The University of New Mexico Department of Biology

26th ANNUAL RESEARCH DAYS

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

March 30 & 31, 2017

KEYNOTE LECTURE: *New Perspectives on Future Climate Change Risk & Ecosystem Change,* 3:30 p.m., March 31st,
Science & Math Learning Center

KEYNOTE SPEAKER:

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

SCHEDULE OF EVENTS

WEDNESDAY, MARCH 29

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

THURSDAY, MARCH 30

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

9:30–11:30 a.m. **Student Poster Presentations, Session 1**, first-floor hallways of Casetter Hall (odd-numbered posters judged).

1:30–3:20 p.m. **Student Poster Presentations, Session 2,** first-floor hallways of Casetter Hall (even-numbered posters judged).

3:30–4:20 p.m. **Department Research Presentation:** *"The Avian Tree of Life in the Phylogenomics Era,"* by **Dr. Michael Andersen**, UNM Assistant Professor of Biology, 100 Castetter Hall.

4:30–6:00 p.m. **Museum of Southwestern Biology (MSB) Open House.** CERIA (Bldg. 83).

4:45–5:00 p.m. **Grand Opening Ceremony and Tour of the MSB Division of Genomic Resources**, CERIA 324.

FRIDAY, MARCH 31

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

9:00 a.m.–Noon **Student Oral Presentations, Session 1**, 55 Castetter Hall.

11:45 a.m.–1:00 p.m.
- **Lunch** provided in the Basement & Courtyard of Castetter Hall.
- **BGSA Lunch** with the Keynote Speaker, 107 Castetter Hall.

1:00–3:00 p.m. **Student Oral Presentations, Session 2**, 51 Castetter Hall.

1:00–3:15 p.m. **Student Oral Presentations, Session 3**, 55 Castetter Hall.

3:30–5:15 p.m. **Keynote Lecture and Scholarship Awards**, Room 102 (auditorium), Science & Math Learning Center (Bldg. 14):
- **Brief Introduction** by **Dr. William T. Pockman**, Professor & Chair |of UNM Department of Biology.
- **Brief Remarks** by **Dr. Craig White**, UNM Acting Provost & Executive Vice President for Academic Affairs.
- **Introduction of the Keynote Speaker** by **Dr. William T. Pockman**, Professor & Chair of UNM Department of Biology.
- **Keynote Lecture: DR. JONATHAN T. OVERPECK**, *"New Perspectives on Future Climate Change Risk and Ecosystem Change."*
- **Presentation of Gift of Appreciation to Dr. Overpeck** by **Dr. Robert B. Waide**, Professor of UNM Biology & Co-Chair of the 2017 Research Day Committee.

—continued on the next page—

FRIDAY, MARCH 31 (continued)

- **Brief remarks** by **Dr. Mark Peceny**, UNM Arts & Sciences Dean.
- **Scholarship Awards** by **Dr. William T. Pockman**, Professor & Chair of UNM Department of Biology.

5:15–8:00 p.m. **Reception for our Keynote Speaker, Research Days Awards Ceremony, and Silent Auction**, foyer and Room 120 of the Science & Math Learning Center (Bldg. 14):

- **Reception**, foyer, **and Silent Auction**, Room 120.
- **Presentation of Research Days Winners** by Research Day Committee.
- 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

Emily Arzate
Catherine St. Clair
Dr. Ben Hanelt
Joanne Kuestner
Dr. Steve Poe
Anne Rice
Kelsey Cook, BGSA
Kellen Paine, BGSA

Judges

Oral Presentations:
Serina Brady
Michelle Facette
Chauncey Gadek
Dave Hanson
Chris Johnston
Diana Northup
Will Pockman
Irene Salinas
Felisa Smith
Steve Stricker
Tina Takacs-Vesbach
Lee Taylor
Jessie Williamson
Blair Wolf

Poster Presentations
Coen Adema
Brian Alfaro
Rachael Alfaro
Lauren Bansbach
Lisa Barrow
Luke Bell-Dereske
Renee Brown
Sarah Buddenborg
Dunbar Carpenter
Anny Chung
Jocelyn Colella
Rae Devan
Tammi Duncan
Bethaney Fehrenkamp
Erika Gendron
Tom Giermakowski
Alesia Hallmark
Kelly Howe
Tom Kennedy
Martina Laidemitt
Jenna McCullough
Seth Newsome
Steve Poe
Aaron Robinson
Steve Ross
Julie Spencer
Catalina Tome
Ernie Valdez
Helen Wearing
Chris Witt

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 Emily Arzate, Catherine St. Clair, the UNM Biology Accounting staff, the Main Office Front Desk student employees, and to the many other staff and students who help throughout the day.

KEYNOTE ADDRESS: ABOUT THE SPEAKER

The invited keynote speaker for our 26th Annual Biology Research Day is **Dr. Jonathan Overpeck** ("Peck"), who will be speaking on "*New Perspectives on Future Climate Change Risk and Ecosystem Change*" at 3:30 p.m in Room 102 (the auditorium) of the Science & Math Learning Center (Bldg. 14).

Dr. Overpeck received his A.B. in Geology from Hamilton College in 1979, and earned his M.Sc. (1981)and Ph.D. (1985) in Geological Sciences from Brown University. He has a strong interest in past, current and future interactions among climate, ice sheets, and sea level, as well as in interactions between climate and ecosystems, and has published more than 200 works in climate and the environmental sciences. He teaches in the areas of environmental science, paleoenvironmental (especially climate) dynamics, and science communication, and he tweets about climate-related issues @TucsonPeck. Peck has active research programs in North America, South America, Australia, Africa, and monsoon Asia, most commonly focusing on providing paleoenvironmental insights into how key aspects of Earth's climate system may change in the future. He collaborates in the area of environmental law, and he works to promote an understanding of science as well as helping scientists understand broader views, particularly those of society's decision makers who must deal with real-world climate variability and change. Thus, Peck has appeared and testified before Congress on multiple occasions.

Dr. Overpeck is the director of the Institute of the Environment (http://www.environment.arizona.edu/jonathan-overpeck), as well the Thomas R. Brown Distinguished Professor of Science and a Regents' Professor of Geosciences, Hydrology and Atmospheric Sciences. Peck is a fellow of the American Association for the Advancement of Sciences, as well as of American Geophysical Union. Before coming to the University of Arizona, Peck was the founding director of the NOAA Paleoclimatology Program and the World Data Center for Paleoclimatology, both in Boulder, Colorado. While in Boulder, he was also a fellow at the Institute of Arctic and Alpine Research at the University of Colorado. He has worked at Columbia University and NASA. Although much of Peck's work focuses on terrestrial systems, he also has participated in research cruises to the Arabian Sea and tropical Atlantic; he was co-chief scientist with Dr. Larry Peterson on the cruise that began the long and rich history of work involving sediments from the Cariaco Basin in the southern Caribbean. He is a co-principal investigator of the Climate Assessment for the Southwest Project (CLIMAS; http://www.climas.arizona.edu/about/people/jonathan-overpeck), one of the several NOAA Regional Integrated Sciences and Assessment (RISA) programs, and is the lead university investigator (University Director) of the Department of the Interior's Southwest Climate Science Center. Peck is also supported by the U.S. Department of Defense to work with their decision makers on issues related to climate variability and change, and is the lead-PI of a large collaborative U.S. National Science Foundation project focused on global drought, how well we simulate drought with Earth System models, and how information about drought can be optimized for use in society.

Dr. Overpeck's CV can be found at http://www.environment.arizona.edu/sites/default/files/overpeck-9PageCVJanuary2017.pdf.

Cover photographs courtesy of EarthSky.org

PAST RESEARCH DAY SPEAKERS

YEAR	SPEAKER	TALK TITLE
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.
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.

YEAR	SPEAKER	TALK TITLE
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.
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.

YEAR	SPEAKER	TALK TITLE
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.

POSTER PRESENTATIONS

Thursday, March 30, 2017

9:30–11:30 a.m., SESSION 1, Odd-numbered

1:30–3:20 p.m., SESSION 2, Even-numbered

The bolded author is the presenter.

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

0 § Development of Mesoporous Silica Supported Lipid Bilayer Nanoparticles for Delivery of Synergistic Activation Mediator Plasmids.

Dominic J. Medina †, Maximizing Access to Research Careers (MARC), Department of Biology, UNM, and Department of Biochemistry and Molecular Biology, School of Medicine, UNM, Ayse J. Muñiz, Department of Chemical and Biological Engineering, The University of Michigan, Ann Arbor MI, Jacob O. Agola, Center for Micro-Engineered Materials (CMEM), UNM, Paul N. Durfee, Department of Chemical and Biological Engineering, UNM, Kimberly S. Butler, CMEM, UNM, and C. Jeffrey Brinker, CMEM, and Department of Chemical and Biological Engineering, UNM, and Self-Assembled Materials Department, Sandia National Laboratories, Albuquerque, NM.

1 The Las Conchas Fire Effects on Dominant Spider Families at Bandelier National Monument.

Wesley Noe †, Museum of Southwestern Biology, UNM, Kay Beeley, Bandelier National Monument, Los Alamos, NM, and Sandra L. Brantley, Museum of Southwestern Biology, UNM.

2 Methods of Microbial Fuel Cell Maximization.

Sergio Herrera †, Initiatives to Maximize Student Development (IMSD), Department of Biology, and Department of Chemical and Biological Engineering, UNM, and Carlo Santoro, Department of Chemical and Biological Engineering, UNM.

3 Comparative Phylogeography of Fijian Birds.

Xena M. Mapel † and Michael J. Andersen, Department of Biology, UNM.

4 Building Critical Infrastructure for Endangered Species Management: An Event-based Model.

Kaylen Jones ‡, Mariel L. Campbell, Jonathan L. Dunnum, Museum of Southwestern Biology, Department of Biology, UNM, Maggie Dwire, Mexican Wolf Recovery Program, U.S. Fish and Wildlife Service, Albuquerque, NM, Dusty MacDonald and Joseph A. Cook, Museum of Southwestern Biology, Department of Biology, UNM.

5 The Diversification of Distinct Lineages of *Neotoma albigula* in Southwestern New Mexico.

Ally Weidner †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, Schuyler Liphardt, Department of Biology, and Joseph A. Cook, Museum of Southwestern Biology, Department of Biology, UNM.

6 Proportions of Alpine Vegetation Types in the Diet of the American Pika.

Kelly Lizewski †, Marie Westover and Felisa A. Smith, Department of Biology, UNM.

§ In the even-numbered (afternoon) session.

7 The Above-ground Fungal Microbiome of a Tropical Tree and Implications for the Canopy Plant Community.

Kelsey Cook‡, Department of Biology, UNM, Jyotsna Sharma, Department of Plant and Soil Science, Texas Tech University, Lubbock TX, Andrew Taylor, Department of Biology, University of Hawaii–Manoa, Honolulu HI, and D. Lee Taylor, Department of Biology, UNM.

8 Plant–Soil Feedbacks in Ring Formation of Blue Grama.

Lance Carlton†, Department of Biology, UNM, and Nora Dunkirk, University of Wisconsin–Madison.

9 Environmental Predictors of Invasive Plant Species Richness in Western United States.

Brian Alfaro, **Elisa Gagliano**†, Jennifer A. Rudgers, Department of Biology, UNM, Kathryn Wilson, U.S. Geological Survey, Scott L. Collins and Diane L. Marshall, Department of Biology, UNM.

10 Biological Communities of Travertine-precipitating Springs on a Gradient of Anthropogenic Disturbance in the Sandia Mountains, New Mexico.

Kathryn Mendoza‡, Department of Water Resources, UNM, Rebecca Bixby, Museum of Southwestern Biology, Department of Biology, UNM, Laura Crossey, Department of Earth and Planetary Sciences, UNM, and Livia Crowley, Cibola National Forest and National Grasslands, Albuquerque, NM.

11 Genetically Distinct Lineages of the Sacramento Mountain Salamander Revealed by Mitochondrial DNA.

Samantha Cordova‡, Megan Osborne and Thomas F. Turner, Department of Biology, UNM.

12 Utilization of a Within-host Model to Determine Optimal Treatment Regimes for *Schistosoma mansoni* Control.

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

13 Comparing Deep Cave Bacteria with Mars Simulation Surviving Bacteria: Implications for Detecting Life on Extraterrestrial Bodies.

Krystal R. Charley, Diana E. Northup, Ara S. Winter, Department of Biology, UNM, and Penelope J. Boston, NASA Astrobiology Institute, NASA Ames Research Center, Moffett Field CA.

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

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

15 Calcium Imaging in the *Danio rerio* Olfactory Organ in Response to Viral Pathogens.

Aurora Kraus‡, Department of Biology, UNM, Michael Paffett, UNM Cancer Center, and Irene Salinas, Department of Biology, UNM.

16 Application of Nasal Vaccines as an Effective Route of Vaccination in Aquaculture.

Ali Sepahi‡ and Irene Salinas, Department of Biology, UNM.

17 Interactions between *Toxoplasma gondii* and Retinoic Acid-Differentiated Neuro-2A Neuroblastoma Cells.

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

18 *Toxoplasma gondii* Infection Triggers a Potent IL-12 Response in the Absence of Toll-like Receptor Adaptor Molecule MyD88.

Heather Mercer ‡ and Eric Y. Denkers, Department of Biology, UNM.

19 *Toxoplasma gondii* Exploits the Host Wnt/β-catenin Pathway to Successfully Establish Intracellular Infection.

Cameron Ranken and Eric Y. Denkers, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM.

20 Demographics and Host Associations of *Plasmodium*, *Haemosporidian* and *Leucocytozoon* Parasites in Birds of Northwestern New Mexico.

Rosario Marroquin-Flores *, FlyBase, Department of Biology, UNM, Christopher C. Witt, Lisa Barrow, Department of Biology, UNM, Andrea N. Chavez, Department of Biology, UNM and Bureau of Land Management Rio Puerco Field Office, Albuquerque, NM, and Jessie Williamson, Department of Biology, UNM.

21 Arsenic and Uranium Induced Oxidative Stress Response in Immune Cells.

Sandra C. Alvarez *, FlyBase, Department of Biology, UNM, Erica J. Dashner-Titus, Deion A. Jackson, Department of Pharmaceutical Sciences, Health Sciences Center, UNM, Jodi Schilz, Department of Physical Therapy, Department of Orthopaedics and Rehabilitation, School of Medicine, UNM, Karen L. Cooper and Laurie G. Hudson, Department of Pharmaceutical Sciences, Health Sciences Center, UNM.

22 Symbiont Derived Sphingolipids: Anti-inflammatory Properties and Application in Adjuvant Model.

Mariah Sanchez †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, Elisa Casadei, Ali Sepahi and Irene Salinas, Department of Biology, UNM.

23 Searching for Natural Defenses (Actinobacteria) Against White-Nose Syndrome, Found on Bats at a Gateway to the West.

Emily Johnson †, Edward Strach, Patrick Lewis, Nicole A. Caimi, Department of Biology, UNM, Ernest W. Valdez, Fort Collins Science Center, U.S. Geological Survey, Albuquerque NM, and Diana E. Northup, Department of Biology, UNM.

24 The EGFR/MEK Signaling Pathway Is a Critical Regulator of HPV Oncogene E7.

Marilyn Cisneros *, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, and Department of Molecular Genetics and Microbiology, School of Medicine, UNM, Anastacia M. Griego, Pamela F. Barraza, Adrian J. Luna, Rosa T. Sterk, Department of Molecular Genetics and Microbiology, School of Medicine, UNM, Julie E. Bauman, Department of Medicine, University of Pittsburgh Cancer Institute, Pittsburgh PA, and Michelle A. Ozbun, Department of Molecular Genetics and Microbiology, School of Medicine, UNM.

25 Immunogenic Cross-talk Causes Viral Competition That Potentially Influences the Incidence of Dengue and Zika Infections.

Noah J.B. Silva ‡, Department of Biology, and Helen J. Wearing, Department of Biology and Department of Mathematics and Statistics, UNM.

26 Impact of Prenatal Alcohol Exposure on Cannabinoid 1 Receptors and Cannabinoid Receptor-effector Coupling in Dentate Gyrus of Adult Rat Offspring.

Kiana Lujan †, Initiatives to Maximize Student Development (IMSD), Departments of Biology, UNM, and Department of Psychology, UNM, Kyle Christensen, Jennifer Wager, Suzy Davies and Daniel Savage, Department of Neurosciences, UNM.

27 Patient Satisfaction: It's Just a Matter of Time.

Ali Salehpoor †, Department of Biology, UNM, Tommy Soudachanh, Benjamin Howse, Department of Biochemistry, UNM, Aaron Segura, Fernando Sinaloa, UNM School of Medicine, Silas Bussmann, Lynne Fullerton and Jon Femling, Department of Emergency Medicine, UNM.

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

Katrina Baca †, Initiatives to Maximize Student Development (IMSD), Department of Biology, and Department of Biochemistry and Molecular Biology, 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 J. Hathaway, Department of Cell Biology and Physiology, Health Sciences Center, UNM.

29 Autophagy Variants in Melanoma Progression.

Sabah Osmani †, Department of Chemistry, UNM, Kirsten A.M. White, Salina M. Torres, Li Luo, Chien-An A. Hu, Jenna Lilyquist, DeAnn Lazovich, Christopher Hughes and Marianne Berwick, Department of Internal Medicine/Molecular Epidemiology, UNM.

30 No Health Insurance, Less Medical Assurance.

Krista Houmpheng, Lucas Winter, Niharika Ravichandran, Cameron Guy, Lynne Fullerton, Silas Bussmann and A. Robb McLean, Department of Emergency Medicine, UNM.

31 How Illicit Drug Users Seeking Treatment Differ in Expectations by Ethnicity.

Nyabang Buom *, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, Pilar Sanjuan and Jeff Scott Tonigan, Center on Alcoholism, Substance Abuse and Addictions, UNM.

32 Tissue Engineered Heart Valve Scaffolds of Oligo (Poly (Ethylene Glycol) Fumerate).

Quan Huynh *, Post-baccalaureate Research and Education Program (PREP), Department of Biology, and Center for Biomedical Engineering, UNM, Kent E. Coombs, Biomedical Sciences Graduate Program, and Center for Biomedical Engineering, UNM, Matthew N. Rush, Center for Biomedical Engineering, and Chemical and Biological Engineering, UNM, Olivia Bell, Chemical and Biological Engineering, UNM, and Elizabeth L. Hedberg-Dirk, Center for Biomedical Engineering, and Chemical and Biological Engineering, UNM.

33 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 Development (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.

34 Effects of Knockout of Cold-Inducible RNA Binding Protein (CIRP) on Breast Tumorigenesis.

Joey L. Ochoa †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, and Department of Biochemistry and Molecular Biology, UNM, Daniel A. Lujan, Melanie N. Peterson, Helen J. Hathaway and Rebecca S. Hartley, Department of Cell Biology and Physiology, Health Sciences Center, UNM, and UNM Cancer Research and Treatment Center.

35 Novel Sensors for Detecting Alzheimer's Disease Related Tau Protein Aggregates.

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

36 Altered Expression of Angiogenesis-associated miR-150-5p and its Target Vezf1 in Mouse Models of Prenatal Alcohol Exposure.

Gabriela Perales *, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, Amy S. Gardiner, Andrea M. Allan and Nora Perrone-Bizzozero, Department of Neurosciences, Health Sciences Center, UNM.

37 Axonal Conductance across Corpus Callosum in a Third-trimester Equivalent Mouse Model of Prenatal Alcohol Exposure.

T. Martinez *, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, J. Newville, C.F. Valenzuela and L.A. Cunningham, Department of Neuroscience, Health Sciences Center, UNM.

38 The Role of Relaxin-H2 in Mediation of Cystic Renal Epithelial Cell Recruitment of Fibroblasts.

Elena Delgado †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, and Heather Ward, Department of Internal Medicine, Health Sciences Center, UNM.

39 Histone Deacetylase Inhibition as a Means of Increasing Sensitivity to Platinum Based Chemotherapeutics.

Alejandra Rosales *, FlyBase, Department of Biology, UNM, Michaela L. Granados and Sabrina Samudio-Ruiz, Department of Pharmaceutical Sciences, College of Pharmacy, UNM.

40 CD82 Regulation of Hematopoietic Stem Cell Adhesion and Migration.

Erica Pascetti †, Chelsea Saito-Reis and Jennifer Gillette, Department of Pathology, Health Sciences Center, UNM.

41 The Role of CD82 Expression and Post-translational Modifications on c-Kit Signaling in Acute Myeloid Leukemia.

Erin E. Lucero †, Department of Biology, UNM, Christina M. Termini and Jennifer M. Gillette, Department of Pathology, Health Sciences Center, UNM.

42 MRTF Constitutively Active and Dominant Negative Line Analysis.

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

43 Contribution of Acid-sensing Ion Channels to Ventilatory Control in Conscious, Unrestrained Mice.

Kenneth G. Vigil †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, Neil D. Detweiler and Nikki L. Jernigan, Vascular Physiology Group, Department of Cell Biology and Physiology, Health Sciences Center, UNM.

44 Classification of Four mi-RNA Genes Involved in Muscle Development in *Drosophila melanogaster*.

Daniel L. Wilson †, Tracy E. Dohn and Richard M. Cripps, Department of Biology, UNM.

45 Protein Dysregulation in the Isolated Extracellular Matrix of Failing Human Hearts with Dilated Cardiomyopathy.

Joshua L. DeAguero *, FlyBase, Department of Biology, UNM, Elizabeth N. McKown and Dawn A. Delfin, Department of Pharmaceutical Sciences, UNM.

46 Myosins: Motor Proteins Influencing Cell Polarization in Maize during Asymmetric Cell Division.

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

47 Single Stranded Transposon Insertion.

Emily Alden *, FlyBase, Department of Biology, and Department of Molecular Genetics and Microbiology, UNM.

48 Toward Programmable Amplification Using DNA Strand Displacement.

David Arredondo*, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, and Department of Biomedical Engineering, UNM, and Matthew Lakin, Department of Chemical and Biological Engineering, and Department of Computer Science, UNM.

49 Characterization of Cardiac and Somatic Muscle Genes in *Drosophila*.

Sam McKitrick†, Tyanna Lovato and Richard M. Cripps, Department of Biology, UNM.

50 Silica Sol-Gel Encapsulation Effects on Cell Division Rates and Chlorophyll Fluorescence and Content in *Chlorella sorokiniana*.

Bianca Serda†, John Roesgen and David T. Hanson, Department of Biology, UNM.

51 Amphiphilic Cyclodextrins for Biocompatible Targeted Gene Delivery.

Valerie Perea†, Initiatives to Maximize Student Development (IMSD), Department of Biology, and Department of Chemistry and Chemical Biology, and UNM Comprehensive Cancer Center, Ping Zhang, Alberta Glycomics Centre, University of Calgary, Alberta, Canada, Kunlun Yin, Department of Chemistry and Chemical Biology, and UNM Comprehensive Cancer Center, Chang-Chun Ling, Alberta Glycomics Centre, University of Calgary, Alberta, Canada, and Lina Cui, Department of Chemistry and Chemical Biology, and UNM Comprehensive Cancer Center.

52 Using Dye Encapsulating Liposomes to Study Protein-Induced Membrane Disruption.

Anthony M. Garcia†, Initiatives to Maximize Student Development (IMSD), Department of Biology, and Department of Chemistry and Chemical Biology, UNM, Adeline M. Fanni, Biomedical Engineering Graduate Program, Center for Biomedical Engineering, UNM, and Eva Y. Chi, Center for Biomedical Engineering, Department of Chemical and Biological Engineering, UNM.

53 Effect of Pangloss and Brick Mutations on Stomatal Function.

Marissa Harjoe†, Maximizing Access to Research Careers (MARC), Department of Biology, UNM, David T. Hanson and Michelle R. Facette, Department of Biology, UNM.

54 Systematic Screening for Transcriptional Regulators of Adult Myogenesis in *Drosophila* by RNAi.

Tommy Soudachanh†, Department of Biochemistry, UNM, Sandy Oas, Department of Biology, UNM, Tyler Mendes, Department of Cellular, Molecular and Developmental Biology, Ohio State University, Columbus OH, Anton Bryantsev, Department of Molecular and Cellular Biology, Kennesaw State University, Kennesaw GA, and Richard M. Cripps, Department of Biology, UNM.

ORAL PRESENTATIONS

Friday, March 31, 2017

9:00 a.m.–Noon, SESSION 1, 55 Castetter Hall

1:00–3:00 p.m., SESSION 2, 51 Castetter Hall

1:00–3:15 p.m., SESSION 3, 55 Castetter Hall

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

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

9:00 a.m.–Noon, SESSION 1, 55 Castetter Hall

Moderators: Christian Denny & Tammi Duncan

9:00 55 Branch Movements in Creosote (*Larrea tridentata*) Are Related to Plant and Environmental Water Stress.

Alesia Hallmark‡, Marcy Litvak, Robert Pangle and Gregory Maurer, Department of Biology, UNM.

9:15 56 Reproductive Success of Bonytail (*Gila elegans*) Reared in Off-channel Habitats Assessed via Parent–Offspring Genotyping.

Megan Osborne, **Alyssa Sanchez**† and Thomas F. Turner, Museum of Southwestern Biology, Department of Biology, UNM.

9:30 57 What Does a Prudent Pika Pick? Spatial and Temporal Dietary Trends of an Alpine Mammal.

Marie L. Westover‡ and Felisa A. Smith, Department of Biology, UNM.

9:45 58 Consequences of Shrub Encroachment on a Bee Community.

Julieta Bettinelli‡ and Diane Marshall, Department of Biology, UNM.

10:00 59 Evaluating the Relationship of Temperature and Growth of Larval Colorado River Suckers (Catostomidae) Through Otolith Aging and Stable Isotopes ($\delta^{18}O$).

Adam L. Barkalow‡, Thomas F. Turner, Department of Biology, UNM, Nicu-Viorel Adutorei, Center for Stable Isotopes, UNM, Seth D. Newsome, Department of Biology, UNM, Mark C. McKinstry, U.S. Bureau of Reclamation, and Steven P. Platania, American Southwest Ichthyological Researchers, Albuquerque NM.

10:15 Break.

10:30 60 Islands as Drivers of Diversity: A Genomic Perspective on Meso-carnivore Diversity and Hybridization

Jocelyn P. Colella‡, Department of Biology, UNM, Tianying Lan, Department of Biological Sciences, SUNY, Buffalo, NY, Sandra L. Talbot, U.S.G.S., Alaska Science Center, Anchorage, AK, Joseph A. Cook, Department of Biology, UNM, and Charlotte Lindqvist, Department of Biological Sciences, SUNY, Buffalo, NY.

10:45 61 Adaptive Phenotypic Variation in Native, Invasive, and Crop Populations of *Brassica tournefortii*.

Brian Alfaro‡ and Diane L. Marshall, Department of Biology, UNM.

11:00 62 Estimating Levels of Introgression between Gila Trout (*Oncorhynchus gilae*) and Rainbow Trout (*O. mykiss*) using Next-generation Sequencing Data.

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

11:15 63 Comparative Population Genetics of Two Congeneric Duck Schistosomes, *Trichobilharzia querquedulae* and *T. physellae*.

Erika T. Ebbs‡, Eric S. Loker, Veronica Flores and Sara V. Brant, Department of Biology, UNM.

11:30 64 Adaptive Polynomial Expansion Method for the Numerical Solution of the Lenard-Balescu Equation.

Justyna Tafoya †, Initiatives to Maximize Student Development (IMSD), Department of Biology, and Department of Mathematics, UNM, Abby Hickok, Princeton University, Princeton NJ, Loek Van Heyningen, University of California–Berkeley, Bilyana Tzolova, Johns Hopkins University, Baltimore MD, Omer Tekin, University of California–Los Angeles, Chris Scullard and Frank Graziani, Lawrence Livermore National Labs, Livermore CA.

11:45 65 Combining δ13C, δ15N, and δ2H to Better Understand the Ecology of Eastern Pacific Green Sea Turtles (*Chelonia mydas*).

Laura Pagès Barceló ‡, Department of Biology, UNM, Jeffrey A. Seminoff, Southwest Fisheries Science Center, NOAA, National Marine Fisheries Service, La Jolla CA, Calandra Turner-Tomaszewicz, Southwest Fisheries Science Center, NOAA, National Marine Fisheries Service, La Jolla CA, and Division of Biological Sciences, Ecology, Behavior and Evolution Section, University of California, San Diego, La Jolla CA, David Aurioles, Centro Interdisciplinario de Ciencias Marinas, Instituto Politécnico Nacional, La Paz Baja California Sur, Mexico, and Seth D. Newsome, Department of Biology, UNM.

1:00–3:00 p.m., SESSION 2, 51 Castetter Hall

Moderators: Janette Mendoza & Cathy Cumberland

1:00 66 Sex-stratified DNA Repair SNPs in Melanoma Risk and Survival.

Christopher Hughes †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, Jenna Lilyquist, Mayo Clinic, Rochester, MN, Kirsten White, Department of Epidemiology, UNM, Salina Torres, Center for HPV Prevention, Health Sciences Center, UNM, Li Luo, Department of Epidemiology, UNM, Eszter Erdei, Pharmaceutical Sciences, Health Sciences Center, UNM, DeAnn Lazovich, University of Minnesota, Minneapolis, MN, and Marianne Berwick, Department of Epidemiology, UNM.

1:15 67 Investigating Protein Function in Living Cells by Proximity-based Protein Labeling.

Larisa Breden †, Initiatives to Maximize Student Development (IMSD), Department of Biology, and Department of Biochemistry, UNM, Yabin Song, Guihua Zeng and Fu-Sen Liang, Department of Chemistry and Chemical Biology, UNM.

1:30 68 Effect of Terrestrialization of the Proteome of the Skin Mucus of African Lungfish (*Protopterus dolloi*).

Ryan D. Heimroth ‡ and Irene Salinas, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM.

1:45 69 Detail Not Easily Visible with X-ray Computed Tomography Revealed in Neutron Computed Tomography of Cretaceous Tyrannosauroid Dinosaur *Bistahieversor sealeyi* and Paleocene Phenacodontid Mammal *Tetraclaenodon puercensis* Skulls.

Katlin Schroeder ‡, Department of Biology, UNM, Thomas E. Williamson, N.M. Museum of Natural History & Science, Albuquerque NM, Stephen L. Brusatte, University of Edinburgh, Scotland, Michelle A. Espy, Cort Gautier, James Hunter, Adrian S. Losko, Ronald Nelson and Sven Vogel, Los Alamos National Laboratories, Los Alamos NM.

2:00 Break.

2:15 70 Activation of the Signaling Intermediates β-catenin, STAT3, STAT5, and SOCS2 by the Intracellular Protozoan Parasite *Toxoplasma gondii*.

Hoang Bui †, Initiatives to Maximize Student Development (IMSD), Department of Biology, UNM, and Eric Y. Denkers, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM.

2:30 71 Forensic Magnetic Resonance Imaging: Can We Predict Time of Death Based on Diffusion?

Jordan Weisend †, Maximizing Access to Research Careers (MARC), Department of Biology, UNM, and Department of Biochemistry, UNM.

2:45 72 Gene–Environment Interaction between a BDNF Polymorphism and Developmental Ethanol Exposure.

C.W. Bird, B.C. Baculis, J.J. Mayfield, G.J. Chavez, Department of Neuroscience, Health Sciences Center, UNM, **T. Ontiveros** *, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, and Department of Neuroscience, Health Sciences Center, UNM, D.J. Paine, A.J. Marks, A.L. Gonzales, D. Ron and C.F. Valenzuela, Department of Neuroscience, Health Sciences Center, UNM.

1:00–3:15 p.m., SESSION 3, 55 Castetter Hall

Moderators: Tom Kennedy & Julie Spencer

1:00 73 Small Mammal Community Dynamics in Two Stable States: A Twenty Year Record.

Jennifer Noble ‡, Sydney Jones, and Scott L. Collins, Department of Biology, UNM.

1:15 74 A Comparative Study of Island and Mainland *Anolis* Lizard Assemblages.

Chris Anderson ‡ and Steven Poe, Department of Biology, UNM.

1:30 75 Submerged Aquatic Macrophytes (SAMs) in the Sky: At Home in High Elevation Streams.

Virginia F. Thompson ‡ and Clifford N. Dahm, Department of Biology, UNM.

1:45 76 Microbial Community Diversity and Composition across a Latitudinal Gradient along the Antarctic Peninsula.

Kelli Hughes ‡, David Van Horn, Department of Biology, UNM, Uffe Neilsen, Hawkesbury Institute for the Environment, University of Western Sydney, Sydney, Australia, and Rebecca Ball, School of Mathematical and Natural Sciences, Arizona State University, Phoenix AZ.

2:00 Break.

2:15 77 Race against Time: Documenting Hairworm (Nematomorpha: Gordiida) Species Diversity of the Madrean Sky Islands.

R.J. Swanteson-Franz †, B. Hanelt, Center for Evolutionary and Theoretical Immunology (CETI), Department of Biology, UNM, A. Schmidt-Rhaesa, Biocenter Grindel, Zoological Museum and Institute, University of Hamburg, Hamburg, Germany, and M.G. Bolek, Department of Zoology, Oklahoma State University, Stillwater, OK.

2:30 78 Study of Stomatal Response in Corn Plants.

Michelle R. Facette, David T. Hanson, and **Oscar Huamani Jimenez** †, Department of Biology, UNM.

2:45 79 Inactivation of the Anterior Thalamus Disrupts Directional Discrimination in an Object-place Paired Associate Memory Task.

Shannon M. Thompson *, Postbaccalaureate Research and Education Program (PREP), Department of Biology, UNM, Shawn S. Winter, Center for Cognitive Neuroscience, Depart-

ment of Psychological and Brain Sciences, Dartmouth College, Hanover NH, and Benjamin J. Clark, Department of Psychology, UNM.

3:00 80 Understanding Carbon Flow in a Complex Intertidal Ecosystem Using Amino Acid $\delta^{13}C$ Analysis.

Emma A. Elliott Smith‡, Department of Biology, UNM, Chris Harrod, Instituto de Ciencias Naturales, Universidad of Antofagasta, Chile, and Seth D. Newsome, Department of Biology, UNM.

ABSTRACTS: POSTER PRESENTATIONS

The bolded author is the presenter.

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

0 § Development of Mesoporous Silica Supported Lipid Bilayer Nanoparticles for Delivery of Synergistic Activation Mediator Plasmids.

Dominic J. Medina†, Ayse J. Muñiz, Jacob O. Agola, Paul N. Durfee, Kimberly S. Butler and C. Jeffrey Brinker.

Recent developments in gene editing and modulation through the CRISPR/Cas9 system are enabling rapid advancements in gene therapy technologies; however, delivery of nucleic acid cargoes to specific cell types remains a significant challenge. While viral delivery vectors are commonly used to overcome physiological barriers, their non-viral counterparts, including liposomes, inorganic nanoparticles, polymeric nanoparticles, peptides, dendrimers, and other constructs, offer attractive properties such as reduced risk of immunogenicity, increased biocompatibility, and reduced toxicity. Mesoporous silica nanoparticles (MSNPs) have emerged as a multi-functional non-viral platform for drug and nucleic acid delivery due to their unique structure enabling for loading multiple types of cargo, easy surface modification, and low toxicity. Presence of a supported lipid bilayer on MSNPs significantly enhances their functionality by facilitating cell uptake, increasing loading capacity, and enhancing nanoparticle stability. While small molecule delivery has been achieved, the delivery of large biomolecules has met with little success. Recently, Synergistic Activation Mediator (SAM) plasmids have been developed for short-term modulation of gene expression. Three large plasmids encode for a dCas9 enzyme, a sgRNA that recruits the enzyme upstream of a target gene, and transcriptional activator recruiter proteins assemble and force expression of the target gene. Herein we have applied mesoporous silica-supported lipid bilayer nanoparticles, termed "protocells," as a novel delivery method for these large nucleic acid constructs that involves a porous silica core encapsulated within a lipid bilayer that becomes internalized by a host of prostate cancer cell lines. Upon successful transfection, the chosen SAM plasmids should temporarily force expression of *TP53*, a gene that is heavily involved in cell regulation through p53 protein production.

1 The Las Conchas Fire Effects on Dominant Spider Families at Bandelier National Monument.

Wesley Noe†**,** Kay Beeley and Sandra L. Brantley.

§ In the even-numbered (afternoon) session.

Severe wildfires are becoming more common in the southwestern U.S., affecting plant and animal numbers and species composition, including many arthropod groups. In 2011, a catastrophic wildfire burned through a large part of Bandelier National Monument and the Jemez Mountains, in northern NM. Thirty pitfall traps were already in place in each of three habitats (piñon–juniper (PJ), ponderosa pine (PP), and mixed-conifer (MC)). PP and MC sustained moderate to severe fire damage, while PJ did not burn, but was included for comparison. With data from three years before (2008–2010), the fire year, and after the fire (2012–2014), we asked the following questions about the two dominant spider families: wolf spiders (Lycosidae) and ground spiders (Gnaphosidae). (1) Did the two families respond differently to the fire in terms of abundance and species composition? (2) Is post-fire abundance approaching pre-fire numbers? Based on mean relative abundance per trap per year, we used multidimensional scaling to visualize similarity between families and among habitats and years; and PERMANOVA to test for statistical significance of the effects of family, habitat, or years. Family and habitat were significant, but not years. Environmental temperature and precipitation are likely to affect yearly abundances, making it difficult to detect the effect of the fire itself, which is also influenced by these two factors. The two spider families showed that they are not interchangeable; each family responds to habitat type and conditions independently. Our results also showed the importance of long-term monitoring, especially for species with large year-to-year variation in abundance.

2 Methods of Microbial Fuel Cell Maximization.

Sergio Herrera † and Carlo Santoro.

The investigation of this work is focused on the study and characterization of PGM-free catalyst for ORR based on bimetallic catalysts. The addition of the second metal generally increased the performance of Co-based catalysts, while for Fe-based catalysts, only Fe-Mn had a positive effect on the performances. The catalysts were then integrated in air breathing cathodes and then tested in a membrane-less single chamber microbial fuel cell (SCMFC). Experimentation of bimetallic catalysts were conducted to determine superior power output. Bimetallic combinations proved to be a feasible means to supply greater output when compared to single metallic catalysts in the case of Co-based materials. Considering Fe-based materials, only Fe-Mn catalyst overcome Fe-based catalyst. For example, Co-Mn had a power output of 188 $\mu W\ cm^{-2}$ and Co- as a singular catalysts, produced a power output of approximately 162 $\mu W\ cm^{-2}$. In parallel, Fe as a singular catalyst had a power output peaking at approximately 192 $\mu W\ cm^{-2}$ and Fe-Mn had a power peak of 221 $\mu W\ cm^{-2}$. A general trend is observed that Co power output is increased significantly in the presence of another metal, beginning with Co as a singular catalyst, then with Ni, and finally with Mn, the power output steadily increases from 148 $\mu W\ cm^{-2}$ in intervals approximately equal to 20 $\mu W\ cm^{-2}$. In light of this, Fe still stands as the most secure means to maximize power output, particularly in combination with other metals, furthermore, it is an economically sound and accessible catalyst to utilize.

3 Comparative Phylogeography of Fijian Birds.

Xena M. Mapel † and Michael J. Andersen.

A fundamental goal of biology is to understand how species colonize and evolve on islands. The guiding principal from the theory of island biogeography suggests that species colonize islands from a mainland source population; thus, islands often are considered evolutionary 'dead-ends.' However, this long-standing idea of one-way colonization from mainland to island does not address how island populations evolve once they arrive. We studied the phylogeographic history of Fijian birds to assess patterns of insular diversification in a remote, oceanic archipelago. We used mitochondrial DNA from four species that co-occur on Fiji's major islands to test whether these species share coincident evolutionary histories within the archipelago. Here, we present time-calibrated phylogenies, generated in the program BEAST, of *Foulehaio carunculatus*, *Myiagra azureocapilla*, *M. vanikorensis*, and *Cettia ruficapilla* and show that each species has different topologies. These idiosyncratic patterns suggest unique evolutionary histories of colonization and diversification in Fiji's landbirds. For example, *Myiagra vanikorensis* shows no genetic differentiation, whereas the remaining three species show marked genetic differentiation, but with dif-

ferent branching patterns among island populations. These results support a complex phylogeographic history of Fiji's birds, which warrants further study to tease apart species-specific mechanisms of differentiation. I will do just this for my senior honors thesis next year. Namely, I will leverage the latest sequencing technology to produce thousands of loci from ultraconserved elements across the genomes of these species. This approach promises a more comprehensive genomic survey that will allow us to explore patterns of gene flow and dispersal across Fiji's birds.

4 Building Critical Infrastructure for Endangered Species Management: An Event-based Model.

Kaylen Jones[‡], Mariel L. Campbell, Jonathan L. Dunnum, Maggie Dwire, Dusty MacDonald and Joseph A. Cook.

The Museum of Southwestern Biology (MSB) has maintained a multi-decadal collaboration and repository agreement with the USFWS Endangered Species Recovery Program to accession, process, curate, and archive Mexican Grey Wolf (*Canis lupus baileyi*) specimens. MSB's database (Arctosdb.org) provides an online archive for linking associated data through multiple identifiers (e.g., catalog, studbook, and GenBank numbers) associated with complex systems including live sampling and archiving of museum specimens. Due to the endangered status of the Mexican Grey Wolf, multiple and diverse samples (e.g., serial blood samples, tissue, skin and skeletal material) are associated with each specimen and linked to derivative data (e.g., gene sequences, isotopes, publications) that must be discoverable. In the past, each blood sample collected from live wolves and subsequent traditional specimens from deceased wolves were cataloged separately in Arctos. Samples collected from the same wolf, but at different times and by different facilities were difficult to track. Over the last five years, we have worked with Arctos developers to create an event-based model for specimen data whereby all information from a single wolf, including time series samples, can be tracked under a single unified record. As new specimens from wild and captive populations enter the repository, their information is now databased using these new protocols established by MSB and USFWS personnel. This project streamlines specimen curation, discoverability, and accessibility and represents a model for how museums and federal agencies can collaborate to build powerful data management and archival infrastructure for critical wildlife management and endangered species recovery efforts.

5 The Diversification of Distinct Lineages of *Neotoma albigula* in Southwestern New Mexico.

Ally Weidner[†], Schuyler Liphardt and Joseph A. Cook.

Neotoma albigula, the white-throated woodrat, is widely distributed across the Southwest and exhibits relatively high levels of infraspecific genetic divergence between geographically defined subspecies. High genetic divergence led to the recognition of the newly described and closely related species, *N. leucodon* (Edwards et al., 2001) and *N. melanura* (Bradley et al., 2016). Previous work by Jones et al. (in prep.) based on mtDNA identified two distinct clades of white-throated woodrat in southwestern New Mexico. The aim of our study is to resolve fine-scale phylogeographic relationships within *N. albigula* in southwestern New Mexico and explore the dynamics of potential contact zones between distinct genetic lineages. The mitochondrial gene, cytochrome b (cytb), was sequenced for 68 specimens from the Museum of Southwestern Biology for this study, with an additional 88 cytb sequences acquired from GenBank to provide greater geographic breadth. A Bayesian phylogenetic tree was constructed for cytb to provide a basis for subsampling individuals representing distinct genetic clades. These hypothetical species clades were tested using three nuclear loci, BFIB, ADH, and MYH6, and that work is currently underway. Our mitochondrial tree suggests deep divergence, roughly 7% sequence divergence, of two populations of *N. albigula* that are sympatric in Southwestern New Mexico. The combination of mitochondrial and nuclear genes provides the means to test previous taxonomic hypotheses and explore the evolutionary history, population level relationships, and dynamics of introgression within distinctive lineages of *Neotoma albigula* of southwestern New Mexico.

6 Proportions of Alpine Vegetation Types in the Diet of the American Pika.

Kelly Lizewski†, Marie Westover and Felisa A. Smith.

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 that eats a variety of vegetation, including flowers. The diet of pikas may be impacted by climate change due to changing alpine vegetation communities. A key to understanding this relationship is identifying changes in diet through stable isotopes, an accepted method to analyze dietary composition. However, the isotopic signatures of alpine plants, particularly differences in flowers and leaves, are largely unknown. We hypothesize that different vegetation functional groups in alpine areas vary in the proportions that they contribute to pika diets. We predict that forbs, gramminoids, woody vegetation and flowering portions of plants will carry different isotopic signatures. We analyzed carbon and nitrogen stable isotopes from forbs, gramminoids and woody plants collected from alpine regions of northern New Mexico. We analyzed flowers and leaves from the same individuals of gramminoids and forbs to determine if flowering portions of plants have different isotope values. Preliminary results suggest that different plant groups and plant structures vary in carbon and nitrogen isotopic values. We will use data from this project to calculate the proportions of plant types in pika diets over space and time. Our research is instrumental in estimating the dietary niche of the pika and other alpine animals.

7 The Above-ground Fungal Microbiome of a Tropical Tree and Implications for the Canopy Plant Community.

Kelsey Cook‡, Jyotsna Sharma, Andrew Taylor and D. Lee Taylor.

Few molecular surveys have been conducted on the diverse fungal communities found in the tree canopies of tropical forests. To our knowledge, none have examined the spatial structure of these communities. In this study, we use a hierarchical spatial sampling design together with high-throughput Illumina amplicon sequencing to address these gaps in tropical ecology and to better understand the small-scale distributions of tropical fungi. Samples were collected from 135 points, located between one centimeter and seven meters apart, from five branches of *Saurauia montana* in Tapanti National Park, Costa Rica. Samples were subdivided based on substrate type, including wood, bark, moss, and litter. ITS sequence analyses revealed high alpha and beta diversity of fungal communities at a small spatial scale. Fungal communities were distinct at points as little as a half meter apart. Fungi were also different across substrates, with each substrate type hosing a distinct community. The spatial heterogeneity and substrate specificity of these fungi suggest that they may play a role in structuring canopy plant communities. In ongoing research, we examine how fungal distributions affect distributions of epiphytic plants, with a focus on orchids.

8 Plant–Soil Feedbacks in Ring Formation of Blue Grama.

Lance Carlton† and Nora Dunkirk.

Plants are known to cultivate root-inhabiting microorganisms that often alter plant host performance. This process is known as plant–soil community feedback (PSF). Negative PSFs, which result when a plant performs worse in association with its own soil community than with the soil communities from other plant species, have been hypothesized to explain why some plants, such as the grass blue grama (*Bouteloua gracilis*), form patches in the shape of rings. Host-specific pathogens could build up in the center of the plant, causing plant dieback and the formation of a ring as the plant grows outward toward pathogen-free soil. The mechanisms for grass-ring formation have been minimally studied in the field, and none, to our knowledge, have directly tested for a role of PSFs in ring formation. This study tested the effect of negative PSFs on ring formation by comparing the plant response of blue grama seedlings when grown in soils taken from either inside or outside grass rings in the field to sterile controls. We found higher rates of germination, survival, and growth for seedlings grown on live soil from inside the ring than from live soil outside the ring. Microscopy was used on roots obtained from the experimental

plants to determine if levels of root colonization by fungi differed between the different soil locations. The levels of colonization were not significantly different, which suggests that there is still more to look at in order to understand ring formation in blue gramma.

9 Environmental Predictors of Invasive Plant Species Richness in Western United States.

Brian Alfaro, **Elisa Gagliano**†, Jennifer A. Rudgers, Kathryn Wilson, Scott L. Collins and Diane L. Marshall.

The distribution of organisms is affected by many limiting biotic and abiotic factors. Introduced species that become invasive can become opportunistic and especially competitive for these resources. Therefore, understanding how species richness interact to environmental factors can be important in understanding invasion patterns. In our study, we analyzed data collected on invasive species richness (in both annuals and perennials), nutrient deposition, human disturbance, and environmental factors, in the Southwestern United States and surrounding regions. In our preliminary analyses, we found through model selection that human disturbance is a strong predictor for invasive species richness. We reassessed our dataset to account for sampling bias and spatial autocorrelation by implementing rarefaction and spatially corrected regression, respectively.

10 Biological Communities of Travertine-precipitating Springs on a Gradient of Anthropogenic Disturbance in the Sandia Mountains, New Mexico.

Kathryn Mendoza‡, Rebecca Bixby, Laura Crossey and Livia Crowley.

Carbonate-rich waters of travertine-precipitating springs facilitate unique physiochemical environments that support distinct diatom species assemblages adapted to the environmental stress of constant carbonate precipitation. Spring systems are further limited by the impacts of historical and ongoing anthropogenic disturbance which includes recreational activity and hydrologic modification of springs using spring boxes and wells. This study focused on impacts of water chemistry and anthropogenic disturbance on diatom assemblages found in travertine-precipitating springs. Data were collected in the fall and spring at eight spring sites, including six known to precipitate travertine, in the Sandia Mountains of central New Mexico. Water chemistry, benthic diatoms and macroinvertebrate abundances, sediment composition, percent organic matter, and categorical disturbance variables were analyzed. Hydrochemical analysis showed seven springs are dominated by Ca-HCO_3 and one was mixed Ca-Mg-Cl type. Common diatom taxa include indicators of high conductivity (e.g., *Diploneis parma*, *Pinnularia* spp.), flowing water (e.g., *Meridion circulare*), and sediment substrates (e.g., *Surirella* spp., *Planothidium* spp.). Diatom assemblage analysis, disturbance characterization, and other biological assessments can be used to prioritize restoration of springs with unique habitats, such as travertine-precipitating springs.

11 Genetically Distinct Lineages of the Sacramento Mountain Salamander Revealed by Mitochondrial DNA.

Samantha Cordova‡, Megan Osborne and Thomas F. Turner.

Southwestern United States plethodontids including *Aneides hardii* (Sacramento Mountain salamander) are restricted to high-elevation mixed conifer habitat that is often fragmented by roads and low-elevation Piñon–Juniper woodland. Short-term seasonal oscillations of temperatures and moisture affect abundance and distribution, and *A. hardii* persistence is at long-term risk due to disease and climate change. Previous studies based on allozymes suggested that Sacramento, White, and Capitan Mountains populations of *A. hardii* were genetically distinct. Sampling, however, was limited to single sites representing each mountain range, and allozyme loci are typically not variable enough to allow inferences about the scale of movement within and between populations. In this study, we used mitochondrial DNA to identify the scale of population subdivision by sampling across the range of *A. hardii*. Twenty-seven haplotypes and three distinct lineages were identified using cytochrome b. About 89% of the total genetic variance was explained by differences between populations. Some *A. hardii* populations exhibited low genetic diversity, particularly the west Capitan Mountain population. Isolated and small populations with low genetic diversity are vulnerable to localized extirpation and should be managed appropriately.

Mitochondrial data indicate that there is higher genetic diversity and less population structure in the more contiguous areas of habitat. Divergence between the populations on the Sacramento, White, and Capitan Mountains are consistent with Pleistocene climatic changes that have isolated salamanders to 'sky island' habitats.

12 Utilization of a Within-host Model to Determine Optimal Treatment Regimes for *Schistosoma mansoni* Control.

Larissa Anderson[‡] and Helen Wearing.

Schistosomiasis is a neglected parasitic disease caused by various trematode species of the genus *Schistosoma* for which 218 million people needed treatment in 2015. Many mathematical models of *Schistosoma mansoni* transmission incorporate the effect of chemoprophylaxis on parasite burden within the human host. While praziquantel is the most commonly implemented pharmaceutical used to control of schistosomiasis, due to its applicability over several species and its negligible side effects, it is not very effective against juvenile schistosomes in humans. This limited efficacy on the juvenile life-stage of the parasite may be an important factor in the persistence of the disease. The demographic consequences of praziquantel use on schistosome population age and sex composition within the human host may obfuscate the effectiveness of these chemoprophylactic control strategies. Furthermore, the effectiveness of this treatment is heavily dependent on the force of infection to humans, the initial schistosome population size and structure, and the frequency at which these pharmaceuticals are administered. Using a stochastic ordinary differential equation based model, we investigated the effects of inconsistent drug efficacy among parasite life-stages, varying parasite population structure within the human host, and treatment regimes alternative to the prevalent once yearly treatment strategy. This allowed us to identify the reduction in infection prevalence under differing infection risk scenarios, parasite population structure at the time of treatment, and treatment schedules and consequently to determine optimal treatment strategies under each scenario.

13 Comparing Deep Cave Bacteria with Mars Simulation Surviving Bacteria: Implications for Detecting Life on Extraterrestrial Bodies.

Krystal R. Charley, Diana E. Northup, Ara S. Winter and Penelope J. Boston.

Caves on Mars are a likely place to host extant or fossil microbial life owing to the sheltered environment from harsh surface conditions. Previous studies have not compared cultures that have survived under simulated Martian conditions to cultures from Mars analog sites. Lechuguilla Cave, in southeastern New Mexico, is a good analog for Mars because the microorganisms exist in an aphotic, oligotrophic environment with only limited liquid water. I hypothesize that cultured bacteria from Mars simulation experiments, collected from various caves, will be similar to those found in Lechuguilla Cave and may share metabolic strategies. I obtained 30 putatively pure subcultures each from Lechuguilla Cave and the Mars Survivors; mixed cultures that could not be purified were cloned and sequenced. I identified the bacterial consortia using full-length 16S rRNA gene sequences, which provide taxonomic information and hints to metabolic strategies employed. Sequenced isolates from Lechuguilla cultures show species closely related to *Stenotrophomonas* spp., *Bacillus* spp., *Ochrobactrum* spp., *Cupriavidus* sp., *Microbacterium* sp., *Pseudoxanthomonas* sp., *Sphingopyxis* sp., and *Brevundimonas* spp. Sequenced results of the Mars Survivors revealed the presence of *Sphingomonas* sp., *Achromobacter* spp., *Alcaligenes* spp., *Micromonospora* sp., *Lysobacter* sp., *Gloeocapsopsis* sp., *Neorhizobium* sp., *Mesorhizobium* sp., *Luteimonas* sp., *Pusillimonas* sp., *Devosia* sp., and *Bacillus* spp. Putative metabolic strategies of Mars simulation survivor cultures will be compared to Lechuguilla Cave cultures. This culture-based and phylogenetic approach will assess whether a deep cave, like Lechuguilla Cave, is a good analog for Martian caves and improve our chances of detecting life on other planets.

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

Alissa Cabada-Gomez[†], Ryan Heimroth, Susana Magadan and Irene Salinas.

T-cells have a central role in the adaptive immunity of all jawed vertebrates. T lymphocytes express a membrane bound T cell receptor (TCR) that recognizes antigens presented to T cells in the context of MHC molecules. There are two conventional subsets of T cells in gnathastomes based on the type of TCR expressed on their surface: αβ T cells and γδ T cells. In mammals, γδ T cells display unique features such as the limited variability of their TCR repertoire, predominantly innate-like function and their abundance at mucosal sites. However, when the dichotomy between mucosal and systemic γδ T cells first appeared in evolution is unknown. African lungfish (*Protopterus* sp.) are the closest living relative to all tetrapods. In response to unfavorable environmental conditions, lungfish can adapt to terrestrial life in a process known as aestivation. 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. Targeting the 5′ ends of TCR sequences using Rapid Amplification of cDNA ends (5′RACE), we cloned γ and δ V domain sequences and 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. Ongoing analysis of aestivated animals will reveal if adaptation to land results in changes in skin γδ T cells. Our results suggest that the dichotomy and specialization of dermal γδ T cells predates the origin of tetrapods.

15 Calcium Imaging in the *Danio rerio* Olfactory Organ in Response to Viral Pathogens.

Aurora Kraus ‡, Michael Paffett and Irene Salinas.

Olfactory sensory neurons (OSNs) of bony fish directly contact both the pathogen-rich aqueous environment and the olfactory bulb in the central nervous system (CNS). Therefore, olfactory epithelium requires a rapid defense mechanism to combat potential infections and protect the brain from pathogen invasion. We hypothesize that crypt olfactory neurons' TRPV4 calcium channels are activated by viral pathogens in a dose-dependent manner, causing a subsequent influx of calcium, which elicits both action potentials and transcription of immunity genes in OSNs. Previous research in our laboratory has shown that intranasal delivery in trout with the attenuated infectious hematopoietic necrosis virus (IHNV) leads to significant upregulation of nasal immune genes as rapidly as 15 minutes post-delivery. The goal of this study is to measure calcium responses of the teleost model zebrafish (*Danio rerio*) olfactory organ to live viruses and to determine whether TRPV4 is involved in those responses. Explants containing intact olfactory rosettes, olfactory nerve, and brain were bolus injected with Rhod-2AM. Intracellular calcium responses are live imaged under a resonant scanner confocal microscope while continuously perfusing with aCSF at 5% CO_2/95% O_2 with a flow rate of 1 ml/min. Treatments include appropriate positive and negative controls and serial dilutions of live IHNV with or without pharmacological blockage of TRPV4. Images were taken in five 2μm-thick stacks every 0.5s for ~150ms. Analysis of action potentials will be assessed based on their quantity, location in the olfactory epithelium, and fluorescent intensity. The results will help elucidate a novel mechanism of immune activation.

16 Application of Nasal Vaccines as an Effective Route of Vaccination in Aquaculture.

Ali Sepahi ‡ and Irene Salinas.

The presence of a nasal immune system in finfish represents a great opportunity for vaccine delivery. Vaccination is used to prevent fish-disease outbreaks worldwide. Injection, immersion and oral vaccination are the most common routes of vaccination in the fish industry; however, nasal vaccination may offer advantages over injected, immersion and oral vaccines. The goal of this study was to evaluate vaccine efficacy and safety of nasal vaccines in trout (*Oncorhynchus mykiss*). Our results showed that nasal vaccination against some of the most common diseases in rainbow trout, such as infectious hematopoietic necrosis virus (IHNV) and enteric red mouth (ERM), can give up to 100% protection 7 days and 28 days post vaccination. We also observed that a dual-delivery method of nasal vaccines (IHNV and ERM) resulted in high protection (between 80 to 100%) when each vaccine is delivered into separate nares. Next, in a separate experiment, we tested how early the nasal vaccines can be delivered into young rainbow trout. Intranasal administration of IHNV and ERM vaccine in 24, 30 and 70 days post-hatch rainbow trout resulted in high protection in all age groups 28 days post vaccination. Finally, we showed that nasal vaccination is safe in trout and does not cause inflammatory responses in the brain, but leads

to strong immune responses in systemic immune tissues. In conclusion, the application of nasal vaccines against viral and bacterial pathogens is effective, safe, elicits systemic immunity and can be applied to very young fingerlings.

17 Interactions between *Toxoplasma gondii* and Retinoic Acid-Differentiated Neuro-2A Neuroblastoma Cells.

Alicia Romero[†] and Eric Y. Denkers.

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, parasites differentiate into the slow-growing bradyzoite stage and they initiate encystation in tissues of the central nervous system. Recent evidence indicates that neurons are preferentially targeted 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 both are susceptible to infection, as demonstrated by parasite-specific immunofluorescence microscopy. Furthermore, we found that Toxoplasma preferentially targets dendrite regions of differentiated N2A cells. Future studies will focus on tachyzoite-to-bradyzoite conversion and the role of host signaling in these cells. The importance of this work is that encysted parasites in the brain are currently resistant to elimination, and understanding the interactions between *Toxoplasma* and host neuronal cells may provide new clinical strategies to eliminate the parasite.

18 *Toxoplasma gondii* Infection Triggers a Potent IL-12 Response in the Absence of Toll-like Receptor Adaptor Molecule MyD88.

Heather Mercer[‡] and Eric Y. Denkers.

Toxoplasma gondii is an opportunistic pathogen whose control is critically dependent upon the Th1-inducing cytokine IL-12. A major innate immune recognition pathway in mice involves sensing of *Toxoplasma* by Toll-like receptors (TLR) 11 and 12, which then signal through adaptor molecule MyD88 to instruct dendritic cell IL-12 production. Yet, in humans both TLR11 and TLR12 are nonfunctional and populations genetically deficient in MyD88 show no evidence of increased susceptibility to many microbial infections, including *T. gondii*. We hypothesize there is an alternate IL-12 pathway that proceeds independently of MyD88. To address this hypothesis, we measured parasite-triggered IL-12 production in wild-type (WT) and MyD88 knockout (KO) mice. Accordingly, we collected splenocytes from WT and KO mice, incubated with *Toxoplasma* tachyzoites, then measured IL-12 release. While there was robust *Toxoplasma*-induced IL-12 production in WT splenocytes, this response was completely dependent upon functional MyD88. Subsequently, we infected WT and KO mice by intraperitoneal inoculation with high (RH strain) and low (PTG strain) virulence *Toxoplasma*, collected peritoneal exudate cells (PEC) four days later, then measured *ex vivo* IL-12 production. In this case, WT and KO PEC from RH infected mice produced equivalent amounts of IL-12. For the case of PTG, WT PEC produced lower amounts of IL-12, which was partially dependent upon MyD88. Our results identify a MyD88-independent route of IL-12 production triggered by *Toxoplasma*, and they further reveal a role for parasite strain in activation of this pathway.

19 *Toxoplasma gondii* Exploits the Host Wnt/β-catenin Pathway to Successfully Establish Intracellular Infection.

Cameron Ranken and Eric Y. Denkers.

The microbial pathogen *Toxoplasma gondii* is an intracellular protozoan that actively invades host cells and simultaneously creates a specialized parasitophorous vacuole within which the parasite lives and replicates. The parasite molecular machinery that drives establishment of the intracellular niche is relatively

well known. However, it is now emerging that *Toxoplasma* exploits less well-understood host cell components to enable successful infection. Here, we examined the role of host Wnt/β-catenin during *T. gondii* infection. Using human fibroblasts and a mouse dendritic cell line, we found that infection with Toxoplasma stimulated both upregulation and nuclear localization of β-catenin. Using a transwell experimental approach, we obtained data indicating that direct contact between parasites and cells is required for increased β-catenin expression. To examine the functional consequences of augmented β-catenin levels, we determined the effect of a panel of Wnt/β-catenin inhibitors on the ability of *T. gondii* to successfully establish infection. Using both dendritic cells and fibroblasts, we found up to 90% inhibition of infection in the presence of the small molecule inhibitors. Current efforts are directed towards determining whether host β-catenin is required for the invasion event itself, or whether its role is in maintenance of the parasitophorous vacuole in newly invaded cells.

20 Demographics and Host Associations of *Plasmodium*, *Haemosporidian* and *Leucocytozoon* Parasites in Birds of Northwestern New Mexico.

Rosario Marroquin-Flores *, Christopher C. Witt, Lisa Barrow, Andrea N. Chavez and Jessie Williamson.

Lineages of the genera *Plasmodium*, *Haemosporidan* and *Leucocytozoon* are widespread malarial parasites found in many bird communities, but vary in host-specificity, pathogenicity, and transmission by vector species. Infection by these parasites can affect host immune function, survivorship, distribution, and hatchling/fledgling success in infected birds. Climate change is re-establishing the ranges of some birds and arthropod vector species, forcing novel intra- and interspecific interactions and potentially introducing novel malarial strains to endemic populations. The diversity and host associations of avian malaria in northwestern New Mexico have not yet been evaluated. We have used Polymerase Chain Reaction (PCR) and microscopy techniques to describe malarial communities in avian specimens (n = 186) collected at three sites on public lands within the jurisdictional boundary of the Bureau of Land Management's the Rio Puerco Field Office. Mitochondrial DNA sequences derived from PCR screening were used to detect malarial infections in birds native to piñon–juniper and Ponderosa pine habitats in northwestern New Mexico. We identified an overall infection rate of 33%, and a co-infection rate of 10%. We expect to see host associations by avian taxonomic family. The present study is a partnership with the BLM to survey bird populations for the purposes of management decision-making and to monitor emerging diseases as conservation threats to native bird populations in New Mexico. Data describing the diversity, distribution, and host-associations of avian malaria parasites will inform land and wildlife management agencies of infection rates and evidence for local transmission of these parasites in native bird communities.

21 Arsenic and Uranium Induced Oxidative Stress Response in Immune Cells.

Sandra C. Alvarez *, Erica J. Dashner-Titus, Deion A. Jackson, Jodi Schilz, Karen L. Cooper and Laurie G. Hudson.

Groundwater contamination by environmental metals is a global health concern. Chronic arsenic exposure causes many adverse effects such as immunotoxicity. Less is known about the health effects of exposure to uranium or combined arsenic and uranium exposures. One mechanism of metal toxicity is metal-induced oxidative stress. For these studies, a human monocyte cell line (THP-1) and a human T lymphocyte cell line (Jurkat) were exposed to arsenic, uranium or both. Cell viability was measured using PrestoBlue and oxidative stress response markers included Heme oxygenase-1 (HO-1), superoxide dismutase (SOD) and catalase (Cat) as detected by immunoblot analysis and RT-qPCR. Results from cell viability assays reveal no cytotoxicity of uranium at any dose tested up to 72 hours of exposure and no cytotoxicity of arsenic until treatments surpass 10 μM. Metal combinations did not alter the toxicity when compared to single metal exposures. Immunoblotting reveals a dose and time dependent induction of HO-1 protein after arsenic exposure. Dose and time dependent induction of HO-1, SOD and Cat were detected by RT-qPCR in THP-1 cells. Jurkat cells displayed a similar magnitude of SOD and Cat induction. In this study we detect transcriptional changes of oxidative stress response genes at non

cytotoxic doses of arsenic and uranium. Because abandoned uranium mines are prevalent in the western U.S., it is important to better understand the contributions of mining associated metals and metal mixtures exposures to oxidative stress response. Supplemental zinc may play a protective role against the effects of metal exposure.

22 Symbiont Derived Sphingolipids: Anti-inflammatory Properties and Application in Adjuvant Model.

Mariah Sanchez †, Elisa Casadei, Ali Sepahi and Irene Salinas.

Symbiotic bacteria products are known to play a major role in the regulation and homeostatic maintenance of the host immune system. Studies in our laboratory have demonstrated that *Flectobacillus major*, the predominant commensal species in the gills and skin of rainbow trout, produces a uniquely structured sphingolipid. Moreover, *F. major* sphingolipids are able to modulate antibody responses in rainbow trout. Here, we hypothesize that *F. major* sphingolipids have anti-inflammatory properties in rainbow trout by regulating cytokine expression. A current method used to control diseases in fish hatcheries is through use of vaccines and adjuvants. Adjuvants are often used to enhance the immunological response elicited by the vaccines and although they prove to be exceptionally useful, they often cause undesired side effects, including local inflammation and granuloma formation. In order to test our hypothesis, rainbow trout received an intraperitoneally injection of the Freund's Complete Adjuvant (FCA) alone, FCA + sphingolipids or sphingolipids alone. Fish were sampled three weeks later, and macroscopic and histological examinations were performed. Internal organ adhesion, wound size, infiltration of immune cells and size and number of granulomas were scored in each fish. Our results indicate that *F. major* sphingolipids are able to greatly reduce harmful side effects of FCA at the injection site and in the visceral organs and therefore can potentially be used as anti-inflammatory agents in the aquaculture industry.

23 Searching for Natural Defenses (Actinobacteria) Against White-Nose Syndrome, Found on Bats at a Gateway to the West.

Emily Johnson †, Edward Strach, Patrick Lewis, Nicole A. Caimi, Ernest W. Valdez and Diana E. Northup.

Since 2006, millions of eastern North American bats have died from white-nose syndrome (WNS), caused by the fungus *Pseudogymnoascus destructans* (*P.d.*). This disease has spread westward across 29 states and five provinces in the United States and Canada, respectively. A recent study on the external microbiota of bats from the Southwest revealed the presence of many Actinobacteria, some of which produce antifungal properties against *P.d*. All of the sample sites in that study came from southern and western New Mexico, as well as from northern and southeastern Arizona. Despite this, we believe that one pathway for WNS to enter into the Southwest would be through northeastern New Mexico and southeastern Colorado, which we regard as the northeast corridor of New Mexico. In 2016, we sampled bats for external bacteria, targeting Actinobacteria, from Capulin Volcano National Monument (CAP), and Pecos National Historic Park (PEC), and Bent's Old Fort National Historic Site (BEOL) within this northeast corridor. Herein we document new records of occurrence of bats and bacteria found on 23 bats belonging to seven different bat species occurring on CAP, PEC, and BEOL. From our analyses of bacteria, we found that our bat samples contained seven dominant bacterial phyla including Acidobacteria, Actinobacteria, Bacteroides, Cyanobacteria, Firmicutes, Proteobacteria, and Synergistetes. NMDS plots showed that microbiota within a location were similar. Some bat species, however, share common microbiota despite being from different locations. Upon closer examination of Actinobacteria, we documented 324 isolates with Streptomyces representing the dominant genus and comprising about one-third of these.

24 The EGFR/MEK Signaling Pathway Is a Critical Regulator of HPV Oncogene E7.

Marilyn Cisneros *, Anastacia M. Griego, Pamela F. Barraza, Adrian J. Luna, Rosa T. Sterk, Julie E. Bauman and Michelle A. Ozbun.

Human papillomaviruses (HPVs) are the most common sexually transmitted infectious agents, and a subset of HPVs (HPV16, HPV18) are associated with cervical, anogenital, and oropharyngeal cancers.

The mechanism whereby HPVs cause cancer is by uncontrolled expression of the viral oncoproteins, E6 and E7. The E6 and E7 oncoproteins induce transformation by disrupting many cellular proteins, most notably by inactivating tumor suppressor proteins, p53 and pRb, respectively. Previous studies suggest a positive relationship between the EGFR pathway and the oncogenic HPV activities, including the ability of viral oncoproteins to augment EGFR signaling and the ability of EGFR's downstream effectors to stimulate HPV oncogene expression. Our hypothesis is that EGFR/MEK/ERK inhibition leads to reduction of HPV oncogene expression, subsequent restoration of p53 and pRb, and thereby increased susceptibility to chemotherapeutic or radiation treatment. Our goal is to determine how the disruption of the EGFR signaling pathway regulates the expression of E6 and E7 and their cellular targets. To test our hypothesis, we are using HPV-negative and HPV16 positive cell lines that maintain the replicating HPV16 genome as well as HPV16 positive head and neck cancer cell lines. We find that inhibition of EGFR, MEK, and ERK proteins downregulates the expression of HPV16 E7 protein and p16, a cellular protein that accumulates in response to E7 expression. These results suggest that EGFR, MEK and ERK are potential therapeutic targets for HPV-related neoplasia and may have clinical anti-HPV effects that can reduce tumor growth and may increase susceptibility to chemo- or radiation therapies.

25 Immunogenic Cross-talk Causes Viral Competition That Potentially Influences the Incidence of Dengue and Zika Infections.

Noah J.B. Silva[‡] and Helen J. Wearing.

The burden of disease caused by the four serotypes of dengue virus has long posed a global health problem. A related virus, Zika, which shares the same mosquito vector, is now emerging in areas where dengue is endemic. Recent *in vitro* studies support some measure of immunogenic cross-talk between these viruses, but the potential for viral cross-enhancement and/or cross-immunity is not yet fully understood. Complicating interactions further, an imperfect dengue vaccine recently has been developed and currently is being implemented in nine countries. Mathematical modeling can provide insights into potential future viral dynamics of these diseases. Thus, we created a deterministic, five-serotype model for the dengue-Zika viral system that can examine the consequences of different assumptions about viral competition. This model incorporates dengue vaccination, cross-immunity between dengue serotypes, and cross-talk between dengue and Zika. Using this model, we show that there is potential for an increase in Zika incidence following dengue vaccination. We investigated the role that the timing of dengue vaccination and Zika introduction play in both short- and long-term patterns of Zika incidence. We also show a potential risk of increasing the rate of severe infections, both of dengue and Zika, when vaccination is implemented. The implications of the patterns we observe emphasize the need for further studies on the interactions between Zika and dengue, and illustrate the potential perils of imperfect vaccine implementation within a set of closely related, competing viruses.

26 Impact of Prenatal Alcohol Exposure on Cannabinoid 1 Receptors and Cannabinoid Receptor-effector Coupling in Dentate Gyrus of Adult Rat Offspring.

Kiana Lujan[†], Kyle Christensen, Jennifer Wager, Suzy Davies and Daniel Savage.

Previous studies from our lab suggest that a deficit in activity-dependent potentiation of glutamate release from the entorhinal cortical perforant path projection to the dentate gyrus is one mechanism contributing to the synaptic plasticity and learning deficits we have observed in moderate prenatal alcohol-exposed (PAE) rat offspring. We have observed that ABT-239, a histamine H_3 receptor inverse agonist, ameliorates these synaptic plasticity and learning deficits. Given that H_3 receptors mediate an inhibition of glutamate release and PAE elevates H_3 receptor-effector coupling in dentate gyrus, we speculate that the mechanistic basis for ABT-239's beneficial effect in PAE rats is to blunt this heightened inhibitory influence. Cannabinoid 1 (CB_1) receptors, like H_3 receptors, are G_i/G_o protein-coupled receptor residing on glutamatergic nerve terminals, where they mediate their effects through the same receptor-effector coupling system as H_3 receptors. We examined whether PAE affects CB_1 receptor density or receptor-effector coupling in the dentate gyrus. PAE did not affect the density of [^{3}H]-WIN 55,212 binding to CB_1 receptors in any brain region measured. In contrast, CB_1 receptor-effector coupling, as measured by

WIN-55,212-stimulated [^{35}S]-GTPγS binding, was significantly elevated in dentate gyrus and cortical brain regions of PAE rats compared to saccharin controls. Further, LY-320,135, a CB_1 receptor inverse agonist, inhibited WIN-55,212-stimulated [^{35}S]-GTPγS binding to a greater extent in PAE rats when compared to controls. The differential effect of PAE on CB_1 receptor-effector coupling suggests that CB_1 receptor inverse agonists such as LY-320,135, may have some efficacy for ameliorating the synaptic plasticity and behavioral deficits observed in PAE offspring. (Supported by 1 R01AA19984 and 1 P50 AA22534 and GM060201.)

27 Patient Satisfaction: It's Just a Matter of Time.

Ali Salehpoor †, Tommy Soudachanh, Benjamin Howse, Aaron Segura, Fernando Sinaloa, Silas Bussmann, Lynne Fullerton and Jon Femling.

We examined the effect of a Patient Liaison in the UNMH Emergency Department (ED) waiting room. The Liaison provided patients with information about average ED wait times and general processes upon request. A cross-section of ED patients was surveyed later about their satisfaction and understanding of their experience of care. Patients who spoke to the Liaison in the waiting room did not report a significant difference in their satisfaction. However, we found a negative relationship between time spent in the waiting room and patient satisfaction ($p < 0.001$) and a positive relationship between patient understanding and satisfaction ($p < 0.001$). This data suggests that a more active intervention targeting patients with the longest waiting room times and providing patients with specific updates about the steps being taken to provide them care may be more effective in improving patient satisfaction.

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

Katrina Baca †, Niki Marjon, Eric Prossnitz and Helen J. Hathaway.

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 a 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 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.

29 Autophagy Variants in Melanoma Progression.

Sabah Osmani †, Kirsten A.M. White, Salina M. Torres, Li Luo, Chien-An A. Hu, Jenna Lilyquist, DeAnn Lazovich, Christopher Hughes and Marianne Berwick.

In 2017, an estimated 10,130 people will die from melanoma, the deadliest form of skin cancer. Autophagy is an intracellular catabolic recycling pathway that has been linked with melanoma progression. Several single nucleotide polymorphisms (SNPs) in autophagy-related (*ATG*) genes have a known functional impact on the autophagic flux and potentially melanoma risk or histopathological factors. Previously, a SNP in *ATG16L* has shown an inverse association with Breslow thickness (Coeff 0.87, 95% CI 0.97-0.99, $p = 0.03$), anatomic site (OR 0.20, 95% CI 0.05-0.86, $p= 0.03$), earlier stage at diagnosis

(OR 0.47, 95% CI 0.27-0.81, p = 0.02) and younger age at diagnosis (p = 0.02) in melanoma patients. However, variants in *ATG16L* have not been investigated for association with melanoma risk and survival. Here, we examined *ATG16L* (rs2241880) in a large population-based case–control study. The participants were diagnosed between 2004 and 2007, aged 25-59, with invasive cutaneous melanoma. Controls were randomly selected from the state drivers' license list and frequency-matched to cases on the basis of age and gender. Altogether, 1,753 individuals submitted DNA samples for genotyping: 893 cases and 766 controls and completed a self-administered questionnaire and telephone interview. In summary, our data examines the role of *ATG16L* with age at diagnosis and histopathological factors as well as melanoma risk and survival. These associations may contribute to our current understanding of the significant role of autophagy in melanoma progression.

30 No Health Insurance, Less Medical Assurance.

Krista Houmpheng, Lucas Winter, Niharika Ravichandran, Cameron Guy, Lynne Fullerton, Silas Bussmann and A. Robb McLean.

Emergency Departments are busy. According to nationwide data gathered by ProPublica, the average length of stay for patients who visit the University of New Mexico Hospital Emergency Department (ED) is more than five hours and 46 minutes. Despite the efforts of the Affordable Care Act, many individuals still remain uninsured. According to the U.S Department of Health and Human Services, in 2015, 10.9% of New Mexicans remained uninsured. We hypothesize that uninsured patients have fewer options for primary care, and are thus more likely to use the ED for non-emergent treatment, aggravating the busy nature of the ED. We recruited a convenience sample of more than 800 adult patients from the UNMH ED. We surveyed patients about their insurance status, reasons for seeking care in the ED, and their perception of access to a primary care facility. Our findings showed insured patients were twice as likely than uninsured patients to have been referred to the ED by another provider. Furthermore, insured patients were also twice as likely than uninsured patients to consider going elsewhere for treatment. Only seven out of 108 uninsured patients considered going somewhere other than an ED, indicating that uninsured individuals sought out Emergency Departments as a primary source of care. Additionally, a higher proportion of uninsured patients were assigned as low acuity. Taken together, these results suggest that uninsured patients are more likely to be confined to an Emergency Department for non-emergent treatment, which increases the strain on the healthcare system.

31 How Illicit Drug Users Seeking Treatment Differ in Expectations by Ethnicity.

Nyabang Buom*, Pilar Sanjuan and Jeff Scott Tonigan.

It is well documented that client change readiness and the meeting of expectations of substance use disorders (SUD) treatment are important considerations in terms of treatment compliance, retention, and outcome. Unfortunately, with a few notable exceptions, (e.g., Milligan, 2004), ethnic differences in motivation and expectations of SUD treatment remain unclear and are understudied. This secondary analysis examined Hispanic (n = 72) and non-Hispanic Whites (n = 109) differences in motivation and treatment expectations among illicit drug users seeking outpatient treatment (R01DA009864, Miller). Measures central to this study included the Form90D (Westerberg et al., 1998), What I Want from Treatment Inventory (Miller, et al., 1994), and the SOCRATES (Miller and Tonigan, 1991). Few between-group pre-treatment differences were found on measures of motivation, substance use, and life functioning. Likewise, with a few exceptions, the ethnic groups did not differ in their expectations of SUD treatment; both ethnic groups reported enthusiasm for skills-based therapy and increased knowledge of 12-step programs, while both groups also reported low enthusiasm for medications. Findings indicated that, in general, Hispanics and non-Hispanic Whites approached treatment with similar expectations of treatment and change readiness. Future investigations need to examine how, if at all, the pre-treatment measures of interest in this study may predict treatment outcomes.

32 Tissue Engineered Heart Valve Scaffolds of Oligo (Poly (Ethylene Glycol) Fumerate).

Quan Huynh *, Kent E. Coombs, Matthew N. Rush, Olivia Bell and Elizabeth L. Hedberg-Dirk.

Aortic heart valve disease affects approximately 1.5 million Americans, resulting in reduced pumping efficiency and blood flow to the rest of the body. Currently, the only effective treatment is surgical replacement; however, options are limited due to degradation and blood clotting. In the aortic valve, valvular interstitial cells (VICs) are the predominant cell population and are responsible for valve formation, repair, and disease development. In order to overcome the limitations of current replacement options, our goal is to develop tissue engineered heart valve (TEHV) scaffolds for the controlled growth of valve tissue. Previous studies have shown that surface chemistry can control cell behavior in two-dimensional environments, but three-dimensional scaffolds are required to mimic the growth of new tissues. The degradable polymer, oligo (poly (ethylene glycol) fumerate) (OPF), provides a platform to study how VICs behave in 3D environments. We have developed a nitrogen sparge OPF synthesis reaction for the creation of OPF that is more efficient than previous methods and yields a better product for tissue engineered studies. By functionalizing OPF to control for surface chemistry, this 3D system will allow for a more realistic TEHV material. We hypothesize VICs grown in hydrogels created from OPF functionalized with carboxyl chemistry will induce a healthy phenotype, while VICs encapsulated in OPF functionalized with amine groups will induce an osteoblastic phenotype. Overall, this work will provide for better environments for the growth and repair of aortic valve disease.

33 Moderate Prenatal Alcohol Exposure Produces Deficits in the Extinction of Contextually Conditioned Fear Learning in Adult Female Rat Offspring.

A.H. Moezzi †, J.L. Wagner, N.S. Graham, K.H. Christensen, D.R. Barto, S. Davies, D.A. Hamilton and D.D. Savage.

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. The experimental group consumed 5% ethanol, whereas the control group consumed saccharin for four hours per day throughout pregnancy. 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 3 ½ 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 moderate PAE rat offspring that may be attributable to functional damage in the frontal cortex. (Supported by NIAAA R01-AA019884.)

34 Effects of Knockout of Cold-Inducible RNA Binding Protein (CIRP) on Breast Tumorigenesis.

Joey L. Ochoa †, Daniel A. Lujan, Melanie N. Peterson, Helen J. Hathaway and Rebecca S. Hartley.

RNA binding proteins (RBPs) are essential to processes that involve RNAs, beginning from their transcription through to their degradation. In this study, we utilize the polyomavirus middle T antigen (PyMT) mouse model to evaluate the role of cold-inducible RBP (CIRP) in breast tumorigenesis. When PyMT is expressed in the mammary epithelium of mice, it causes aggressive tumorigenesis. CIRP has been shown to incite the translation of mRNAs encoding stress-induced proteins, and has been observed to increase expression in breast cancer. We have shown that human CIRP overexpression in the PyMT mouse appears to impede breast tumorigenesis during early and late stages of tumor development. Based

on these results, the current study set out to evaluate the effects of CIRP knockdown on tumor development. We expect knockdown to allow greater progression of tumor growth, as well as a higher rate of metastasis. To address this hypothesis, CIRP will be knocked out using CRISPR cas-9 in a PyMT —mammary tumor—derived cell line. CIRP deficient PyMT cells will be injected into the mammary fat pad of a wild type mouse, and tumor growth will be assessed. CIRP knockout in PyMT cells will be analyzed via RT-qPCR and western blotting to determine the effective timing tor mammary fat pad injections. Tumor growth will be monitored for 3-6 weeks. Final tumor burden and metastasis will be determined, and tumor proliferation and apoptosis will be evaluated by histopathological analysis. The results of this study will tell us if CIRP overexpression has the potential to protect against breast cancer.

35 Novel Sensors for Detecting Alzheimer's Disease Related Tau Protein Aggregates.

Salomon Alires †, Florencia Monge, David G. Whitten and Eva Y. Chi.

The pathological hallmarks of Alzheimer's Disease are the accumulation of extracellular amyloid-beta fibrils and intracellular tau tangles. Currently, there is no reliable method to detect these plaques and tangles. We have developed a new class of synthetic sensors based on an oligo phenylene-ethynylene scaffold (OPE) that can selectively bind to the fibrillar conformer of model amyloid proteins. Upon binding, the OPEs become highly fluorescent for optical detection. In this study, we tested the sensing capability of OPEs on a synthetically derived six amino acid tau peptide VQIVYK. The 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. We hypothesize that OPEs can selectively bind to the fibrillar conformer of tau. Tau has been synthesized and purified. Incubation of tau in water at 70°C and 2 mg/mL reproducibly resulted in fibril formation. Tau samples were then mixed with an OPE or Thioflavin-T and analyzed with fluorescence spectroscopy, circular dichroism, and ultraviolet-visible spectroscopy. Anionic OPE displayed the highest affinity for the fibril conformer and generated enhanced fluorescence over cationic OPE. Alternatively, Thioflavin-T did not positively sense fibril formation. The goal of this study is to determine that OPEs are also effective biomarkers towards the disease-related tau protein.

36 Altered Expression of Angiogenesis-associated miR-150-5p and its Target Vezf1 in Mouse Models of Prenatal Alcohol Exposure.

Gabriela Perales *, Amy S. Gardiner, Andrea M. Allan and Nora Perrone-Bizzozero.

Fetal alcohol spectrum disorders (FASD) occurs to an individual whose mother consumed alcohol during pregnancy. Prenatal alcohol exposure (PAE) is difficult to diagnose early on because problems start to arise as an individual develops over time, which can lead to a wide range of birth defects and developmental disabilities later in life. These deficits can be caused by alterations in gene expression that are regulated by microRNAs (miRNAs). miRNAs are small non-protein-coding ~22 nucleotide single-stranded RNA molecules that regulate gene expression by binding to the 3′UTR of targeted mRNA and prevent translation. Using a mouse model of PAE, analysis of the dam's plasma for extra cellular circulating miRNAs was done using MicroRNA sequencing. A miRNA of interest, miR-150-5p was found to be altered. Then we collected cortices of alcohol-exposed pups at embryonic day 18 (E18) and, through RT-qPCR, found that miR-150-5p was significantly increased compared to control. Previous studies suggest miR-150-5p is involved in angiogenesis in embryonic brain development. We identified a potential angiogenic target of miR-150-5p, vascular endothelial zinc finger 1 (Vezf1), which is an endothelial-specific transcription factor required for vascularization. Through RT-qPCR, we found Vezf1 to be significantly decreased in these same cortices of alcohol-exposed pups. We hypothesis that miR150-5p is regulating Vezf1 expression during neuronal development and altering brain vasculature when alcohol exposed. To demonstrate that miR-150-5p is directly binding to the 3′UTR of Vezf1, we will be cloning the 3′UTR into the pISO firefly luciferase reporter and perform dual luciferase assays.

37 Axonal Conductance across Corpus Callosum in a Third-trimester Equivalent Mouse Model of Prenatal Alcohol Exposure.

T. Martinez *, J. Newville, C.F. Valenzuela and L.A. Cunningham.

Recent human imaging studies have found white matter abnormalities in the corpus callosum (CC) of children diagnosed with fetal alcohol spectrum disorder (FASD). Using a third-trimester equivalent alcohol exposure model in mice, we have discovered persistent microstructural changes in white matter as assessed by diffusion tensor imaging. Mothers and their pups were placed in alcohol inhalation chambers, allowing the mean pup blood ethanol concentration to reach 160.4 ± 12.0 mg/dl (NM legal limit: 80 mg/dl). To determine if functional deficits resulted from alcohol exposure, postnatal day 50-60 mice were deeply anesthetized with ketamine, promptly decapitated and brains sliced coronally at 400 µm thick using a vibratome. Slices were incubated in artificial cerebrospinal fluid at 25°C prior to electrophysiological assessment. Conduction velocity was estimated across the CC by measuring peak latency of compound action potentials at constant stimulus intensity, while decreasing distances between electrodes from 1,125 µm to 375 µm in steps of 125 µm. The conduction velocity (CV) of myelinated axons (N1 peak) of air-exposed mice was 1.061 ± 0.1744 m/s (n = 4), and of ethanol-exposed animals was 0.717 ± 0.0620 m/s (n = 4). The CV of unmyelinated axons (N2 peak) of air-exposed mice was 0.290 ± 0.0237 m/s (n = 4), while the ethanol exposed mice CV was 0.262 ± 0.0046 m/s (n = 4). A t-test revealed that neither the N1 nor the N2 CVs was significantly different between treatment groups (N1, $p = 0.1128$; N2, $p = 0.2902$).

38 The Role of Relaxin-H2 in Mediation of Cystic Renal Epithelial Cell Recruitment of Fibroblasts.

Elena Delgado † and Heather Ward.

Autosomal dominant polycystic kidney disease (ADPKD) is a hereditary condition that affects more than 12 million people worldwide and is characterized by cyst enlargement, scarring, and increased production of transforming growth factor-beta (TGF-β1) within both kidneys. TGF-β-mediated signaling alters matrix metabolism and affects epithelial cell-fibroblast interactions that contribute to fibrogenesis. The anti-fibrotic hormone relaxin-H2 inhibits TGF-β signaling and matrix synthesis, but its effects on fibroblast behavior within ADPKD kidneys are unknown. We hypothesized that ADPKD renal epithelia recruit a greater number of fibroblasts than normal epithelia under control conditions, while relaxin-H2 treatment of ADPKD epithelia limits fibroblast migration under normal and fibrotic conditions. Normal and ADPKD kidney epithelial cells were treated with vehicle control, relaxin-H2, TGF-β1, or a combination of relaxin-H2 and TGF-β1, then co-incubated with fibroblasts in a transwell migration system. Fibroblast migration was quantified via colorimetric assay. We found that fibroblast migration was dependent on the epithelial cell line used and the relaxin-H2 concentration. Further analysis revealed that myofibroblast conversion occurred by passage 3 in culture; thus, the state of fibroblast activation may have affected the response to treated epithelia. Our epithelial cell lines exhibited varied levels of relaxin receptor, RXFP1, which regulates relaxin-H2 mediated signaling. Therefore, we generated a RXFP1-GFP expression vector to increase relaxin-receptor expression in cultured cells. Data from these experiments will determine how relaxin-mediated signaling in renal epithelia affects epithelial-fibroblast communication. Limiting fibrogenesis by decreasing fibroblast recruitment would indicate that the relaxin-H2 receptor could serve as a therapeutic target to combat fibrosis in ADPKD.

39 Histone Deacetylase Inhibition as a Means of Increasing Sensitivity to Platinum Based Chemotherapeutics.

Alejandra Rosales *, Michaela L. Granados and Sabrina Samudio-Ruiz.

Ovarian cancer is the leading cause of death arising from gynecological malignancies. Low survival rates can be attributed to the frequent acquisition of resistance to platinum-based chemotherapeutics. Previous studies have shown that platinum resistance in ovarian cancer cells is associated with increased expression of histone deacetylases (HDACs), thereby suggesting that resistant cells have decreased histone acetylation. Histone acetylation is an epigenetic mechanism important in the regulation of chromatin structure

and gene expression. Decreased histone acetylation is associated with a closed chromatin structure and decreased gene expression. Furthermore, there is evidence that HDAC inhibitors (HDACi) can partially restore platinum sensitivity in cisplatin resistant cells. We hypothesize that *in vitro* models of platinum resistant cells will display decreased histone acetylation accompanied by increased HDAC activity and that HDACi can restore platinum sensitivity. Using our previously developed resistant model (OV-CA433-CPR) and a commercially available resistant line (A2780-cis), we verified resistance to cisplatin by cell viability assay and measured basal levels of histone acetylation by immunoblotting. Initial dose-response studies using a pan-HDACi, Belinostat showed that increasing doses of the HDACi increased histone acetylation from basal levels without affecting cell viability. Our current focus is on evaluating how Belinostat affects response to cisplatin in resistant cells. These findings show that Belinostat is able to inhibit HDACs and increase histone acetylation, while maintaining cell viability. If our hypothesis is correct, HDACi may be a promising therapeutic approach in reversal of platinum resistance in ovarian cancer, thereby making platinum-based chemotherapeutics more effective.

40 CD82 Regulation of Hematopoietic Stem Cell Adhesion and Migration.

Erica Pascetti†, Chelsea Saito-Reis and Jennifer Gillette.

Hematopoietic stem and progenitor cells (HSPCs) are responsible for the continued production of new blood and immune cells. Self-renewal and differentiation of HSPCs is tightly regulated by interactions with the bone marrow microenvironment or "niche." Therefore, the ability of HSPCs to migrate and adhere to the bone marrow dictates their repopulation potential and the success of a stem cell transplant. The tetraspanin scaffold protein CD82 is enriched on the surface of HSPCs and previous work from our laboratory identified a potential role for CD82 in modulating bone marrow migration and repopulation of HSPCs. In the present study, we are testing the hypothesis that CD82 expression specifically regulates HSPC adhesion and migration. Isolating primary HSPCs from wildtype (WT) and global CD82 knockout (CD82KO) mice, we are analyzing how the loss of CD82 impacts adhesion and migration behaviors using *in vitro* assays. Measuring cell adhesion in a fluorescence-based assay, we find that HSPCs have increased adhesion to OP9 stromal cells and the Vascular Cell Adhesion Molecule-1 (VCAM-1), with minimal adhesion to extracellular matrix components collagen I and laminin. When comparing cell adhesion abilities of WT and CD82KO HSPCs, we detect no differences. In contrast, fibronectin cell-spreading assays indicate that CD82KO HSPCs have a significant increase in cell area and expanded lamellipodia when compared to WT cells. The Rho GTPase family memberRac-1 regulates the polymerization of actin to produce lamellipodia, thus current studies are directed at analyzing potential increases in Rac-1activity. Together with time-lapse migration experiments, these data are providing insight into how CD82 may be targeted to regulate HSPC/niche communication.

41 The Role of CD82 Expression and Post-translational Modifications on c-Kit Signaling in Acute Myeloid Leukemia.

Erin E. Lucero†, Christina M. Termini and Jennifer M. Gillette.

c-Kit is a receptor tyrosine kinase found on hematopoietic cells where interactions with its ligand, stem cell factor (SCF), stimulates c-Kit dimerization and signal transduction. Upon overexpression, c-Kit can lead to cancers such as acute myeloid leukemia (AML). Previous studies suggest that c-Kit associates with tetraspanin proteins, which are multi-spanning membrane scaffold proteins that regulate protein trafficking, cellular adhesion and signaling. Previously, we demonstrated that the post-translational modifications of palmitoylation and glycosylation of the tetraspanin CD82 regulate membrane protein organization, modifying protein expression and activity. We hypothesize that CD82 expression and post-translational modifications regulate c-Kit expression and downstream signaling that modulates AML cell behavior. To test this, we generated CD82 overexpressing AML cell lines with wild-type CD82 (CD82OE), a palmitoylation deficient CD82 (Palm-OE), and a N-linked glycosylation deficient CD82 (Ngly-CD82OE) tagged to the mCherry fluorescent protein. Control cells expressing the mCherry protein also were generated. Using Western blot analysis, we analyzed c-Kit expression under resting and SCF stimulated conditions. Densitometry analysis indicates higher c-Kit expression in CD82OE and

Ngly-CD82OE under resting conditions compared to control cells. Under resting conditions, the Palm-OE cells decreased c-Kit expression. Additionally, when cells are stimulated with SCF, we found that the Ngly-CD82OE cells exhibit increased phosphorylation of c-Kit compared to control cells. These data suggest that the scaffolding properties of CD82 regulate the overall protein expression of c-Kit. This ability of CD82 and its post-translational modifications to regulate c-Kit expression may serve as a therapeutic target to control c-Kit expression and aberrant AML signaling.

42 MRTF Constitutively Active and Dominant Negative Line Analysis.

Praveen Paudel†, Tracy Dohn and Richard Cripps.

MRTFs, a family of conserved transcriptional co-activators, are expressed in cardiac and smooth muscles where they regulate cell differentiation via transactivation of differentiation marker genes. As important mediators in muscle differentiation, MRTFs have been implicated in fruit fly (*Drosophila melanogaster*) flight muscle development, and appear to have an essential role in early muscle cell progenitor development. However, the mechanism through which MRTF is regulating muscle development is not yet understood. Therefore, I obtained and characterized the phenotypes of transgenic *Drosophila* lines that cause MRTF to be always "on" (constitutively active) or always "off" (dominant negative). I used the UAS-Gal4 system to overexpress these transgenes specifically in adult muscle progenitor cells through an 1151-Gal4 driver. The functional flight test showed that the transgenic flies have a weaker flight. Moreover, I cryosectioned and fluorescent immunostained these flies, and analyzed the specific muscle disruptions through confocal imaging. The dominant negative MRTF appears to transform indirect flight muscles, a fibrillar muscle, to a structure more similar to the jump muscle, a tubular muscle type. 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.

43 Contribution of Acid-sensing Ion Channels to Ventilatory Control in Conscious, Unrestrained Mice.

Kenneth G. Vigil†, Neil D. Detweiler and Nikki L. Jernigan.

The chemoreceptor reflex modulates respiration to ensure arterial partial pressures of oxygen (pO_2), carbon dioxide (pCO_2), and pH are maintained at relatively constant levels. Peripheral chemoreceptors, located in the carotid and aortic bodies, directly sense changes to the concentrations of O_2, CO_2, and H^+ in the blood; however, the mechanisms that stimulate chemoreceptor activity is not well-understood. Acid-sensing ion channels (ASIC1-3) are activated by extracellular acidosis, expressed in carotid body glomus cells, and have been implicated as potential chemoreceptors. However, the importance of ASICs to chemoreceptor responses in conscious, unrestrained animals remains unconfirmed. We hypothesize that ASICs contribute to the hypercapnic and hypoxic chemoreceptor response. To examine the contribution of ASIC2 to hypoxic and hypercapnic ventilatory responses, we exposed wild-type (WT) and ASIC2 knockout (ASIC2KO) mice to normoxia (21% O_2, O% CO_2), isocapnic hypoxia (7% O_2, 3.2% CO_2), hypocapnic hypoxia (7% O_2, 0% CO_2), and hypercapnia (21% O_2, 6% CO_2). Respiratory rate, tidal volume, and minute ventilation were measured using whole-body plethysmography. We additionally assessed arterial pO_2, pCO_2, and pH. We found that changes to ventilation in ASIC2KO mice in response to hypocapnic hypoxia and hypercapnia were similarly to WT mice, but minute ventilation during isocapnic hypoxia was decreased in ASIC2KO mice compared to WT. This decrease in minute ventilation was not reflected in changes to pO_2, suggesting the difference in minute ventilation between WT and ASIC2KO mice may not be great enough to cause difference in arterial oxygen tension.

44 Classification of Four mi-RNA Genes Involved in Muscle Development in *Drosophila melanogaster*.

Daniel L. Wilson†, Tracy E. Dohn and Richard M. Cripps.

Micro-RNAs (mi-RNA) are highly conserved post-transcriptional regulators essential to development and maintenance in many organisms. These small, non-coding RNA molecules prevent maturation of protein-coding genes by inhibiting transcription or mediating mRNA degradation in a sequence-specific

manner. Previous research has linked mi-RNAs to both muscle development and maintenance, however the specific mechanism is unknown. Here, we study four genes previously implicated in myogenesis in the hopes of further elucidating the role of mi-RNA in muscle development. In order to do this, we used the UAS/Gal4 system in *Drosophila* to over-express and under-express our four mi-RNAs of interest. Functional tests measuring flight and jump ability showed decreased muscle function in both over-expression and under-expression as determined by weak or absent flying and reduced jump distance at 10 days after eclosion. Flies were cryo-sectioned at 16h, 24h, 48h, and 96h after puparium formation (APF). Sections were fluorescent antibody stained and shown to have significant developmental defects in muscle organization. Therefore, this data implies that these four mi-RNAs are influential in proper muscle development and function in *Drosophila melanogaster*.

45 Protein Dysregulation in the Isolated Extracellular Matrix of Failing Human Hearts with Dilated Cardiomyopathy.

Joshua L. DeAguero*, Elizabeth N. McKown and Dawn A. Delfin.

Damage to the heart from a multitude of cardiovascular diseases leads to pathological cardiac remodeling. Long-term effects of this pathological remodeling greatly reduces cardiac function and can lead to the development of cardiomyopathy and heart failure. Pathological cardiac remodeling can lead to changes in the extracellular matrix (ECM) of the heart as the ECM is a dynamic structural and regulatory cardiac component and is highly responsive to cardiovascular stress. The ECM is composed of an intricate network of proteins that offer structural support while also regulating the functions of cells attached to it, including cell proliferation, differentiation and survival. Changes in the ECM by pathological cardiac remodeling not only affects protein composition, but it also affects rates of protein synthesis and degradation, which causes disruption of the heart's ECM structure and content leading to an alteration in mechanical support of the heart. Failing hearts with dilated cardiomyopathy are known to have extensive pathological cardiac remodeling, an increase in ECM volume and an altered ECM protein expression profile. For the purposes of our research, it was important to understand and characterize the protein composition of the isolated ECM from failing human hearts with dilated cardiomyopathy relative to that of non-failing hearts. As there are relatively few treatments for end-stage heart failure, besides heart transplant, therapies are needed. The goal of this study is to aid the understanding of the pathology of heart failure with dilated cardiomyopathy and how changes in ECM content might afford insight into possible therapeutics.

46 Myosins: Motor Proteins Influencing Cell Polarization in Maize during Asymmetric Cell Division.

Janette Mendoza‡ and Michelle R. Facette.

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 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.

47 Single Stranded Transposon Insertion.

Emily Alden *.

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 at 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 commonly used 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 either a phosphate or 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.

48 Toward Programmable Amplification Using DNA Strand Displacement.

David Arredondo * and Matthew Lakin.

DNA can be synthesized with an arbitrary nucleic acid sequence, and through design this can be exploited for the DNA to serve as the building blocks of complex networks. DNA nanotechnology is a particularly powerful tool in the fields of nanomedicine and nanorobotics within biochemical systems. Examples of possible implementation include autonomous diagnosis and treatment of disease, observation of enzyme function, and molecular cargo transport. Toehold mediated strand displacement (TMSD) reactions are a class of reactions within the realm of DNA nanotechnology capable of using two domain single stranded DNA (ssDNA) as inputs and outputs, recognized by top nicked double stranded DNA (dsDNA) gates. Due to the modular nature of the gates and signals, complex multi-layered networks comprised of different DNA species are theoretically capable of creating any logical circuit. We present the design of a signal transducer with variable gain. An initial concentration of input species X is converted to scaled concentration of fluorescent output species Y based on a pre-programmed gain factor. The gain is determined by the degree of competition between the catalytic gate that releases signal and a sink gate that absorbs input and releases no output. We focus here on preliminary experimental work characterizing various components of the circuit to validate the behavior of the designed system in practice. Future work entails the utilization of this circuit within a larger circuit that may benefit from a variable gain such as a trainable neural network or diagnosis requiring detection of low concentration molecules.

49 Characterization of Cardiac and Somatic Muscle Genes in *Drosophila*.

Sam McKitrick †, Tyanna Lovato and Richard M. Cripps.

The HIM (Holes in Muscles) and CG7033 (CCT2) genes are expressed in muscle and heart cells in *Drosophila* and are predicted to be important for muscle and heart development. In the HIM gene there are no known conserved protein domains, but it is known that it plays a role as an inhibitor of muscle transcription factors during myogenesis. HIM is of interest because it may be a crucial gene involved in myogenesis, and may hold insight into the mechanisms involved in muscle remodeling during pupal development. CG7033 is a gene that has conserved domains associated with Chaperonin proteins; however, there is still much to learn about it. CG7033 is primarily of interest because Chaperonin proteins are involved in the folding of other proteins, which is a crucial factor in muscle development. In order to investigate the function of these genes, we have hijacked the bacterial CRISPR-Cas9 system to create

knock out mutants. We hope that the resulting phenotypes will provide insight into their role during development.

50 Silica Sol-Gel Encapsulation Effects on Cell Division Rates and Chlorophyll Fluorescence and Content in *Chlorella sorokiniana*.

Bianca Serda†, John Roesgen and David T. Hanson.

The goal of the experiment was to compare the encapsulated silica sol-gel and liquid cultures with respect to cell growth and function over 28 days. A freshwater green alga, *Chlorella sorokiniana*, liquid cultures were grown in parallel with encapsulated silica sol-gel cultures. Cell counts, chlorophyll fluorescence (for assessing photosynthetic electron transport) and chlorophyll content were measured daily. The preliminary testing showed that silica sol-gel samples increased slightly in cell density and chlorophyll content relative to liquid cultures and maintained photosynthetic function for all 10 days. This is consistent with our expectations that encapsulation limits cell division but not metabolic activity.

51 Amphiphilic Cyclodextrins for Biocompatible Targeted Gene Delivery.

Valerie Perea†, Ping Zhang, Kunlun Yin, Chang-Chun Ling and Lina Cui.

The clinical success of targeted gene therapy against cancer depends on the use of safe, efficient delivery systems that circumvent immunogenicity. In previous attempts, responses to viral vector-based gene therapy were problematic and associated with treatment toxicity, acquired drug resistance possibly due to intrinsic mechanisms and/or genetic heterogeneity in cancer cells. Therefore, drug carriers that bypass such unwanted side effects are highly desired. Cyclodextrins (CDs) are a class of cyclic oligosaccharides consisting of 6, 7, or 8 (α-1,4)-linked α-D-glucose units with an inner-outer amphiphilic nature. They have emerged as an important tool in gene delivery systems because of their stabilizing and shielding effects, high specificity, and biocompatibility. We have developed CD molecules JG108 and JG140 for successful delivery of chemotherapeutics to cancer cells. This study investigates the toxicity and mechanism of gene transfection of CDs JG108 and JG140. Green Fluorescent Protein (GFP) was used as readout moiety to evaluate transfection efficiency of the CDs. Transfection efficiency and cytotoxicity were assessed 24 hours post transfection. HeLa cells transfected with JG108 nitrogen to GFP pDNA phosphate ratio (N/P) of 20/1 had a 4.2 fold increase of fluorescence compared to HeLa cells not transfected with CDs. Flow cytometry corroborated these results, as fluorescence increased with an increase in N/P ratio for JG108. MTT assay results indicated cell viability decreased with a higher N/P ratio for JG 108 (for 20/1 viability = 15%, for 2/1 viability = 74%, n = 5). Prospective work will test newly synthesized CD molecules for gene transfection efficiency.

52 Using Dye Encapsulating Liposomes to Study Protein-Induced Membrane Disruption.

Anthony M. Garcia†, Adeline M. Fanni and Eva Y. Chi.

The misfolding and aggregation of certain proteins, such as amyloid-beta (Aβ) and tau, are linked to the pathogenesis of neurodegenerative disorders, including Alzheimer's and Parkinson's diseases. Although it remains unclear how protein aggregates cause toxicity that leads to neurodegeneration, it has been hypothesized that the ability of protein aggregates to perturb the lipid membrane can serve as a toxicity pathway. This study aims to investigate the capability of both the tau hexamer VQIVYK and Aβ40 peptide to cause membrane disruption by using a dye leakage assay with small unilamellar vesicles (or liposomes) (~100 nm) containing a high concentration of quenched fluorescent dye and incubated with Aβ or tau. Disruption of the membrane leads to leakage of encapsulated dye into the solution and thereby increases the solution's fluorescence. Previous studies have shown that both Aβ40 and tau proteins insert into lipid monolayers at the air/water interface, suggesting that both proteins may cause membrane disruption. To assess the protein's membrane disruption ability, we have prepared dye-encapsulated liposomes and have used two different methods, dialysis and size-exclusion High Performance liquid-chromatography (SE-HPLC) to isolate the liposomes from free dye in solution. Isolated dye-encapsulated liposomes will then be incubated with the proteins of interest. Dye leakage resulting from protein-induced membrane disruption will be monitored by fluorescence. To date, the dye leakage

assay has been unsuccessful and optimization of the method is necessary. Once the method is optimized, this study could be expanded to test how polyphenols, such as curcumin, affects the proteins' ability for membrane disruption.

53 Effect of Pangloss and Brick Mutations on Stomatal Function.

Marissa Harjoe†, David T. Hanson and Michelle R. Facette.

Asymmetric cell division is important in the formation of the stomatal complex. The stomatal complex of *Zea mays* is composed of guard cells and subsidiary cells that are formed by asymmetric divisions and is a useful model for exploring these types of divisions. The proper divisions of guard mother cells (GMC) and subsidiary mother cells (SMC) that form the stomatal complex relies on proper cell polarization. The process of polarization in these cells is disrupted in certain mutants. Pan and brk mutants express aberrant subsidiary cells. Pan1 and pan2 code for a catalytically inactive receptor-like kinases important in triggering cell polarization. Brk1 and brk3 are components of the complex that prompts the actin-nucleating complex, Arp2/3, causing the nucleus to migrate to one side of the cell. These mutants have high percentages of aberrant subsidiary cells in juvenile leaves, but are only present at about 5% in adult leaves. It is unclear to what degree these mutations have on stomatal function. To functionally characterize these mutations, pan1, pan2, brk1, brk3 and wild type, B73, were grown and their rates of stomatal opening and closure were assessed on a juvenile and adult leaf. The goals of this project are to better understand the role of subsidiary cells as they relate to stomatal function and further explore the process of the asymmetric cell divisions that create the stomatal complex.

54 Systematic Screening for Transcriptional Regulators of Adult Myogenesis in *Drosophila* by RNAi.

Tommy Soudachanh†, Sandy Oas, Tyler Mendes, Anton Bryantsev and Richard M. Cripps.

The genome of *Drosophila melanogaster* has 60% of its genes in common with the human genome, and 77% of known human disease causing genes have a similar match to genes in the *Drosophila* genome. In addition, the muscles of *Drosophila* show similar structure and pathway of development to the muscles of humans, which allows **Drosophila** to model human muscle disorders. However, little is known about many of the genes and their potential role in muscle development. Thus, the focus of this project is to efficiently screen for potential transcriptional regulators of muscle development and identify associated disorder phenotypes. Genes were selected based on having a potential role in transcriptional regulation, which were silenced using RNA inhibition (RNAi). The flies with the RNAi were collected and assayed to measure the effects of this genetic loss in the flight and jump muscles by measuring a readout of enhancer activity in these flies. Those with significant differences in muscle development were immunostained to visualize the muscles. All 101 genes in the latest set have been assayed for a change of enhancer activity in flight muscles; where severe loss, moderate loss, no change, and gain were 15%, 23%, 44%, and 18%, respectively. In previous sets, genes with a severe loss showed unfused myoblasts and genes with a moderate loss showed thin myofibrils. Therefore, the results demonstrate that the screen is efficient in identifying potential transcriptional regulators and muscle disorder phenotypes.

ABSTRACTS: ORAL PRESENTATIONS

The bolded author is the presenter.

† Undergraduate Student, * Postbaccalaureate Student, ‡ Graduate Student

55 Branch Movements in Creosote (*Larrea tridentata*) Are Related to Plant and Environmental Water Stress.

Alesia Hallmark‡, Marcy Litvak, Robert Pangle and Gregory Maurer.

Near-surface, repeat digital photography has emerged as a powerful tool to collect continuous observations of plant traits. To date, this technology has largely been used to detect patterns of vegetative phenology. Little work has been done to use digital photographs to quantify changes in canopy structure or shifts in canopy function on shorter time scales. In this study, we tracked the position of creosote (*Larrea tridentata*) branches using time-series photos taken in a creosote-dominated shrubland in central New Mexico. Temperature, humidity, soil water content, soil water potential, and stem water potential also were measured. We found that both living and dead woody branches displayed dramatic diurnal patterns of movement, with some branches displaying vertical movements of more than 0.25m. Although movements in plants are often attributed to cyclical patterns of photoperiod, we found that creosote branch movements were best correlated with changes in humidity and temperature. Branch position may alter precipitation interception and soil temperature around creosotebush. To our knowledge, this is the first study to describe diurnal patterns of branch movements in creosote and is the most extensive dataset of observations of diurnal movements in any woody plant. It provides more knowledge about the biology of a desert shrub, but also offers novel methods for using repeat digital photography to gain inferences about plant form and function.

56 Reproductive Success of Bonytail (*Gila elegans*) Reared in Off-channel Habitats Assessed via Parent–Offspring Genotyping.

Megan Osborne, **Alyssa Sanchez**† and Thomas F. Turner.

Bonytail chub (*Gila elegans*), once a prominent species in the Colorado River, has experienced the most dramatic declines of the Colorado's four "big river" fishes due to the introduction of non-natives, installation of mainstem dams, and water development. Bonytail is now considered functionally extinct in the wild and efforts to reestablish the species have thus far been unsuccessful. An alternative management strategy was proposed in 2002 that proposed using isolated and protected backwaters for reproduction and rearing. Our aim was to understand effects of demographic factors, such as breeding behaviors, on genetic diversity in fish reared in isolated habitats. For three years, two backwaters, Nevada Egg and North Nine Mile, were stocked with equal numbers of male and female adult bonytail. Over the course of the summer, larvae and age-0 fish were collected. To facilitate parentage analysis and to obtain estimates of genetic diversity, all fish were genotyped at 18 microsatellite loci. The results indicated that 23-97% of adults contributed to offspring and genetic effective size ranged from 70-156. Variance in reproductive success did not differ by males and females and genetic diversity is maintained from the parents to the progeny. Recruitment success appears to be driven by water quality differences among backwaters. When conditions are favorable, most individuals contribute to progeny production.

57 What Does a Prudent Pika Pick? Spatial and Temporal Dietary Trends of an Alpine Mammal.

Marie L. Westover‡ and Felisa A. Smith.

Climate change is driving changes in species and communities worldwide, including range shifts, local extirpation, and population declines. The specific mechanisms remain unclear, but may include physiological limits or the reduction in food sources. Previous research has shown that the American pika

(*Ochotona princeps*) is sensitive to increased temperatures, but whether their population declines are directly due to temperature stress or indirectly due to their dietary change is debated. Pikas are central-place foragers that do not hibernate, but instead store food for the winter in hay piles, and thus may be particularly sensitive to changes in vegetation. We hypothesize that variation in diet may be an important factor influencing pika populations. We predict that pika populations' diets will have changed in response to climate change, and that pikas will exhibit seasonal variation in their diet. Using carbon and nitrogen stable isotopes, we characterize the isotopic dietary niche of nine populations of pikas from the southernmost limit of their range to central populations in the southern Rocky Mountains and compare historical to modern populations. We use bone isotope values to compare populations over space and historical time, and fur isotope values to study seasonal variation in diet. We find that there is no significant change in dietary niche space over historical time or latitude. We find that populations tend to exhibit more variation seasonally than over decades. While limited to the southern Rocky Mountains, our findings suggest that pika are constrained in their diet composition across space and historical time.

58 Consequences of Shrub Encroachment on a Bee Community.

Julieta Bettinelli‡ and Diane Marshall.

Over the past 150 years, numerous populations of native shrubs worldwide have increased in density and cover, effectively invading neighboring grassland communities. In the American Southwest, desert grasslands have been extensively replaced by *Larrea tridentata*, causing decreased plant cover and diversity. This reduction in floral reward diversity is likely to affect pollinators, which in turn have a major role in plant reproduction. *L. tridentata*, however, provides considerable floral resources. Therefore, the consequences of shrub encroachment in this habitat are likely to be complex, and will depend on the extent that *L. tridentata* can be utilized by the pollinator community, as well as on whether the decreased abundance of forb species can successfully attract and sustain those pollinators which cannot rely on the shrub. This study evaluates the effect of *L. tridentata* encroachment on the diversity and abundance of bee communities. Thirty-minute bee surveys were conducted at side-by-side plots (grassland vs. shrubland) weekly from July to September 2015 to evaluate differences in overall bee community composition. Overall bee abundance was higher in the grassland sites compared to shrubland sites and community composition was markedly different. Shrubland sites were dominated by *L. tridentata* and its associated bees. In contrast, several plant species had high number of bee visitors in the grassland, contributing to an overall increased diversity. Bee diversity worldwide is highest in arid-temperate areas, such as the American Southwest. Therefore, shrub encroachment and the consequent displacement of the unique grassland bee community, effectively reducing overall diversity, is cause for concern.

59 Evaluating the Relationship of Temperature and Growth of Larval Colorado River Suckers (Catostomidae) Through Otolith Aging and Stable Isotopes ($\delta^{18}O$).

Adam L. Barkalow‡, Thomas F. Turner, Nicu-Viorel Adutorei, Seth D. Newsome, Mark C. McKinstry and Steven P. Platania.

It is well understood, through laboratory experiments, that growth rates of larval fishes are related to environmental temperature. However, assessing the relationship between growth and environmental temperature of riverine fish larvae in the wild is confounded by larval movement (e.g., via drift and diel movements) and because larvae can actively seek thermally heterogeneous mesohabitats. Isotopic analysis of otoliths from larval Colorado River fishes could facilitate better understanding of thermal ecology of larvae in natural settings. For example, analysis of oxygen isotope ratio ($\delta^{18}O$) of an otolith is a validated method for evaluating the environmental temperature experienced by a fish. Here we present a method of obtaining $\delta^{18}O$ individual larval otoliths and compare these results with daily growth rates based on counts of otolith annuli and body size. We used specimens of two Colorado River catostomids, Flannelmouth Sucker *Catostomus latipinnis* and Bluehead Sucker *Pantosteus discobolus* collected in the lower Grand Canyon in 2015. Hypolimnetic releases from Glen Canyon dam have lowered mainstem water temperatures compared to historical values of the Colorado River within the Grand

Canyon. Colder water temperatures lead to decreased growth rates of ectothermic larval fishes and prolong larval period duration. However, analysis of $\delta^{18}O$ of otoliths and growth rates from larval suckers suggests that larvae use thermal refugia within the Grand Canyon and these warmer environments offset negative effects of colder temperature on growth and development. Nonetheless, larval growth rates are much slower compared to those in warmer systems.

60 Islands as Drivers of Diversity: A Genomic Perspective on Meso-carnivore Diversity and Hybridization

Jocelyn P. Colella‡, Tianying Lan, Sandra L. Talbot, Joseph A. Cook and Charlotte Lindqvist.

Contemporary mammalian biodiversity in North America has been shaped by cycles of population isolation and divergence driven by Quaternary glacial advances, and subsequent population expansion and contact during glacial retreats. As a consequence of expansion, divergent lineages, previously isolated in independent glacial refugia, came into secondary contact, but the extent to which climate-mediated admixture contributed to contemporary diversity remains poorly explored. Using Illumina whole-genome sequence data, I investigated the role of hybridization in the genomic evolution of a Holarctic carnivore, the ermine (*Mustela erminea*). I demonstrated divergence among four lineages coincident with known North American refugial centers: Beringia (Alaska–Siberia), West, East, and North Pacific Coast (NPC). I identified multiple bouts of hybridization, including contemporary hybridization at a contact zone along the Alaska–Yukon Territory border, between East and Beringia lineages, and an earlier episode of East-Beringia admixture spurring the evolution of the genetically distinct and insular endemic, NPC Island lineage. Isolated in a coastal refugium during the Last Glacial Maximum (~21 Kya), the NPC Island lineage subsequently diverged, suggesting an alternative model of hybrid speciation that may be especially common in high-latitude mammals: allopatric divergence after ephemeral gene flow. While hybrid-based divergence in this coastal environment has immediate evolutionary consequences and conservation implications for ermine, it also offers an alternative lens for viewing the role of islands or glacial refugia as engines of biological diversification.

61 Adaptive Phenotypic Variation in Native, Invasive, and Crop Populations of *Brassica tournefortii*.

Brian Alfaro‡ and Diane L. Marshall.

Contrasting evolutionary mechanisms among discrete groups of plant populations can produce disparate patterns in variation, and these patterns may predict evolutionary trajectories of wild, agricultural, or invasive populations. Potential differences can depend on genetic and environmental factors that are present in each population. Depending on how these factors interact, correlations between trait values and fitness or trait values and environmental gradients may result in adaptive clinal variation. These clinal patterns, however, can change in organisms dispersed accidentally or intentionally by humans to new habitats. Here, we examine phenotypic variation in an important cosmopolitan desert species to determine whether its evolutionary patterns have changed in invasive and agricultural populations.

62 Estimating Levels of Introgression between Gila Trout (*Oncorhynchus gilae*) and Rainbow Trout (*O. mykiss*) using Next-generation Sequencing Data.

David Camak‡ and Thomas F. Turner.

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 Gila River and San Francisco River drainages based on various genetic markers. Understanding levels of introgression is crucial for management and conservation of genetic diversity. Previous genetic data suggested admixture with nonnative Rainbow Trout (*O. mykiss*) and native Gila Trout individuals from the Iron Creek lineage through illegal stocking or movement over barriers. Despite shared allozyme and microsatellite alleles between the Iron Creek lineage and Rainbow Trout, mtDNA analyses indicate no shared haplotypes. Gila and Rainbow Trout are close relatives and shared alleles could result from common recent ancestry rather than introgression. We used next-generation sequencing and SNP genotyping to increase resolution of genetic variation and gain a better insight into levels of introgression

between Gila and Rainbow Trout lineages. About 30 individuals from each relict Gila Trout lineage and source Rainbow Trout lineages were sequenced and genotyped. Initial results are consistent with previous data, indicating five distinct Gila Trout lineages with varying levels of diversity within each lineage. Results show no indication of substantial introgression among the five relict Gila Trout lineages and Rainbow Trout. Initial results, however, are based on averages across and within lineages, which may underrepresent hybrid origins, especially if introgression has been low.

63 Comparative Population Genetics of Two Congeneric Duck Schistosomes, *Trichobilharzia querquedulae* and *T. physellae*.

Erika T. Ebbs ‡, Eric S. Loker, Veronica Flores and Sara V. Brant.

Host–parasite systems exist across complex and ecologically heterogeneous landscapes; they evolve at the population level and are shaped by many co-occurring factors (immunology, evolutionary constraints, ecology). Host ecology is thought to be important in shaping parasite microevolution; however, identifying relevant ecological factors is challenging as it is unknown to what extent evolutionary history has determined contemporary microevolutionary patterns. In an effort to control for this, we assessed the population genetics of two congeneric trematodes (*T. querquedulae* and *T. physellae*), assumed to have evolved under similar evolutionary constraints. These worms infect ducks and freshwater snails; both *T. querquedulae* and *T. physellae* infect *Physa* spp. snails, which are common snails throughout North America and one species (*Physa acuta*) is globally invasive. These worms are associated with different duck groups in distinct lineages and with different habitat preferences and distribution. *Trichobilharzia querquedulae* is found globally, while *T. physellae* is restricted to North America. In comparing *T. querquedulae* and *T. physellae* from 20 different localities, we see strong discordance of population genetic patterns and intraspecific variation, based on CO1 and ND4 genetic markers. *Trichobilharzia querquedulae* maintains greater genetic diversity and effective population sizes than *T. physellae*. Within host diversity of *T. querquedulae* is equal to between host diversity, suggesting a well-mixed and genetically diverse metapopulation. These data represent populations' sampled across the range of two widely distributed congeneric trematodes and reveal strikingly different microevolutionary stories, suggesting the importance of evolutionary and ecological forces in shaping the evolutionary potential of *Trichobilharzia* populations.

64 Adaptive Polynomial Expansion Method for the Numerical Solution of the Lenard-Balescu Equation.

Justyna Tafoya †, Abby Hickok, Loek Van Heyningen, Bilyana Tzolova, Omer Tekin, Chris Scullard and Frank Graziani.

The National Ignition Facility (NIF), at Lawrence Livermore National Laboratory, carries out experiments in nuclear fusion. The experiments' goal is to create ignition with a larger energy output than input. Given the physical conditions occurring in the experiments at NIF, the nuclear fuel becomes a plasma. The plasma consists of protons and electrons which are well described by the quantum Lenard-Balescu equation. This project attempts to provide a mathematical model of a system when these two particle types are set at different initial temperatures that then reach equilibrium. The approach consists of expanding the solution in orthogonal polynomials and simplifying the quantum Lenard-Balescu equation to the Landau equation by taking the classical limit of $\hbar \to 0$. We start with a system of coupled ordinary differential equations governing the distribution functions of each particle type. In a previous study this equation was solved for a one particle system, however, a problem occurs when the initial temperatures of the particles are too far from the equilibrium temperature of the system. In this case, the system of differential equation solver crashes due to a loss of resolution as the coefficients become too large. We propose to remedy this problem by periodically re-projecting the coefficients onto a new basis of polynomials in order to avoid them growing too large. We call this the adaptive method. These re-projected coefficients can then be used to solve for the distribution functions of each particle type given initial conditions, regardless of separation of initial temperatures.

65 Combining $\delta^{13}C$, $\delta^{15}N$, and $\delta^{2}H$ to Better Understand the Ecology of Eastern Pacific Green Sea Turtles (Chelonia mydas).

Laura Pagès Barceló ‡, Jeffrey A. Seminoff, Calandra Turner-Tomaszewicz, David Aurioles and Seth D. Newsome.

Sea turtles have been severely impacted by numerous anthropogenic activities and yet we know little about their ecology because their elusive nature makes them difficult to study. Two aspects we still know little about are their resource and habitat preferences, and how these vary among individuals or age classes. Carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope analysis has proven to be a useful tool for characterizing sea turtle diet composition and habitat use. Here we compare $\delta^{13}C$ and $\delta^{15}N$ data with hydrogen isotopes $\delta^{2}H$) to assess if $\delta^{2}H$ can be used to characterize resource and habitat use in green sea turtles living along the Pacific coast of Baja California Sur, Mexico. We measured skin $\delta^{13}C$, $\delta^{15}N$ and $\delta^{2}H$ values from 82 green sea turtles collected from two open ocean and three lagoon sites. Using a logistic regression model, we found that $\delta^{2}H$ values, in conjunction with $\delta^{13}C$ and $\delta^{15}N$ isotopes, can help differentiate sea turtle habitat into either open ocean or lagoon habitats; for this model, the residual deviance for lack-of-fit was 0.99 with a classification threshold of 0.9, indicating a strong fit and high classification accuracy. Thus, our preliminary results show that $\delta^{2}H$ can be used in three-factor models to more accurately interpret sea turtle habitat use. Furthermore, $\delta^{13}C$ values for lagoon sites cluster together indicating an individual habitat-diet specialization. Our results suggest that the use of hydrogen stable isotope as a third variable may be a valuable tool for understanding sea turtle ecology in coastal settings.

66 Sex-stratified DNA Repair SNPs in Melanoma Risk and Survival.

Christopher Hughes †, Jenna Lilyquist, Kirsten White, Salina Torres, Li Luo, Eszter Erdei, DeAnn Lazovich and Marianne Berwick.

Cutaneous melanoma utilizes a complex and dynamic route to pathogenesis that is not entirely understood. Over the past several decades incidence rates have risen and fueled investigations to elucidate the causes of melanoma. In 2017, 87,110 new melanoma cases are predicted, with an estimated 9,730 deaths. Males experience higher mortality and incidence rates than females, but little is known about the sex-dependent biological differences for risk and survival. As melanoma confers the highest mutational burden of any cancer, DNA repair capacity is an ideal etiology target. DNA repair variants, or single nucleotide polymorphisms (SNPs), within these genes may influence sex-disparities in melanoma risk and survival. We genotyped 893 melanoma cases and 766 control participants from the Minnesota Skin Health Study for 92 SNPs in 20 DNA repair genes. Males had four SNPs in three genes associated with melanoma risk, while five SNPs in two genes were associated with female risk. Multiplicative SNP interactions with environmental exposures identified 17 SNPs in six genes for male risk and 21 SNPs in 10 genes for female risk. Survival analyses revealed two homozygous SNPs in males and one homozygous SNP in females that negatively impacted patient survival. This study establishes the epidemiological plausibility for a putative causal role of DNA repair variants in sex-dependent risk and survival in melanoma patients. Further studies are needed to fully evaluate the potential mechanistic role of these SNPs in melanoma sex-disparities.

67 Investigating Protein Function in Living Cells by Proximity-based Protein Labeling.

Larisa Breden †, Yabin Song, Guihua Zeng and Fu-Sen Liang.

New methods for investigating protein functions in live cells are needed because fluorescence protein tags are bulky and can potentially interfere with normal structure and/or function of the tagged proteins. Although chemical probes—another labeling option—are smaller, they have limited targeting specificity and coupling efficiency onto chosen proteins. To address the current hurdles in protein labeling, we plan to develop a novel technology, Proximity-Based Protein Labeling, that enables the self-catalyzed labeling of proteins of interest (POI) in live cells. The technology mimics the posttranslational modification process of the Hedgehog (Hh) protein and could be used to couple different

chemical probes with high efficiency and specificity to any chosen POI. The Hedgehog system contains a Hedgehog-Hint domain (HH), which induces the formation of an activated thioester linkage that can be targeted through nucleophilic attack. In our system, HH is fused to the C-terminus of a chosen POI and to a "probe transfer domain" (PTD). The PTD recognizes a unique synthetic ligand linked to a protein-labeling probe and facilitates the coupling between the POI and the protein-labeling probe. Once optimized, this technique can be used to investigate or manipulate protein functions in live mammalian cells.

68 Effect of Terrestrialization of the Proteome of the Skin Mucus of African Lungfish (*Protopterus dolloi*).

Ryan D. Heimroth‡ and Irene Salinas.

Transitioning to life in terrestrial environments was a fundamental step in the success and diversification of the vertebrate lineage. Terrestrialization imposed many strenuous and novel challenges that ancestral vertebrates had never previously encountered. The outermost organ of the vertebrate body, the skin, underwent extreme functional and histological modifications in order to cope with these new challenges, such as desiccation stress, UV radiation and novel pathogens. Lungfish are the last extant relatives to the first tetrapods that are able to go through situational terrestrialization, making them the ideal model to study. We hypothesize that African lungfish will increase the amount of resources allocated to skin immunity early in the process of terrestrialization. In order to understand how lungfish cope with all of these novel aggressors, we collected skin mucus samples before and 10 days after entering terrestrialization, solubilized them and performed LC-MS/MS analysis of in-gel trypsin digested whole protein mixtures. We observed different protein patterns before and after terrestrialization, with 460 proteins in the control and 452 in the terrestrialized mucus sample. Gene ontology analysis revealed that 202 proteins were present in both samples, whereas 127 were unique to terrestrialized mucus. Moreover, terrestrialization resulted in an increase in the percentage of immune related proteins from 17.2% in the control to 25.5% after terrestrialization. Our results provide a first glance to the skin proteome composition of sarcopterygian fish and adaptation to terrestrial life.

69 Detail Not Easily Visible with X-ray Computed Tomography Revealed in Neutron Computed Tomography of Cretaceous Tyrannosauroid Dinosaur *Bistahieversor sealeyi* and Paleocene Phenacodontid Mammal *Tetraclaenodon puercensis* Skulls.

Katlin Schroeder‡, Thomas E. Williamson, Stephen L. Brusatte, Michelle A. Espy, Cort Gautier, James Hunter, Adrian S. Losko, Ronald Nelson and Sven Vogel.

Three-dimensional (3D) visualization of x-ray computed tomography (CT) has revolutionized the study of paleontology over the last decade, allowing paleontologists to gain essential insights into the anatomy, development and preservation of important specimens. Only rarely applied to vertebrate fossils, neutron computed tomography (NT) is an exciting new frontier in 3D visualization. Based on the interaction of neutrons and the nuclei of materials, NT is able to penetrate fossils impregnated with dense, iron-rich minerals otherwise impervious to traditional CT. We have applied NT to two specimens: the skull of the holotype of the Cretaceous tyrannosauroid *Bistahieversor sealeyi* and a nearly complete skull of the Paleocene phenacodontid *Tetraclaenodon puercensis* were scanned using high- and low-energy neutrons. To reduce attenuation due to scattering by hydrogen, a common component of plaster, a carbon fiber support jacket was constructed to hold the *Bistahieversor* skull. To allow a comparison of the two scanning techniques, the *Bistahieversor* skull also was scanned using 10MeV microtron CT at 100x100µm resolution, which to our knowledge is the highest resolution CT of an entire tyrannosaur skull ever made. Preliminary NT results revealed details of the internal bone structure of both specimens not readily visible with CT. NT showed that *Bistahieversor* possesses the extensive tympanic sinuses and elongate, tubular endocast that were once thought to diagnose only the largest-bodied, most derived tyrannosaurids like *T. rex*, whereas thermal NT scans showed *Tetraclaenodon* has an endocast that was not as proportionally large, and overall more primitive, than the brains of modern placentals.

70 Activation of the Signaling Intermediates β-catenin, STAT3, STAT5, and SOCS2 by the Intracellular Protozoan Parasite *Toxoplasma gondii*.

Hoang Bui† and Eric Y. Denkers.

Toxoplasma gondii is a globally distributed parasite that commonly infects humans and other warm-blooded animals. While infection in most cases is asymptomatic, *T. gondii* causes life-threatening disease in individuals with weakened immune systems, notably HIV/AIDS patients. In normal individuals, Toxoplasma elicits a strong protective immune response that facilitates 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 signaling pathway, activated STAT3 and STAT5 proteins are each involved in unique aspects of the immune response, and SOCS2 is known to be a suppressor of cytokine signaling. Previously, we found that β-catenin expression is increased during *Toxoplasma* infection in mouse dendritic cells and human fibroblasts. Here, we employed Western blotting to study expression of β-catenin, and the additional signaling molecules SOCS2, phospho-STAT3, and phospho-STAT5 over time following infection with *Toxoplasma* tachyzoites. In experiments employing mouse bone marrow-derived macrophages, we detected expression of SOCS2 after infection. Regarding β-catenin activation, when mouse dendritic cells were infected, we found increasing β-catenin levels throughout the nine-hour incubation time. STAT3 and STAT5 were similarly activated during infection. Our findings suggest that β-catenin, SOCS2, STAT3 and STAT5 are molecular components that act at the host–parasite interface during the intimate association of *Toxoplasma* with the mammalian cell.

71 Forensic Magnetic Resonance Imaging: Can We Predict Time of Death Based on Diffusion?

Jordan Weisend†.

Magnetic resonance (MR) imaging allows for the acquisition of a highly soft-tissue-sensitive image. This sensitivity cannot be reproduced using x-ray computed tomography (CT), a widely-used imaging technique. MR obtains primarily measurements of time, relating to the difference between time of release and recapture of a signal, whereas CT responds only to changes in density. User implemented changes in the signal timing schemes allow for the optimization of procedures for specific settings. This difference enables modifications for different applications of MR, where we apply MR to medico-legal death investigation. While this application is attractive for the non-invasive nature, there are still many questions regarding implementation procedures and optimization. Current literature shows that although MR can be highly sensitive to differences in soft tissue composition, this difference is also highly dependent on temperature. Here, we use animal decedents to access the relationship between petrification and temperature, analyzed using post mortem MR imaging. We initially analyzed the relationship between post mortem interval (PMI) and the applied diffusion coefficient, where we found what seemed to be a trend linking the two. Upon further analysis controlling for temperature, we found the relationship between PMI and the applied diffusion coefficient to be based solely on temperature. While we concluded that we cannot predict PMI based on diffusion, this study has contributed to the current understanding of MR applications in medico-legal death investigation.

72 Gene–Environment Interaction between a BDNF Polymorphism and Developmental Ethanol Exposure.

C.W. Bird, B.C. Baculis, J.J. Mayfield, G.J. Chavez, **T. Ontiveros***, D.J. Paine, A.J. Marks, A.L. Gonzales, D. Ron and C.F. Valenzuela.

Prenatal alcohol exposure is associated with learning, memory, attention, social, and mood deficits in humans, which are categorized as Fetal Alcohol Spectrum Disorders (FASD). There are many factors such as genetics, timing and pattern of exposure that play a role in susceptibility to FASD. Brain-derived neurotrophic factor (BDNF) plays a key role in neuronal development and synaptic plasticity. Here, we characterized the modulation of FASD severity by a polymorphism in the human BDNF

gene (val66met). The Val66Met genotype has been known to disrupt the secretion of BDNF, as well as increase the frequency of neuropsychiatric disorders such as depression and anxiety. We hypothesized that developmental alcohol exposure more severely disrupts behavior in mice carrying the $BDNF^{met/met}$ polymorphism. We used transgenic mice homozygous for either valine (val/val) or methionine (met/met) in the mouse equivalent of human residue 66. These were exposed to ethanol during the second and third trimesters of human pregnancy. We used traced fear conditioning, an associative learning task, which engages the hippocampus, to examine anxiety-like behavior, as well as modifying the task to minimize non-associative plasticity related to the aversive test. We found that, in adulthood, ethanol exposure reduced anxiety-like behavior and disrupted trace fear conditioning only in $BDNF^{met/met}$ mice, and that trace fear conditioning behavior was normalized with the modified paradigm. These studies suggest that the $BDNF^{met/met}$ polymorphism increases vulnerability to hippocampal damage due to prenatal alcohol exposure, and could be seen as a novel genetic risk factor that may aid in determining the severity of FASD.

73 Small Mammal Community Dynamics in Two Stable States: A Twenty Year Record.

Jennifer Noble‡, Sydney Jones, and Scott L. Collins.

In the American Southwest, grassland and shrubland co-occur as alternative stable states under a similar climatic regime. Over the next century, this region is expected to increase in aridity due to higher temperatures and longer periods between precipitation events. Climate models predict a ~10–20% decrease in winter precipitation, more variable precipitation, and a shift toward late season monsoon rains. The dominant grass (*Bouteloua eriopoda*) is detrimentally affected by drought and the dominant shrub (*Larrea tridentata*) is metabolically active at cooler temperatures, benefiting from late season rains, therefore climate change is expected to favor the expansion of shrubland, altering the boundary between these two stable states. To enhance our understanding of the biological drivers in this system, we used community dynamic metrics and structured equation modeling of long-term data on precipitation, standing biomass, net primary production, and small mammal presence/absence (1989 to present) to quantify temporal changes in the small mammal community in each stable state. Herbivores utilize the two states differently; tracking primary production, omnivores and carnivores utilize both states similarly irrespective of primary production. The ability to forage on multiple trophic levels to meet energetic demands reduces dependence on primary production. Changes in 29% of mice species explain 90% of the differences in landscape utilization. The shrubland community is historically more specious, but less populated, due to increased landscape heterogeneity, which increases the number of available niches in comparison to the grassland. Small mammal communities are not exhibiting directional change in either stable state, just a temporal reordering of the dominant species.

74 A Comparative Study of Island and Mainland *Anolis* Lizard Assemblages.

Chris Anderson‡ and Steven Poe.

The mechanisms by which assemblages of closely related species form have become a primary focus of evolutionary ecology. Comparative studies of island and mainland communities may provide novel insight into assemblage evolution. Differences between island and mainland ecosystems may cause differing evolutionary patterns in island and mainland assemblages. Adaptive radiations on islands are expected to result in assemblages that are phylogenetically clustered, but phenotypically diverse, whereas predator- and competitor-rich mainland environments may produce phenotypically uniform assemblages. Here we utilize a nearly complete phylogeny and a morphological dataset for 336 species of *Anolis* lizards (anoles) comprising 168 assemblages to test for differences in phenotypic and phylogenetic structure in mainland versus island assemblages. We present three main conclusions: (1) both mainland and island assemblages are phylogenetically and phenotypically clustered; (2) mainland assemblages tend to be more clustered than island assemblages, according to both phylogenetic and phenotypic measures; and (3) differences in degree of phenotypic clustering between mainland and island assemblages are not explained by differences in phylogenetic clustering alone.

75 Submerged Aquatic Macrophytes (SAMs) in the Sky: At Home in High Elevation Streams.

Virginia F. Thompson‡ and Clifford N. Dahm.

Submerged aquatic macrophytes (SAMs) are key species when present in aquatic ecosystems, but are not a ubiquitous aquatic ecosystem component. When present, they perform multiple ecosystem functions, including water quality enhancement, habitat structure, direct and indirect food sources, and nutrient cycling. Normally studied in low-elevation, low-gradient, often highly impacted river systems, SAMs were found in multiple high-elevation (2,500 m) stream systems in the Jemez Mountains, where they experience few human impacts; however, little was known about SAM communities in the area and at high elevation. We studied physical (geomorphology: depth, width, velocity, estimated discharge, and stream gradient) and biological parameters (percentage cover and biomass) of three Jemez Mountain river systems that contained SAM species in some locations to assess the SAM community of the Jemez. A Principal Components Analysis (PCA) and Mann-Whitney U tests showed that the physical parameters in surveyed systems differ in sites with and without macrophyes present. While no statistical differences in biomass were found in each system, different species compositions were found from river to river. Although elevation is a common limiting factor in biogeographic ranges of other plants, these results imply that elevation alone may not be key to shaping the geographic range of these macrophyte communities.

76 Microbial Community Diversity and Composition across a Latitudinal Gradient along the Antarctic Peninsula.

Kelli Hughes‡, David Van Horn, Uffe Neilsen and Rebecca Ball.

The Antarctic Peninsula is experiencing rapid changes due to global warming, which will likely alter species diversity and distribution as well as above- and belowground community linkages. We sought to evaluate the influences of sampling site latitude (as a proxy for warming changes) and soil vegetation cover type over bacterial community composition and diversity. Across all sampling sites and cover types, microbial communities were dominated by *Proteobacteria*, *Bacteriodetes* and *Acidobacteria*. The Random Forests (RF) machine learning classification algorithm could correctly distinguish microbial communities within sampling locations with 91% accuracy, with no decrease in accuracy associated with latitudinal changes. Similarly, we can distinguish between microbial communities associated with the five vegetation cover types with 77% overall accuracy. RF revealed grass to be the most distinctive cover type, while lichen- and algae-associated communities were indistinguishable from others. Grass also had the highest number of microbial species and lichen the lowest. However, lichen-associated communities were more distinguishable in the colder, more southern latitudes, indicating that lichen became more influential to microbial communities, while bare ground, grass, and moss-associated communities became less distinct. Additionally, more southern latitudes supported more diverse bacterial communities, particularly within lichen, grass, and bare soil associated communities. Our large-scale analysis of spatial diversity patterns indicates that aboveground vegetation impacts on belowground microbial communities change with latitude, and thus we have a better understanding of potential microbial community responses to global changes in maritime Antarctica.

77 Race against Time: Documenting Hairworm (Nematomorpha: Gordiida) Species Diversity of the Madrean Sky Islands.

R.J. Swanteson-Franz†, B. Hanelt, A. Schmidt-Rhaesa and M.G. Bolek.

Within parasitology, there is a lack of diversity surveys. Horsehair worms (Phylum Nematomorpha), which parasitize arthropods, are paradigms of this. Twenty-five thousand species are hypothesized to exist, but only 350 species have been described. There also has been inadvertent sampling bias, creating substantial hairworm data in some regions, while others remain virtually unstudied. Here, we focus on the diversity within the Madrean Sky Islands, a complex of high-altitude, pine-oak woodlands separated by lower-elevation Sonoran and Chihuahuan deserts, where, until recently, hairworm diversity surveys have not occurred. Sky Islands have ecological separation between mountains caused by abiotic

variation that mimics that of oceanic islands. This causes Sky Islands to become cradles of evolution and biodiversity hotspots due to a plethora of exceptional ecosystems and microhabitats. The Madrean Sky Islands are host to almost 7,000 plant and animal species, making it likely that similar diversity should exist for Nematomorphs. Using data from four years of specimen collections, we will describe the species found in the Madrean Sky Islands, specifically the Chiricahua Mountains of southern Arizona, using primarily molecular data. Previously described *Chordodes morgani* and *Neochordodes occidentalis*, and four new species (three *Gordius* n. spp. and one *Paragordius* n. sp.) have been identified. As far as we know, two species represent endemics. Since collections began, all sites have been consumed by wildfire—the impact of these fires on the life cycle and survival of these parasite species will be discussed, addressing the need for a paradigm shift in conservation to include parasites.

78 Study of Stomatal Response in Corn Plants.

Michelle R. Facette, David T. Hanson, and **Oscar Huamani Jimenez** †.

Leaves in plants have numerous small pore-like structures called stomata where most of gas exchange take place. Stomata in plants play a major role in carbon dioxide uptake and water loss through evaporation. To maximize CO_2 uptake and minimize water loss, plants open and close their stomata in response to environmental stimuli such as light, CO_2 concentration, atmosphere humidity and temperature. Fast stomatal responses (both opening and closing) due to environmental changes are favorable, since the rate of opening and closing determines plant water-use efficiency and CO2 uptake, thereby affecting drought tolerance and biomass accumulation. This study measured the rate of stomatal opening and closing in 10 different genetic inbred lines of corn in response to changing light conditions. These genetic variants present differences in stomatal morphology, leading to the hypothesis that they will present differences in the stomatal opening and closing rates. Initial rates of photosynthesis and stomatal conductance were measured and differed amongst the different inbred lines. Moreover, different corn inbreds have clear differences in stomatal opening and closing rates. Currently, quantitative measures describing stomatal morphology are underway to determine if there is a possible mathematical correlation between the stomatal shape and the rate of opening and closing. Identification of morphological features that promote fast stomatal response has potential for plant breeding. Moreover, the observation that there are differences in different genetic isolates of corn paves the way for future studies to determine the underlying genes promoting fast stomatal response.

79 Inactivation of the Anterior Thalamus Disrupts Directional Discrimination in an Object-place Paired Associate Memory Task.

Shannon M. Thompson *, Shawn S. Winter and Benjamin J. Clark.

The recollection of previous experiences and events, which include representations of what, where, and associations between these elements, has been extensively evaluated in procedures such as object-place paired associate (OPPA) tasks. This experiment rewards rodents when selecting an object encountered in a specific location, but not in other locations. Our laboratory has shown that representations of directional orientation, based on vestibular cues, facilitate the disambiguation of spatial locations in OPPA. The precise neural mechanisms underlying directional discrimination, however, is poorly understood. It is well known that the anterior thalamus contains large populations of head direction cells, which fire as a function of an animals' directional orientation. In the present study, we addressed the hypothesis that the anterior thalamus contributes to directional discrimination by inactivating the anterior thalamus with muscimol, a GABA agonist, and measuring subsequent performance in a previously trained OPPA task. Briefly, the task requires that rats learn to discriminate between an identical pair of objects presented in 180° opposite arms of a radial arm maze over 14 days. Twenty-four hours after the rats reached criterion in the, animals received either muscimol or saline infusion to the anterior thalamus and were tested in a 20-trial session. Our results indicate that muscimol inactivation of the anterior thalamus significantly reduced object choice accuracy relative to saline treated rats. Therefore, these observations provide confirmatory evidence that the anterior thalamus contributes to

directional discrimination in OPPA tasks and supports the notion that subcortical limbic circuits have a fundamental role in the recollection of previous events.

80 Understanding Carbon Flow in a Complex Intertidal Ecosystem Using Amino Acid $\delta^{13}C$ Analysis.

Emma A. Elliott Smith‡, Chris Harrod and Seth D. Newsome.

Understanding how energy moves through foodwebs, which sources of production support consumers, and the variation in these dynamics is a fundamental area of ecological research. Recently, stable isotope analysis of individual essential amino acids (AA_{ESS}) has become utilized in this regard. Because only primary producers and microbes synthesize AA_{ESS}, consumers typically route them directly into tissues, and they are minimally altered through food chains. Moreover, previous studies have found different producer taxa have highly distinct $\delta^{13}C$ AA_{ESS} values, which can provide a carbon 'fingerprint' in consumers. We analyzed marine producers and intertidal macroinvertebrates collected at a single site in Alaska in 2012. We characterized the $\delta^{13}C$ AA_{ESS} 'finerprints' for four marine producers: a kelp (*Laminaria* sp.), green algae (*Ulva* sp.), red algae (*Neorhodomela* sp.) and particulate organic matter (POM). We also analyzed four species of invertebrate consumers: *Mytilus*—a filter feeder; *Strongylocentrotus*—a grazer; *Nucella*—a secondary consumer; and *Pycnopodia*—a tertiary consumer. We used linear discriminant analysis (LDA) and isotope mixing models (MIXSIAR) to test how well $\delta^{13}C$ AA_{ESS} values could distinguish between our producer groups, as well as to classify the source of our consumer AA_{ESS} carbon. Our LDA analysis showed an 88% successful reclassification rate between our producers. The LDA and MIXSIAR indicated that POM/red algae was most important for *Mytilus* and *Strongylocentrotus*, whereas kelp was the most important AA_{ESS} carbon source for *Pycnopodia* and *Nucella*. Our study demonstrates the utility of $\delta^{13}C$ AA_{ESS} analysis in disentangling complex marine foodweb dynamics.

THE UNIVERSITY *of*
NEW MEXICO

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