions also displayed defective β-catenin up-regulation, further supporting a requirement for parasite invasion. Our results suggest that *Toxoplasma* exploits β-catenin signaling to promote establishment of the intracellular niche in cells.

---

## SESSION 2, 9:00–10:45 a.m., 57 Castetter Hall

**The bolded author is the presenter.**

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

9:00 8 Developing an Essential Amino Acid δ13C Library for Tracing the Importance of Biofilms and Biocrusts in Aquatic and Terrestrial Ecosystems.

**Alexi C. Besser** ‡, Emma A. Elliott Smith, Department of Biology, UNM; Adam Barkalow, American Southwest Ichthyological Researchers, LLC, Albuquerque NM; David Camak, Thomas F. Turner and Seth D. Newsome, Department of Biology, UNM.

Aquatic biofilms and soil biocrusts are ecologically important microbial assemblages that transform recalcitrant organic and inorganic energy into bioavailable forms. For example, heterotrophic biofilms may be an important mechanism by which terrestrial organic matter is made available to freshwater aquatic consumers. Similarily, exchanges of nutrients between soil biocrusts (which share inorganic N) and adjacent terrestrial plants (which share photosynthate) in aridland ecosystems likely constitute an important symbiotic relationship for dealing with limited resources. Until now, most studies examining heterotrophic biofilms and soil biocrusts have emphasized the *elements* exchanged (C, N, or P), not the specific molecules. This elemental focus has overlooked possible exchanges of amino acids in aquatic and terrestrial food webs. Here, we show that carbon stable isotope ($\delta^{13}C$) analysis of individual essential amino acids ($AA_{ESS}$) provides enhanced discriminatory power to trace the flow of heterotrophic biofilm- and soil- biocrust-derived energy. Characterizing $AA_{ESS}$ $\delta^{13}C$ patterns in autotrophs and heterotrophs that synthesize

$AA_{ESS}$ *de novo* is a critical step for addressing these hypotheses; however, no study to date has done this at the local scale. We are analyzing instream and riparian producers from the Middle Rio Grande (MRG) and adjacent desert plants from the northern Chihuahuan Desert in New Mexico, USA. Our data indicates $AA_{ESS}$ $\delta^{13}C$ patterns provide high discriminatory power among producers. This library of freshwater aquatic and terrestrial producer $AA_{ESS}$ $\delta^{13}C$ patterns will be invaluable for ongoing local studies on the role heterotrophic biofilms and soil biocrusts play in the MRG food web and adjacent nutrient-limited desert ecosystem.

9:15 9 Defining the Role of CG1674 in Adult Muscle Development.

**Emily Czajkowski †**, Marilyn Cisneros and Richard M. Cripps, Department of Biology, UNM.

*Drosophila* provides us with an excellent model for studying muscle related diseases in humans. By identifying and classifying genes involved in muscle development, we can better understand the mechanisms responsible for muscle growth and deterioration, and help us discover treatments and therapies for muscle-related diseases. Proteome sequencing of flight muscle confirmed that the CG1674 protein is present in the sarcomere, suggesting it plays a role in sarcomere assembly, and may be a functional component of the flight muscle. To further characterize CG1674, we identified its role in normal muscle formation by creating an RNAi that targeted CG1674 transcript. When crossed with muscle drivers Mef2-Gal4 and 1151-Gal4, the flies became flightless due to defects in myofibril formation, as confirmed by immunofluorescent staining, identifying CG1674 as a major component in normal flight-muscle formation. In addition, the expression of a UAS-CG1674-FLAG construct confirmed that the CG1674 protein is localized to the Z-disc, a structural component between adjacent sarcomeres. This localization suggests that Z-disc formation is the major function of CG1674 within the sarcomere.

9:30 10 Adult Muscle Formation in *Drosophila melanogaster* Is Influenced by *miR-31b* and *miR-987*.

**Daniel Lloyd Wilson †**, Tracy Dohn and Richard M. Cripps, Department of Biology, UNM.

Micro-RNAs (miRNAs) are post-transcriptional regulators essential to muscle development and homeostasis. These small, non-coding RNA molecules prevent maturation of protein-coding genes by inhibiting translation or mediating mRNA degradation in a sequence-specific manner. Previous research has linked miRNAs to both muscle development and its maintenance; however, the roles of many miRNA are unknown. Based on a previous screen, we proposed *miR-31b* and *miR-987* to play a role in adult muscle formations. To examine this hypothesized role, we used the UAS/Gal4 system in *Drosophila* to over-express and under-express the respective miRNAs during adult muscle formation. Functional tests measuring flight and jump ability showed decreased muscle function in both over-expression and under-expression adults as determined by weak or absent flying and reduced jump distance at 10 days after eclosion. Over- and under-expression individuals were cryosectioned at 48h, 72h, and 96h after puparium formation (APF) to observe muscle development and organization. Sections were fluorescent antibody stained, and displayed significant developmental defects in muscle fiber organization, including visible holes in the indirect flight muscle (IFM) myofibrils, and an abnormal cell number in the trochanter (TDT) for *miR-31b* and *miR-987*, respectively. Computer analysis using multiple miRNA target prediction databases revealed potential miRNA target genes. These targets were identified on at least three miRNA target prediction databases and were refined further by analyzing expression patterns recorded in literature. Quantitative PCR (qPCR) will confirm these potential molecular interactions, illuminating the role that these miRNA plays in influencing proper muscle development in *Drosophila melanogaster*.

9:45 11 Quantification and Visualization of DNA Single Strand Transposon Insertions.

**Emily Alden***, Flybase, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM; and Jeremy Edwards, Department of Chemistry and Chemical Biology, UNM.

Transposase is an enzyme that catalyzes the cleavage and insertion of segments of DNA from one location on the genome to another. Transposase has an application in next-generation sequencing (NGS) library preparation in a process called tagmentation, where two transposases are assembled with end sequences (ES) only, but no linking donor DNA. This creates a double-stranded DNA break with the ES attached to the ends of the resulting DNA fragments. Tagmentation activity can be increased by replacing the wild type ES with a synthetic mosaic end sequence (MES). This hyperactive variant of the Tn5 transposase is used commonly in NGS library preparation to both tag and fragment (tagment) double-stranded DNA. In an effort to better understand the mechanisms of Tn5 insertion, we studied the ability of transposase to tagment only a single DNA strand when chemical modifications were added to the 3' end of one of the complex's MES. We found that the addition of a dideoxy nucleotide can prevent complete tagmentation and results in one MES-tagged DNA strand and one intact, unmodified DNA strand. This approach may allow us to block specific steps of transposase enzymatic activity, which can be used to improve our understanding of the exact mechanisms of Tn5 transposase insertion events. Furthermore, this "asymmetrical" tagmentation could be useful in the development of new library preparation methods.

10:00 12 Synthesis and Characterization of Colloidal ZnT/ZnSe Quantum Dots.

**Gavin Gonzales** †, Maximizing Access to Research Careers (MARC), Department of Biology, and Center for High Technology Materials, UNM, and Department of Physics and Astronomy, UNM; Arjun Senthil, Nathan Withers, Gema Alas, Alejandro Sandoval III, Christina Minetos, Center for High Technology Materials, UNM; Sergei A. Ivanov, Center for Integrated Nanotechnologies, Los Alamos National Laboratory, Albuquerque NM; Gennady A. Smolyakov, Center for High Technology Materials, UNM; Dale L. Huber, Center for Integrated Nanotechnologies, Sandia National Laboratories, Albuquerque NM; and Marek Osiński, Center for High Technology Materials, UNM.

Quantum dots (QDs) emitting in the visible spectrum are of interest for many biomedical applications, including bioimaging, biosensing, drug targeting, and photodynamic therapy. A significant limitation, however, is that QDs typically contain cadmium, which makes prospects for their FDA approval very unlikely. Previous work has focused on indium phosphide and zinc oxide as alternative semiconductor materials for QDs. These nanoparticles, however, also have been shown to be cytotoxic. High-efficiency luminescent ZnTe QDs could be a reasonable alternative to Cd-containing QDs. Here, we report on our recent studies of ZnTe QDs, including their synthesis, structural characterization, and optical properties. The final product was monodisperse ZnTe/ZnSe colloidal QDs, which displayed an orange photoluminescence under UV excitation.

10:15 13 Isolation and Gene Flow Affect the Diversification of a South Pacific Bird: The *Foulehaio* Honeyeater Complex.

**Xena M. Mapel** †, Department of Biology, UNM; Alice Cibois, Muséum National d'Histoire Naturelle, Paris, France; Tejashree H. Modak, Department of Biology, Boston University, Boston MA; Robert G. Moyle, Biodiversity Institute, University of Kansas, Lawrence KS; Aliverti Naikatini, Institute of Applied Science, University of the South Pacific, Suva, Fiji; Joshua O. Seamon, Department of Marine and Wildlife Resources, American Samoa Government, Pago Pago, American Samoa; Michael D. Sorenson, Department of Biology, Boston University, Boston MA; Jean-Claude Thibault, Muséum National d'Histoire Naturelle, Paris, France; Ruth B. Utzurrum, University of Hawaii, Hilo HI; and Michael J. Andersen, Department of Biology, UNM.

Islands are natural barriers that prevent gene flow between populations and promote allopatric diversification. Birds in the South Pacific are an excellent model to explore the interplay between isolation and gene flow due to the region's extensive archipelagos and relatively well-characterized avian communities. The Wattled Honeyeater complex (*Foulehaio* spp.) comprises three allopatric taxa that are widespread and common across Fiji, Tonga, Samoa, and Wallis and Futuna. Previous work using mitochondrial DNA found three well-differentiated lineages that are up to 8% diverged, but questions remain about what, if any, genetic structure exists within the nuclear genome of *Foulehaio*. Here, we explore patterns of gene flow within and between these lineages using a dataset of ultraconserved elements (UCEs). We sampled 134 individuals (132 ingroup plus two outgroup taxa: *Xanthotis provocator* and *Gymnomyza viridis*) from 21 islands across the entire range of *Foulehaio*. Our 95% complete datamatrix comprised 1,341 UCEs (mean contig length = 1,077 bp; total alignment = 1.4 Mb) from which we called SNPs. We used tree-based and population genetic approaches in a multispecies coalescent framework to study patterns of gene flow within *Foulehaio*. We found strong support for three lineages of *Foulehaio*, each pertaining to previously identified mitochondrial lineages (*F. carunculatus*, *F. procerior* and *F. taviuensis*). There is minimal gene flow between these lineages, supporting treatment as three species; however, we detected interesting patterns of gene flow between populations of *F. carunculatus*, the most widespread taxon from Eastern Fiji to Samoa.

10:30 14 Evolutionary Dynamics of Elevational Ranges in Andean Birds.

**Chauncey R. Gadek** ‡ and Christopher C. Witt, Department of Biology, UNM.

Andean uplift reorganized the South American climate since the mid-Miocene, creating steep environmental gradients and novel habitats. This period of geologic dynamism coincided with diversification into the Andes by many avian groups. Bird lineages that successfully colonized and persisted in the Andes are marked by physiological adaptations and restricted elevational ranges. Genera and families tend to have similar elevational ranges, suggesting constraints on evolutionary shifts in elevation. Here, we used phylogenies and elevational range data for Andean birds to estimate the history of elevational transitions and elevational stasis. We asked three questions that have implications for evolutionary mechanisms: (1) Have the timing of elevational transitions indeed coincided with Andean uplift? (2) Do the rate and magnitude of elevational transitions vary according to their ancestral starting point, suggesting threshold effects? and (3) Do upward and downward shifts occur with equal probability? We present evidence that elevational ranges are continuing to shift in conjunction with recent diversification, that the rate of elevational shifts changes with elevation, and that downward shifts are less common than upward shifts during the history of Andean bird diversification.

# ABSTRACTS: POSTER PRESENTATIONS

## SESSION 1, 11:00 a.m.–12:30 p.m.

**The bolded author is the presenter.**
† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

15 Lipid Production by Bacteria in the Pyloric Caeca and Intestine of Trout.

**Alejandra De La Cruz** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; Seth D. Newsome and Irene Salinas, Department of Biology, UNM.

The vital role that commensal bacteria play within their hosts has become increasingly clearer. Symbiotic bacteria are known to provide immunological, metabolic and developmental advantages to the host (Kelly and Salinas, 2017). Increasing evidence suggests that the host uses microbiota to synthesize proteins; however, very little is known regarding the contribution of bacteria from teleost fish to the host protein and lipid metabolism. Here we propose that that the communities within the pyloric caeca (PC) are more diverse than the ones found in the rest of the intestine. Previous sequencing of trout intestine has shown that it is dominated by *Mycoplasma* sp., small genomic bacteria. Additionally, we hypothesize that these diverse communities in the PC contribute to the host metabolism to a greater extent than the intestine microbiota. Additionally, we predict that the intestinal bacteria play a previously unrecognized role in host lipid synthesis. Based up DNA sequencing of the pyloric caeca, which had not been done to date, the diversity of the microbial community does not appear to be more diverse than the intestinal communities of trout. Both tissues are home primarily to *Mycoplasma* sp. These results reveal the bacterial communities residing in the PC and intestine of trout as well as their metabolic relationship.

16 How Will Climate Change Induced Microbial Migration Effect Alpine Plants?

**Danielle A. Duarte** †, Department of Biology, UNM; Jennifer A. Rudgers and Joshua S. Lynn, Department of Biology, UNM, and Rocky Mountain Biological Laboratory, Gothic CO.

Climate change is causing species with previously disparate ranges to come in contact. A key challenge in ecology is to predict the consequences of climate change caused species reshuffling. Experiments aimed at addressing this issue have focused on competition, but other interactions, like plant–microbe interactions, are less studied. In this glass house study, we tested the effects of low-elevation microbial communities interacting with novel alpine restricted grasses from the West Elk Mountains, CO, USA. The climate currently occupied by the low-elevation microbes is expected to occupy the high-elevation range of the grasses over the next century of climate change. We compared the effects of microbes from within and below the elevation range of focal plants and from three different mountains (six microbial communities, total) on plant tiller growth and competitive ability (height) of three populations of three grass species (*Poa alpina*, *Festuca brachyphylla*, *Elymus scribneri*). Each microbial treatment was compared with a sterile control. We fitted mixed effects models with a glass house block random effect and compared models of the interactions among the three treatments (elevation, mountain, sterilization). Plant height for all three species was best predicted by mountain. Till number was higher in sterile soil for *P. alpina* and *F. brachyphylla*, while *E. scribneri* growth varied by peak. The results suggest that novel microbes may have little effect on alpine grass species growth and competitive ability. Future work will analyze treatment effects on root colonization, root and shoot biomass, and leaf investment traits.

17 The Brown Garden Snail *Cornu aspersum*: A Model to Broaden the Scope of Snail Immunity.

**Erin Watson-Chappell** ‡ and Coenraad Adema, Department of Biology UNM.

The brown garden snail, *Cornu aspersum*, is a globally invasive species and pest originally from the Mediterranean. Accordingly, *C. aspersum* likely has a robust immune system that allows it to thrive despite encountering ever-changing pathogen landscapes in invaded ecosystems. As a host for several significant parasites, and as representative of Stylommatophora (terrestrial pulmonate gastropods), *C. aspersum* is an interesting candidate for study as the current understanding of snail immunity is mostly restricted to the phylogenetically distant aquatic snails (*Hygrophila*). Considering their potential threat to agriculture, ranching, and human health, we have begun to explore field populations found in New Mexico by genetically characterizing *C. aspersum* populations as well as their immune cells to develop comparative immunology studies. Snails were collected from two distinct field sites in Albuquerque, NM: the foothills of the Cibola National Forest and the bosque along the Rio Grande. Physical inspection and microscopy indicate that *C. aspersum* interacts with pathogenic intrusion through cellular responses. Parasites and bacteria will be used to evoke and study *C. aspersum* immune responses.

18 Immobilization of Enzymes on Carbonaceous Materials for Catalytic Cascades Enhancement.

**Jose Monclova** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, and Department of Chemical and Biological Engineering, UNM; Madelaine Seow Chavez, Ivana Gonzales and Plamen Atanassov, Department of Chemical and Biological Engineering, UNM.

In nature, complex fuels are oxidized by successive catalytic reactions, where the product of one reaction is often channeled to the next reactive site without diffusion into the bulk. While in nature cascade reactions are catalyzed by biomolecules, synthetic cascades can involve three types of catalysts: biomolecular, organic, and inorganic. The overarching goal of this project is to design an efficient system where different types of catalysts are used to catalyze cascade reactions, such as the oxidation of glycerol. This project focuses on the immobilization and spatial orientation of a bio-catalyst on carbonaceous supports and its effect on the enzyme's activity. More specifically, we studied the tethering of oxalate decarboxylase (OxDC) from *Bacillus subtilis* on the conductive platforms based on carbon nanotubes and 3D-Graphene nanosheets, using an amphoteric 1-pyrenebutanoic acid succinimidyl ester that attaches to both the enzyme and the support. OxDC oxidizes the conversion of oxalate to formate, a key reaction in the glycerol oxidation cascade. Optimal concentration of the tether will be determined that yields the highest activity of the immobilized OxDC. In addition, ultraviolet-visible spectroscopy is used to determine the kinetics of immobilized OxDC by using the formate dehydrogenase assay. By characterizing this reaction, we can determine the amount of formate produced from the tethered enzyme and determine the kinetic parameters vmax and Km. Successful immobilization of OxDC on carbonaceous supports will enable the incorporation of this enzyme with inorganic catalysts to create more efficient catalytic cascades for oxidation of complex fuels.

19 Creating Cellular Patterns Using Genetically Engineered, Gold- and Cell-binding Polypeptides.

**Dominic J. Medina***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, and Biomedical Engineering, UNM; Linying Li, Chia-Kuei Mo, Ashutosh Chilkoti, Department of Biomedical Engineering, Duke University, Durham NC; Gabriel P. Lopez, Department of Chemical and Biological Engineering, UNM; and Nick J. Carroll, Biomedical Engineering, UNM, and Department of Chemical and Biological Engineering, UNM.

Mammalian cell pattering on material surfaces is of interest for the study of fundamental cell biology, tissue engineering, and cell-based bioassays. Current methods of cell patterning are complex and do not allow for the study of cell-to-cell communication. We propose a simple approach in which use gold patterned surfaces that adsorb to an Elastin Like Polypeptide (ELP) biopolymer that has both gold and cell biding motifs. Genetic incorporation of gold-binding domains enables C-terminal chemisorption of polypeptides onto gold regions with enhanced accessibility of N-terminal cell binding domains. To create the gold pattern, a photoresist pattern is developed onto a silicon wafer, then gold evaporation is

used to deposit a layer of gold at roughly 500 Å. The excess photoresist is then chemically etched away, leaving behind gold micro-islands measuring 10 μm apart. The surface is then exposed to ELPs, which bind to the gold micro-islands. HUVEC cells are cultured onto the material surface and allowed to adsorb to the ELPs. The size of the micro-islands only allows for one cell per island, making this system perfect for the cell to cell communication via Tunneling Nanotubes (TNTs). This study demonstrates an innovative surface-engineering approach for cell patterning by exploiting distinct ligand accessibility on heterogeneous surfaces.

20 Generation of Gene-edited Conditional *Hnrnph1* Knockouts with an HA-Tag Reporter to Understand the Role of *Hnrnph1* in Methamphetamine Sensitivity.

**Diego Trujillo**, UNM; Qiu Ruan, School of Medicine, Boston University, Boston, MA; and Cameron Bryant, School of Medicine, Boston University, Boston, MA.

Understanding the genetic basis and neurobiological mechanisms of drug addiction is a necessary step towards engineering an efficient treatment. *Hnrnph1* was identified by The Laboratory of Addiction Genetics at Boston University as a quantitative gene underlying Methamphetamine (MA) sensitivity. *Hnrnph1* was validated using TALENS mediated deletion in the first coding exon of *Hnrnph1*. Mice carrying one copy of the *Hnrnph1* deletion (*Hnrnph1* +/- ) showed reduced sensitivity to the stimulant properties of MA. After successfully finding that the *Hnrnph1* gene is responsible for MA sensitivity, the lab is now investigating the mechanism that links *Hnrnph1* dysfunction with reduced sensitivity. The genetic basis of addiction is still not fully understood, which complicates engineering an effective treatment. *Hnrnph1* is expressed ubiquitously in the brain. An important question is where *Hnrnph1* acts in the reward-circuit to influence MA behaviors. Understanding the brain-region and cell-type specific function of this gene would help elucidate its mechanism of action. For this analysis, a knock-in mouse model was engineered with loxP sites flanking the first coding exon of Hnrnph1 via TALENS-mediated gene editing. The Cre-loxP system will be used to finely manipulate the expression of *Hnrnph1* in specific brain regions and cell type within the reward circuitry. We first needed to optimize our PCR assay to detect the presence of the loxP sites and HA tag for confirmation using PCR-genotyping and gene sequencing. Optimization of the PCR assay included designing primers, as well as adjusting the annealing temperatures, DNA concentration, and type of DNA polymerase used.

21 The Impact of Introgression.

**Jocelyn P. Colella** ‡, Department of Biology, UNM; Tian-ying Lan, Department of Biology, State University of New York–Buffalo; Robert E. Wilson, Sandra L. Talbot, Molecular Ecology Laboratory, USGS, Anchorage AK; Charlotte Lindqvist, Department of Biology, State University of New York–Buffalo; and Joseph A. Cook, the Museum of Southwestern Biology, Department of Biology, UNM.

How does hybridization and the transfer of genetic material between species (i.e., introgression) influence evolution in vertebrates? The consequences of hybridization are relatively well studied in plants, with outcomes ranging from hybrid vigor followed by speciation to the complete fusion of previously distinct lineages. Once thought to play a relatively minor role in vertebrate evolution, recent genomic investigations have highlighted the ubiquity of hybridization, suggesting that identifying instances of introgression (e.g., humans and Neanderthals) may be critical for understanding vertebrate evolution. Here, I investigate introgression dynamics at multiple locations between North American martens (*Martes americana* and *M. caurina*). These species diverged in isolated glacial refugia (east, west) during the Late Pleistocene, but are now naturally hybridizing along the northern Rocky Mountain cordillera and on Kuiu Island off the North Pacific Coast. Martens also have been the subject of multiple wildlife translocations, which function as iterative experiments to test how hybridization impacts mammalian evolution across geography (mainland/insular), demography, and time. We found evidence of biased introgression, with genes diffusing from *M. caurina* into *M. americana*, which may result in the genetic swamping and loss of endemic *M. caurina*. Residual signatures of admixture in peripheral populations in the Southwest and far North suggest hybridization in these species previously was more widespread. Ultimately, it appears that, although the consequences of hybridization can vary across time and space, introgression created a lasting impact on the evolution of this mesocarnivore.

22 Medicinal Plant Extraction and Analysis.

**Shania Sanchez** †, Victor French, Department of Biology, UNM; and Tracy Terry, Department of Chemistry, UNM–Valencia Campus.

We have begun a survey of the medicinal properties of common plants of the southwest. For this study, steam distillation for essential oils have been carried out on various locally sourced plants. These extracts have been analyzed for antimicrobial properties via Kirby-Bauer assay using *Escherichia coli* and *Staphylococcus aureus* on Mueller Hinton agar. Zones of inhibition were analyzed and compared to a Ciprofloxacin control and a blank BBL disk. Extracts have shown antimicrobial properties via Kirby-Bauer assay. Other assays for biological activity will be conducted in the future. As active agents are identified, further isolation and analysis of compounds for possible synergistic effects will occur.

23 Regulation of Long Noncoding RNA during *Toxoplasma gondii* Infection.

**Breanne E. Haskins** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; Kayla L. Menard and Eric Y. Denkers, Department of Biology and Center for Evolutionary and Theoretical Immunology (CETI), UNM.

Long noncoding RNAs (lncRNAs) are >200 nucleotide, non-translated molecules that regulate gene expression either at the transcriptional or post-transcriptional level. There is an emerging, but poorly understood role for lncRNAs in the immune response to infection. Here, we examined lncRNA activity during intracellular infection with *Toxoplasma gondii*, a medically and agriculturally important opportunistic pathogen in humans and animals. RNA was isolated from mouse macrophages infected with high- and low-virulence strains of T. gondii and was subjected to analysis on a microarray (a technique to measure which genes are up- or down-regulated). The microarray results identified greater 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 selected a panel of six lncRNAs and six mRNAs regulated by *Toxoplasma* for in-depth analysis by semi-quantitative, real-time PCR. Our results supported the preliminary microarray data, thus validating the microarray values and providing a foundation for further study on a subset of highly regulated lncRNAs. Recently, we have begun to determine the role of Rop16 in the molecular function of lncRNAs by utilizing Rop16 mutant parasite strains. Rop16 is a parasite protein that is important in the activation of host cell signaling leading to changes in host gene expression. Future work will continue to focus on lncRNA molecular function within the cell and the downstream consequences of infection.

24 A Biomechanical Justification for Conservative Management of Partial Extensor Tendon Lacerations.

**Darielys Mejías Morales***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, and Department of Orthopaedics and Rehabilitation, UNM; Jasmin Regalado, Department of Mechanical Engineering, School of Engineering, UNM; Patrick Gilligan, Deana Mercer and Christina Salas, Department of Orthopaedics and Rehabilitation, UNM.

The current (anecdotal) indication for surgical intervention of extensor tendon injuries is a tear that exceeds 50% of the total width of the tendon. The goal of our study is to determine the threshold at which partial extensor tendon lacerations can be treated with conservative management. Six cadaver hands were used for testing. For each hand, the index, middle and ring fingers were lacerated with either a 50–74% tear or a 75–90% tear. To simulate post-operative motion, each finger was loaded with 25 lb. and cycled from full extension to flexion for 5,000 cycles. Then each specimen was loaded to failure. Tendons in both laceration groups experienced an insignificant drop in force (< 0.5N). No specimens suffered a complete rupture of the tendon during cyclic testing and there was no significant loss in the range of motion. During the failure testing, the tendons with 75–90% lacerations failed at an average of 61.9 N. The tendons with incisions that ranged from 50–74% did not experience complete rupture. We suggest that patients with lacerations of less than 75% can be managed conservatively (no surgical repair); how-

ever, patients with incisions of 75–90% should receive surgical intervention to avoid complete rupture of the tendon.

25 Horizontal Gene Transfer in the *Mycobacterium tuberculosis* Complex.

**Julie Allison Spencer** ‡, Department of Biology, UNM.

The emergence of extensively drug-resistant tuberculosis highlights the need to understand evolutionary mechanisms leading to drug resistance in the *Mycobacterium tuberculosis* complex (MTBC). In this study, we examine whether horizontal transfer events in the slow-growing MTBC clade of the *Mycobacterium* genus have affected known drug-resistance genes. We selected 50 conserved genes in 88 representative taxa to construct a reference tree for genus *Mycobacterium*, and used SplitsTree and fastGEAR to identify ancestral and recent recombination events. We found recombination hotspots associated with five loci. These results suggest that, although there has been a widespread assumption of clonality in MTBC, horizontal gene transfer and antigenic variation could play a role in the evolution of drug resistance in this unusual clade. These results may lead to insights conducive to new drug target strategies.

26 Detection of the Human Parasite *Schistosoma mansoni* and Intermediate Host *Biomphalaria glabrata* in Water by Using eDNA.

**O.L. Weinbaum** *, Flybase, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM; B.K. Hanna and E.S. Loker, Department of Biology, UNM.

About 240 million people are infected with digenetic trematodes of the genus *Schistosoma*. An urgent need is for sensitive and specific techniques for detecting low levels of transmission in the aquatic habitats supporting the snail hosts of schistosomes. Detection of schistosome DNA in environmental samples (eDNA) taken from these habitats offers considerable promise. Water from a laboratory habitat used in the maintenance of *Schistosoma mansoni* and *Biomphalaria glabrata* life cycles was sourced for eDNA. Samples were cleaned using inhibitor removal columns prior to amplification. *S. mansoni* cytochrome oxidase 1 (CO1) and *B. glabrata actin* genes were targeted. PCR products were checked using agar gel electrophoresis. Amplification of *Schistosoma* CO1 and *Biomphalaria* actin produced gel bands of expected size (about 300 bp and 500 bp, respectively), matching those of positive controls, with sample concentrations ranging from 0.4 to 85.6 ng/ul. Inhibitor removal proved to be an important step, allowing amplification of otherwise intractable samples. Our protocol shows robustness against organic inhibitors and background DNA populations present in environmental samples. With further development, eDNA could be a sensitive method, ideal for assessing risk in natural bodies of water. (This research project has been reviewed and approved by the UNM Institutional Animal Care and Use Committee [IACUC]. All investigators/assistants in this study have attained animal-use certification regarding the ethical treatment of animals. Biology of Trematode-Snail Associations, #16-200551-MC.)

27 The Role of Fructose-1,6-bisphosphate as an Assembly Factor for Vacuolar ATPase.

**Casey T. Simoes***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, and Department of Biochemistry and Molecular Biology, School of Medicine, UNM; Summer R. Hayek and Karlett J. Parra, Department of Biochemistry and Molecular Biology, School of Medicine, UNM.

Vacuolar ATPase (V-ATPase) is a proton pump found on eukaryotic membranes. The primary function of V-ATPase is to manage intra-organelle and cytosolic pH. Defects in V-ATPase have been associated with numerous human disease states and are tied to fungal pathogenicity. V-ATPase is regulated by the reversible disassembly of its membrane-bound complex (Vo) and its cytosolic complex (V1), a process influenced by the presence of carbon sources. It is known that following nutrient starvation, glucose will induce V-ATPase assembly and activation, but it is unknown whether glucose itself is the direct signaling molecule responsible. We hypothesized that fructose-1,6-bisphosphate (F1,6bP), a downstream glycolytic intermediate, serves as the signaling molecule. For these studies, we used a pH-sensitive fluorescent dye (BCECF) to measure the vacuolar pH change that occurs after the addition of various carbon sources to starved 5Aα *Saccharomyces cerevisiae* cells. We compared glucose, F1,6bP, and 2,5-anhydro-D-mannitol (2,5AM), an analogue of F1,6bP. If the carbon source assembles and activates V-ATPase,

the enzyme will pump protons into the vacuole, thus lowering the vacuolar pH. Results from these pH assays showed that comparable to glucose addition, vacuolar pH decreased upon the introduction of F1,6bP, and to a lesser extent upon the addition of 2,5AM. This suggests that F1,6bP serves as the reassembly signal for V-ATPase and implies that glycolytic flow through F1,6bP is essential for glucose-induced activation of V-ATPase. Because of V-ATPase's role in disease states and pathogenicity, it is important to establish its key regulatory components for use in more specific drug design.

28 Nanopillar Analysis for the Manipulation of Indium Gallium Arsenide Quantum Well Compositions Using Stress Transfer.

**Kimberly Toddy** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, and Department of Chemical and Biological Engineering, UNM; Brian D. Rummel, NanoScience and MicroSystems Engineering, and Center for High Technology Materials, UNM; and Sang M. Han, Department of Chemical and Biological Engineering, and NanoScience and MicroSystems Engineering, and Center for High Technology Materials, UNM.

Previously, our group demonstrated a stress transfer method to locally manipulate the composition of compound semiconductor materials. In this experiment, a silicon nanopillar array was used to apply an elastic compressive stress field, which serves to locally manipulate the composition of indium atoms in a GaAs/InGaAs/GaAs quantum well structure to produce a patterned arrangement of indium depleted regions within the well. Our goal is to determine the necessary parameters that are needed to produce optimal applied pressure to diffuse Indium atoms, or the plastic limit under elastic loading of the substrate, at a given temperature. It is expected for the set temperature to be less than 600°C to prevent thermal diffusion of the indium atoms, and the optimal pressure to be lower than the applied pressure that would activate plastic deformation of the GaAs substrate. Using this method, an appropriate pillar design can be produced and pressed into the structure, causing indium atoms to be locally confined to regions surrounded by pure GaAs, eventually producing a quantum dot. Modeling software is used to translate applied pressures to resulting stress fields to determine the characteristic stress necessary to induce diffusion. Additionally, various modifications will be made to the nanopillar shape and diameter to achieve better-quality quantum dots. Lateral quantum confinement in quantum dots are particularly difficult to produce with current manufacturing techniques, and this technique offers variable sizes of uniformly arranged dots, as opposed to randomly placed, which could improve current technology and generate superior technologies in numerous fields.

29 TNF-α Priming Regulates CD82 Expression and Bone Marrow Homing of Hematopoietic Stem and Progenitor Cells.

**Erica M. Pascetti***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, and Department of Pathology, UNM; Christina M. Termini, Muskan Floren and Jennifer M. Gillette, Department of Pathology, UNM.

Hematopoietic stem/progenitor cell (HSPC) transplantation is a primary clinical therapy for the treatment of blood cancers, immunodeficiency disorders, and high-dose chemotherapy patients. For effective HSPC transplantation, stem cells must traffic through the blood and home to the bone marrow, which provides support and instructional cues to balance stem cell properties. Despite the clinical successes of HSPC transplantation, the molecular mechanisms that regulate HSPC trafficking remain unclear. Tetraspanins are molecular scaffolds that function to organize adhesion and signaling proteins into membrane microdomains, which impacts cell adhesion and signal transduction. Our previous work identified the tetraspanin, CD82, as a regulator of HSPC adhesion and bone marrow homing. Therefore, we hypothesize that the upregulation of CD82 expression may promote bone marrow homing and improved transplantation. In the current study, we describe the use of tumor necrosis factor α (TNFα) to modulate CD82 expression on the surface of HSPCs. A dose response analysis of TNFα primed HSPCs identified a significant increase in the surface expression of CD82. Additionally, we find that HSPC TNFα priming promotes increased cell adhesion. Finally, our data suggest that TNFα priming of HSPCs enhances bone marrow homing of HSPCs in preclinical animal models. Together, we anticipate

that these studies have the potential to offer new molecular targets and treatments to improve HSPC transplantation.

30 Comparison among Sky-island Haemosporidian Communities Reveals Dynamics of Parasite-species Turnover and Host-switching.

Lisa N. Barrow, Department of Biology, UNM; **Selina M. Bauernfeind***, Flybase, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM; Christopher C. Witt, Matthew J. Baumann, Serina S. Brady, Department of Biology, UNM; Andrea N. Chavez, Bureau of Land Management, Albuquerque NM; Paxton A. Cruz, John E. Ford, Chauncey R. Gadek, 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, and Jessie L. Williamson, Department of Biology, UNM.

Birds and their haemosporidian parasites (*Haemoproteus*, *Plasmodium*, and *Leucocytozoon*) comprise a diverse multi-host, multi-parasite system that is uniquely suited for studying evolutionary dynamics of host–parasite relationships. However, because of the challenges of surveying entire bird communities for parasites, few studies to date have been able to fully characterize parasite diversity, rates of species turnover, and variation in host–parasite relationships across geographic space. To address these questions, we conducted community-level surveys of haemosporidians within a narrow elevational zone (2100–2500 m) in three adjacent mountain ranges in New Mexico. We screened 776 specimens using PCR and sequencing of an mtDNA 'barcode' (*cytb*), as well as microscopy of thin blood smears. We used phylogenies of parasite and host lineages, respectively, to compare community composition and host–parasite relationships among the three mountain ranges. We found 268 infected birds (34.5% of birds). The majority were *Haemoproteus* (57.8%), followed by *Leucocytozoon* (39.2%), and *Plasmodium* (23.1%). Compared to previously published sequences, 61.6% were novel. We found conserved host specificity at the avian clade and species level, but host range varied strikingly by parasite genus. Host-switching by haemosporidian lineages was common, particularly between closely related hosts. Infection rates also varied strikingly among hosts, with vireos and nuthatches exhibiting nearly universal infection and non-infection, respectively. Haemosporidian species turnover among mountain ranges was modest overall, but high in specific host species. Host specificity appears to be fleeting over evolutionary time and variable across space, although certain hosts may be critical to the maintenance of overall parasite diversity.

31 Characterization of Rapid Nasal Antiviral Immune Responses in Zebrafish.

**Aurora Kraus** ‡ and Irene Salinas, Department of Biology, UNM.

The nasal epithelium contains the only sensory neurons that are exposed to external pathogen-rich environments, yet infection of these neurons rarely spreads to the brain. Infectious hematopoietic necrosis virus (IHNV) infects multiple types of bony fish, and when attenuated IHNV vaccine is delivered to the nose of trout, there is a rapid upregulation of immune genes in the nasal epithelium and no detection of virus in the central nervous system (CNS). The swiftness with which IHNV infection is contained in the nose leads us to hypothesize that sensory neurons play a role in activating the immune system to clear the virus and protect the CNS. The goal of this project is to establish a model for intranasal IHNV delivery in zebrafish (*Danio rerio*) in order to understand how neurons and immune cells orchestrate antiviral immune responses. Preliminary studies show that nasal delivery of live attenuated IHNV results in decreased locomotor activity during the first 15 min, suggesting that olfactory sensory neurons recognize IHNV and send the information to the CNS, changing behavior. Histological examination of the olfactory epithelium shows significant edema, enlargement of the lamina propria and infiltration of immune cells 15 mins after nasal viral delivery. Together these results indicate that both neurons and the mucosal immune system are immediately activated when attenuated IHNV is given to the olfactory epithelium, meaning the zebrafish is a sufficient model for further investigation into how neurons and immune cells are communicating.

32 Response of Grasshoppers and Crickets to Low-severity Wildfire in a Ponderosa Pine Forest of the Jemez Mountains: Can Low-severity Wildfires Be Beneficial?

**Marlo G. McCarter †** and Mark A. Ward, Division of Arthropods, Museum of Southwestern Biology (MSB), Department of Biology, UNM.

In the Southwestern U.S., a history of fire suppression and over-grazing has disrupted natural fire regimes and resulted in dense forests prone to high-severity fires. A collaborative restoration project in the Jemez Mountains of New Mexico was established to address this concern and monitor ecosystem responses to thinning or prescribed burn treatments. An unplanned wildfire in 2013 provided the opportunity to assess the effects of low-severity fire as a proxy for a prescribed burn. In this study, we report on the effect on ground-active invertebrates, specifically grasshoppers and crickets (Orthoptera), with the hypothesis that the composition and relative abundance (activity-density) of Orthoptera will remain unchanged, or will recover quickly to pre-fire conditions. Orthoptera are a good indicator of ecosystem response due to their large population sizes and relatively quick life cycles. They play an important role as a food source for invertebrates and vertebrates, and in nutrient cycling as primary consumers (grasshoppers) or detritivores (camel crickets). Pitfall traps to collect ground-active arthropods were in place two years before the fire through two years after the fire. Our preliminary results do not suggest significant differences in species composition or activity-density of Orthoptera populations as a result of low-severity wildfire. These results are in sharp contrast to observed changes in both composition and activity-density of Orthoptera in nearby ponderosa pine stands subjected to high-severity wildfire.

33 Abnormal Brain Structure in Adults Who Commit Homicide.

**Ashly Sajous-Turner***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, and The Mind Research Network, Albuquerque NM; and Kent Kiehl, Department of Psychology, UNM, and The Mind Research Network, Albuquerque NM.

Violent and aggressive behaviors are significant social problems. They hold great costs and consequences not only for the perpetrator, victims and their families, but also for the communities they were committed in. DeLisi (2010) found that the average cost per murder surpassed $17.25 million. Using a mobile MRI unit, we have collected brain data from thousands of incarcerated individuals. In this study, we used voxel-based morphometry (VBM), which is an automated way to quantify grey matter volume and density, to examine grey matter in individuals who have committed homicide (n = 89) compared to incarcerated individuals who have not committed homicide (n = 876). We predicted that we will see gray matter volume reductions in the prefrontal cortex (PFC), due to its role in executive functioning as well as planning and decision making. We also predicted that we will see reductions in the temporal lobes due to limbic structures, such as the amygdala, as well as the anterior temporal cortex, which is connected to the amygdala and the PFC. This research will help us better understand the pathophysiology of criminal behavior. (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.)

34 The Paradoxical Giant Hummingbird: Comparison of Andean and Coastal Subspecies with Respect to Blood, Migration, and Genes.

**Jessie L. Williamson ‡**, Selina M. Bauernfeind, Chauncey R. Gadek, Museum of Southwestern Biology (MSB), Department of Biology, UNM; Natalia Ricote-Martinez, Francisco Bozinovic, Departamento de Ecología, Pontificia Universidad Católica de Chile, Santiago, Chile; and Christopher C. Witt, MSB, Department of Biology, UNM.

The Giant Hummingbird (*Patagona gigas*) is twice as large as the next largest hummingbird species and has long been considered paradoxical with respect to flight biomechanics. It is also an extreme outlier in other respects. For example, it is the only hummingbird species that breeds above 4,000 m elevation and also along the beaches of the Pacific Ocean. The high Andean populations of Giant Hummingbird (*P. g.*

*peruviana*) that we have studied previously have a beta-hemoglobin genotype (serine at beta-hemoglobin A positions 13 and 83) that is characterized by high $O_2$-affinity and is only shared with four unrelated hummingbird taxa that also are restricted to extreme high altitudes. Here, we report that lowland-breeding populations of Giant Hummingbird (*P. g. gigas*) are genetically highly similar to their high-elevation counterparts; they even share the same beta-hemoglobin genotype, a unique characteristic among lowland hummingbirds. We found that hemoglobin concentration is lower and red blood cell volume is higher in the lowland *P. g. gigas* compared to their high Andean relatives. Complicating this comparison is the possibility that coastal *P. g. gigas* may be a seasonal elevational migrant, but neither the geographic range nor elevation of non-breeding *P. g. gigas* are known at present. We describe our efforts to describe its migratory behavior using geolocators.

35 *FcRN* Gene Expression within the Gut of Developing *Monodelphis domestica*.

**Kimberly Morrissey** †, Bethaney D. Fehrenkamp and Robert D. Miller, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM.

All mammals receive passive immune protection during development; this is primarily in the form of maternal antibodies. A role for lactation in acquiring maternal antibodies is most evident in marsupials, a lineage of mammals known for a brief gestational period with limited placental development and an increased reliance on an extended lactation period to complete fetal development outside the womb. Most newborn marsupials do not receive passive maternal immunity *in utero* and therefore are entirely dependent upon factors within the milk for immune protection until capable of mounting their own responses. Early exposure to potential pathogens, prior to the development of a functional immune system, requires a complex strategy for providing immunological protection. To investigate potential transfer of IgG from the milk to neonates, the transcripts of the IgG transporter, the Neonatal Fc Receptor (*FcRN*), were quantified within the gut of developing opossums, *Monodelphis domestica*. Intestinal samples were collected from *M. domestica* offspring from eight time points following birth as well as after weaning. Adult intestinal tissue was used as a control. *FcRN* transcripts were quantified using quantitative real-time PCR (qRT-PCR) and individual transcript levels were normalized to *ACTR2* as a reference gene. *FcRN* expression within the gut appears to coordinate with maternal expression of FcRN within the mammaries, as well as with the appearance of IgG transcripts within the offspring. This provides evidence of offspring acquisition of maternally derived IgG antibodies during development.

36 Triploid Atlantic Salmon (*Salmo salar* L.) Gill Microbiome Is More Resilient to Bacterial Infection than That of Diploid Atlantic Salmon.

**Ryan M. Brown** †, Department of Biochemistry, UNM; Sonal Patel, Institute of Marine Research, Bergen, Norway; and Irene Salinas, Department of Biology, UNM.

The composition of the microbial communities that live in symbiosis with a host is an important marker in assessing the host's health. Both the host genetics and the environment are known to shape the microbial communities that inhabit every barrier tissue of vertebrates. Recent studies in teleost fish have begun to characterize the microbiome in commercially important species such as Atlantic salmon (*Salmo salar* L.). Atlantic salmon farmers have developed sterile triploid animals that cannot reproduce if they escaped to the wild. Triploid salmon have several physiological differences compared to diploid salmon, yet the differences in their microbiome have not been characterized. In this study, we aimed to evaluate the gill microbiome of diploid and triploid Atlantic salmon at two different time points (0 and 21 days). Throughout the experiment, fish from both groups were supplied with the same water. Interestingly, we identified *Candidatus Branchiomonas*, a known pathogen in salmon gill tissue, in both groups, while the abundance of this pathogen was 7% in triploid and 52% in diploid fish at day 0. At day 21, *C. Branchiomonas* dominated the gill microbiome of both groups, while commensal species with known beneficial properties to the host such as *Oleispira* sp. and *Sphingomonas* sp. were effectively wiped out. These results give insights into how host genetics selects for the gill microbiome in Atlantic salmon and suggest that diploid salmon are more susceptible to *C. Branchiomonas* epitheliocysts than triploid fish.

37 Plant Mating Strategy Affects Probability of Island Colonization.

**Timothy Ohlert** ‡, Department of Biology, UNM; and Emma Goldberg, Department of Ecology, Evolution, and Behavior, University of Minnesota, St. Paul MN.

Evolution has led to a diversity of traits related to plant reproduction. A self-compatible (SC) plant is capable of fertilizing its own ovules, while a plant that is self-incompatible (SI) requires pollen of another individual in order to reproduce. Self-compatibility in plants creates a colonization advantage since only a single individual colonization event is necessary in order to establish a population. The dispersal of plants is also dependent upon the distance of an island away from the nearest mainland. Rates of colonization are much higher in islands nearer the mainland than further away. In order to test the interactions of distance and mating system in colonization, we compiled a database of plant presence on islands comprised of species from three plant families: Asteraceae, Brassicaceae, and Solanaceae. We found that species richness decreased in all three of the families as island distance increased. Additionally, in the Brassicaceae and Solanaceae families, SC plants were more common than SI plants across the distance gradient. In the Asteraceae family, the frequency of SI plants decreased at a faster rate than SC plants. This evidence supports the hypothesis that SC plants exist on islands at greater rates than SI plants and that the ratio of SC to SI on islands is magnified by island distance from mainland.

38 Role of the G Protein-Coupled Estrogen Receptor in Breast Cancer Metastasis.

**Katrina Baca** †, Initiatives to Maximize Student Diversity (IMSD), and Department of Biology, Department of Biochemistry, and Department of Cell Biology and Physiology, Health Sciences Center, UNM; Niki Marjon, Department of Cell Biology and Physiology, Health Sciences Center, UNM; Eric Prossnitz, Department of Internal Medicine, Health Sciences Center, UNM; and Helen Hathaway, Department of Cell Biology and Physiology, Health Sciences Center, UNM.

Breast cancer is the second leading cause of cancer-related death in women, and estrogen (E2) exposure promotes breast cancer. The estrogen receptor G Protein-Coupled Estrogen Receptor (GPER) correlates with poor prognosis in breast cancer patients. Inhibition or loss of GPER represses breast cancer progression and metastasis in a mouse model. In this study, we begin to determine mechanisms by which GPER contributes to metastasis by examining metastasis markers in mice treated with E2 (GPER agonist) or E2 + G36 (GPER antagonist). We hypothesize that G36 abrogation of E2-dependent GPER activation will suppress specific metastasis markers; these findings will provide clues to GPER function in promoting metastasis. The polyoma middle T antigen transgenic mouse model (PyMT Tg) was treated with vehicle, E2, or E2+G36. Tumors were harvested at 13 weeks and used in immunofluorescence/ immunohistochemistry assays to quantitate vasculature (anti-CD31 antibody) and two markers of epithelial-mesenchymal transition (EMT), vimentin and smooth muscle actin (SMA). There was no difference in CD31 immunostaining, suggesting GPER does not promote metastasis through increased angiogenesis. Vimentin and SMA expression were increased in tumors from mice treated with E2 + G36. This suggests increased EMT, which is paradoxical to the reduced metastasis we observe. One intriguing possibility is that the overexpression of vimentin and SMA promotes EMT in the tumor, but prevents mesenchymal-epithelial transition (MET) when tumor cells colonize distant sites, reducing metastasis. Future research will examine co-expression of EMT markers with cell lineage markers to understand how GPER inhibition decreases metastasis.

39 The Role of OPAQUE1 Myosin in Asymmetric Cell Division in Maize.

**Janette Mendoza** ‡ and Michelle R. Facette, Department of Biology, UNM.

Asymmetric cell division (ACD) is important because it determines cell fate and tissue patterning. However, many aspects of ACD in plants are still unclear. Stomatal development in maize has proven to be a useful model for understanding the ACD mechanism. Previous studies have identified several actors in subsidiary mother cell (SMC) polarization including BRK proteins (regulators of actin nucleation), PAN proteins (receptor-like molecules), and ROP (a GTPase). A dense actin patch also polarizes in SMCs, and the nucleus polarizes via an actin-based mechanism. After polarization, the preprophase

band marks the division plane, followed by cytokinesis. Mutations also have been identified in division plane establishment and maintenance (*dcd* and *tan*). Previously, *Opaque1* was identified as a maize myosin XI important for protein body localization in seeds. Plants have two types of myosins: myosin VIII and myosin XI. Myosin XIs are required for organelle movement and cytoplasmic streaming. Thus, we hypothesize that myosin is required for ACD in maize and has several potential roles in ACD. We speculate that myosins can play a role during the perception of the polarizing cue, during polarization of organelles in the cell, or during formation of the spindle alignment. Preliminary data showed *opaque1* has abnormal subsidiary cells. The shapes of the abnormal subsidiary cells closely resemble *dcd* mutants, rather than *pan* or *brk* mutants, suggesting *opaque1* may have defects post-polarization. Currently, we are examining nuclear migration, actin, and PAN protein polarization in *Opaque1* mutants to determine if they have defects during polarization.

40 Assessment of Intra- and Interregional Genetic Variation in the Eastern Red-backed Salamander, *Plethodon cinereus*, via Analysis of Novel Microsatellite Markers.

**Alexander C. Cameron** ‡, Department of Biology, UNM; Jeffry J. Anderson, Medical College of Wisconsin, Milwaukee WI; and Robert B. Page, Department of Science and Mathematics, Texas A&M University, San Antonio TX.

The red-backed salamander has long served as a model system in ecology, evolution, and behavior, and studies surveying molecular variation in this species have become increasingly common over the past decade. However, difficulties are commonly encountered when extending microsatellite markers to populations that are unstudied from a genetic perspective due to high levels of genetic differentiation across this species' range. To ameliorate this issue, we used 454 pyrosequencing to identify hundreds of microsatellite loci. We then screened 40 of our top candidate loci in populations in Virginia, Pennsylvania, and Ohio—including an island population off the shore of Lake Erie (South Bass Island). We identified 25 loci that are polymorphic in a well-studied region of Virginia, and 11 of these loci were polymorphic in populations located in the genetically unstudied regions of Ohio and Pennsylvania. Use of these loci to examine patterns of variation within populations revealed that South Bass Island has low diversity in comparison to other sites. However, neither South Bass Island nor isolated populations around Cleveland are inbred. Assessment of variation between populations revealed three well defined genetic clusters corresponding to Virginia, mainland Ohio/Pennsylvania, and South Bass Island. This work provides novel genetic resources that will facilitate population genetic studies in a part of the red-backed salamander's range that previously has not been studied in this way and refines our understanding of how neutral variation is distributed in this ecologically important organism.

---

## SESSION 2, 1:30–3:00 p.m.

### The bolded author is the presenter.

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

41 Characterization of Somatic Muscle Gene, Holes in Muscles (Him), in *Drosophila*.

**Samuel Mckitrick** †, Department of Biology, UNM.

Understanding the regulatory mechanisms involved in myogenesis is of crucial importance when attempting to comprehend the processes that drive developmentally derived diseases. We generated a null mutant of the Him (Holes in Muscles) gene to better understand its contribution to myogenesis. Him is a myogenic repressor gene that previously was shown to inhibit Myocyte enhancer factor-2 (MEF2) activity, and is expressed in myoblasts, but not differentiating myotubes. Through this inhibition of MEF2, Him additionally is predicted to act as a block on cell differentiation and proliferation. Using a

line of *CRISPR-Cas9* (*III*) flies and a Him sgRNA targeting plasmid, we successfully obtained a knock-out mutant caused by a frameshift mutation. The Him mutant is able to persist in the homozygous state, but shows distinct differences in muscles morphology leading to a reduced ability or inability to fly, as well as a lessened ability to jump. Using fluorescent staining of muscle sections, we observed that the jump muscle has a distinctly different phenotype than observed in yw control flies. The muscle fibers of the TDT in Him mutants have significantly more fibers than the wild type and contain less nuclei per fiber; additionally, the fibers are not distinctly organized. Currently, ongoing research is being performed to further classify this mutation. This data helps to provide insight into the mechanisms of cell development and the role Him plays as a possible regulatory agent of cell differentiation.

42 Pramipexole, a Dopamine D2/D3 Receptor Agonist, May Act to Modulate Pain Signaling in the Dorsal Horn Spinal Cord to Reduce Chronic Neuropathic Pain.

**Jacob Sanchez***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, and Department of Neurosciences, UNM; Arden Vanderwall, Melody Sun, Jayapriya Chandrasekaren, Monique Nysus, Department of Neurosciences, UNM; Rodrigo Escalona, Department of Psychiatry, UNM; and Erin Milligan, Department of Neurosciences, UNM.

During the onset of neuropathic pain, glial cells (astrocytes and microglia) in the spinal cord are activated and mediate the release of pro-inflammatory cytokines that act to enhance neuronal sensitivity. New evidence suggests that glial cells express dopamine receptors, which may play a key role in modulating neuropathic pain. Spinal glia are known to facilitate pro-inflammatory signaling leading to neuropathic pain. In the spinal cord, the predominant dopamine receptor is the D2 receptor subtype (D2DR), which is an inhibitory G protein-coupled receptor that decreases astrocyte activation. Prior evidence suggests that a decrease in spinal astrocyte activation results in suppression of pain signaling. Pramipexole (PPX) is a D2/D3 receptor agonist that acts in the brain to increase dopamine signaling for the treatment of Parkinson's disease to restore normal motor coordination. PPX also is known to reduce inflammation. We hypothesize that PPX activates D2DRs in the spinal cord to inhibit both astrocyte activation and the release of pro-inflammatory mediators that contribute neuropathic pain. Our study utilizes a mouse model of neuropathic pain to assess changes in sensitivity to light touch in response to PPX. The results show that following a PPX intrathecal injection (a peri-spinal infusion into the cerebrospinal fluid) or an intravenous injection, decreases in sensitivity to light touch (pain suppression) for three hours post-injection was observed. Ongoing studies will explore whether PPX acts to modulate dopamine signaling specifically on spinal astrocytes, which may uncover a new therapeutic approach for the treatment of neuropathic pain.

43 Fluorescence Lifetime Imaging of Senescence-associated Beta-Galactosidase.

**Ashton L. Sigler**†, Maximizing Access to Research Careers (MARC), Department of Biology, UNM; Jun Liu, Paul Henderson, Philip Deenik and Lina Cui, Department of Chemistry and Chemical Biology, UNM.

In 2018, there are expected to be more than 1.8 million new cancer cases and more than 600,000 cancer deaths in the United States alone. While cancer treatment options have become increasingly effective over the years, determining the efficacy of specific treatments remains difficult. Treatment of cancer often involves DNA damage via chemotherapeutic drugs that may cause cancerous cells to enter senescence, a permanent state where cells remain metabolically active, but will no longer divide and proliferate. In this state, senescence-associated beta-galactosidase (SABG) is overexpressed and is frequently used as a senescence indicator. The aim of our study is to use fluorescence lifetime imaging (FLI) of an SABG probe to measure cellular senescence. FLI has shown promise in multiple studies as a method for detecting and diagnosing cancerous or otherwise diseased tissues through endogenous fluorophores. Using fluorescence lifetime imaging microscopy (FLIM) and spectroscopy (FLIS), both senescent and non-senescent cancerous mammalian cell lines will be observed after incubation with the fluorescent probes. We hypothesize that there will be a significant, measurable difference in the fluorescence lifetimes between: (a) the bound and unbound probes, and (b) senescent and non-senescent cells. Preliminary results from western blots

using beta-galactosidase have suggested that the binding efficiencies vary based on the substituents of the linking group and that, while the probe is cleaved by beta-galactosidase, it does not bind specifically to the cleaving protein. We anticipate FLI applications will be useful in evaluating the efficacy of cancer treatments, and therefore providing clinical tools in precision medicine.

44 Cardiac Fibroblasts as Modulators of the Failing Heart ECM.

**Steven Guerin***, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, and Department of Pharmaceutical Sciences, College of Pharmacy, UNM; Dawn A. Delfín and Elizabeth McKown, Department of Pharmaceutical Sciences, College of Pharmacy, UNM.

Treatment of heart failure via stem cell therapy has proven challenging, and thus far clinical trials have had mixed success. Past research has indicated that ABI3BP, a protein in the extracellular matrix (ECM), may play a role in stem cell attachment to the ECM and transdifferentiation of the cells into mature cardiomyocytes. We hypothesized that increasing ABI3BP levels in the ECM from failing hearts will both increase their attachment and differentiation ability. To increase the prevalence of ABI3BP in ECM, first we used cardiac fibroblasts stimulated with ascorbic acid, known to be involved in the increased production of the ECM. Treatment of fibroblasts with ascorbic had mixed success, and it is still unclear if it increases ECM protein production. Next, we transfected fibroblasts with an ABI3BP expression vector and grew the cells on human heart ECM in order to test whether the fibroblasts could modulate ABI3BP levels in existing ECM, and whether the failing heart ECM would have an effect on the fibroblasts. We observed that the ECM has no effect on the fibroblasts. Currently, a stably transfected line of fibroblasts is in development. In the future, the fibroblast-modulated ECM with increased expression of ABI3BP could be used to create a potential testing ground for future experiments involving stem cells, and hopefully will shed light on the role of ABI3BP in stem cell attachment.

45 Quantifying Consumer Forage, Flower, and Fruit Availability Using Plant Phenology Data.

**Alesia Hallmark** ‡, Department of Biology, UNM.

Plant phenology, the timing of important life events such as leaf growth or reproduction, dictates when critical resources may be available for higher trophic levels within a food web. In aridlands, plant growth is controlled by stochastic rain events, leading many individuals to fail to grow or reproduce in some seasons or years. This extreme intra- and interannual variation in resource availability cascades throughout arid food webs; however, most studies fail to go beyond qualitative descriptions of "good" or "bad" years for consumer populations. Here, we leverage plant phenology and biomass datasets to create Forage, Flower, and Fruit Availability Indices for three semi-arid biomes spanning two decades. We then relate these indices to the abundance and richness of three consumer taxa at the same sites—herbivorous grasshoppers, pollen- or nectar-dependent bees, and granivorous rodents—in order to answer the following questions: (1) Are some plant functional types more important in determining the stability of consumer populations? (2) Are there identifiable lags between Availability Indices and consumer community metrics? and (3) Which consumer taxa are most at risk in the face of increasing aridity?

46 Rac1 Overexpression Changes Cell Growth and Morphology in Ovarian Cancer Cell Lines.

**Sara Asfan** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, and Department of Biochemistry and Molecular Biology, UNM; Martha Grimes, Dayna Dominguez, Michaela Granados, Department of Pharmaceutical Sciences, College of Pharmacy, UNM; Angela Wandinger-Ness, Department of Pathology, School of Medicine, UNM; and Laurie G. Hudson, Department of Pharmaceutical Sciences, College of Pharmacy, UNM.

Ovarian cancer affects more than 20,000 women annually, and the 70% percent of women who receive treatment after late-stage diagnosis will relapse within three years. Clinical studies report that overexpression of certain members of small Rho family GTPases, specifically Rac1 and Cdc42, are associated with a worse prognosis in ovarian cancer patients. Our lab is investigating a new Rac1 inhibitor, R-Ketorolac, which was identified by high throughput screening of FDA approved drugs. To study the effects of Rac1 expression in ovarian cancer cells, we analyzed cell growth characteristics in a colony formation assay.

We found that elevated expression of Rac1 in ovarian cancer cells increased mean area and mean perimeter per colony, but decreased mean colony number after seeding equivalent cell numbers. In addition, overexpression of Rac1 changed colony morphology to a less compact phenotype with more elongated cell characteristics. This morphological change is consistent with epithelial to mesenchymal transition (EMT). Increased Rac1 expression led to decrease in certain epithelial markers such as Claudin and increased expression of the EMT regulatory protein Slug/Snail2. Ongoing studies include testing the effects of known Rac1 inhibitors and R-ketorolac on ovarian cancer cell lines colony characteristics and EMT. Since R-Ketorolac inhibits Rac1 GTPase activity it could have promising benefits as an ovarian cancer therapy.

47 Effects of Wildfire on Climate Sensitive Species *Ochotona princeps*.

**Kelly A. Lizewski †**, Marie L. Westover, Department of Biology, UNM; Erik A. Beever, Northern Rocky Mountain Science Center, USGS, Bozeman MT; and Felisa A. Smith, Department of Biology, UNM.

Alpine environments are among those most at risk from climate change, due to high rates of endemism, containing many cold-adapted species with limited dispersal ability. Among these species of conservation concern is the American pika (*Ochotona princeps*), a small mammal found in mountainous regions of 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 increased the probability of severe wildfire occurrences. Changes to vegetation following fires have been shown to influence small mammal populations such as woodrats and deer mice, but limited information is known about the impact of fires on pikas. To examine these effects, we collected surveys during the summers of 2016 and 2017 on pika habitat across the Jemez and Sangre de Cristo Mountains. We collected data regarding pika abundance, species and proportion of vegetation, percent habitat burned, and additional abiotic variables. We used geographic information systems caltopo.com and mtbs.gov to determine the date and extent of fires from 1984 to the present. Using these programs and gps points obtained during surveys, we were able to determine the fires that affected pika habitat. We analyzed the data to determine the extent to which fires impact the distribution and abundance of pikas in New Mexico. Our research will allow us to gain further insight into fire ecology, including the role of fire on vegetation communities and pika populations in New Mexico.

48 High Reproductive Success of Bonytail Reared in Off-channel Habitats.

Megan Osborne, Brian Fitzgerald, and **Charisa Bell †**, Division of Fishes, Museum of Southwestern Biology, Department of Biology, UNM.

Bonytail (*Gila elegans*) is a highly endangered freshwater fish native to the Colorado River basin. It is considered functionally extirpated in the wild as adult fish are extremely rare and there is virtually no recruitment due to predation pressure. An alternative conservation strategy involves releasing adults into off-channel habitats where they can breed in the absence of predators. A potential risk of using this strategy is that few adults may produce the majority of offspring. This can lead to low genetic effective size and a loss of diversity. In 2017, we collected genetic data from adults and offspring stocked into three ponds at the Imperial National Wildlife refuge. Parentage analysis revealed that more than 80% of both males and females contributed at least one offspring. Consequently, genetic diversity was transmitted faithfully between adult and offspring generations. The majority of adults had more than one mate and the number of mates was strongly positively correlated with the number of offspring attributed to individuals. There was also a positive relationship between female size and measures of reproductive success. The results from this study reveal aspects of the reproductive ecology of Bonytail and will help guide future conservation plans.

49 Characterization of the T-cell Receptor Repertoire in *Protopterus dolloi*: Searching for the Evolutionary Origins of Dermal γδ T Cells.

**Alissa Cabada-Gomez** †, Ryan Heimroth, Gabriela Padial, Susana Magadan and Irene Salinas, Department of Biology, UNM.

T lymphocytes have a central role in the adaptive immunity of all jawed vertebrates. Two conventional subsets of T cells in gnathastomes are distinguished by the type of T cell receptor (TCR) expressed on their surface: αβ T cells and γδ T cells. In mammals, γδ T cells are abundant at mucosal sites and display features such as limited variability of their TCR repertoire, innate-like immune functions, and wound healing properties. Additionally, peripheral γδ T cells have unique repertoires compared to populations within central tissues. African lungfish (*Protopterus* sp.) are the closest living relative to all tetrapods and lungfish adapt to terrestrial life in a process known as aestivation. Aestivation occurs in the wild in response to unfavorable environmental conditions and can be mimicked in the laboratory. The goal of this study was to characterize the TCR repertoire of the skin and pre-pyloric spleen of *P. dolloi* before and after aestivation in central (spleen) and peripheral (skin) tissues. We cloned α, β, γ, and δ V domain sequences from control skin and spleen tissue and then analyzed the length and diversity of their hypervariable region 3 (CDR3). Results indicate a more restricted repertoire in skin γδ T cells compared to their systemic counterparts in freshwater lungfish. Preliminary analysis from aestivated animals indicate a different and more diverse repertoire in skin γδ T cells compared to controls. Our results suggest that the dichotomy and specialization of epidermal γδ T cells predates the origin of tetrapods.

50 Optimizing Schistosomiasis Treatment Timing with Respect to Seasonal Fluctuations in the Force of Infection.

**Larissa Anderson** ‡, Department of Biology, UNM; and Helen J. Wearing, Department of Biology, and Department of Mathematics and Statistics, UNM.

Schistosomiasis is a neglected parasitic disease caused by trematode species of the genus *Schistosoma*. A common schistosoma species, Schistosoma mansoni, utilizes humans as its obligate definitive host and freshwater planorbid snails of the genus *Biomphalaria* as its intermediate host. Despite relatively stable temperature regimes in sub-tropical and tropical regions, the wet and dry seasons can drastically change the aquatic environment that provide habitat for the snail intermediate host and the two free-living stages of schistosomes. The changes in water body size may also concentrate exposure in the human and snail hosts or periodically eliminate suitable habitat. Substantive variation in snail population size or infection level may impact the force of infection to humans and a reduction in this would present an opportunity to maximize the impact of current control measures. To quantify seasonal variation in snail abundance, we collected absolute and relative snail density and *S. mansoni* infection prevalence data bimonthly from a perennial stream in the Kisumu, Kenya area from July 2015–January 2018. Daily rainfall and temperature date also was obtained for January 2013–January 2018. We used time-series analysis, including the analysis of varying time-lags, to identify the temperature and rainfall events most predictive of snail density and infection prevalence. In future work, we will use these data to parameterize periodic seasonal forcing of snail population size and infection prevalence in a dynamic model of schistosomiasis. The goal of this model will be to assess the impact of seasonal timing on the outcome of control measures.

51 Water Source Analysis Utilizing Sap Flux and Budyko Analysis.

**Devon Fisher-Chavez** †, Marcy E. Litvak, William T. Pockman, Cheng-Wei Huang and Robert Pangle, Department of Biology, UNM.

Given the abundance of *Pinus ponderosa* (Ponderosa Pine) in New Mexican forests, we explored the water resources that allow them to survive in semi-arid, high-elevation environments. We observed a stand of Ponderosa pine in the Valles Caldera from 2014 to 2017 and measured sap flux, stand-level evapotranspiration (ET), precipitation (P) and soil water availability to determine the timing of water uptake from groundwater (GW) or precipitation (P). We performed a Budyko analysis of ET, P and potential

evapotranspiration (PET) to identify energy and water-limited periods. We also analyzed the sensitivity of sap flux across water-limited and water-surplus periods. We hypothesized that GW is the main water resource for Ponderosa Pine at this site when sap flux is not sensitive to soil water status and P. We found that the dependence on GW mainly occurred during the dry period prior to the summer monsoon (i.e., May–July), while the utilization of P mainly occurred during wet monsoon period (August–September/ October). We also found that snow melt determined a threshold of GW required to sustain ecosystem-level ET during the following pre-monsoon dry period. Ecosystem function was limited during extended droughts when GW was below the threshold. These results suggest that Budyko analysis alone may not sufficiently demonstrate the energy-limited or water-limited regime for an ecosystem when GW is accessible, sap flux (i.e., transpiration) also must be considered.

52 Microbes that Masquerade as Minerals.

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

Caves contain many secondary minerals, which we are discovering may harbor microorganisms and have important implications for life detection on extraterrestrial bodies. Preliminary investigations of microorganisms within secondary mineral deposits, or "microbes that masquerade as minerals," have yielded promising results in lava caves of Hawaii. Microbes inhabiting these mineral deposits are fitting targets in the search for extraterrestrial life as their morphologies can be described, quantified, and differentiated from other deposits lacking microbial communities. With my mentors, Drs. Diana Northup and Michael Spilde, I am investigating basalt lava caves in New Mexico and Hawaii, in semi-arid region with low precipitation. While I will employ techniques in analytical geochemistry to analyze substrate composition, electron microscopy to document putative microbial morphologies, and genetic sequencing to characterize microbial diversity, this presentation will focus on the continuum as established using electron microscopy. My ultimate goal is to create a continuum of mineral morphologies from least microbial to most microbial in composition. These results will provide scientists at NASA with information necessary to program rovers to identify and analyze secondary mineral deposits that are likely to possess evidence of life. In 1992, Dr. Penelope Boston, of NASA's Astrobiology Institute, proposed we search life in the subsurface of Mars, given the inhospitable environment on the surface. To provide a good analogue for the Martian subsurface, we are examining basalt lava caves on Earth, as they are similar in formation and provide good microbial habitats.

53 From Our Collections: Mammals Evolving Our Knowledge.

**Lindsey Frederick** ‡, Department of Biology, UNM.

Caves contain many secondary minerals, which we are discovering may harbor microorganisms and have important implications for life detection on extraterrestrial bodies. Preliminary investigations of microorganisms within secondary mineral deposits, or "microbes that masquerade as minerals," have yielded promising results in lava caves of Hawaii. Microbes inhabiting these mineral deposits are fitting targets in the search for extraterrestrial life as their morphologies can be described, quantified, and differentiated from other deposits lacking microbial communities. With my mentors, Drs. Diana Northup and Michael Spilde, I am investigating basalt lava caves in New Mexico and Hawaii, in semi-arid region with low precipitation. While I will employ techniques in analytical geochemistry to analyze substrate composition, electron microscopy to document putative microbial morphologies, and genetic sequencing to characterize microbial diversity, this presentation will focus on the continuum as established using electron microscopy. My ultimate goal is to create a continuum of mineral morphologies from least microbial to most microbial in composition. These results will provide scientists at NASA with information necessary to program rovers to identify and analyze secondary mineral deposits that are likely to possess evidence of life. In 1992, Dr. Penelope Boston, of NASA's Astrobiology Institute, proposed we search life in the subsurface of Mars, given the inhospitable environment on the surface. To provide a good analogue for the Martian subsurface, we are examining basalt lava caves on Earth, as they are similar in formation and provide good microbial habitats.

54 Dark Septate Endophyte and Host Relationship Responses under Simulated Future Climates.

**Katherine Anderson** †, Jennifer A. Rudgers and Katlin Beaven, Department of Biology, UNM.

High temperatures and drought are expected to become more frequent in the near future, creating harsh growing conditions for rangeland grasses, which feed highly in-demand livestock. In response to these limiting conditions, the agricultural industry must find innovative ways to deliver a stable supply of crops. Creation of drought and heat-tolerant plants by means of genetic engineering has a high cost. Instead, using fungal symbionts to benefit their grass hosts may reach the same result. By artificially creating high-heat and low-water conditions and inoculating *Bouteloua gracilis* with strains of Dark Septate Endophytes (DSE), we can observe how *B. gracilis* hosts and their DSE symbionts respond. In addition to gauging responses, we also can test the stress-gradient hypothesis, which states that as conditions become more stressful, symbioses will yield more positive results for both the host and the symbiont. Thus, the goal of this study was to observe the responses of DSE symbionts and their plant hosts to a range of simulated drought conditions. In a novel experimental design, 24 chambers were created to simulate warmer temperatures and varying levels of precipitation through a strict watering regime. We hypothesized that DSE dampen the harsh effects from high temperature and drought for *B. gracilis*, resulting in higher than normal growth rates and biomass.

55 Development of a SNP Assay for Assessment of Genetic Diversity and Parentage Assignment in Gila Trout.

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

Gila trout (*Oncorhynchus gilae*) is a federally protected species in the family Salmonidae and is confined to headwater streams in the Gila and San Francisco Rivers in New Mexico and Arizona. Currently, there are five recognized relict and genetically distinct lineages of Gila trout found in the upper reaches of the Gila and San Francisco Rivers. Although genetically distinct, Gila trout populations show relatively low genetic diversity, effective sizes, and possible local adaptions. Climate change and nonnative introductions of Rainbow trout (*O. mykiss*), among other sources, threatens this cold-water species. Therefore, it is imperative to understand the sources of genetic variation available to effectively conserve the genetic diversity and structure within Gila trout. Using a restriction site associated 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 lineages of Rainbow trout stocked in NM. We have identified variable SNPs in putatively neutral areas and areas under selection in the genome in an effort to create a 100–200 SNP locus assay. Specifically, we have targeted lineage-specific and species-specific loci that provide overall population genetic diversity, diversity within ecologically significant genes, and pedigree tracking. Ultimately, we want to provide a high-throughput assay for managers to cheaply and efficiently genotype all Gila trout individuals that gives a higher resolution of the genetic resources available for effective captive breeding programs in a changing climate and the ability to identify any nonnative hybrids.

56 Probing Photosynthesis.

**Estania Jean Charles** †, John Roesgen and David T. Hanson, Department of Biology, UNM.

To assess $CO_2$ response and Rubisco activation, we used a LI-6800 Portable Photosynthesis System. I tested this by measuring photosynthetic function via $CO_2$ uptake of discs of algae using a leaf-style gas exchange system and using variable chlorophyll fluorescence measurements of quantum yield. Rapid $CO_2$-response curves were used to determine the level of Rubisco activity at saturating and sub-saturating light (as determined by the light-response curve). A faster response time to the changing $CO_2$ concentrations under saturating light suggests Rubisco activase activity is higher (Stinziano *et al.*, 2017). The Li-Cor also was used to measure the photosynthetic gas exchange under various light intensities from 50–1,000 PAR. This proof-of-concept project shows that we can use a Li-Cor 6800 portable photosynthesis system to collect various measurements on living microalgal cells by collecting them onto a porous filter and measuring them as we would a leaf.

57 Fleas of Beringian Shrews (*Sorex* spp.).

Laurel Cenac, **Lizon Cenac** †, Division of Genomic Resources, Museum of Southwestern Biology, Department of Biology, UNM; Ralph Eckerlin, Animal Parasitic Diseases Laboratory, Agricultural Research Service, U.S. Department of Agriculture, Beltsville, MD; Mariel L. Campbell and Joseph A. Cook, Division of Genomic Resources, Museum of Southwestern Biology, Department of Biology, UNM.

The Collaborative & Integrative Inventories of Biomes of the Arctic (CIIBA) is a research effort that focuses on the flora and fauna of Beringia, the vast territory (larger than the continental U.S.) that occupies NE Asia and NW North America, and which was the gateway for biotic expansion between the Palearctic and Nearctic through much of the Tertiary. Over the last decade, the Cook lab has conducted comparative evolutionary studies of mammals, parasites and pathogens to address the extent and timing of host/parasite differentiation and cospeciation in Beringia. In conjunction with this research, we have assembled a collection of more than 4,000 small mammals and associated ecto- and endoparasites through field expeditions in Beringian Pleistocene refugia encompassing much of eastern Yukon, interior Alaska, and eastern Siberia. The results presented here are an initial inventory of fleas from shrews (Sorex spp.) collected by the CIIBA project from Alaska, Canada, and Russia.

58 Are Caves a Source of Bat Microbiota? A Comparison of Bacterial and Fungal Communities in Caves and Cave Roosting Bats in El Malpais National Monument, New Mexico.

**Nicole A. Caimi** ‡, Jennifer J.M. Hathaway, Department of Biology, UNM; Debbie C. Buecher, Buecher Biological Consulting, Tucson AZ; and Diana E. Northup, Department of Biology, UNM.

In the aftermath of the discovery of white-nose syndrome (WNS), documented patterns of infection and mortality in bats with WNS showed that some bat species may be less vulnerable than others, possibly due to natural microbial defenses. Research into which natural defenses bats have and where they are acquiring these defenses is important in predicting which western bats species may be most vulnerable to WNS. To address this research area, we are investigating to what extent bat microbiota are acquired from the cave walls on which the bats roost. Two caves in El Malpais National Monument (ELMA) were sampled for bat microbiota and wall microbial mats. In each cave, the external surfaces of six roosting bats of four different species and their associated microbial mats were sampled. Bat swabs and microbial mat samples were sent to MR DNA in Shallowater, TX for genomic DNA extraction and sequencing. Samples were sequenced using Illumina MiSeq sequencing of the 16S rRNA gene for bacterial diversity and the ITS region for fungal diversity. Both the bacterial and fungal sequences were processed and analyzed using Qiime, USEARCH, and R Studio. Bacterial analyses showed 1,591 taxa were present on the bats and 1,425 taxa in the microbial cave mats, with 120 shared taxa overall between bats and microbial mats. The fungal analyses showed 405 taxa on the bats and 196 taxa found in the microbial mats, with 187 shared taxa overall. Our results contribute to our understanding of the possible sources of bat external microbiota.

59 The Role of *Shigella sonnei* in Intranasally Infected Non-Transgenic Mice (C57BL6/J).

**Gabriela Padial** †, Elisa Casadei, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM; Devon Chisholm, Department of Molecular Genetics and Microbiology, Health Sciences Center, UNM; Kiran Bhaskar, Neurobiology Research Facility, Department of Molecular Genetics and Microbiology, Health Sciences Center, UNM; and Irene Salinas, CETI, Department of Biology, UNM.

Tauopathy induced neurodegenerative diseases, such as Alzheimer's disease (AD), affect millions of people worldwide. The rapidly rising prevalence of AD and other neurodegenerative diseases signify the immediate need for understanding these pathologies. Anosmia is a known early symptom of the onset of neurodegeneration. Preliminary studies of the brain microbiome of AD and tauopathy patients have found the presence of the enterobacterium *Shigella sonnei*. We hypothesize that this pathogen may penetrate the CNS via the olfactory route. The aim of this research is to establish a *S. sonnei* infection

model in mice by intranasal administration and to determine whether *S. sonnei* invades the CNS, causing cognitive impairment in non-transgenic mice. One-month-old and three-month-old female and male C57BL6/J mice received *S. sonnei* or PBS (phosphate-buffered saline) by intranasal administration every other day for a total of six doses. Samples of the olfactory bulb, olfactory epithelium, and feces were collected for a period of 10 days. Behavioral assays were performed 20 days after the first infection. *S. sonnei*-specific PCR indicate the presence of S. sonnei in all the tissues, but only in the feces sampled from the mice that had been administered *S. sonnei*, but not control mice. Our results indicate that nasal infection with *S. sonnei* results in shedding of the pathogen in the feces, which suggests a fecal-oronasal-fecal mode of transmission. Additionally, *S. sonnei* nasal infection resulted in altered cognitive behavior. Future analyses will evaluate whether behavioral changes are associated with tau pathology in the CNS.

60 R-Ketorolac Inhibition of Rho GTPases in Ovarian Cancer.

**Alejandra Rosales***, Flybase, Post-Baccalaureate Research and Education Program (PREP), UNM; Martha Grimes, Dayna Dominguez, Michaela Granados, Department of Pharmaceutical Sciences, College of Pharmacy, UNM; Melanie Rivera, Angela Wandinger-Ness, Department of Pathology, School of Medicine, UNM; and Laurie Hudson, Department of Pharmaceutical Sciences, College of Pharmacy, UNM.

Epithelial Ovarian Cancer is the leading cause of death in gynecological malignancy, despite advances in therapy. Studies show Rho-family small GTPases, specifically Rac1 and Cdc42, play critical roles in tumor growth and metastasis. Rac1 and Cdc42 regulate cancer-relevant signaling pathways and gene expression, and are up-regulated in many human tumors. Our lab identified the R-enantiomer of a non-steroidal anti-inflammatory drug, Ketorolac, as an inhibitor of Rac1 and Cdc42. R-Ketorolac inhibits cell proliferation, adhesion, migration, and invasion in cell culture, plus decreases tumor growth in xenograft studies. Elucidating the roles of GTPases during tumor promotion may provide critical evidence for the best use of R-Ketorolac as a therapeutic. We measured changes from Rac1 overexpression, such as cell growth/proliferation, morphology, and biomarkers, for Epithelial-Mesenchymal Transition (EMT) as determined by qPCr and western blot analysis. Vector control and Rac1 overexpressing SKOV3ip cells (ovarian cancer cell line) were analyzed. Rac1 overexpression resulted in EMT biomarker changes. Up-regulation of HMOX-1, SLUG, CXCR4, N-CAD, ZEB2, and PAN-KERATIN were detected at transcript and protein levels. Other EMT markers were down-regulated, E-CAD, CYCLIND, and TWIST. Interestingly, preliminary xenograft studies in R-Ketorolac treated mice demonstrated a decrease in similar EMT biomarkers in tumor samples compared to tumors isolated from placebo control mice. These findings show Rac1 overexpression enhances EMT, associated with aggressive tumors, and suggest that Rac1 is an important therapeutic target in ovarian cancer. We hypothesize R-Ketorolac will reduce the effects from Rac1 overexpression, indicating R-Ketorolac as a potential therapeutic for ovarian cancer patients.

61 The Involvement of the Myogenic Gene *nautilus* in Muscle Development.

**Jonathon Cordova †**, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; and Richard M. Cripps, Department of Biology, UNM.

In vertebrates, MyoD belongs to a family of Myogenic Regulatory Factors (MRFs) that are essential for muscle differentiation. In *Drosophila*, the only MyoD homolog, *nautilus*, plays a role in the differentiation of progenitor cells into mature muscle fibers. There is a controversy, however, about the requirement for MyoD in this process. To resolve this controversy, we investigated the requirement and sufficiency of *nautilus* to promote muscle development. Individuals homozygous for *nautilus* mutations were examined at stage 16 of embryonic development so that the *nautilus* mutant phenotype could be characterized. These mutant embryos exhibited slight to severe alterations in a subset of muscles, indicating that a deficiency of *nautilus* leads to poor muscle development. In order to visualize the importance of *nautilus* for myogenic conversion, we transfected a line of *Drosophila* cells with cDNA expressing *nautilus*, *daughterless*, and *Mef2*, which allowed us to observe myogenic conversion of the cells. We hope to determine if *nautilus* is able to initiate myogenic conversion in tissue culture by itself or when co-expressed with other

basic-Helix-Loop-Helix (bHLH) or MADS-domain box transcription factors. In addition, we hope to obtain a better understanding of how these transcription factors interact with one another, which will help us decipher the overall mechanism of muscle differentiation in *Drosophila*. In preliminary data, we found that the expression of *nautilus*, *daughterless*, and *Mef2* was sufficient to induce myogenesis, which will give us a basic understanding of how orthologous genes for muscle development function in various organisms.

62 Maximization of Microbial Fuel Cell Power Output Utilizing Bimetallic Cathode Catalysts.

**Sergio Herrera** †, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM, and Department of Chemical and Biological Engineering, UNM; Carlo Santoro, Mounika Kodali and Plamen Atanassov, Center for Micro-Engineered Materials, Department of Chemical and Biological Engineering, UNM.

The investigation of this work is focused on the study and characterization of platinum group metal free (PGM-free) bimetallic catalyst effects on oxidation reduction reactions (ORR) in a single chamber microbial fuel cell (SCMFC). To provide a bit of background SCMFCs are bio-electrochemical systems used to produce power; that is, biological organisms, in this case bacteria, are used to produce power (electricity) via chemical reactions (ORR) provided by the consumption of introduced organic compounds. Digressing, experimentation of bimetallic catalysts was conducted to determine superior power output. In general, the results show that the addition of a second metal increased the performance of Co-based catalysts, while for Fe-based catalysts, only Fe-Mn had a positive effect on the performances. Specifically, Co-Mn had a power output of 188 μW cm-2 and Co- as a singular catalyst, produced a power output of approximately 162 μW cm-2. In parallel, Fe as a singular catalyst had a power output peaking at approximately 192 μW cm-2 and Fe-Mn had a power peak of 221 μW cm-2. In light of the fact that every bimetallic combination with Co- produced greater power then Co- as a singular catalyst, it may be observed that, ultimately, Fe- based materials still surpass the power output of Co-, even when Co- is combined with another metal. Furthermore, Fe- is a much more cost-effective metal to utilize in practice. In all, however, bimetallic combinations stand to be a feasible means to supply greater power output when compared to single metallic catalysts.

63 A Shifting Baseline: δ15N Analysis of Individual Amino Acids to Track Ecosystem Changes across the Late Pleistocene Extinction.

**Emma A. Elliott Smith** ‡, Catalina P. Tome, Department of Biology, UNM; Thomas W. Stafford Jr., Stafford Research LLC, Lafayette, CO; S. Kathleen Lyons, Department of Biology, University of Nebraska, Lincoln NE; Felisa A. Smith and Seth D. Newsome, Department of Biology, UNM.

One of the likely consequences of the late Pleistocene megafauna extinction was a reorganization of mammalian communities, including trophic niche shifts of medium- and small-bodied mammals. Traditionally, nitrogen isotope ($\delta^{15}N$) analysis of bulk tissues has been used as a proxy for trophic level. Interpreting temporal or spatial changes in consumer $\delta^{15}N$ values, however, is complicated by potential concurrent shifts in (baseline) $\delta^{15}N$ values of primary producers. Recently, $\delta^{15}N$ analysis of individual amino acids (AAs) has emerged as a new technique to simultaneously track trophic level and changes in baseline $\delta^{15}N$ values. 'Source' AAs are routed directly from diet to consumer and so their $\delta^{15}N$ values do not change with trophic level, whereas 'trophic' AAs show a strong relationship between trophic level and $\delta^{15}N$. Here, we apply this approach to mammalian fossils sourced from Hall's Cave in west-central Texas, a site that spans from the late Pleistocene through the Holocene. We analyzed 35 individuals from two mammalian species: the cotton rat (*Sigmodon hispidus*), and the coyote (*Canis latrans*). For both species, we found a similar and significant decline in $\delta^{15}N$ of both source and trophic AAs through time from the mid to late-Holocene. However, the offset in $\delta^{15}N$ between source and trophic AAs remained constant, indicating that there was a shift in the base of the food web rather than a trophic shift of either species. Our study demonstrates that AA $\delta^{15}N$ analysis of ancient consumers may provide a useful way of quantifying both ecosystem shifts and trophic dynamics.

64 Myocardin Related Transcription Factors (MRTFs) Transgenic Lines: 'Dominant Negative' and 'Constitutively Active' Analysis in *Drosophila melanogaster*.

**Praveen Paudel †**, Tracy Dohn and Richard M. Cripps, Department of Biology, UNM.

Studies have shown that Serum Response Factor (SRF) and its co-activator Myocardin Related Transcription Factors (MRTFs) are regulators of myogenesis and signaling regulation. SRF is an essential regulator of skeletal muscle differentiation and numerous components of the muscle sarcomere. Cellular stimuli allow for shuttling of MRTFs to the nucleus where they activate SRF. SRF and MRTFs work together late in muscle development to promote flight muscle structure and maturation in *Drosophila melanogaster*, though potential involvement of MRTFs in early fight muscle still not well understood. Therefore, we obtained and characterized the adult muscle phenotypes of transgenic *Drosophila* lines that cause MRTF to be constitutively active or dominant negative. We used the UAS-Gal4 system to overexpress these transgenes specifically in adult muscle progenitor cells through an 1151-Gal4 driver. Furthermore, the specific muscle disruptions were analyzed through confocal imaging and functional flight tests. Molecular and genetic tools like cryosectioning and fluorescent immunostaining were used in analysis. The flight test data showed that transgenic dominant negative (UAS-DMRTFΔC) flies have weak flight muscle phenotypes. Furthermore, our analysis of flight muscle structure suggests that truncation of C-terminal results in disruption of Indirect Flight Muscles (IFMs) resulting in the weaker flight in DMRTFΔC flies. Similar to *Drosophila*, the vertebrate muscle system comprises several types of muscle fibers, indicating that MRTF may have an important conserved role in muscle fiber differentiation not only in *Drosophila*, but also in vertebrates. Therefore, this project leads to a better understanding of the role of MRTF in early muscle development.

65 The Role of the Vacuolar Ion Transport Genes VCX1 and VNX1 in *C. Albicans* Filamentation, Secretion, and Virulence.

**Esteban Abeyta †**, Initiatives to Maximize Student Diversity (IMSD), Department of Biology, UNM; Samuel Lee, Hallie Rane and Stella Bernardo, New Mexico VA Healthcare System, Albuquerque NM.

*Candida albicans* is a major cause of hospital-acquired infections and the main cause of invasive candidiasis in most clinical settings. Therapeutic options for *C. albicans* remain limited, with continued high mortality rates from invasive infection. Recent studies have shown that cellular pH homeostasis plays a vital role in *Candida* virulence. It is unknown, however, what components of pH homeostasis are necessary for maintenance of virulence. To understand whether vacuolar pH homeostasis can interfere with *C. albicans* virulence, we chose to investigate the predicted vacuolar, proton-ion transporter genes VNX1 and VCX1. Based on studies in Saccharomyces cerevisiae, we hypothesize that loss of these transporters will cause vacuolar pH disruption and a reduction in the ability of *C. albicans* to cause infection. If disrupting these transporters decreases virulence, they could have potential as drug targets. Using a PCR-based gene disruption strategy, we gene rated vcx1Δ/Δ and vnx1Δ/Δ null mutants in *C. albicans*. Reintegrant control strains are being constructed by cloning the wild-type VCX1 and VNX1 genes into bacterial vectors containing an auxotrophic marker, followed by lithium acetate transformation. Null mutants were assayed for pH and cation-dependent growth, filamentation, secretion of virulence proteins, and biofilm formation. Standard growth showed no difference between the wild-type and vcx1Δ/Δ and vnx1Δ/Δ mutant strains. Phenotypic analysis of these mutants, however, revealed surprising differences between the vcx1Δ/Δ and vnx1Δ/Δ strains, despite similarities in protein function and cellular localization. Further work will be done to examine these differences and their contribution to pH homeostasis and virulence.

66 ABA-ontrolled Chemically Induced Proximity Approach to Control CAR T Cells Activity Targeting GD2 Antigen Presenting Solid State Tumors.

Fu Sen Liang, Huong Nguyen, Department of Chemistry and Chemical Biology, UNM; **Brynn E. Cullander †**, Maximizing Access to Research Careers (MARC), Department of Biology, UNM, and Department of Chemistry and Chemical Biology, UNM.

Cancer remains one of the most difficult human diseases to combat, due to the resilient and unique nature of the disease. Immunotherapeutic approaches to treating various malignant and devastating human cancers have been developing quickly. While there have been encouraging cases of success, there still remains a substantial challenges associated with immunotherapies, especially the toxicity issues due to the lack of specific antigens and the diminished efficacy due to the repressive microenvironment of solid tumors. To address these hurdles, currently, we are developing a method using chemically caged abscisic acid (ABA) that is activated by cancer signals to control protein proximity and thus induce the activation of chimeric antigen receptor (CAR) T cells and the production of immune checkpoint inhibitors. This method is highly customizable for a variety of cancers. Currently, we are focusing on engineering CAR T cells targeting Disialoganglioside 2 (GD2) expressed on tumors of neuroectodermal origin, including neuroblastoma and melanoma. We are cloning constructs to express GD2-specific ABA-inducible CAR T cells. If successful, this method could have a significant impact on both future cancer research and treatment.

67 Fabrication of a Smart Hydrogel for Encapsulation of Poly(Ethylene Glycol).

**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 4L electrolyte lavage solution with poly(ethylene glycol) (PEG-ELS) for preparation. One in three patients are non-compliant to their colonoscopy schedules, with many patients who abstain reporting refusal due to significant discomfort associated with this preparation. We hypothesize that an alternative to this negative experience will improve patient adherence and patient experience with colonoscopies. The proposed method is a novel hydrogel system, no larger than the typical over-the-counter drug, used to encapsulate PEG-3350 (the active agent) to reduce patient discomforts. Various release test have been completed in increasing pH to ensure these hydrogels are pH responsive and swell to release PEG-3350 and other contents into pH environments similar to those found in the stomach (pH 1.0–3.0). H NMR has confirmed release of PEG-3350 in pH = 2.14. Biocompatibility of hydrogel extracts were assessed using Bovine Aortic Endothelial Cells. BAECs are biocompatible with low concentrations of poly(ethylene glycol), but higher concentrations show signs of cytotoxicity.

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).

Department of Biology, MSC03 2020
1 University of New Mexico
Albuquerque, NM 87131-0001
(505) 277-3411
http://biology.unm.edu