



Program & Faculty Guide

UNLV School of Life Sciences

UNLV

UNIVERSITY OF NEVADA, LAS VEGAS



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UNLV School of
Life Sciences



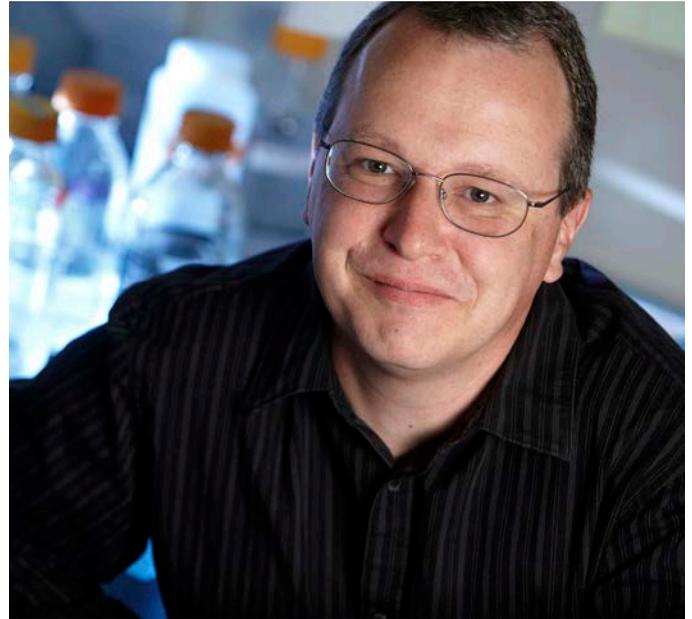
From the Director

The School of Life Sciences (SoLS) is one of the largest academic units on the University of Nevada, Las Vegas (UNLV) campus. It has 30 full-time faculty members, 10 adjunct and research faculty, more than 1,900 undergraduate majors, and approximately 55 graduate students. The school's offices and laboratories are located in four buildings: Juanita Greer White Hall (WHI), the Science and Engineering Building (SEB), the White Hall Annex (WHA2), the Campus Lab Building (CLB). Research facilities on campus include centers for bioinformatics/biostatistics with access to supercomputer facilities, confocal and biological imaging core with a new a high-speed laser-scanning microscope, genomics center, greenhouses, tissue culture facilities, environmental chambers and modern animal care facilities.

The faculty research and graduate programs are organized into Bioinformatics, Cell & Molecular Biology, Ecology & Evolutionary Biology, Integrative Physiology, and Microbiology. SoLS faculty are recruited from some of the best research institutions and currently collaborate with the Nevada Institute of Personalized Medicine (NIPM), Lou Ruvo Center, Desert Research Institute (DRI), BLM, USGS, US National Park Service, and with faculty and researchers at many universities and government agencies throughout the nation and international institutions, providing expanded opportunities for our students. The faculty compete successfully for funding from BLM, DOE, DOI, FWS, NASA, NIH, NSF, USDA, USGS and other agencies. Given the high research productivity, the high current and potential synergy with important regional entities, and the large number of majors, the School of Life Sciences is uniquely poised to contribute to the UNLV Top Tier Goals.

The UNLV campus is located near the intersection of the Mojave, Sonoran, and Great Basin deserts and is also situated in close proximity to broad elevation gradients (600-3600m) with snowcapped mountains in the winter. Within a one-hour drive are numerous recreation and scenic areas, including two National Recreation Areas (Lake Mead and Spring Mountain), Red Rock Canyon Natural Conservation Area, and Valley of Fire State Park. Within a three to five hour drive are many other natural areas, including several famous National Parks (Death Valley, Grand Canyon, Zion, Bryce).

Las Vegas is best known as a center for entertainment and recreation and is a rapidly growing Southwestern city with a broad economic and cultural base. UNLV is an integral part of the Las Vegas culture and environment with nationally recognized musical, dramatic, dance, and artistic performers regularly visiting campus. Several popular lecture series bring in well-known politicians, newsmakers, and scientists. The 135-ha campus is characterized by modern facilities, and surrounded by both traditional lawns and desert landscaping.



School of Life Sciences Director Frank van Breukelen

About UNLV

Since its first classes were held in 1957, the University of Nevada, Las Vegas (UNLV) has transformed from a small branch college into a thriving urban research institution. Along the way, UNLV has become an indispensable resource in one of the country's fastest-growing and most enterprising cities.

Today, UNLV is a doctoral-degree-granting institution of nearly 30,000 students, 3,000 faculty and staff, and more than 100,000 alumni. A federally designated Minority Serving Institution, UNLV has nationally recognized programs in the arts, sciences and health sciences, hospitality, law, and liberal arts.

Mission

The University of Nevada, Las Vegas is a public research institution committed to rigorous educational programs and the highest standards of a liberal education

UNLV's Top Tier Mission

UNLV's diverse faculty, students, staff, and alumni promote community well-being and individual achievement through education, research, scholarship, creative activities, and clinical services. We stimulate economic development and diversification, foster a climate of innovation, promote health, and enrich the cultural vitality of the communities that we serve.

Diversity

At UNLV, we have come together and created one of the most affirmative and dynamic academic environments in the country. UNLV continues to rise in U.S. News & World Report's annual listing of the nation's most diverse universities for undergraduates. The university is tied for first in the publication's annual Best Ethnic Diversity listing. UNLV has placed in the top 10 for the past six years and continues to show our commitment to serving our wonderfully diverse population and building the future for Las Vegas and Nevada.

UNLV is accredited by the Northwest Commission on Colleges and Universities.



Programs

Bachelor of Science in Biological Sciences

Biology is the study of life. The earth is filled with an enormous variety of living organisms; therefore, an understanding of the basic biological processes common to all organisms is essential to understanding the world. In recent decades, great strides have been made in understanding important biological processes, particularly those at the molecular, cellular, and ecosystem levels. An understanding of biological systems depends, in part, on the principles of physics and chemistry; thus a firm background in the physical sciences is also important in the study of biology. For many, an undergraduate major in biology (Bachelor of Science (B.S. Degree)) serves as a basis for postgraduate study in the life sciences. School of Life Sciences graduates have gone on to advanced graduate study, leading to careers in college or university teaching, basic and applied research, and public health. Many have entered professional programs in medicine, veterinary medicine, and dentistry. Other graduates have gone directly into secondary (high school) science teaching, the biomedical industry, independent laboratory research, natural resources management, or environmental education.

The Biological Sciences undergraduate degree program aims to diversely train its students, enabling graduates to pursue careers or advanced degrees in life and health sciences, research, education, industry, or governmental work. Based on their individual interests, students may select from the following concentrations: **Cell and Molecular Biology, Ecology and Evolutionary Biology, Integrative Physiology, Microbiology,** and **Pre-Professional Studies**. All biology undergraduate students must complete a minimum of 120 credit hours. Each concentration may require specific upper division courses; therefore the number of upper division electives may vary across concentrations.

Master of Science in Biological Sciences

The Master of Science (M.S.) degree in Biological Sciences within the School of Life Sciences (SoLS) consists of four sectional research concentrations that reflect the scope of modern biology: **Ecology and Evolutionary Biology (EEB), Integrative Physiology (IP), Cell and Molecular Biology (CMB), Microbiology (MB),** and **Quantitative Biology and Bioinformatics (QBB)**. The degree is research centered and requires the defense of a thesis that describes a novel research project that can serve as the basis for the publication of at least one paper in a peer-reviewed journal. The M.S. degree in Biological Sciences prepares students for careers in education, government, and industry as well as preparing them for more advanced degrees in the life sciences. Students must complete a minimum of 30 credit hours from a list of core and approved courses within their section.

All students graduating with a Master's of Science in Biological Sciences should be able to:

- Master a critical set of key concepts specific for each sectional concentration.
- Become familiar with key methodologies specific for each sectional concentration.
- Comprehend and critically evaluate the current published scientific literature.
- Engage in scientific research in which the individual can formulate hypotheses, generate high quality data, and evaluate that data for reasonable scientific conclusions.
- Communicate scientific results effectively in oral presentations to general and specialized audiences.
- Communicate scientific results effectively in written reports suitable for publication.
- Instruct and engage students and members of the community at all levels to appreciate the importance of biology in their lives.

Programs Continued

Doctor of Philosophy in Biological Sciences

The Doctor of Philosophy (Ph.D.) in Biological Sciences within the School of Life Sciences (SoLS) consists of four sectional research concentrations that reflect the scope of modern biology: **Ecology and Evolutionary Biology (EEB)**, **Integrative Physiology (IP)**, **Cell and Molecular Biology (CMB)**, **Microbiology (MB)**, and **Quantitative Biology and Bioinformatics (QBB)**. The degree is research intensive and designed to prepare students for careers in academia, government, and industry as engaged scholars who are experts in their chosen field. Students must complete a minimum of 60 credit hours from a list of core and approved courses within their research section. They must engage in independent research that is novel and exciting culminating with a dissertation that makes an important contribution to their chosen field. As such, it is expected that their dissertation work will be published in peer reviewed journals with the student listed as first author. Successful students are also trained and expected to develop as effective teachers and educators, and each student must serve as a teaching assistant for two semesters as part of the degree program.

All students graduating with a Ph.D. in Biological Sciences should be able to:

- Master a critical set of key concepts specific for each sectional concentration.
- Gain expertise with key methodologies and experimental techniques specific for each sectional concentration.
- Read, comprehend, and critically evaluate the current published scientific literature.
- Evaluate a scientific question and formulate testable hypotheses.
- Independently design experiments to effectively test hypotheses.
- Generate and collect reproducible data.
- Access up-to-date methods for analyzing and tabulating data.
- Communicate scientific results effectively in oral presentations to general and specialized audiences.
- Communicate scientific results effectively in written reports for publication in peer-reviewed journals.
- Apply and be competitive for extramural monies to fund research.
- Instruct and engage students and members of the community at all levels to appreciate the importance of biology in their lives.



Facilities

Biocomputing Center

The Biocomputing Center supports the teaching and research missions of faculty at the School of Life Sciences and their associates in bioinformatics, biostatistics, biomathematics and biomodelling. Located in Room 204, Juanita Greer White Hall, this center is equipped with servers and work stations and is directly linked to the supercomputer clusters in the National Supercomputing Institute on campus (<https://www.nscee.edu/>). Software available for research and teaching includes Matlab (with Bioinformatics, Statistics, and Simulation Biology modules), Mathematica, CLC Genomics Workbench, and free, open source packages such as MACS, Trinity, Bowtie/Tophat/Cuffdiff/CummeRbund, and HISAT/StringTie/Balgon. The center fosters collaborations among faculty members and students for analyzing “big data” from Next-Generation Sequencing (RNA-seq, Chip-seq, and Exome sequencing), Genome-Wide Association Studies, Network Analyses, and modeling of water transport in plants. The software at the Center can also be used in general for addressing a wide variety of models based on ordinary or partial differential equations.

UNLV Confocal and Biological Imaging Core

Laser scanning microscopy (LSM) has revolutionized our ability to investigate complex biological processes with light microscopy. These capabilities have vastly broadened the scope of questions being addressed in biological systems to the extent that LSM has become a basic tool for the advancement of research. The UNLV Confocal and Biological Imaging Core (CBI Core) is a fee-for-service, multi-user facility committed to providing access to both confocal and multiphoton microscopy for all Nevada researchers. The Confocal and Biological Imaging Core has had a profound impact on infrastructure and enhances our ability to develop innovative and timely research products. Current users are from research groups in the UNLV College of Engineering, College of Liberal Arts, College of Nursing, and College of Sciences.

The current instrument is a state-of-the-art Nikon A1R CLSM with a resonance scanner for high-speed imaging of living samples and spectral unmixing for advanced applications. This system is mounted on a Nikon Eclipse Ti body equipped with a CLSM imaging resonance scanner, for rapid acquisition of images from living samples. Two additional digital imaging systems are available for epifluorescence and other types of light microscopy: a high resolution charge-coupled device (CCD) and a highly sensitive electron-multiplying CCD (EMCCD). The CBI core operates a separate image processing workstation that runs the commercial image processing and analysis application Volocity. A multiphoton fluorescence microscope system will be installed in early 2018.

The core operates both as a shared instrument facility and re-charge center. Every new user must demonstrate proficiency with the CLSM before receiving access to the facility. A web-based reservation program is used to schedule time in the Imaging Core. User fees are revised on a yearly basis, and assessed quarterly. The microscope is located in the UNLV Science and Engineering Building.

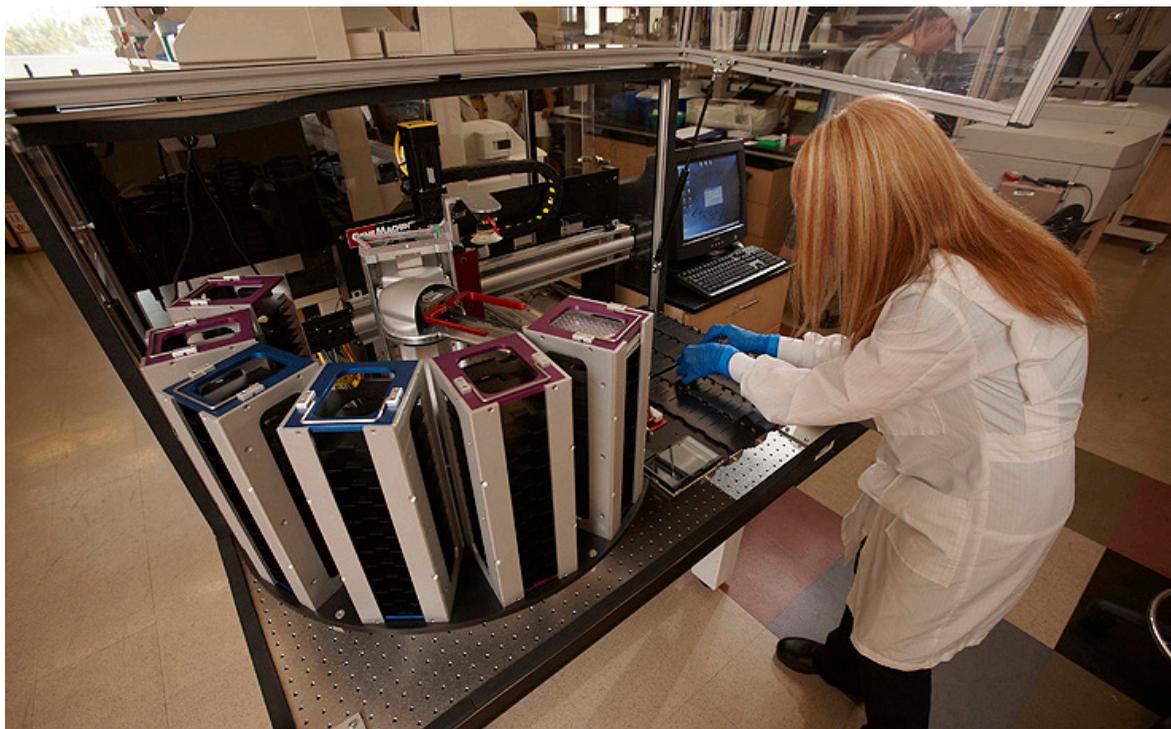
UNLV Genomics Core Facility

The UNLV Genomics Core Facility is a non-profit recharge laboratory designed to aid biomedical, biotech, and genomic research endeavors by providing users with access to essential instrumentation, services and technical expertise at the lowest cost possible. The UNLV Genomics Facility is

Facilities Continued

designed to aid researchers in studying the properties and functions of genes and their products. Our goal is to provide quality, timely, and reliable services to research laboratories and to serve as a training platform for scientists wishing to learn nucleic acid and protein techniques. Our services include: ABI 3130 DNA Sequencing, Affymetrix GeneChip® Microarray, Agilent 2100 Bioanalyzer RNA analysis, BD FACSCalibur Flow Cytometry.

We also offer a wide variety of state-of-the-art equipment on either a recharge basis, or free of charge. We are committed to helping scientists from all disciplines in life science take advantage of our services in order to answer questions enabled by genomics approaches. The UNLV Genomics Core Facility is a non-profit recharge laboratory designed to aid biomedical, biotech, and genomic research endeavors by providing users with access to essential instrumentation, services and technical expertise at the lowest cost possible.



Greenhouse

The SEB greenhouse is a core facility with four individually controlled bays and a communal headhouse. The headhouse contains the controls for an iGrow system that monitors the environment and adapts the mechanical systems to control conditions in each bay. The iGrow system uses information from its outside weather station and sensors in each bay to predict energy load. The program then calculates the best way to maintain a stable environment in each bay with minimal fluctuation. A system manager can also make changes remotely to each bay to help maintain or change conditions. In the event of a system failure and environmental condition falls outside of required specifications, the greenhouse is wired to the SEB Programmatic Alarm System which sends out an alarm so research will not be lost. The headhouse also contains space for small storage of items and work benches for preparation of materials.

Facilities Continued

The greenhouse bays each contain sensors monitoring temperature and humidity so the iGrow system will be able to monitor and adjust conditions to remain within user defined specifications. Bays are also equipped with domestic and RO water systems, movable benches and retractable solar shades.

UNLV National Supercomputing Institute

To provide computing, networking, and supercomputing resources for support of academic and research programs of Nevada's universities, community colleges, secondary and primary schools, advanced technology companies, and local, state and federal governmental agencies. To provide high-performance computing and networking resources for research and development programs requiring collaboration at the state, national and international levels. To facilitate high-technology economic diversification in Nevada by providing services not available in the private-sector and by promoting partnerships between university faculty and external entities.

In collaboration with Switch Communications and Cisco, there is a dedicated high-speed network available for research users. Currently, the research network connects the UNLV NSI data centers located in the UNLV Science and Engineering Building with our resources at SWITCH's SUPERNAP7 colocation facility. This connection consists of an aggregated 200Gb/s link over dedicated fiber. There is also a 10Gb/s connection to the Internet. In collaboration with Intel, Penguin Computing, and Switch Communications, the Cherry Creek supercomputer is now available for use.

Wesley E. Niles Herbarium

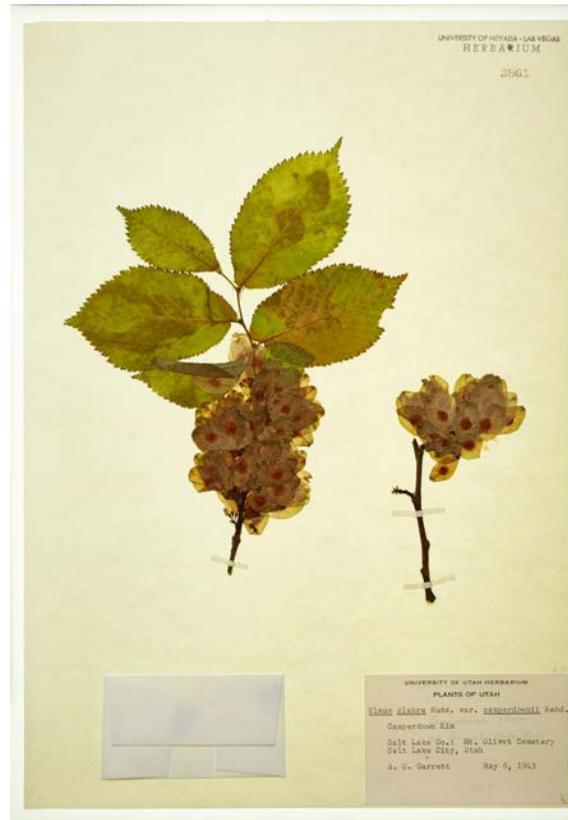
The Wesley E. Niles Herbarium is a collection of dried, pressed plant specimens mounted on sheets of archival paper, enclosed in species folders, and stored in airtight, metal cabinets for future reference



Facilities Continued

and long-term preservation. These specimens and the collection data accompanying them provide documentation for the past and present occurrence, distribution, and diversity of flowering plants, conifers, and mosses in the southwestern United States, especially the deserts and mountains of the Mojave ecoregion. The herbarium also serves as a center for research and teaching, and provides botanical support to governmental agencies and to the general public.

Dr. Wesley E. Niles (now faculty emeritus) founded the herbarium in 1970 soon after he arrived at UNLV. Four years after its inception, the herbarium was designated a "National Research Collection" by the Advisory Committee for Systematic Resources in Botany. Although 1200 herbaria in the United States were surveyed at the time, the UNLV herbarium was one of only 105 to be judged as essential and of such importance that its "loss or inaccessibility" would compromise taxonomic research in the United States and worldwide. It was the only herbarium in the state of Nevada and the Mojave ecoregion to be so designated.



The herbarium currently is comprised of a vascular plant collection of approximately 65,000 specimens, all of which are accessible in a digital database, and a smaller, but expanding collection of more than 4,000 bryophytes. As the herbarium grows in specimen numbers and value, its importance as a scientific resource has continued to extend beyond traditional taxonomic and systematic studies. It increasingly serves as a significant, if not an essential, resource for genetic sampling, conservation biology, understanding biogeographic patterns, and addressing environmental concerns such as natural and anthropogenic disturbances and climate change.

Graduate Students

Cellular and Molecular Biology

Victoria Amato - Ph.D. student
Advisor: Jeffery Shen

Santiago Bataller - Ph.D. student
Advisor: Jeffery Shen

Adrienne Bugayong - Ph.D. student
Advisor: Nora Caberoy

Jennifer Clark - Ph.D. student
Advisor: Allen Gibbs

Randolph Grell - Ph.D. student
Advisor: Kelly Tseng

Jesus Guerrero - M.S. student
Advisor: Mo Weng

Rosey Le - M.S. student
Advisor: Frank van Breukelen

Sheila Mosallaei - Ph.D. student
Advisor: Laurel Raftery

Nicholas Nelson - M.S. student
Advisor: Andrew Andres

Lorena Samentar - Ph.D. student
Advisor: Nora Caberoy

Anne Villacastin - Ph.D. student
Advisor: Jeffery Shen

Ecology and Evolutionary Biology

Maryam Hadi - Ph.D. student
Advisor: Elizabeth Stacy

Sotodeh Ebrahimi - M.S. student
Advisor: Lloyd Stark

Elizabeth (Wendy) Jones - Ph.D. student
Advisor: Donald Price

Carolyn Koehn - M.S. student
Advisor: Matthew Petrie

Corina Ledbetter - M.S. student
Advisor: Philippos Tsourkas

Robert Pelletier - Ph.D. student
Advisors: Frank van Breukelen and Jef Jaeger

Nikki Pirtel - M.S. student
Advisor: Matthew Petrie

Rebeca Rivera - M.S. student
Advisors: Scott Abella and Jef Jaeger

Tomoko Sakishima - Ph.D. student
Advisor: Elizabeth Stacy

Vivian Sam - M.S. student
Advisor: Scott Abella

Neil Savage - M.S. student
Advisor: Matthew Petrie

Katie Schultz - M.S. student
Advisor: Allen Gibbs

Matthew Simes - Ph.D. student
Advisor: Daniel Thompson

Casey Stamereilers - Ph.D. student
Advisor: Philippos Tsourkas

Chenoa Wilcox - M.S. student
Advisor: Scott Abella

Tamara Wynne - Ph.D. student
Advisor: Dale Devitt

Integrative Physiology

Dylan Guerin - Ph.D. student
Advisor: Kelly Tseng

Michael Isaacs - Ph.D. student
Advisor: David Lee

Cindy Kha - Ph.D. student
Advisor: Kelly Tseng

Austin McKenna - Ph.D. student
Advisor: Allen Gibbs

Claudia Silva Rubio - M.S. student
Advisor: Frank van Breukelen

Emma Weitzner - Ph.D. student
Advisor: Allyson Hindle

Microbiology

Timothy Alba - Ph.D. student
Advisor: Eduardo Robleto

Erin Cassin - Ph.D. student
Advisor: Boo Tseng

Molly Devlin - Ph.D. student
Advisors: Brian Hedlund and Duane Moser

Tatiana Ermi - M.S. student
Advisor: Eduardo Robleto

Ariel Friel - Ph.D. student
Advisor: Brian Hedlund

Dengxun Lai - Ph.D. student
Advisor: Brian Hedlund

Holly Martin - Ph.D. student
Advisor: Eduardo Robleto

Joy McKenna - Ph.D. student
Advisor: Helen Wing

Nancy Nou - M.S. student
Advisor: Brian Hedlund

Melissa Schofield - Ph.D. student
Advisor: Boo Tseng

Cale Seymour - M.S. student
Advisor: Brian Hedlund

Jillian Socea - Ph.D. student
Advisor: Helen Wing

Carmen Vallin - Ph.D. student
Advisor: Eduardo Robleto

Quantitative Biology and Bioinformatics

Dylan Barth - Ph.D. student
Advisor: Mira Han

Corinne Sexton - M.S. student
Advisor: Mira Han

Faculty Research Guide

UNLV School of
Life Sciences



Scott Abella

Assistant Professor
Ph.D., Northern Arizona University

Research Interests

- Restoration Ecology
- Fire Ecology
- Plant Ecology



Our lab's mission is producing and distributing high-quality ecological science that can help inform the conservation and restoration of ecosystems. To accomplish this mission, we have expertise in botany, plant ecology, soil science, fire science and management, restoration ecology, experimental and monitoring design, statistical analysis, and information synthesis.

Some examples of our current projects include:

- M.S. student project developing techniques for restoring native plants, including plants culturally important to Native Americans, in Glen Canyon National Recreation Area with the National Park Service.
- PhD student project assessing the long-term (multi-decade) effects of novel fire regimes on Mojave Desert ecosystems.
- Undergraduate research projects restoring riparian habitat along receding Lake Mead and evaluating visitation of pollinator insects to restored flowering plants.
- Using dendroecology to evaluate long-term forest change and forest health.
- Synthesizing the effectiveness of restoration and conservation practices and projects across U.S. national parks.

Selected Publications

Book

- Abella, S.R. 2015. *Conserving America's National Parks*. CreateSpace, Charleston, SC. 200 pp.

Journal Articles

- Abella, S.R., R.J. Guida, C.L. Roberts, C.M. Norman, and J.S. Holland. 2019. Persistence and turnover in desert plant communities during a 37-year period of land use and climate change. *Ecological Monographs* 89:e01390. (M.S. students second, third, and fifth authors when the research was performed).
- Abella, S.R., and L.P. Chiquoine. 2019. The good with the bad: when ecological restoration facilitates native and non-native species. *Restoration Ecology* 36:284-294.
- Abella, S.R., C.E. Hausman, J.F. Jaeger, K.S. Menard, T.A. Schetter, and O.J. Rocha. 2019. Fourteen years of swamp forest change from the onset, during, and after invasion of emerald ash borer. *Biological Invasions* 21:3685-3696.

Selected Awards

- 2017: Robert C. Stebbins research award by the Desert Tortoise Council
- 2016: Faculty mentor for first and second place undergraduate student posters, Society for Ecological Restoration chapter conference
- Distinguished Alumnus-in-Residence, Grand Valley State University



The Caberoy Lab has two major areas of focus:

Molecular Mechanisms of Retinal Degeneration and Age-Related Macular Degeneration

The retina is a thin, multi-layer, light-sensitive tissue that is found all the way at the back of the eye. It contains special type of neurons called photoreceptors- cells responsible for reception and processing of light and sending the signal to the brain. Because the photoreceptors are constantly exposed to light, they become susceptible to photo-oxidation damage. The oxidized photoreceptors are shed and rapidly eaten by specialized cells underneath them called retinal pigment epithelium (RPE) cells through the process of phagocytosis. Defect in phagocytosis results in accumulation of the shed photoreceptors and toxic products. This eventually leads to the death of the photoreceptors and other cells of the retina resulting to progressive loss of vision such as in *Retinitis pigmentosa* and age-related macular degeneration. We study the role of RPE phagocytosis in photoreceptor death that leads to retinal dysfunction and then blindness. We also identify factors and pathways associated with damage of the retina, in the hope to develop ways to prevent or treat blindness.

Development of a Novel Alzheimer's Therapy

Alzheimer's disease is a progressive, neurodegenerative disease that is poorly understood and has no cure; existing treatments produce modest cognitive enhancement addressing behavioral symptoms. Thus, effective disease-modifying pharmacological intervention for prevention and treatment are essential.

One of the major disease hallmarks of Alzheimer's is the buildup of harmful amyloid beta protein aggregates in the Alzheimer's brain. Amyloid betas are normally removed by specialized cells in the brain called microglia. However, the removal of these aggregates leads to activation of the inflammatory pathway that eventually results to death of the brain cells.

Using genetic engineering, we have created new types of "molecular bridges": hybrid proteins that are capable of "snatching" harmful amyloid beta and "re-channeling" them to an alternative degradation route that will not instigate a toxic response in the brain. We use 3D culture systems to test the efficacy of the hybrid proteins in removing amyloid beta. At the same time, we administer our hybrids in mice with Alzheimer's disease and determine if the treatment can prevent accumulation of amyloid beta and reduce production of inflammatory factors. Furthermore, we assess whether the treatments can improve learning and ameliorate memory deficits in mice with Alzheimer's disease. Our long-term goal is to use our hybrid proteins to treat humans diagnosed with Alzheimer's disease.

Selected Awards

- 2017: Association for Research in Vision and Ophthalmology (ARVO)/ National Eye Institute Travel Award.
- 2016: 1st Office of Undergraduate Research — Outstanding Faculty Research Mentor Award (UNLV).
- 2014, 2017: Top Tier Doctoral Graduate Research Assistant Award (UNLV)
- 2012-2015: Lincy Assistant Professorship (UNLV)
- 2011-2016: Pathway to Independence Award (K99/R00; National Eye Institute/NIH)

Nora Caberoy

Associate Professor
Ph.D., Washington State University

Research Interests

- Phagocytosis
- Retinal degeneration and age-related macular degeneration
- Alzheimer's Disease



Selected Publications

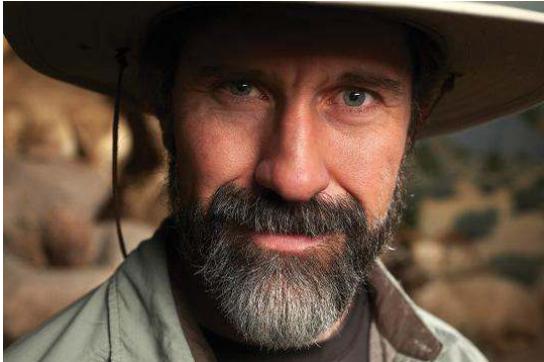
- LeBlanc M, Wang W, Chen X, Caberoy NB, Guo F, Shen C, Ji Y, Tian H, Wang H, Chen R, Li W. (2017) Secretogranin III as a disease-associated ligand for anti-angiogenic therapy of diabetic retinopathy. *Journal of Experimental Medicine*. pii: jem.20161802. doi: 10.1084/jem.20161802. [Epub ahead of print].
- Caberoy, NB. (2014). Synergistic interaction of tubby and tubby-like protein 1 (Tulp1). *Advances in experimental medicine and biology*. 801, 503-9.
- Caberoy NB, Alvarado G & Li W. (2012) Tubby regulates microglial phagocytosis through MerTK. *J Neuroimmunol*. 2012 Nov 15;252(1-2):40-8. doi: 10.1016/j.jneu roim.2012.07.009. PMID: 22884297.
- Caberoy NB, Zhou Y & Li W. (2010) Tubby and tubby-like protein 1 are new ligands for MerTK. *EMBO J*. 29 (23):3898-3910. PMID: 20978472.

David Choate

Visiting Assistant Professor
Ph.D., University of Notre Dame

Research Interests

- Behavioral Ecology
- Population Dynamics
- Conservation



Selected Publications

- Choate, D. K. Longshore, and D. Thompson. 2018. Cougar dispersal and natal homing in a desert environment. *Western North American Naturalist*. 78:221-235.
- Stoner, D., Sexton, J., Choate, D., Nagol, J., Bernales, H., Sims, S., Ironside, K., Longshore, K., Edwards, T. 2018. Climatically driven changes in primary production propagate through trophic levels. *Global Change Biology*. 24:4453-4463.
- Robinson, H., T. Ruth, J. Gude, D. Choate, R. DeSimone, M. Hebblewhite, K. Kunkel, R. Matchett, M. Mitchell, and K. Murphy. 2015. Linking resource selection and mortality modeling for population estimation of mountain lions in Montana. *Ecological Modelling*. 312:11-25.
- Choate, D., C. Prather, M. Michel, A. Baldrige, M. Barnes, D. Hoekman, C. Patrick, J. Rüegg, and T. Crowl. 2012. Integrating theory: a graphical model for graduate students and researchers. *BioScience*. 62:594-602.

Life requires trade-offs: the most definitive involves predation. Fear of being killed drives hungry herbivores to avoid vegetation containing the best foods when the same patches may conceal an equally hungry predator. In addition to losing energy, prey often trade-off reproduction for safety. While an attack can trigger an acute response resulting in either survival (e.g., for a deer) or a meal (for a cougar), chronic stress may lead to dysregulation, disease, and ultimately lower fitness for the survivors. In comparison to killing, these 'risk-effects' influence every aspect of prey and predator behavior, from habitat use to foraging decisions, yet linking individual behavioral plasticity to population dynamics remains a key challenge in ecology.

As a wildlife ecologist, I have studied species (rodents to raptors) in diverse environments (rainforests to deserts) in collaboration with state and federal agencies as well as private institutions (consulting, NGOs). Primarily, I have investigated cougar-prey ecology in several ecosystems including the urban/suburban interface of southern California, mountains in Utah and Montana, and Nevada deserts. My research focuses on understanding how behavioral decisions influence predator-prey population dynamics, how these dynamics structure communities, and bringing this understanding to bear on conservation issues. My research philosophy is grounded in two worlds. First, I approach problems using the best available theoretical framework and statistical tools (e.g., foraging theory, habitat modeling, population estimation and projection). Second, theory and predictive models need to be tested and informed by data and direct field experience, these can only be gained by spending hours in the field tracking animals. Working with students and collaborators, I have applied these principles to address cougar movement, dispersal, predation, population estimation, and risk effects on: deer and elk diet optimization, and mule deer and bighorn sheep use of water sources in desert environments. Results from this work support management efforts by both state and federal agencies.

In SoLS, my primary responsibility is teaching large enrollment, first year biological sciences courses, as well as upper division courses in animal behavior and endocrinology. Throughout my career I have taught both in classroom and various field settings. My goal in teaching is to inspire through active engagement, enthusiasm, and a passion for the outdoors.



I am a soil and water scientist with expertise in the area of soil plant water relations. I am the Director of the Center for Urban Water Conservation. My research is primarily field based with some controlled greenhouse experimentation. I am particularly interested in how plants use water and how they adjust growth and physiological response to stress. I do research in both natural systems such as riparian, mixed shrubland and forest ecosystems but I also study plants under irrigated conditions in an urban setting (golfcourses and residential landscapes). Recent research includes quantifying evapotranspiration at the basin level using an energy balance approach (Devitt et al. 2010), quantifying groundwater extraction by phreatophytes (Devitt et al. 2015) and investigating the ecohydrologic connectivity between mountains and valley (Devitt et al. 2017). Other research I have been doing relates to the fate and transport of contaminants in soil plant systems, such as the fate of selenium in an urban watershed (Devitt et al. 2014), fate and transport of pharmaceuticals in irrigated turfgrass systems (Wright et al. 2012) and the fate of deicing salts in mountain ecosystems (Devitt et al 2014). I am currently assessing the impact of large scale solar development on adjacent desert ecosystems, quantifying surface hydrology decoupling and heat transport.

Current funded projects include an NSF EPSCoR project on solar energy, a USGA/USGS project assessing tree to grass water use ratios and a BLM restoration project associated with a desert tortoise habitat burn site.

I enjoy hiking and making wine and I am actively involved in local groups that address social injustice in the community.

Selected Publications

- Devitt D.A., L.F. Fenstermaker, M.H. Young, B. Conrad, M. Baghzouz and B. Bird. 2010. Evapotranspiration of mixed shrub communities in phreatophytic zones of the Great Basin region of Nevada (USA). *Ecohydrology* 4:807-822.
- Wright L. D.A. Devitt, M.H. Young, J.Gan, B. Vanderford, S.Snyder and M McCullough. 2012 Fate and Transport of 14 Pharmaceutical and Personal Care Products in an Irrigated Turfgrass System. *Agronomy Journal*. 104(5);1244-1254.
- Leinauer Bernd and Dale Devitt. 2013. Irrigation Science and Technology. In: *Turfgrass Science*, American Society of Agronomy.
- Scott Mensing, Scotty Strachan, Jay Arnone, Lynn Fenstermaker, Franco Biondi, Dale Devitt, Brittany Johnson, Brian Bird, Eric Fritzing. 2013. A network for observing Great Basin Climate Change. *EOS, Transactions For American Geophysical Union*. 94(11);105-106 DOI: 10.1002/2013EO110001.
- Devitt D.A., L. Wright and M.H. Young. 2013. Water and salt status of bare soil and turfgrass systems irrigated with recycled water. *Agronomy Journal* 105:1051-1060. doi:10.2134/agronj2012.0126.
- Devitt, D. A., Wright, L., Landau, F., Apodaca, L. (2014). Deicing Salts; Assessing Distribution, Ion Accumulation in Plants and the Response of Plants to Different Loading Rates and Salt Mixtures. *Environment and natural resources research*, 4(1).
- Devitt, D. A., Wright, L. E., Shanahan, S. A., Hausrath, E. M. (2014). Fate of selenium in a small urban watershed. *Environmental Monitoring and Assessment*, 186(5), 3181-3197.
- Young, M. H., Green, R. L., Conkle, J. L., McCullough, M., Devitt, D. A. (2014). Field-scale monitoring of pharmaceutical compounds applied to active golf courses by recycled water (2nd ed., vol. 43, pp. 658-670). *Journal of Environmental Quality*. Vol. 43 No. 2, p. 658-670.

Dale Devitt

Professor
Ph.D., University of California,
Riverside

Research Interests

- Soil plant water relations
- Growth and physiological response to stress
- Contaminants in soil plant systems



Selected Award

- Outstanding paper of 2002 for the journal of American Water Resources Association; "A reevaluation of the groundwater budget for Las Vegas Valley Nevada with emphasis on groundwater discharge"

Allen Gibbs

Professor
Ph.D., Scripps Institution of
Oceanography

Research Interests

- Environmental Physiology
- Experimental Evolution



Selected Publications

- Hardy, C.M., M.K. Burke, L.J. Everett, M.V. Han, K.M. Lantz and A.G. Gibbs. 2017. Genome-wide analysis of starvation-selected *Drosophila melanogaster* - a genetic model of obesity. *Molecular Biology and Evolution*. Accepted for publication.
- Etges, W.J., C. de Oliveira, S. Rajpurohit and A.G. Gibbs. 2016. Effects of temperature on transcriptome and cuticular hydrocarbon expression in ecologically differentiated populations of desert *Drosophila*. *Ecology and Evolution* 7: 619-637.
- Rajpurohit, S., L.M. Peterson, A.J. Orr, A.J. Marlon and A.G. Gibbs. 2016. An experimental evolution test of the melanism-desiccation hypothesis in insects. *PLoS One* 11(9): e0163414.
- Hardy, C.M., R.T. Birse, M.J. Wolf, L. Yu, R. Bodmer, and A.G. Gibbs. 2015. Obesity-associated cardiac dysfunction in starvation-selected *Drosophila melanogaster*. *American Journal of Physiology – Regulatory, Integrative and Comparative* 309: R658-R667.

The fundamental question for the Gibbs lab is: How do organisms interact with and adapt to their environments? For example, the small size of insects results in a relatively high surface area:volume ratio, so that insects face an inherent problem of losing a small volume of water through a relatively large surface. Thus, insects should not tolerate arid conditions very well, yet desert insects are diverse and abundant. How can they survive and thrive in the desert? We study physiological mechanisms of adaptation to stressful environments, including deserts. Organisms studied have included ants, grasshoppers, scorpions and many other taxa. In each case, we ask: What problems does the environment pose; what are the potential solutions; and what solutions are actually used?

Fruit flies in the genus *Drosophila* are a major research focus. They occupy a wide range of habitats across the world, and the desert fruit fly, *Drosophila mojavensis*, is especially tolerant of desiccation, heat and other environmental stresses. It was also the first desert organism with a sequenced genome, information we have used to investigate how gene expression in these flies is affected by environmental conditions.

Most current research uses experimental evolution in *Drosophila melanogaster* as a model for environmental adaptation in nature. For example, we have created an artificial desert in the laboratory and selected for desiccation-resistant flies. They generally have the same desert adaptations as *Drosophila mojavensis*, but not always. These results have generated new hypotheses to be tested. Another research program uses selection for starvation resistance. The most straightforward mechanisms to survive starvation are increased energy storage (survival of the fattest) and reduced metabolism. Starvation selection has yielded extremely obese and inactive *Drosophila*. Other phenotypes of these flies mimic those of obese humans (e.g. cardiac dysfunction, disrupted sleep patterns). In the past decade, *Drosophila* has emerged as a new model for obesity research. Our flies provide a unique system with which to investigate physiological and genetic mechanisms of obesity.

Fed Control



Starvation Selected



Our research activities are focused on questions related to structural variations in the genome, and its phenotypic and evolutionary consequences. Structural variations arise from large scale mutations such as insertions and deletions or segmental duplications. Sometimes insertions are created by transposable elements and contain repeat sequences. Other times the insertions or deletions are large enough to even contain multiple genes. Because they are likely to be deleterious, many of these mutations cause disease. In rare cases when they are not too deleterious, they can shape the genome architecture, create new genes, and lead to an expansion or contraction of gene families.

Some of the current research questions we are pursuing are:

1. Transposable element activity in somatic cells.
Transposable elements (TEs) comprise more than 40% of the human genome. Although most of the copies have lost their ability to move, some families of TEs (notably, LINE-1 and Alu) are currently active in human populations with deleterious effects on human health. We are studying genomic data from cancer cells, to understand how TEs are controlled in the somatic cells.
2. Evolutionary constraint on insertions and deletions.
Comparing closely related genomes provides us with clues about where changes tend to happen in the genome. There are parts of the genome that have experienced many changes in evolutionary history, while some parts do not show any sign of change. Based on this information we can infer how insertions and deletions are tolerated in a specific region of a genome, and in turn predict the effect of those mutations in humans.
3. Impact of structural variants on laboratory evolution of fruit flies.
Fruit flies in Rose lab at UC Irvine have been bred to have different generation times ranging from less than 10 days to 5 weeks. Fruit flies in Gibbs lab at UNLV have been bred to be resistant to starvation. We are working with different groups to analyze the structural variants found in these different stocks of flies, hoping to pinpoint the genetic variation that led to the different phenotypes in these experimentally evolved flies.



Mira Han

Assistant Professor
Ph.D., Indiana University

Research Interests

- Molecular Evolution
- Genomics
- Bioinformatics



Selected Publications

- Graves, J., Hertweck, K., Phillips, M., Han, M.V., Cabral, L., Barter, T., Greer, L., Burke, M., Mueller, L., Rose, M., Genomics of Parallel Experimental Evolution in *Drosophila*. 2017. *Molecular Biology and Evolution*. 34(4): 831-842.
- Navarro Leija, O., Varghese, S., M.V. Han, Measuring Accelerated Rates of Insertions and Deletions Independent of Rates of Nucleotide Substitution. 2016. *Journal of Molecular Evolution*, 83(3-4), 137–146.
- Neafsey, D. E., R. M. Waterhouse, ... M.V. Han, ..., N. J. Besansky, Highly evolvable malaria vectors: The genomes of 16 *Anopheles* mosquitoes. 2014. *Science*, 347(6217).
- Han, M.V., G.W.C. Thomas, and M.W. Hahn, Estimating gene gain and loss rates in the presence of error in genome assembly and annotation using CAFE 3. 2013. *Molecular Biology and Evolution*. 30(8): 1987-1997.

Brian Hedlund

Professor
Ph.D., University of Washington

Research Interests

- Microbial Ecology
- Thermophiles
- Biodiversity Exploration



My lab studies microorganisms in a variety of contexts and habitats, including animal models of *Clostridium difficile* infection, desert springs, and a variety of biotechnological applications. Our best-known work focuses on terrestrial geothermal springs in the western US and abroad. One major research thrust examines the ecological consequences of high temperatures. For example, we and others have recently established quantitative relationships between biological diversity and temperature. We are now following these studies up by probing relationships between extreme temperature and the nitrogen biogeochemical cycle and other microbial functions. A second major research thrust strives to explore microbial biodiversity. Currently, only half of the major lineages (phyla) of bacteria have been cultivated in a laboratory or carefully described in the scientific literature. Many of these “dark” lineages are abundant in terrestrial geothermal systems. We work with a variety of collaborators to learn about these organisms by combining microbial cultivation efforts with environmental systems biology approaches such as environmental genomics (single-cell genomics and metagenomics), meta-transcriptomics and -proteomics, and targeted and whole-community stable isotope approaches such as fluorescence in situ hybridization coupled with nano-scale secondary ion mass spectrometry (FISH Nano-SIMS), quantitative stable isotope probing (SIP), and SIP-metagenomics.

My lab is also engaged in microbial biodiversity exploration through microbial cultivation. We have recently isolated and taxonomically described two new classes and one new phylum of the bacterial phylum Chloroflexi. To understand these organisms in more detail, we combine traditional microbial systematics with modern approaches such as genomics, environmental genomics, and exometabolomics. I am also engaged in the international microbial systematics community as an editor for Bergey’s Manual of Systematics of Archaea and Bacteria.

Selected Awards

- 2006-2011 National Science Foundation Early Career Grantee (CAREER)
- 2010 Nevada Regents’ Rising Researcher Award
- 2012-2015 UNLV Angel Professorship
- 2014 UNLV College of Sciences Distinguished Researcher Award
- 2015-present Trustee and Editor for Bergey’s Manual of Systematics of Archaea and Bacteria

Selected Publications

- Bowers RM, Kyrpides NC, Stepanauskas R, Harmon-Smith M, Doud D, Reddy TBK, Schulz F, Jarett J, Rivers AR, Eloe-Fadrosh EA, Tringe SG, Ivanova NN, Copeland A, Clum A, Becraft ED, Malmstrom RR, Birren B, Podar M, Bork P, Weinstock GM, Garrity GM, Dodsworth JA, Yooseph S, Sutton G, Glöckner FO, Gilbert JA, Nelson WC, Hallam SJ, Jungbluth SP, Ettema TJG, Tighe S, Konstantinidis KT, Liu WT, Baker BJ, Rattei T, Eisen JA, Hedlund B, McMahon KD, Fierer N, Knight R, Finn R, Cochrane G, Karsch-Mizrachi I, Tyson GW, Rinke C, Lapidus A, Meyer F, Yilmaz P, Park, DH, Eren AM, Schriml L, Banfield JF, Hugenholtz P, Woyke T. 2017. Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. *Nature Biotechnology*. 35:725-731.
- Nobu, MK, Dodsworth JA, Murugapiran SK, Rinke C, Gies EA, Webster G, Schwientek P, Kille P, Weightman A, Parkes J, Sass H, Liu WT, Hallam SJ, Tsiamis G, Woyke T, Hedlund BP. 2015. Phylogeny and physiological potential of the candidate phylum “Atribacteria” (OP9/JS1) inferred from single-cell genomes and metagenome bins. *ISME Journal*. 10:273-286.
- Dodsworth JA, Blainey PC, Murugapiran SK, Swingley WD, Ross CA, Tringe SG, Chain PS, Scholz MB, Lo CC, Raymond J, Quake SR, Hedlund BP. 2013. Single-cell and metagenomic analyses indicate a fermentative, saccharolytic lifestyle for members of the OP9 lineage. *Nature Communications* 4:1854.
- Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson IJ, Cheng JF, Darling A, Malfatti S, Swan BK, Gies EA, Dodsworth JA, Hedlund BP, Tsiamis G, Sievert SM, Liu WT, Eisen JA, Hallam SJ, Kyrpides NC, Stepanauskas R, Rubin EM, Hugenholtz P, Woyke T. 2013. Insights into the phylogeny and coding potential of microbial dark matter. *Nature*. 499:431-437.

I am interested in the neurobiology of stress, brain circuitry, and pharmacology. I utilize animal models of stress and addiction to tie behavior with changes in brain organization. Some of my work focused on the role of early life stress in developing sensitivities to psychostimulants and drugs of abuse in adulthood. My research focused on understanding modulation and plasticity of brain circuitry in regions important for decision-making processes, reward, and stress, such as the dorsal striatum, cortex and the mesocorticolimbic pathway. I used a combination of molecular, biochemical, electrophysiological, and behavioral techniques. My data indicate males are more affected by early life stress, which influenced drug effects on neural circuits later in life. Understanding these pathways and relationships to behavior is key in assisting with these disorders and furthering our knowledge of brain function.

Today, my primary role involves instructing biology students from freshman to seniors and post-baccalaureates. To date, I have taught entry level to upper division courses focusing on introductory topics to neurobiology and pharmacology. Courses change every semester and I aim to continually adapt to new students and changing course dynamics. I research the brain because I have an unyielding enthusiasm for the topic. The biological basis of learning occurs through the strengthening of neuronal connections. As an instructor, I aim to enhance these connections and ignite an interest in the Fundamentals of Life Science and neurobiology. Through my presentation of the material and excitement for science, I hope to motivate students so they leave the classroom with an enhanced knowledge and curiosity for the subject. I plan to integrate myself into existing research programs in SoLS and continue to study the brain and neurobiology.

My research and teaching covers several areas. As I continue to instruct a wide range of students, I incorporate my experiences into current and future work. Neurobiology is my passion and Eric Kandel summed up the importance of research of the mind as follows: "The biology of the mind bridges the sciences – concerned with the natural world – and the humanities – concerned with the meaning of human experience."

Selected Publications

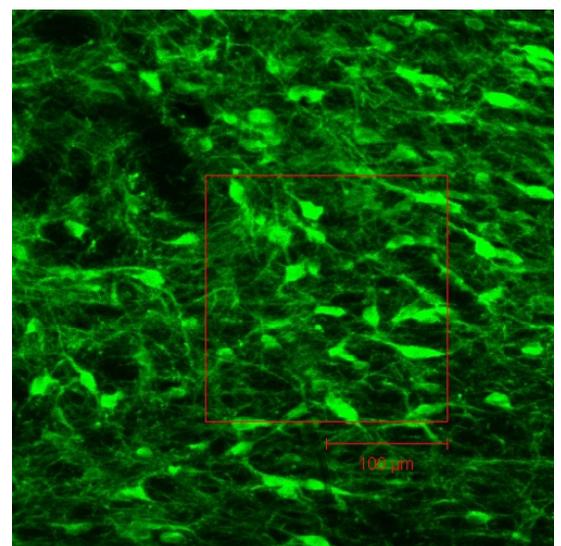
- Hensleigh, E. & Pritchard, L.M. (2015). Maternal separation increases methamphetamine-induced damage in the striatum in male, but not female, rats. *Behavioral Brain Research*, 295, 3-8. PMID: 25535855.
- Hensleigh, E. & Pritchard, L.M. (2014). The effect of early environmental manipulation on locomotor sensitivity and methamphetamine conditioned place preference reward. *Behavioral Brain Research*, 268, 66-71. PMID: 24713150.
- Hensleigh, E. & Pritchard, L.M. (2013). Glucocorticoid receptor expression and sub-cellular localization in dopamine neurons of the rat midbrain. *Neuroscience Letters* 556, 191-195. PMID: 24121048.
- Hensleigh, E., Smedley, L., & Pritchard, L. M. (2011). Sex, but not repeated maternal separation during the first postnatal week, influences novel object exploration and amphetamine sensitivity. *Developmental Psychobiology* 53(2), 132-140. PMID: 20886535.

Emily Hensleigh

Visiting Assistant Professor
Ph.D., University of Nevada,
Las Vegas

Research Interests

- Neurobiology of Stress and Addiction
- Neurotransmitter Systems and Circuits
- Science Education



Allyson Hindle

Assistant Professor
Ph.D., Texas A&M University

Research Interests

- Comparative Physiology
- Physiological Telemetry
- Cellular Metabolism



Selected Awards

- Early Career Advocacy & Policy Fellowship, American Physiological Society 2015-2017
- Astronaut Finalist, Canadian Space Agency 2009, 2017



My research program investigates wild species that naturally possess extreme physiological traits. This work focuses on the molecular mechanisms that control blood flow, cellular metabolism and tissue-specific protective strategies, primarily in two animal systems: marine vertebrates and hibernators. Both groups contain many species that challenge conventional definitions of mammalian homeostasis by naturally tolerating low oxygen and low temperature conditions.

Breath-hold divers such as seals are exceptionally tolerant to hypoxia, and execute coordinated cardiovascular adjustments during diving in order to conserve on-board oxygen for critical tissues. Small-bodied hibernators cycle between bouts of cold torpor lasting several weeks and rapid rewarming arousal periods of less than a day. They must therefore orchestrate rapidly reversible metabolic depression, and undergo dramatic changes in body temperature, oxygen consumption and tissue perfusion without harm. Using varied approaches for each species and question, we combine whole-animal telemetry measurements (including field work) with molecular biology and cell culture systems, and also use comparative genomics to identify themes and gene targets across lineages.

The broad goal is to both to learn more about, as well as learn from, these impressive animals. By investigating the molecular mechanisms that regulate tissue perfusion and protection from low oxygen conditions, we hope to identify novel pathways with therapeutic potential in humans. We are also interested in understanding how and when physiology is the limiting factor for wild populations to thrive. This will help resource managers and policy makers identify likely outcomes from ecosystem disturbance and change, and to enable more informed decisions for managing land use and ocean economy.

Selected Publications

- Bagchi, A., A.J. Batten, M. Levin, K.N. Allen, L.A. Huckstadt, D.P. Costa, E.S. Buys and A.G. Hindle (2018) Intrinsic anti-inflammatory properties of serum in two species of deep-diving seal. *J Exp Biol.* 221, doi:10.1242/jeb.178.
- Thoonen, R., A.G. Hindle and M. Scherrer-Crosbie (2016) Brown adipose tissue: the heat is on the heart. *Am J Physiol-Heart Circ Physiol* 310:H1592-605.
- Hindle, A.G., M. Horning and J.E. Mellish. (2015) Estimating total body heat dissipation in air and water from skin surface heat flux telemetry in Weddell seals. *Anim Biotelem* 3:50 /10.1186/s 40317-015-0081-4.
- Grabek, K.R., S.L. Martin and A.G. Hindle. (2015) Proteomics approaches shed new light on hibernation physiology. *J Comp Physiol B.* 185:607-627.
- Hindle, A.G., Rosen, D.A.S. and A.W. Trites (2010) Swimming depth and ocean currents affect transit costs in Steller sea lions (*Eumetopias jubatus*). *Aquat Biol* 10: 139-148.

My interests are predominately conservation biology and population ecology, and while I have worked across taxonomic groups and questions, in recent years, my research efforts have increasingly focused on anurans (frogs and toads). Many amphibian species world-wide are declining, with numerous species already having gone extinct. This amphibian crisis has been suggested as foreshadowing a potential sixth mass extinction. As part of my professional service, I am active on two voluntary conservation teams focusing on rare anuran species, and I am the meeting coordinator for the California/Nevada Amphibian Population Task Force.

In support of local, state, and federal agencies, my research group has been leading monitoring efforts for the relict leopard frog, a species endemic to the Southern Nevada region. We also conduct a program of headstarting and translocation which has reestablished wild populations of this rare species. The relict leopard frog was once on the verge of extinction, but our conservation efforts have successfully kept it off the federal list of endangered and threatened species. These efforts have also been a catalyst for synergistic research funding for projects ranging from field studies on anuran population dynamics to laboratory studies on the impact of a pathogenic amphibian chytrid fungus. These efforts provide experiential opportunities for graduate and undergraduate students, and often allow our students direct and insightful interactions with resource and management agency personnel.

As my position in SoLS is primarily teaching, I specialize on large enrollment, introductory biological sciences for non-science majors, and I also occasionally teach upper division ecology courses. I am an active lecturer with a Socratic-teaching style. My goals for introductory courses are to provide students with a fundamental appreciation for the science being taught and a basic framework of concepts and principles that allows further learning.

Selected Publications

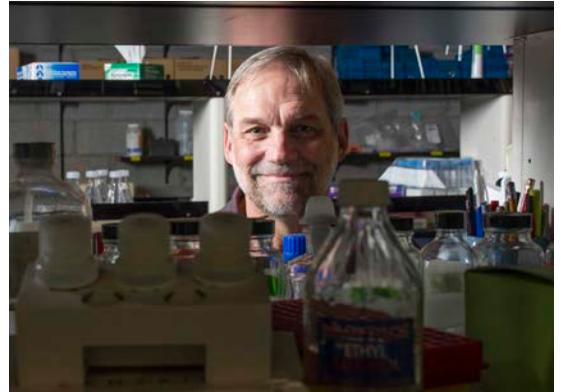
- Jaeger JR, Waddle AW, Rivera R, Harrison DT, Ellison S, Forrest MJ, Vredenburg VT, and van Breukelen F (2017) *Batrachochytrium dendrobatidis* and the decline and survival of the relict leopard frog. *Ecohealth* 10.1007/s10393-017-1240-2.
- Jezkova T, Jaeger JR, Oláh-Hemmings V, Jones BJ, Lara-Resendiz RA, Mulcahy DG, and Riddle BR (2015) Range and niche shifts in response to past climate change in the desert horned lizard (*Phrynosoma platyrhinos*). *Ecography* 38:001-012.
- Graham MR, Jaeger JR, Prendini L, and Riddle BR (2013) Phylogeography of the Arizona hairy scorpion (*Hadrurus arizonensis*) supports a model of biotic assembly in the Mojave Desert and adds a new Pleistocene refugium. *Journal of Biogeography* 40:1298-1312.
- Bryson RW, Jaeger JR, Lemos-Espinal JA, and Lazcano D (2012) A multilocus perspective on the speciation history of a North American aridland toad (*Anaxyrus punctatus*). *Molecular Phylogenetics and Evolution* 64:393-400.

Jef Jaeger

Assistant Professor-in-Residence
Ph.D., University of Nevada,
Las Vegas

Research Interests

- Conservation Biology
- Population Ecology
- Phylogeography



David V. Lee

Associate Professor
Ph.D., University of Utah

Research Interests

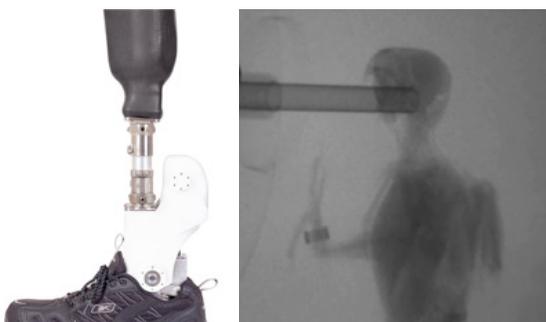
- Comparative Biomechanics
- Locomotion and Limb Dynamics
- Robotic and Prosthetic Gait

My research investigates pure and applied questions of mechanical function in animals, with an emphasis on legged locomotion. These studies in comparative biomechanics span muscle-tendon, joint, limb, and whole-body dynamics. My current research follows three main lines of inquiry: (1) Collision-based analysis to quantify the dynamics of locomotion in quadrupeds and bipeds; (2) The influence of biomechanics on age-related osteoarthritis in animal models; (3) Structure-function relationships across diverse modes of animal locomotion. My laboratory (locb.org) houses a 3D X-ray motion analysis system with integrated force-torque transducers for small animals biomechanics and we use a shared gait lab facility with 3D motion capture and multiple force platforms for human and canine studies. My teaching at UNLV is in comparative vertebrate anatomy, biomechanics, and physiology.

I completed B.S. and M.S. degrees at Cornell University, where I began research in canine hip dysplasia/osteoarthritis at the College of Veterinary Medicine. I completed my Ph.D. at the University of Utah, where I combined experimental and modeling approaches to investigate the influence of body mass distribution, leg geometry and incline/decline on quadrupedal locomotion. As a post-doc at Harvard's Concord Field Station, I continued to work on quadrupeds in collaboration with Boston Dynamics, as they engineered the original BigDog robot. I was recently an Alexander von Humboldt Fellow at Technische Universität Darmstadt, where I focused on economy, dynamics, and control of bipedal animals and robots (including human gait with prosthetics), as well as contributed chapters to *Bioinspired Legged Locomotion* (Elsevier, 2017).

Selected Publications

- Lee, D. V., Isaacs, M. R., Higgins, T. E., Biewener A. A. and McGowan, C. P. (2014). Scaling of the spring in the leg during bouncing gaits of mammals. 54 (6) 1099-1108. *Integr. Comp. Biol.* doi:10.1093/icb/icu114.
- Lee, D. V., Comanescu, T. N., Butcher, M. T. and Bertram, J. E. A. (2013). A comparative collision-based analysis of human gait. *Proc. R. Soc. Lond. B* 280(1771), 20131779; doi: 10.1098/rspb.2013.1779.
- Lee, D. V. and Biewener A. A. (2011). BigDog-inspired experiments in the locomotion of goats and dogs. *Integr. Comp. Biol.* 51, 190-202. doi:10.1093/icb/icr061.
- Lee, D. V., Bertram, J. E. A., Anttonen, J. T., Ros, I. G., Harris, S. L. and Biewener, A. A. (2011). A collisional perspective on quadrupedal gait dynamics. *J. R. Soc. Interface.* 8, 1480-1486.
- Lee, D. V. (2011). Effects of grade and mass distribution on the mechanics of trotting in dogs. *J. Exp. Biol.* 214, 402-411.



SpringActive, Inc.

As modern scientists, by necessity are becoming ever more specialized in their fields, I'd like to think I managed to find my niche as a generalist. My research would be most appropriately defined very broadly as organismal biology with a primary interest in the evolution and ecology of all things furry, referencing of course the group of organisms that have hair as a defining feature: mammals. My expertise is in mammals but my interests in biology are as eclectic as living organisms are diverse and I have been lucky enough to be involved in research projects ranging from the endoparasites of 3 genera of skunks to restoration of bat and rat habitat along the most disturbed riparian corridor in the southwest US; from "desert" rodents living in the Canadian Great Plains to the same species living in subtropical central Mexico; to my current focus, determining the effects of human activity and naturally occurring asbestos on lung fibrosis in native bats and rodents. As varied as they are, all of my research fits within a conservation theme by asking how native animals interact with that ever present and most ubiquitous mammal, humans. To address such varied questions requires the use of a diverse array of techniques that integrate the modern molecular laboratory with classic field-based studies.

My background is equally scattered but allows me to connect to all reaches of society. My background includes employment with a conservation agency following my Ph.D. and private consulting as a biologist, in addition to academic research and education. My undergraduate and graduate studies began with museum work and anyone visiting my office will quickly see that influence is still deeply ingrained in me. The outreach, education, and conservation agenda common among museums, zoos, and aquaria have always aligned well with my particular passion for biology. I am incredibly fortunate in having recently become the science advisor for the Shark Reef at Mandalay Bay. This opportunity has allowed me to once again pursue my original interests in public education and exploring the amazing diversity of life. It has the added benefit of feeding my eclectic tendencies by offering collaborative opportunities for undergraduate and graduate research projects in marine biology centered in the driest desert in North America! Who could ask for anything more?



Sean Neiswenter

Assistant Professor-in-Residence
Ph.D., University of Nevada,
Las Vegas

Research Interests

- Ecology
- Evolution
- Conservation of Mammals



Selected Publications

- Sean A. Neiswenter, David J. Hafner, Jessica E. Light, Gabriella D. Cepeda, Kathleen C. Kinzer, Lois F. Alexander, Brett R. Riddle. 2019. Phylogeography and taxonomic revision of Nelson's pocket mouse (*Chaetodipus nelsoni*), *Journal of Mammalogy* 100:1847–1864.
- A. W. Calvert and S. A. Neiswenter. 2012. Bats in riparian-restored sites along the lower Colorado River, Arizona. *Southwestern Naturalist* 57:340-342.
- Neiswenter, S. A. and B. R. Riddle. 2010. Evolution of silky pocket mice in the *Perognathus flavus* species group: diversification associated with emerging arid grasslands in western North America. *Journal of Mammalogy* 91:348-362.
- Matthews, A. K., S. A. Neiswenter, L. K. Ammerman. 2010. Trophic ecology of free-tailed bats *Nyctinomops femorosaccus* and *Tadarida brasiliensis* (Chiroptera: Molossidae) from Big Bend National Park, Texas. *Southwestern Naturalist* 55:340-346.

Joseph Nika

Assistant Professor-in-Residence
Ph.D., University of Texas at Dallas

Research Interests

- Student Retention and Promotion
- Graduate Program Admission Trends



Selected Publications

- Nika, Joseph (2011) Rescuing the Problem Student: Suggestions for Assisting Students with Extreme Academic Deficiencies, *The Advisor* 31(3): 36-39.
- Nika, J., (2013) Findings of the Task Force on Standardized Letters of Recommendation, Workshop Presentation, WAAHP/WGEA/WGSA Regional Conference, University of California, Irvine, California.
- Nika, J. and Ferguson, C., (2012) Rescuing the Problem Student, Workshop Presentation, NAAHP National Conference, Baltimore, Maryland.
- Anita Taylor, MA Ed; Molly Osborne, MD, PhD; Peggy Dupey, PhD; Joseph Nika, PhD (2011) How Prepared are Third Year Students for Choosing a Specialty? WAAHP/WGSA/WGEA Regional Conference, Stanford, California.

My scientific training is varied and spanned a variety of disciplines. While earning my doctoral degree at the University of Texas at Dallas I employed a variety of cell biology techniques to identify the cellular localization of a yeast homolog of a putative tumor suppressor in *Saccharomyces cerevisiae*. Upon determining that the gene product was a large subunit ribosomal protein the direction of my research turned towards basic science as I characterized eIF2B, a guanine nucleotide exchange factor (GNEF) for the eukaryotic translation initiation factor eIF2. While most GNEF's are small single subunit proteins, eIF2B is a heteropentamer with a molecular mass of over 280 kDa. To assess which subunits are structural vs. functional I delved into yeast genetics to construct a strain that was devoid of all structural genes for eIF2B. After constructing the strain, I turned to biochemistry to develop a purification protocol for wild-type eIF2B to characterize the enzyme kinetics governing the exchange reaction, specifically K_m and V_{max} . With wild-type parameters established a partial eIF2 complex was assembled (lacking the alpha subunit) and found to have higher K_m (decreased affinity of interaction with eIF2B) and higher V_{max} (suggests regulatory function for alpha subunit).

After completing my doctoral degree, I changed fields to medical microbiology as I engaged my postdoctoral fellowship at the University of Texas Southwestern Medical Center at Dallas. My primary role was to identify adhesins for *Haemophilus ducreyji*, the leading cause of ulcerative genital disease worldwide and a key risk factor for HIV transmission in sub-Saharan Africa and South America. Adhesins are attractive vaccine candidates as blocking them stops the infectious process at the earliest possible stage. With the genome sequence available, I conducted BLAST searches using gene clusters implicated in attachment in the related organism *Actinobacillus actinomycetemcomitans*. The Flp operon was an attractive candidate as disruptions in this cluster conferred decreased virulence in this periodontal pathogen. After performing a targeted gene disruption in the first gene in the operon I used quantitative real-time RT PCR to confirm that all genes in the cluster exhibited at least a 100-fold decrease in expression at the transcriptional level. The resulting strain was found to be deficient in attachment to both biological and abiotic surfaces and eventually found to be avirulent in human challenge models. Antibodies procured against the presumed adhesin in the operon were both neutralizing and cidal, thus confirming it as a potential vaccine candidate.

My diverse research background allows me to contemplate scientific issues from many perspectives and I strive to incorporate this into my teaching philosophy. I believe it is important to tie basic science concepts into practical application and relate it to issues that are reported in the media. Since coming to UNLV, I have used this approach when developing courses spanning Microbiology, Allied Health Science Microbiology, Immunology, Virology, and most recently Molecular Biotechnology. In addition to serving as an instructor my main focus has also included student affairs and I plan to continue along these lines for the foreseeable future. These plans include outreach and maintaining contact with School of Life Science Alumni to keep track of where our graduates end up and what careers they pursue.

Dryland ecosystems are shaped by the interactive effects of multiple factors including precipitation and temperature, landscape conditions, and environmental setting. Thus, the ecological patterns and responses that we observe have been produced by the interaction of multiple factors both through time and across space. The goal of my research is to better understand the events, multifactor relationships, and physical mechanisms that shape these ecosystems. I strive to use this understanding to predict future ecological conditions and responses across local and regional areas, and to enhance planning for the 21st century through better understanding of ecohydrological dynamics. To do this, my research utilizes and combines multiple information types including long-term measurements, remote sensing, mechanistic modeling, and field experiments.

As one of the newest faculty members in SoLS, I am currently developing new ecohydrological research focused on water resources and climate change in southern Nevada, and am expanding collaborative research on dryland forest regeneration across western North America.

Current research:

- Local-regional patterns and connection of precipitation, land surface properties and vegetation responses.
- Demographic and climactic controls on future forest persistence.
- Soil-plant-water-climate relationships in dryland ecosystems.
- Multiyear precipitation extremes.

Selected Publications

- Petrie MD, Peters DPC, Burruss ND, et al. 2019. Local-regional similarity in drylands increases during multiyear wet and dry periods and in response to extreme events, *Ecosphere* 10: e02939, doi:10.1002/ecs2.2939.
- Petrie MD, Peters DPC, Burruss ND, et al. 2019. Differing climate and landscape effects on regional dryland vegetation responses during wet periods allude to future patterns, *Global Change Biology* 25: 3305-3318, doi:10.1111/gcb.14724.
- Petrie MD, Peters DPC, Yao J, et al. 2017. Regional grassland productivity responses to precipitation during multi-year dry and wet periods, *Global Change Biology* 24: 1935-1951, doi:10.1111/gcb.14024.
- Petrie MD, Bradford JB, Hubbard RM, et al. Climate change may restrict dryland forest regeneration in the 21st century, *Ecology* 98: 1548-1559, doi:10.1002/ecy.1791.

Matthew Petrie

Assistant Professor
Ph.D., University of New Mexico

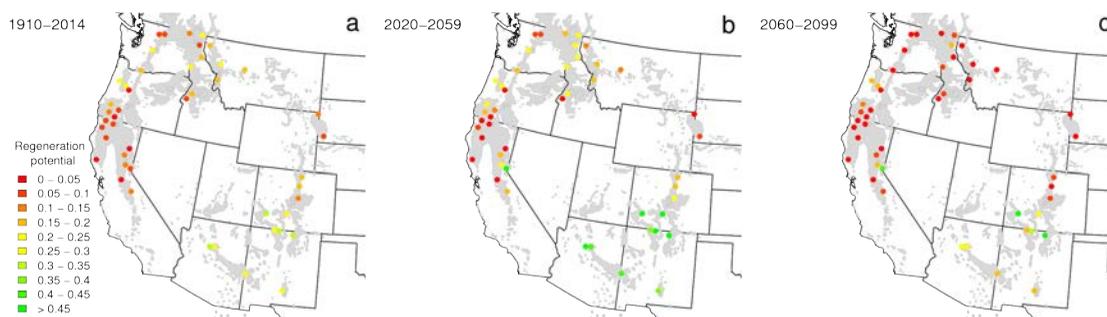
Research Interests

- Dryland Ecohydrology
- Landscape Ecology
- Climate Dynamics
- Forest Regeneration



Selected Awards

- NASA-MSU Professional Enhancement Award, United States Chapter of the International Association for Landscape Ecology, 2018



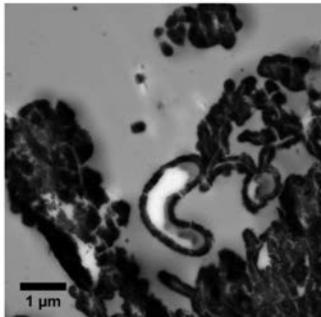
Ponderosa pine regeneration potential may increase in the early 21st century (1910–2014: Panel a versus 2020–2059: Panel b), yet may decline significantly due to higher temperatures and greater moisture stress in the late 21st century (2060–2099: Panel c).

Aude Picard

Assistant Research Professor
Ph.D., University of Lyon, France

Research Interests

- Geomicrobiology
- Astrobiology
- Biogeochemistry



Sulfate-reducing bacteria (SRB) grown in the presence of Fe become encrusted in iron sulfide minerals and influence the properties of minerals. Left image: culture of SRB grown with Fe. Iron-sulfide minerals appear as black precipitates. Right image: transmission electron microscopy image of SRB covered with a layer of iron-sulfide minerals.

Microorganisms drive global geochemical cycles at the surface of the Earth (C, Fe, S, N, O...) and have a tremendous influence on the chemical composition of our environment. The research activities of the geomicrobiology group at UNLV focus on understanding the fundamental aspects of biomineral formation as well as the role of microbe-mineral interactions in the following contexts:

- **Materials & Bioremediation:** Microorganisms influence the formation of minerals; i.e. they affect the physical and chemical characteristics of minerals. Experimental work seeks to understand the complex interface between organic materials and inorganic compounds. Biominerals potentially have unique properties that could be of use for applications in bioremediation or wastewater treatment.
- **Biogeochemistry:** We focus on iron-sulfide (Fe-S) minerals that form in anoxic sedimentary environments, where sulfate-reducing microorganisms (SRM) are ubiquitous. Fe-S minerals formed in the presence of SRM have unique characteristics when compared with minerals formed under abiotic conditions. Experimental studies and field work help understanding how microorganisms affect the transformations of iron sulfide minerals in marine and lacustrine sediments and investigate how minerals contribute to the preservation of organic carbon in sedimentary environments.
- **Astrobiology:** The composition and morphology of microbe-mineral interactions precipitated in the presence of microorganisms could be unique enough to serve as biosignatures for the search of life in the subsurface and at the surface of Mars. Experimental work focuses on the characterization of microbe-mineral aggregates formed in anoxic conditions and subjected to oxidizing conditions as occurring presently at the surface of Mars.

Selected Publications

- Picard A., Gartman A., Cosmidis J., Obst M., Vidoudez C., Clarke D.R., Girguis P.R. (2019) Authigenic metastable iron sulfide minerals preserve microbial organic carbon in anoxic environments, *Chemical Geology*, 530: 119343.
- Meister P., Brunner B., Picard A., Böttcher M.E., Jørgensen B.B. (2019) Sulphur and carbon isotopes as tracers of past sub-seafloor microbial activity. *Scientific Reports*, 9:604.
- Picard A., Gartman A., Clarke D.R., Girguis P.R. (2018) Sulfate-reducing bacteria influence the nucleation and growth of mackinawite and greigite. *Geochimica Cosmochimica Acta*, 220: 364-387.
- Picard A., Obst M., Schmid G., Zeitvogel F., Kappler A. (2016) Limited influence of Si on the preservation of Fe-mineral encrusted microbial cells during experimental diagenesis. *Geobiology*, 14 : 276-292.
- Picard A., Kappler A., Schmid G., Quaroni L., Obst M. (2015) Experimental diagenesis of organo-mineral structures formed by microaerophilic Fe(II)-oxidizing bacteria. *Nature Communications*, 6 : 6277.

A major theme in the life sciences is to understand how species adapt to diverse environmental and biological factors and diverge into new species. The evolutionary changes that permit species to survive and reproduce across a wide range of environments has resulted in a remarkable range of biological complexity.

My research group studies the interplay of behavior, ecology, genetics, and physiology to determine how species adapt to environmental changes and how diversification of populations leads eventually to the formation of new species. One focus of my group is the amazing Hawaiian *Drosophila*, which boasts up to 1,000 species in several taxonomic groups. Using genome sequencing and gene expression analyses coupled with detailed behavioral and physiological measurements we have identified genes that are involved in temperature adaptation between two species and between two populations within one species along an environmental gradient. We have also identified genes and epicuticular hydrocarbons that are involved in behavioral reproductive isolation and hybrid sterility between species. Initial studies have begun on the interaction with microbes, (bacteria and yeasts) that are important for food, internal parasites/symbionts, and possibly host-plant associations. In collaboration with others, we are also investigating the genetics of Hawaiian bats and birds, the invasive *Drosophila suzukii*, and Hawaiian *Metrosideros* trees. We are also initiating projects in the southwestern North America on *Euphilotes* butterflies and their buckwheat host-plants.

Selected Publications

- Eldon, J., M.R. Bellinger, and D.K. Price. 2019. Hawaiian picture wing *Drosophila* exhibit divergent adaptation along a narrow climatic gradient on Hawaii Island. *Ecology and Evolution*. 1-13.
- Billings, A.C., K.E. Schultz, W. E. Jones, E.A. Hernandez, and D.K. Price. 2018. Male courtship behaviors and female choice reduced during experimental starvation stress. *Behavioral Ecology* 30, 231–239.
- 28 co-authors. 2017. Deciphering the routes of invasion of *Drosophila suzukii* by means of ABC random forest. *Molecular Biology and Evolution* 34: 980-996.
- Brill, E., L. Kang, K. Michalak, P. Michalak, D.K. Price. 2016. Hybrid sterility and evolution in Hawaiian *Drosophila*: differential gene and allele-specific expression analysis of backcross males. *Heredity* 117:100–108.
- Kang, L., R. Settlage, K. McMahon, K. Michalak, H. Tae, H. Garner, E.A. Stacy, D.K. Price & P. Michalak. 2016. Genomic signatures of speciation in sympatric and allopatric Hawaiian picture-winged *Drosophila*. *Genome Biology and Evolution* 8: 1482-1488.
- Magnacca, K. and D.K.Price. 2015. Rapid adaptive radiation and host plant conservation in the Hawaiian picture wing *Drosophila* (Diptera: Drosophilidae). *Molecular Phylogenetics and Evolution* 92: 226-242.
- 18 co-authors. 2015. Community assembly on isolated islands: Macroecology meets evolution. *Global Ecology and Biogeography* 25: 769–780.
- Uy, K.L., R. LeDuc, C. Canotte, and D.K. Price. 2015. Physiological effects of heat stress on Hawaiian picture-wing *Drosophila*: genome-wide expression patterns and stress-related traits. *Conservation Physiology* 3 doi:10.1093/conphys/cou062.

Donald Price

Professor
Ph.D., University of Illinois,
Urbana-Champaign

Research Interests

- Behavioral, Ecological, and Evolutional Genetics



Selected Awards

- NSF Dimensions Program: Collaborative Research: A community-level approach to understanding speciation in Hawaiian lineages. 2013-2018, Co-PI.
- NSF Centers for Research Excellence in Science and Technology, University of Hawaii. 2009-2019, PI.
- Gordon and Betty Moore Foundation. Barcoding on Hawaii Island Project. 2008-2014, PI.
- NSF Experimental Program to Stimulate Competitive Research (EPSCoR) Hawaii. 2003-2009, co-PI.
- NSF Faculty Early Career Development Program (CAREER) Grant, PI.

Katie Rafferty

Assistant Professor-in-Residence
Ph.D., Georgia Institute of Technology and Emory University
School of Medicine

Research Interests

- Science Education
- Cardiovascular Pathophysiology



Selected Awards

- 2019: Outstanding Research Mentor by the Office of Undergraduate Research
- 2018-2023: co-PI on NSF Award "Developing the Skill and the Will to Succeed in STEM"
- 2014: Outstanding Faculty Mentor to recipient of the Darwin T. Turner Scholarship, University of Cincinnati
- 2009-2011: American Heart Association Greater Southeast Affiliate Postdoctoral Fellowship
- 2005-2008: American Heart Association Greater Southeast Affiliate Predoctoral Fellowship

I study the Scholarship of Teaching and Learning. My teaching efforts focus on creating a rigorous and supportive classroom environment to cultivate interest and retention in STEM education. My methods impel students to seek their own answers, like detectives, rather than memorize terms. In this way I contribute to UNLV graduates who are ready for careers in the booming technology sector. My instruction employs a number of evidence-based strategies to improve graduation rates in STEM majors for first generation college students, underserved minorities, and women. These include peer-to-peer instruction, facilitating instructor-to-student interaction outside of the classroom, transparent activity design, and frequent quizzing. All of these methods enhance student academic performance and, equally important, the perception of their STEM experience, both of which encourage students to remain in STEM studies and seek employment in industries that require technically skilled employees.

My Ph.D. in Biomedical Engineering combined excellent training in research and teaching. The primary focus of my doctorate and postdoctorate was to determine the earliest detectable mechanical changes in aortic and heart disease. Throughout my academic research career, I found opportunities to teach undergraduate biology and engineering courses. My interest in teaching and supporting future scientists took me out of basic science research and into pedagogic research. I continue to be an enthusiastic Educator because of student interactions such as this one:

A student once spoke up during a lecture on light-activated proteins in the eye to mention an article he read about activating neurons with lasers to treat Parkinson's disease. Because he thought "lasers and mind control are cool," he was able to visualize how biology class concepts directly linked to medical innovation. Students select STEM majors because they are curious. As an Educator my responsibility is to foster that curiosity with opportunities to think critically and brainstorm ideas. In his curiosity, this student illustrates my greatest challenge, motivation, and professional responsibility -- to ensure my students still think science is cool when they leave my courses. Fostering student excitement is critical to promote the graduation of all students who enter STEM disciplines here at UNLV.

Selected Publications

- Maiellaro-Rafferty K, Wansapura JP, Mendsaikhan U, Osinska H, James JF, Taylor MD, Robbins J, Kranias EG, Towbin JA, Purevjav E. Altered regional cardiac wall mechanics are associated with differential cardiomyocyte calcium handling due to nebulosin mutations. *J Mol Cell Cardiol.* 60:151-60, 2013.
- Washington E, O'Donnel R, Maiellaro-Rafferty K, Weiss D, Joseph G, Wan W, Gleason RL, Taylor WR. The Role of Lysyl Oxidase Family Members in the Stabilization of Abdominal Aortic Aneurysms. *AJP: Heart and Circ Phys*, 303(8):H1067-75, 2012.
- Maiellaro-Rafferty K, Weiss D, Joseph G, Wan W, Gleason RL, Taylor WR. Catalase overexpression in aortic smooth muscle prevents pathological mechanical changes underlying abdominal aortic aneurysm formation. *AJP: Heart and Circ Phys*, 301(2):H355-62, 2011.
- Maiellaro (Rafferty) KA and Taylor WR. The Role of the Adventitia in Vascular Inflammation. *Cardiovascular Research.* 75:640-648, 2007.

The Raftery laboratory studies how cells communicate to coordinate the formation and maintenance of functioning organs. In the course of a lifetime, tissues and organs must maintain their function despite environmental insults, disease, and aging. They do so using many of the same genes and proteins that were used to build the tissue during embryonic development. Both development and repair processes are tightly controlled to obtain optimal function and prevent overgrowth. In both processes, cells constantly sense their environment to make decisions about their fate, for example deciding whether to divide, migrate or differentiate. Other cells in the tissue guide these decisions by producing signals that transmit information about the state of the tissue. The resultant combination of signals coordinates individual cell decisions across the tissue to build or maintain functional architecture. We use fruit flies as a model organism, because of the powerful genetic tools available to study cell biology in whole tissues. Current projects in our lab focus on two general approaches to this problem.

First, we are investigating concerted migration of epithelial cells in the fly ovary. Epithelial cells are tightly connected into an organized sheet, and are essential to the function of most organs in both flies and humans. Each fly egg is formed within a structure called a follicle, which includes both germ cells and a somatic epithelium of about 650 follicle cells. This epithelium develops together with the underlying oocyte to create a functional egg. In late oogenesis, neighboring regions of the epithelium undergo distinct migrations: either moving to cover the anterior end of the oocyte or leave the epithelium to cover the apical surface of adjacent follicle cells. To investigate the mechanisms that direct these migrations, we use a variety of techniques to examine genetically manipulated follicle cells, including time-lapse micro-imaging of cultured egg chambers. Our goal is to understand how cell-cell communication mechanisms are fine-tuned to differentiate these two neighboring cell populations and drive two distinct modes of concerted cell migrations.

Second, we are investigating the mechanisms by which ovarian structure evolves in response to environmental stressors, such as a bout of severe starvation in every generation. In this project, we collaborate with the Gibbs lab to study how over 100 generations of selection for starvation-resistance can impact ovarian capacity for egg production.

Selected Publications (Raftery lab members in italics)

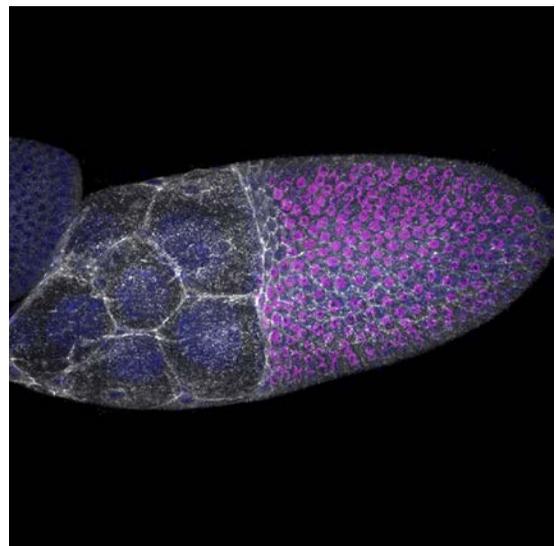
- *Brooks AI**, Dou W*, Pargett M, *Brosnan T*, *Raftery LA*, Umulis DM. BMP signaling in development: A critical analysis of imaging and interpretation. *FEBS Lett.* 2012, 586:1942-1952. *First two authors contributed equally to this publication.
- *Raftery LA*, Umulis, D Generation and interpretation of BMP gradients in *Drosophila*. *Cur. Opin. Cell Biol.* 2012, 24:1-8.
- Nie Y, Li Q, Amcheslavsky A, Veraska A, *Duhart JC*, Stocker H, *Raftery LA*, Ip YT. Bunched and Madm function downstream of Tuberous Sclerosis Complex to regulate the growth of intestinal stem cells in *Drosophila*. *Stem Cell Reviews and Reports* 2015, 11: 813-825.
- *Duhart JC**, *Parsons TT**, *Raftery LA*. The repertoire of epithelial morphogenesis on display: Progressive elaboration of *Drosophila* egg structure. *Mech. Dev.* 2017, doi.org/10.1016/j.mod.2017.04.002. *First two authors contributed equally to this publication.

Laurel Raftery

Professor
Ph.D., University of Colorado,
Boulder

Research Interests

- Cell-Cell Communication
- Epithelial Morphogenesis
- Developmental Genetics



Selected Awards

- 2016-2017 Hermsen Scholarship awarded to **Ph.D. candidate Juan Carlos Duhart**
- 2017 Second Prize Graduate Student Poster awarded to **Ph.D. candidate Tammara Beaghtly** at the 58th Annual *Drosophila* Research Conference

Kurt Regner

Professor-in-Residence
Ph.D., University of Wisconsin,
Madison

Research Interests

- Implementing a problem based approach in biology courses
- Promoting the benefits of undergraduate research
- Using quantitative biology to assess critical thinking



Selected Awards

- UNLV Teaching Academy Fellow

I have been teaching and developing curricula for undergraduate and graduate biology courses in the School of Life Sciences for 12 years. I rotate into introductory biology, microbiology for health science majors, molecular genetics and a graduate course covering molecular biology techniques. My approach to teaching includes introducing lecture topics with a hypothesis to emphasize the process of science over rote memorization. In an effort to encourage critical thinking, my exam questions necessitate the integration of several concepts and all exams include essay questions. I also try to introduce UNLV students to the larger world of science by assigning supplemental readings and arranging guest lectures from local professionals and scientists. I have attended workshops on RNAi technology, microarrays, bioinformatics and the Howard Hughes Medical Institute's Quantitative Undergraduate Biology Education and Synthesis Conference to keep abreast of the latest developments in biology research and education. I also participate in science education activities sponsored by the American Society for Microbiology and the Association of Biology Laboratory Educators.

For the past 10 years, I have been the PI for a National Science Foundation summer Research Experience for Undergraduates site. REU sites provide undergraduates with hypothesis-based projects that promote STEM careers and encourage applications to graduate programs. 53.0% of past-participants have enrolled in a graduate program or work in STEM education and entry-level research positions. To date, 18 participants are authors on 24 accepted publications and 1 book chapter. I am also part of a team that secured a HHMI SEA-Phages award to develop a classroom-based undergraduate research experience. After mastering a basic skill set including annotation, students initiate research projects investigating the nature of bacteriophage genes leading to the publication of phage genomes.

Selected Publications

- Salisbury A, ... Regner K, Strong C, Tsourkas P. 2019. Complete genome sequences of *Mycobacterium smegmatis* phage NihilNomen and Carlyle, isolated in Las Vegas, Nevada. *Microbiol Resource Announc* Sep 19;8(38). e00677-19. doi: 10.1128/MRA.00677-19.
- Salisbury A, ... Regner K, Strong C, Tsourkas P. 2019. Complete genome sequences of *Mycobacterium smegmatis* phages Chewbacca, Reptar3000, and Riparian, isolated in Las Vegas, Nevada. *Microbiol Resource Announc* Feb; 8(6): e01558-18.



My research program is interested in elucidating the molecular mechanisms that produce genetic diversity (mutations) in stressed cells. These mechanisms are novel because they occur in non-dividing cells and add to the well-known mutagenic processes taking place in actively growing cells. These mechanisms are significant because they can explain how cells increase their metabolic capacity, gain the ability to grow uncontrollably, and, in the case of pathogenic cells, evade the immune response, and acquire antibiotic resistance. In particular, we study how the processes of transcription-coupled repair TCR turns mutagenic in stressed cells or cells whose replication is limited. The idea that cells direct mutagenesis towards highly transcribed regions is interesting because it provides a mechanism to produce mutations with high adaptive value. In conditions in which cells are non-dividing these processes lower the risk of genetic load and the occurrence of lethal events. My program has been active for 12 years and has been or is supported by the NIH and NSF. Current areas of research investigate the role of oxidative DNA damage as an intermediate in the formation of mutations. We are also studying the effect of non-B DNA structures, formed during the process of transcription, on the formation of mutations in highly transcribed genes. The third avenue of research examines what factors are important for bacterial pathogens to express pathogenicity factors and acquire antibiotic resistance. My program is powered by an international collaboration and a diverse group of undergraduates and graduate students.

Selected Publications

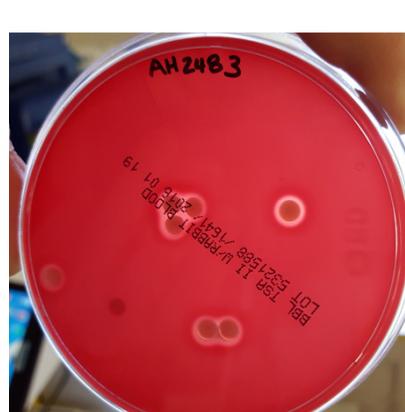
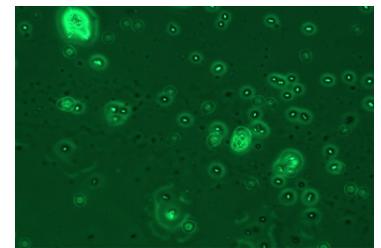
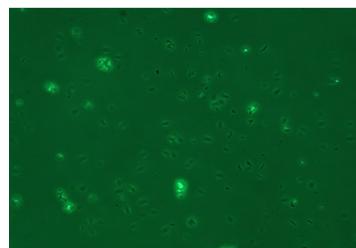
- Castro-Cerritos K, Yasbin R, Robleto E, and Pedraza-Reyes M. 2017. Role of Ribonucleotide Reductase in *Bacillus subtilis* Stress-Associated Mutagenesis. *Journal of Bacteriology*. doi: 10.1128/JB.00715-16.
- Gómez-Marroquín M, Martin H, Pepper A, Girard ME, Kidman A, Vallin C, Yasbin RE, Pedraza-Reyes M, Robleto EA. 2016. Stationary-Phase Mutagenesis in Stressed *Bacillus subtilis* Cells Operates by Mfd-Dependent Mutagenic Pathways. *Genes*. doi: 10.3390/genes7070033.
- Ambriz-Aviña V, Yasbin R, Robleto E, and Pedraza-Reyes M. 2016. Role of Base Excision Repair (BER) in Transcription-associated Mutagenesis of Nutritionally Stressed Nongrowing *Bacillus subtilis* Cell Subpopulations. *Current Microbiology* 73: 721. doi:10.1007/s00284-016-1122-9.
- Gómez-Marroquín M, Vidales LE, Debora BN, Santos-Escobar F, Obregón-Herrera A, Robleto EA, Pedraza-Reyes M. 2015. Role of *Bacillus subtilis* DNA Glycosylase MutM in Counteracting Oxidatively Induced DNA Damage and in Stationary-Phase-Associated Mutagenesis. *J Bacteriol.* 197:1963. PMC4420911.

Eduardo Robleto

Professor
Ph.D., University of Wisconsin,
Madison

Research Interests

- Microbiology
- Microbial Genetics
- Mutagenesis
- Evolution



Paul Schulte

Associate Professor
Ph.D., University of Washington

Research Interests

- Plant Physiology
- Water Transport
- Computational Fluid Dynamics

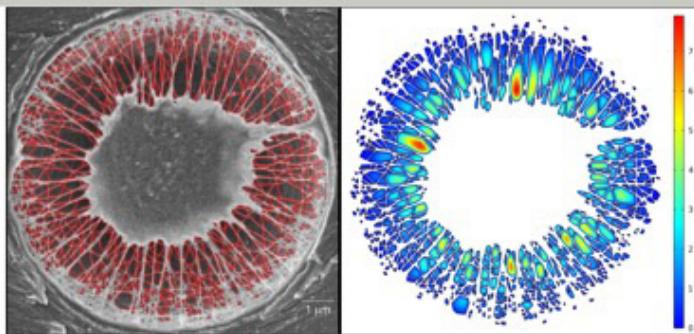
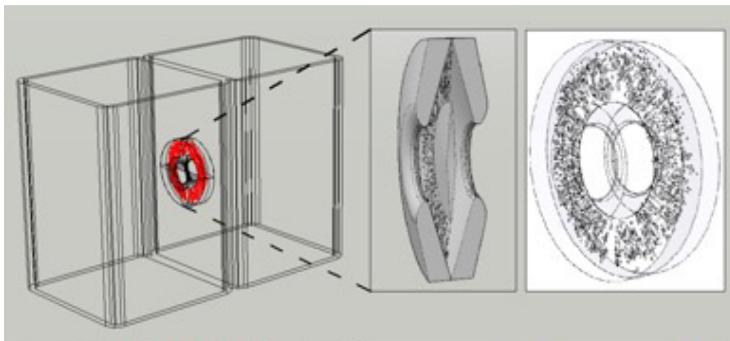


Plants are dependent on water for survival and their ability to acquire water from the soil and transport it throughout the plant is determined in part by the hydraulic properties of the plant's tissues. Therefore in a broad sense, I am interested in the transport of water through plants from a biophysical perspective. My studies of these topics usually involve mathematical or computational approaches.

In the past several years, I have become particularly interested in applying the tools of computational fluid dynamics and solid mechanics to the water transport process. Models describing fluid flow (see image) have been useful for understanding the function of structures found in plant tissues that connect the cells specialized for water transport. Many plant species among the conifers have specialized structures that it is thought act like valves to prevent the spread of air that would block (embolize) the conducting pathway. Models based on a solid mechanics approach can help to understand the forces that may be involved with closing the valve.

In studies of the biophysical aspects of plant water transport, I have been collaborating with a faculty member in the Department of Mathematical Sciences (David G Costa) for many years. Some of this work has involved research on mathematical approaches to transport processes. But we have also been quite interested in efforts to broaden the field of biology with interdisciplinary approaches from mathematics. In this regard, Dr. Costa and I started a biomathematics program with NSF funding and developed a two-part biomathematics course series. These courses bring a mathematical and computational perspective to biological questions, with

students learning to apply software such as *Mathematica* and *MATLAB*. In this regard, our goal is to meld the enormous potential of mathematics that has been so prominent in fields like physics, with the complexity of biological systems – to demonstrate to students that developing a skill set with this integrated STEM approach is important for the future of science in biology.



Selected Publications

- Schulte PJ, UG Hacke, AL Schoonmaker. 2015. Pit membrane structure is highly variable and accounts for a major resistance to water flow through tracheid pits in stems and roots of two boreal conifer species. *New Phytologist* 208:102-113.
- Schulte PJ. 2012. Computational fluid dynamics models of conifer bordered pits show how pit structure affects flow. *New Phytologist* 193:721-729.
- Schulte PJ and DG Costa. 2010. Xylem anisotropy and water transport - a model for the double sawcut experiment. *Tree Physiology* 30:901-913.

With Bioinformatics, Genomics and Proteomics tools, our group studies signal transduction networks mediating plant response to environmental stresses, especially drought and salt stress, and molecular mechanisms controlling seed development, dormancy and germination. In angiosperm, double fertilization initiates the embryogenesis process within a developing seed. The seed is a carrier of a new plant to be dispersed hence they occupy a critical position in the life history of higher plants. Seeds are also desiccation tolerant; understanding this aspect of seed development also helps us decipher the mechanism controlling plant response to environmental stresses. Our focus in the past decade has been identification and isolation of genes involved in drought responses and seed germination, especially those genes encoding transcription factors. We also have addressed the signal transduction pathways mediating the induction or repression of these genes.

Physiological, genetic and biochemical studies demonstrate that plant development is regulated by the interaction of several hormones. The molecular foundation of the interaction is the cross-talk of cell signaling which integrates the independent stimuli using connections between biochemical pathways. Signal cross-talk includes gibberellins, brassinosteroids, and abscisic acid pathways, ethylene and jasmonic acid pathways, ethylene and glucose pathways, sugar sensing and light response pathways, and phytochrome and cryptochrome pathways. The Boolean network model is proposed to integrate genetic data into the logical network of biochemical pathway connections deduced from transcriptome and proteome data.

The third project in Shen lab addresses the molecular basis of leukemia in collaboration with Dr. Jason Cheng at the University of Chicago Medical School. Our contribution is largely on bioinformatic analyses of RNA-seq, ChIP-seq and genome mutation data derived from myelodysplastic syndrome (MDS)-derived erythroid/myeloid line and primary MDS bone marrow cells. Our data support a hypothetical model of epigenetic inactivation of the PU.1 pathway due to increased H3K27me3 in some cases of cytogenetically normal refractory cytopenia with multilineage dysplasia (CN-RCMD).

Selected Publications

- Watanabe, K., Homayouni, A., Gu, L., Huang, K.Y., Ho, T.D., Shen, Q.J.: Transcriptomic analysis of rice aleurone cells identified a novel abscisic acid response element. *Plant Cell Environ.* 2017, 40(9): 2004-2016.
- Xu, H., Watanabe, K., Zhang, L. and Shen, Q. J.: WRKY transcription factor genes in wild rice *Oryza nivara*. *DNA Research*, 2016, 23(4), 311–323.
- Watanabe, K., Ma, K., Homayouni, A., Rushton, P.J. and Shen, Q.J.: Transcript structure and domain display: a customizable transcript visualization tool. *Bioinformatics*, 2016, 32 (13): 2024-2025.
- Tripathi, P., Rabara, R.C., Reese, R.N., Miller, M.A., Rohila, J.S., Subramanian, S., Shen, Q.J., Morandi, D., Bücking, H., Shulaev, V. and Rushton, P.J.: A toolbox of genes, proteins, metabolites and promoters for improving drought tolerance in soybean includes the metabolite coumestrol and stomatal development genes. *BMC Genomics*, 2016, 17:102.
- Cheng, J., Anastasi, J., Watanabe, K., Shen, Q.J., and Vardiman, J.: Genome-wide profiling reveals epigenetic inactivation of the PU.1 pathway by histone H3 lysine 27 trimethylation in cytogenetically normal myelodysplastic syndrome. *Leukemia*, 2013, 27: 1291-1300.

Jeff Shen

Professor
Ph.D., Washington University in
St. Louis

Research Interests

- Development of Database and Bioinformatics Tools for Biological, Agricultural and Biomedical Applications
- Molecular Mechanisms Controlling Seed Dormancy and Germination, and Plant Responses to Abiotic Stresses
- Molecular Basis of Leukemia (in collaboration with Dr. J. Cheng at the University of Chicago Medical School)



Elizabeth Stacy

Associate Professor
Ph.D., Boston University

Research Interests

- Adaptive Divergence and Speciation in Trees



Selected Awards

- NSF Centers of Research Excellence in Science and Technology (CREST) Grant – 2010-2019 [Co-PI].
- NSF Faculty Early Career Development Program (CAREER) Grant – 2010-2016 [PI].
- Moore Foundation Grant – 2008-2014 [Co-PI].
- NSF Research Initiation Grant to Broaden Participation (RIG) – 2006-2009 [PI].



An estimated 100,000 species of trees form the foundation of many terrestrial environments and provide countless ecosystem and commercial services. In spite of the importance of tree diversity, however, little is known about speciation in trees, or how reproductive isolating barriers accumulate between diverging tree populations to generate new species.

I have been fascinated by the origin of tree species ever since my first visit to the Peruvian Amazon decades ago. My lab uses a combination of field, greenhouse, and lab (molecular and microscopy) techniques to better understand how tree populations diverge and evolve reproductive isolating barriers. For over a decade, our studies have been based in Hawai'i, an evolutionary hotspot where ongoing species radiations allow examination of divergence at early stages. The landscape-dominant group, Hawaiian *Metrosideros* ("Ohi'a"), in particular, offers unprecedented opportunities to examine the process of speciation. Over its roughly 4-million-year history in the Hawaiian Islands, this woody genus has diversified into a large number of forms that differ in vegetative traits and are nonrandomly distributed across Hawai'i's heterogeneous landscape, and the group has many traits that make it unusually amenable to evolutionary studies. Our extensive field observations, studies of neutral genetic variation, and experimental studies have established Hawaiian *Metrosideros* as a rare case of incipient radiation in trees and thus as a useful model for studies of divergence and the evolution of reproductive isolating barriers at the early stages of speciation. Importantly, these studies provide insights that are valuable to the management of this foundation woody genus under anthropogenic climate change, which is already affecting Hawai'i. Other studies in my lab focus on the species-rich Hawaiian plant groups, *Clermontia* and *Cyrtandra*, to understand patterns of island colonization and diversification.

Selected Publications

- Choi, J. Y., M. Purugganan, and E. A. Stacy. 2020. Divergent selection and primary gene flow shape Incipient speciation of a riparian tree on Hawaii Island. *Clermontia Molecular Biology and Evolution* <https://doi.org/10.1093/molbev/msz259>.
- Stacy, E. A. and T. Sakishima. 2019. Phylogeography of the highly dispersible landscape-dominant woody species complex, *Metrosideros*, in Hawaii. *Molecular Journal of Biogeography* 46: 2215-2231.
- Ekar, J. M., D. K. Price, M. A. Johnson, and E. A. Stacy. 2019. Varieties of the highly dispersible and hypervariable tree, *Metrosideros polymorpha*, differ in response to mechanical stress and light across a sharp ecotone. *Molecular American Journal of Botany* 106: 1106-1115.
- Stacy, E. A., B. Paritosh^U, M. A. Johnson^U, and D. K. Price. 2017. Incipient ecological speciation between successional varieties of a dominant tree involves intrinsic postzygotic isolating barriers. *Ecology and Evolution* 7: 2501-2512.
- Stacy, E. A., J. B. Johansen, T. Sakishima, and D. K. Price. 2016. Genetic analysis of an ephemeral intraspecific hybrid zone in the hypervariable tree, *Metrosideros polymorpha*, on Hawai'i Island. *Heredity* 117: 173-183.
- Stacy, E. A., J. B. Johansen, T. Sakishima^G, D. K. Price, Y. Pilon. 2014. Incipient radiation within the dominant Hawaiian tree *Metrosideros polymorpha*. *Heredity* 113: 334-342.

My lab studies the ecology and physiology of the trait vegetative desiccation tolerance (DT) in mosses. Desiccation tolerance (DT) is the ability of an organism or structure to survive drying in equilibration with dry air, and among plants is most well developed among the bryophytes. In my lab, various species of mosses are cultured and bred, with experiments on DT normally based on single clonal lines. We are interested in determining the intrinsic ecological strategy of DT employed by a species; this strategy resides along an inducibility gradient, from weakly inducible to nearly constitutive. Current experimental topics include the phenology of DT for both sporophytes and shoots, the linkage of DT to life phase, methods of drying plants for optimal induction of DT, and the influence of rate of rehydration on DT. In essence, my lab investigates how the four factors of desiccation tolerance, (i) the rate of drying, (ii) the equilibrating relative humidity experienced, (iii) the duration spent in the dried state, and (iv) the rate of rehydration, affect the capacity of a plant to tolerate desiccation and influence fitness.

Recent research highlights include the first demonstration that the model moss *Physcomitrella patens* is desiccation tolerant by a Ph.D. student in my lab (2014), the first demonstration that different life phases of a single species exhibit different intrinsic strategies of DT (2016), showing how a prehydration treatment protects against low tissue water contents (2018), and a first illustration of how rate of drying influences low water content in mosses (2019).

Current funded projects include (1) an NSF grant exploring DT in the genus *Syntrichia*, (2) a US Golf Association grant exploring stress effects on a moss that inhabits golfing greens, and (3) a floristic project for Grand Staircase Escalante National Monument. Prospective graduate students should have a background in bryophytes and an interest in moss ecophysiology.

Selected Publications

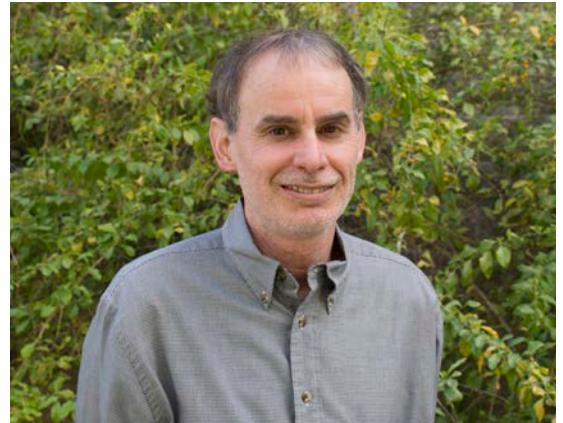
- Greenwood, J.L., L.R. Stark, and L.P. Chiquoine. 2019. Effects of rate of drying, life history phase, and ecotype on the ability of the moss *Bryum argenteum* to survive desiccation events and the influence on conservation and selection of material for restoration. *Frontiers in Ecology and Evolution*, published online 10-18-2019, doi: 10.3389/fevo.2019.00388.
- Coe, K.K., N.B. Howard, M.L. Slate, M. Bowker, B.D. Mishler, R. Butler, J. L. Greenwood, and L.R. Stark. 2019. Morphological and physiological traits in relation to carbon balance in a diverse clade of dryland mosses. *Plant, Cell & Environment* 42: 3140–3151, DOI: 10.1111/pce.13613.
- Raudenbush, Z., J. L. Greenwood, D.N. McLetchie, S.M. Eppley, S.J. Keeley, R.C. Castetter, and L.R. Stark. 2018. Divergence in life-history and developmental traits in Silvery-Thread Moss (*Bryum argenteum* Hedw.) genotypes between golf course putting greens and native habitats. *Weed Science* 66: 642–650. doi: 10.1017/wsc.2018.37.

Llo Stark

Professor
Ph.D., Penn State University

Research Interests

- Ecophysiology of Desiccation Tolerance in Mosses
- Reproductive Biology of Bryophytes



Selected Awards

- Multiple Sullivant Awards (2014, 2016, 2018), presented annually for the outstanding paper published in *The Bryologist*, with the latest paper “Ecology of desiccation tolerance in bryophytes: a conceptual framework and methodology” (2017).

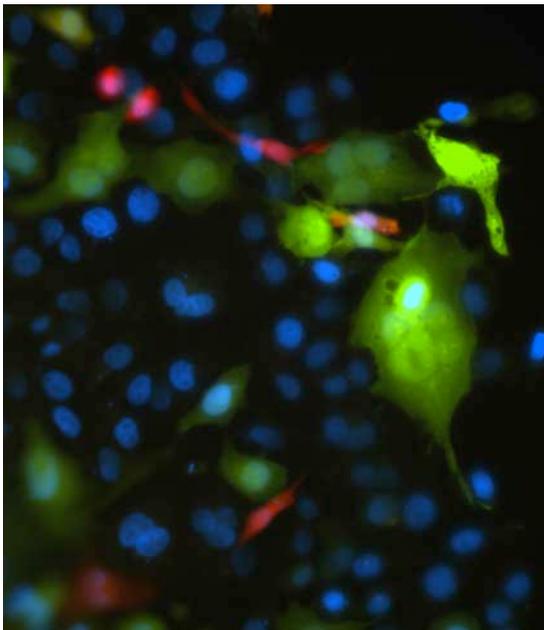


Christy Strong

Assistant Professor-in-Residence
Ph.D., University of Montana

Research Interests

- HIV Biology
- Bacteriophage Biology
- Science Education



Viruses bombard us in our everyday lives. Some successfully establish a toehold in the host leading to an active infection while others pass through our system with humans never being the wiser. The power of a viral blueprint to not only circumvent a host cell's defense but also reprogram the cell to do the virus's bidding is just one of the many fascinating aspects involved in the study of viruses. Dr. Strong's upper division virology course introduces UNLV students to the incredibly diverse world of viruses with the goal of fostering a life-long appreciation of these constructs bordering the definition of life.

Christy Strong earned a B.S. in Biology from Montana State University in 2001, a M.S. in Biology from East Tennessee State University in 2005, and a Ph.D. in Integrative Microbiology and Biochemistry from the University of Montana in 2011. After completing a post-doc at UNLV under the mentorship of Dr. Martin Schiller in 2014, Dr. Strong transitioned to the role of Assistant Professor-in-Residence in the School of Life Sciences.

Dr. Strong's background is in HIV RNA structure and function with an emphasis on understanding how sequences in non-coding regions regulate various steps in the HIV replication cycle. She is currently collaborating with Dr. Philippos Tsourkas on proof of principle experiments to test bioinformatics predictions of bacteriophage gene functions. Dr. Strong, Dr. Tsourkas, and Dr. Regner team-teach the research-oriented undergraduate two-semester course Biol207X Phage Discovery and Bioinformatics.

Selected Publications

- Benjamin R, Berges BK, Solis-Leal A, Igbinedion O, Strong CL, Schiller MR. 2016. TALEN gene editing takes aim on HIV. *Hum. Genet.* Sep;135(9): 1059-70.
- Strong CL, Guerra HP, Mathew KR, Roy N, Simpson LR, and MR Schiller. 2015. Damaging the Integrated HIV Proviral DNA with TALENs. *PLOS ONE.* 10(5):e0125652.
- Sargeant DP, Strong CL, Deverasetty S, Alaniz IJ, Bartlett AN, Brandon NR, Brooks SB, Brown FA, Bufi F, Chakarova M, David RP, Dobritch KM, Guerra HP, Hedden MW, Kumra R, Levit KS, Mathew KR, Matti R, Maza DQ, Mistry S, Novakovic N, Pomerantz A, Portillo J, Rafalski T, Rathnayake V, Rezapour N, Songao S, Tuggle S, Yousif S, Dorsky D, and Schiller MR. 2014. The HIVToobox 2 web system integrates sequence, structure, function, and mutation analysis. *PLOS ONE.*
- Sargeant DP, Hedden MW, Deverasetty S, Strong CL, Alaniz IJ, Bartlett AN, Brandon NR, Brooks SB, Brown FA, Bufi F, Chakarova M, David RP, Dobritch KM, Guerra HP, Levit KS, Mathew KR, Matti R, Maza DQ, Mistry S, Novakovic N, Pomerantz A, Rafalski TF, Rathnayake V, Rezapour N, Ross CA, Schooler SG, Songao S, Tuggle SL, Wing HJ, Yousif S, Schiller MR. 2014. The Geogenomic Mutational Atlas of Pathogens (GoMAP) Web System. *PLOS ONE.* Mar 27; 9(3).
- Strong CL, Lanchy JM, Lodmell JS. 2011. Viral SELEX reveals individual and cooperative roles of the C-box and G-box in HIV-2 replication. *RNA.* Jul;17(7):1307-20.
- Strong CL, Lanchy JM, Dieng-Sarr A, Kanki PJ, Lodmell JS. 2009. A 5'UTR-spliced mRNA isoform is specialized for enhanced HIV-2 gag translation. *Journal of Molecular Biology.* Aug 14;391(2):426-37.
- Baig TT, Strong CL, Lodmell JS, Lanchy JM. 2008. Regulation of primate lentiviral RNA dimerization by structural entrapment. *Retrovirology.* Jul 17;5:65.

My research interests encompass a wide range of organisms and topics in ecology and evolutionary biology. Working with students and several research collaborators I have investigated: spatial ecology of desert shrubs and rodents; habitat selection and movement ecology of bighorn sheep and cougar; the ecology and evolution of phenotypic plasticity and developmental integration in grasshoppers; molecular evolution of gene families; butterfly life-history, habitat selection, and evolutionary ecology; and recovery of alpine butterfly habitat following catastrophic fire.

The research on butterflies, conducted with students and collaborators from federal agencies, is focused on understanding basic characteristics of the life-history, population biology, and larval myrmecophily of several endemic species of conservation concern in the Spring Mountains of southern Nevada. In alpine bristlecone pine environments, we have observed Mount Charleston blue butterfly oviposition (below) on three different species of legume cushion plants and quantified the influence of nectar plant availability and low tree cover on female selection of larval host plants. Portions of this research are described in the Federal Register (Endangered and threatened wildlife and plants; determination of endangered species status for Mount Charleston blue butterfly. Dept of Interior, Fish and Wildlife Service. September 19, 2013, Federal Register 78:57750-57775 and June 30, 2015, Federal Register 80:37404-37430).

In other research, measuring the establishment of plants following the catastrophic Carpenter 1 fire, we have found that the early stages of recovery are dominated by the plants essential for high quality habitat of the endangered Mount Charleston blue butterfly. Using genetic markers and phylogeographic analyses, we are also studying phenological divergence, diapause plasticity, and gene flow in two cohorts of Spring Mountains dark blue butterflies whose larvae feed on the flowers of host plants that bloom at different times. Having found that gene flow between the cohorts of butterflies generates phenological variation, we propose that protecting gene flow should be a focus of conservation efforts.

Selected Publications

- Thompson DB. 2019. Diet-induced Plasticity of Linear Static Allometry is Not So Simple for Grasshoppers: Genotype-Environment Interaction in Ontogeny is Masked by Convergent Growth. *Integrative and Comparative Biology* 59:1382-1398.
- Lowery C, Longshore K, Choate D, Nagol JR, Sexton J, Thompson DB. 2019. Ecological effects of fear: how spatiotemporal heterogeneity in predation risk influences mule deer access to forage in a sky island system. *Journal of Ecology and Evolution* 9:7213–7226.
- Thompson DB, McKelvey K, van Els P, Andrew G, Garrett P, Glenn M, Kallstrom C, Pilgrim K, Opler PA. Conserve the eco-evolutionary dynamic, not the subspecies: Phenological divergence and gene flow between temporal cohorts of *Euphilotes ancilla* endemic to southern Nevada. *Conservation Genetics* (2020, Accepted).
- Sappington M, Longshore K, and Thompson D.B. 2007. Quantifying landscape ruggedness for animal habitat analysis: a case study using bighorn sheep in the Mojave Desert. *Journal of Wildlife Management* 71:1419–1426.

Daniel Thompson

Associate Professor
Ph.D., University of Arizona

Research Interests

- Evolutionary Biology
- Ecology
- Phenotypic Plasticity

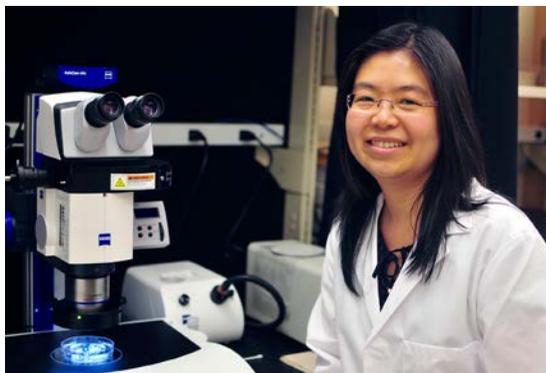


Ai-Sun (Kelly) Tseng

Associate Professor
Ph.D., Harvard University

Research Interests

- Organ Regeneration
- Stem Cells
- Eye



Selected Publications

- Kha, C. X.*, Guerin, D.J.*, and Tseng, K. A.-S. (2020) Studying *in vivo* Retinal Progenitor Cell Proliferation in *Xenopus laevis*. In: Mao CA. (ed) Retinal Development. *Methods in Molecular Biology*, 2092:19-33. Humana, New York, NY.
- Kha, C. X.*, Guerin, D.J. *, and Tseng, K. A.-S. (2019) Using the *Xenopus* Developmental Eye Regrowth System to Distinguish the Role of Developmental Versus Regenerative Mechanisms. *Frontiers in Physiology*, May 8;10:502. doi:10.3389/fphys.2019.00502.
- Kha, C. X., Son, P. H., Lauper, J., and Tseng, K. A.-S. (2018) A Model to Investigate Developmental Eye Repair in *Xenopus laevis*. *Experimental Eye Research*, 169:38-47.
- Tseng, A.-S. (2017). Seeing the future: using *Xenopus* to understand eye regeneration. *genesis: The Journal of Genetics and Development*, 55(1-2), e23003. doi:10.1002/dvg.23003.

Why can some animals regrow organs but humans cannot? It has been known for centuries that animals such as amphibians have the natural ability to regenerate tissues but how this process occurs is still not well known. Understanding regenerative mechanisms can help to provide new strategies to treat damaged tissues in conditions such as nerve degeneration, organ disease, and injuries.

The Tseng lab studies how a highly regenerative animal senses that it has injured or lost tissues and how it responds to repair the damage successfully. We use the powerful and well-characterized vertebrate model, the African clawed frog, *Xenopus laevis*. *Xenopus* embryos and tadpoles can rapidly heal wounds and regrow tissues and organs including limbs, retina, and brain. Like humans, *Xenopus* also shows age-dependent regenerative ability, making it an excellent model for identifying the still unknown mechanisms that underlie the differences between regenerative and non-regenerative responses to injury and disease.

Using interdisciplinary approaches (including molecular, chemical-genetic, physiological, and *in vivo* imaging tools), we seek to elucidate the key mechanisms that enable regeneration and to identify stem cells that can achieve successful repair. In the long term, our goal is to build a blueprint for organ regeneration and to apply this knowledge towards developing novel therapeutics for regenerative medicine

Research Areas

1. Understanding Mechanisms that Drive Neural Regeneration

A main challenge in the regeneration field has been to identify the signaling pathways and suitable cell types needed to enable productive tissue repair. For the eye, the successful generation and maintenance of eye-specific stem cells is a key goal. Although the process of vertebrate eye development is well-characterized, the mechanisms that can induce eye stem cell proliferation following injury remain unknown. We found that *Xenopus* embryos successfully regrew functional eyes after excision. Successful eye regrowth required extended retinal progenitor cell proliferation while delaying eye formation. Eye regrowth is age dependent, providing an ideal animal model to test strategies that can drive successful regrowth. In contrast, other regeneration models lack this feature. Using a combination of cellular, molecular, and bioinformatics approaches, we are: 1) characterizing the stem cells that drive this process and identifying potential new stem cell markers; and 2) systematically defining mechanisms that regulate regenerative stem cell proliferation to drive eye regrowth.

2. Defining Shared Mechanisms of Tissue Repair and Regeneration

Regeneration studies have focused on diverse organs and animal models. Although there is now considerable information about some of the mechanisms that regulate regeneration, it remains unknown whether there are shared mechanisms across different tissues and/or species. If we can identify common mechanisms for initiating regeneration, then this knowledge can streamline approaches for stimulating regeneration in different tissues. By comparing eye regeneration mechanisms with those for limb regeneration, we aim to identify commonalities in repair mechanisms in different vertebrate organs.

A majority of bacteria in the environment reside in complex communities called biofilms. In addition to being an important part of the ecosystem, biofilms impact humans in industry, agriculture, and medicine in ways that can be either beneficial or detrimental. While biofilms can be useful, such as in the treatment of wastewater, they can also be problematic because bacteria in biofilms can cause disease. In fact, the National Institutes of Health have estimated that approximately 80% of all hospital acquired infections are due to biofilm bacteria. Biofilm-based infections are particularly troublesome because bacteria in biofilms are more tolerant against antimicrobial agents than the individual bacteria on their own. Because of this increased tolerance, such infections are often chronic in nature and extremely difficult to eradicate.

My laboratory studies the biofilms of the opportunistic pathogen *Pseudomonas aeruginosa*. This bacterium is commonly found in our environment and does not cause disease in healthy humans. However, *P. aeruginosa* can form biofilms and infect a variety of medically relevant surfaces, such as indwelling medical devices (e.g. contact lenses, catheters, mechanical heart valves and pacemakers), burn wounds, urinary tracts, corneas, ears, and the lungs of people with cystic fibrosis and chronic obstructive pulmonary disease. In the case of those with cystic fibrosis, their *P. aeruginosa* biofilm infections can persist for decades, even though these people are actively taking antibiotics to combat the infection. A main focus of my laboratory is understanding how the biofilm protects the resident bacteria from antimicrobial treatment.

Among the protective mechanisms of biofilm bacteria is their self-produced extracellular matrix, which surrounds the cells. Although proteins have long been known to be an important part of the matrix, very few biofilm matrix proteins of *P. aeruginosa* have been identified and little is known about their functions. Since the biofilm matrix can protect bacteria from antimicrobial attack and is essential for biofilm formation, identifying and characterizing matrix proteins could prove to be critical for treating and preventing biofilm-based infections. We aim to identify matrix proteins and to characterize their roles in biofilm formation and antimicrobial tolerance, using techniques in proteomics, genetics, molecular biology, and microscopy. We expect that our work will provide fundamental information about biofilm formation, which will aid in the development of therapeutics to treat and prevent biofilm-based infections and advance knowledge of *P. aeruginosa* biology.

Selected Publications

- Tseng BS, Reichhardt C, Merrihew GE, Araujo-Hernandez SA, Harrison JJ, MacCoss MJ, Parsek MR. 2018. A Biofilm Matrix-Associated Protease Inhibitor Protects *Pseudomonas aeruginosa* from Proteolytic Attack. *mBio* 9(2): e00543.
- Passos da Silva D, Schofield MC, Parsek MR, Tseng BS. 2017. An Update on the Sociomicrobiology of Quorum Sensing in Gram-Negative Biofilm Development. *Pathogens* 6(4): E51.
- Tseng BS, Majerczyk CD, Passos da Silva D, Chandler JR, Greenberg EP, Parsek MR. 2016. Quorum Sensing Influences *Burkholderia thailandensis* Biofilm Development and Matrix Production. *J Bacteriol* 198(19): 2643.

Selected Grants/Awards

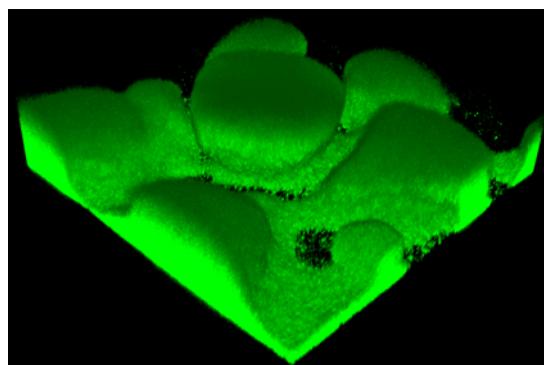
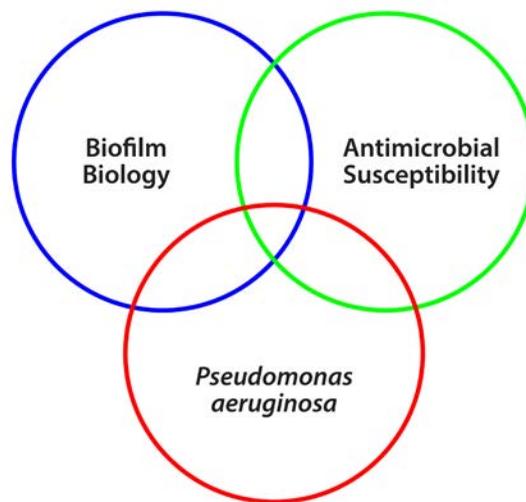
- 2019: Cystic Fibrosis Foundation Pilot Grant
- 2016: NIH NIAID K22 Career Transition Award

Boo Shan Tseng

Assistant Professor
Ph.D., Rockefeller University

Research Interests

- Microbiology
- Bacterial Physiology
- Molecular Biology



Philippos Tsourkas

Assistant Professor
Ph.D., University of California,
Berkeley

Research Interests

- Bioinformatics
- Biostatistics
- Mathematical Modeling
- Bacteriophage Genomics



Selected Publications

- Stamereilers C, LeBlanc L, Yost DG, Amy PS, Tsourkas P (2016) Comparative genomics of nine novel *Paenibacillus larvae* bacteriophages. *Bacteriophage*. 6(3):e1220349. DOI: 10.1080/21597081.2016.1220349.
- Tsourkas P, Yu-Yang P, Liu W, Pierce SK, Raychaudhuri S (2012) Formation of BCR oligomers provides a mechanism for B cell affinity discrimination. *J. Theor. Bio.* 307:174-182.
- Tsourkas P, Liu W, Das S, Pierce SK, Raychaudhuri S (2012) Affinity discrimination in response to membrane antigen in B cells requires that kinetic proofreading predominate over serial engagement. *Cell. & Mol Immunol.* 9:62-74.

Genomics of *Paenibacillus larvae* bacteriophages

Paenibacillus larvae is a Gram-positive, spore-forming bacterium that is the causative agent of American Foulbrood Disease (AFB), one of the leading causes of the global population decline of the honeybee (*Apis mellifera*). As bees lack an adaptive immune system, one potential antibiotic-free AFB treatment is the use of bacteriophages that target *P. larvae*. Phages have several attractive features as a treatment strategy, such as not contaminating honey, being harmless to humans and to important symbiotic bacteria in the larval gut, and co-evolving with their host. My lab is one of the leaders in *P. larvae* phage genomics, having published the largest number of *P. larvae* phage genomes to date. The process of phage genome annotation is ideally suited to undergraduate research and we are currently recruiting talented undergraduate students to annotate *P. larvae* phage genomes for publication.

A meta-tool for bacteriophage gene prediction and genome annotation

Bacteriophages are the most numerous and diverse entities on Earth, with an estimated 1,031 particles in the biosphere. The rapid decrease in cost of sequencing technology has resulted in an explosion in the number of published phage genomes. Manual annotation remains the gold standard for producing accurate phage genome annotations (gene identification, start codon identification, putative function assignment). However, when the number of sequenced phages is large, manual curation becomes prohibitively time-consuming. To this end we are working towards developing a series of tools for bacteriophage genome annotation that combine as many of the advantages of manual curation as possible, while retaining the speed of automation.

Mathematical modeling of lymphocyte receptor signaling

Signaling by receptors is in many cases mediated by a tyrosine kinase domain that transfers a phosphate group from an ATP molecule to a cytosolic signaling molecule, initiating a cascade that eventually leads to gene transcription. Most commonly, the receptor's kinase domain is an intrinsic part of the receptor itself (e.g. in the EGFR family of receptors, insulin receptors, etc...). In lymphocytes however (T and B cells), the intracellular domain of the lymphocyte antigen receptor (the receptor dedicated to detecting foreign pathogens, known as the "B cell receptor" or "BCR" in B cells, and the "T cell receptor", or "TCR" in T cells) does not possess a kinase domain. Rather, kinase activity is carried out by an extrinsic family of molecules known as Src-family kinases that carry out their signaling function by binding to an Immuno-Tyrosine Activation Motif (ITAM) on the intracellular domain of the receptor following antigen ligation to the receptor's extracellular domain. It is currently not known why lymphocyte antigen receptor signaling differs from other receptor families in this respect. One reason could be that lymphocyte antigen receptors, in contrast to other receptor families, encounter an essentially infinite variety of antigenic ligands. We are currently developing mathematical models that we hope will generate useful insight into the differences between extrinsic and intrinsic kinase-mediated signaling cascades.

Selected Awards

- HHMI SEA-PHAGES

My primary responsibility within SoLS is teaching large enrollment undergraduate courses. My most fundamental belief about education is that all students are capable of intellectual growth and development. I seek to facilitate student acquisition of deep and integrated understanding of the material. I encourage students to anchor new information into the foundation of their prior knowledge. I emphasize the idea that critical thinking and analytical problem solving skills are vital components of upholding their future professional duties. I expect my students to take responsibility for their learning; I expect them to invest full effort, to utilize their learning resources, and to ask for guidance when needed.

Effective instruction about the dynamic realm of biology requires ongoing scholarship. My research experience substantially contributes to my success as an instructor. My current research interests include hibernation physiology and science education. Mammalian physiology is widely conserved, thus hibernators provide a relevant paradigm for investigating physiological extremes that are relevant to human health including conditions of hypothermia and hypometabolism, obesity and appetite control, and disuse atrophy. One focus for my current research is investigating the resistance to bone disuse atrophy that occurs in hibernators. Many species of mammals, including humans, experience significant loss of bone mass and bone volume following immobilizations as short as six-weeks. Hibernators may spend 6 to 9 months in an inactive state. Despite this prolonged inactivity, I previously found that bone mass, bone volume, and bone strength are all maintained throughout the hibernation season. Of course the metabolic depression and reduced body temperatures that these animals exhibit during the hibernation season limits widespread application of these findings. Therefore I have continued collaborating with my engineering colleagues to expand our investigation to include animals monitored during the summer, a time when 'standard' mammalian body temperature and metabolic activity are present.

In addition to the bone disuse atrophy project, I have another line of hibernation physiology research that focuses on regulation of the process of warming from torpid body temperatures. I also engage in science education research; my most recent project (conducted by a collaboration of STEM faculty and funded by NSF) investigated the use of Learning Management Systems, like Blackboard, to provide learning strategy and motivational interventions designed to increase student achievement and course completion rates.

Selected Publications

- M. L. Bernacki, L. Vosicka, and J.C. Utz. Can brief, web-delivered training help STEM undergraduates "Learn to Learn" and improve their achievement? Paper presented to American Educational Research Association Annual Meeting, Washington, DC, 2016.
- J.C. Utz and F. van Breukelen. 2013. Prematurely induced arousal from hibernation alters key aspects of warming in golden-mantled ground squirrels, *Callospermophilus lateralis*. *Journal of Thermal Biology*, 38: 570-575.
- J.C. Utz, S. Nelson, B.J. O'Toole, and F. van Breukelen. 2009. Bone strength is maintained after 8 months of inactivity in hibernating golden-mantled ground squirrels, *Spermophilus lateralis*. *Journal of Experimental Biology*, 212: 2746-2752.

Jenifer Utz

Assistant Professor-in-Residence
Ph.D., University of Nevada,
Las Vegas

Research Interests

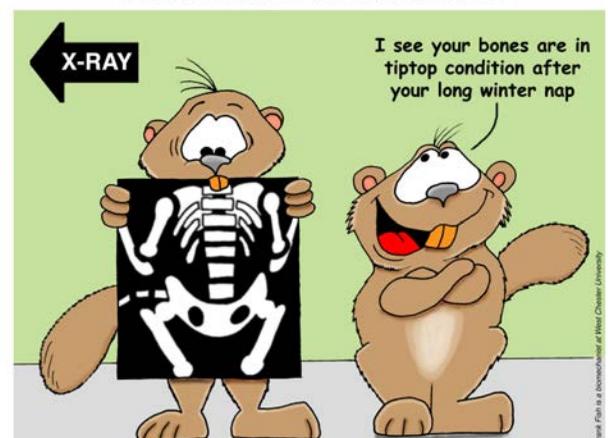
- Hibernation Physiology
- Science Education



Selected Awards

- Professor of the Year Award from the Student Association of Pre-Health Professionals (2016)
- College of Sciences Distinguished Teaching Award (2016)
- National Science Foundation Graduate Research Fellowship (2007-2010)

HIBERNATING SQUIRRELS' BONES WEATHER WINTER WELL



Frank van Breukelen

Director and Professor
Ph.D., University of Colorado,
Boulder

Research Interests

- Animal responses to extreme environments



Selected Awards

- 2009 Nevada Regents' Rising Researcher Award
- 2012 Consolidated Students of the University of Nevada, Las Vegas Faculty of Excellence Award



My laboratory uses techniques and approaches that range from physiology to ecology to biochemistry in addressing significant biological questions about how animals interact with stressful environments. Two areas of particular focus include mammalian hibernation and desert pupfish.

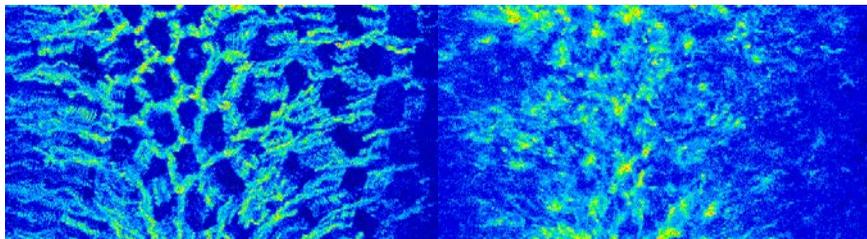
Presumably, in response to limited food availability and harsh environmental conditions, many mammals enter a state of depressed metabolism or torpor. Much of what we learned of hibernation came from a ground squirrel model. Hibernating ground squirrels can maintain body temperatures (T_b) below 0°C for up to three weeks with oxygen consumption rates as low as 1/100th of active rates. The squirrel's hibernation season is comprised of a series of sequential bouts of torpor wherein T_b approaches that of ambient interrupted by periodic rewarmings or interbout arousals to core temperatures near 36°C that usually last less than 24 hours. We found critical homeostatic processes like protein synthesis and degradation are depressed during torpor but resumed during the interbout arousal. Much of our work focused on the implications and mechanisms of that depression. In the end, we assumed a critical role for the interbout arousal in allowing for a resetting of homeostasis.

If ground squirrels represent an elite hibernator, what might we learn if we studied a poor hibernator? More recently, we are challenging our own findings by working with a novel model of hibernation wherein there is no interbout arousal. Many view our early mammalian ancestors as having been nocturnal, insectivorous, with variable T_b and the capacity for metabolic depression or torpor. Common tenrecs (*Tenrec ecaudatus*) are bizarre mammals from Madagascar that have many 'ancestral' features. We hypothesize these animals to possess an ancestral form of hibernation. Their novel hibernation patterns and ability to be active with T_b s that range from below 10 to 32°C will provide unique insight into the evolution and function of hibernation and endothermy.

In another project, we found that pupfish reared at an ecologically relevant temperature (33°C) experience periods of as much as 149 min with no oxygen consumption despite oxygen's availability, a process we call paradoxical anaerobism. Instead, the pupfish produce ethanol as an alternative end product of metabolism. My laboratory is interested in elucidating further the mechanisms that underlie this phenomenon and what this might mean to the evolution of these fishes.

Selected Publications

- P. Pan, M. D. Treat, and F. van Breukelen. (2014) A systems level approach to understanding transcriptional regulation by p53 during mammalian hibernation. *Journal of Experimental Biology*, 217:2489–2498.
- M. Heuton, L. Ayala, C. Burg, K. Dayton, K. McKenna, A. Morante, G. Puentedura, N. Urbina, S. Hillyard, S. Steinberg, and F. van Breukelen (2015) Paradoxical anaerobism in desert pupfish. *Journal of Experimental Biology*, 218:3739-3745.
- F. van Breukelen and S. L. Martin (2015) The hibernation continuum: physiological and molecular aspects of metabolic plasticity in mammals. *Physiology*, 30(4):273-281.



As biological sciences become more and more interdisciplinary, we are starting to appreciate that physical forces, just like biochemical signals, can activate cellular cascades and play an instructive role in regulating cell behaviors. Our long term goal is to understand how mechanical tension is sensed and translated into cellular activities, and eventually impacts the tissue morphology and behaviors.

We study role of tension in cell morphology and behaviors in the context of Epithelial-Mesenchymal Transition (EMT). EMT is a fundamental process that converts a sheet of highly ordered epithelial cells into migratory mesenchymal cells. It is a millstone process during evolution and embryogenesis to generate cell diversity but is also a central process utilized by cancer cells to achieve malignancy. Research in the lab centered on the role of myosin-generated physical tension and related signaling pathways in the progression of EMT and its coordination with morphogenesis. Specific projects includes understanding the tension-dependent remodeling of cell-cell junctions and its impact on EMT, examining the role of conserved transcription factor Snail in regulating adhesion and EMT, exploring the roles of tension-responsive proteins during embryo development.

We use developing *Drosophila* embryos as the model system as there are a lot tension-driven tissue remodeling happening and is an amazing system for live imaging. We employ multidisciplinary approaches such as quantitative live and immunochemistry microscopy, biophysics, computational biology, molecular biology and genetics.

Selected Publications

- Weng M., Wieschaus E.F. (2017) Polarity protein Par3/Bazooza follows myosin-dependent junction repositioning. *Dev. Biol.* 422(2): 125–134.
- Weng M., Wieschaus E.F. (2016) Myosin-dependent remodeling of adherens junctions protects junctions from Snail-dependent disassembly, *J. Cell Biol.* 212:2:219 (Recommended by F1000Prime, commented by: Simoes S., Tepass U. (2016) Muscle versus Snail: Muscle wins, *J. Cell Biol.* 212:2:139)

Mo Weng

Assistant Professor
Ph.D., University of Michigan,
Ann Arbor

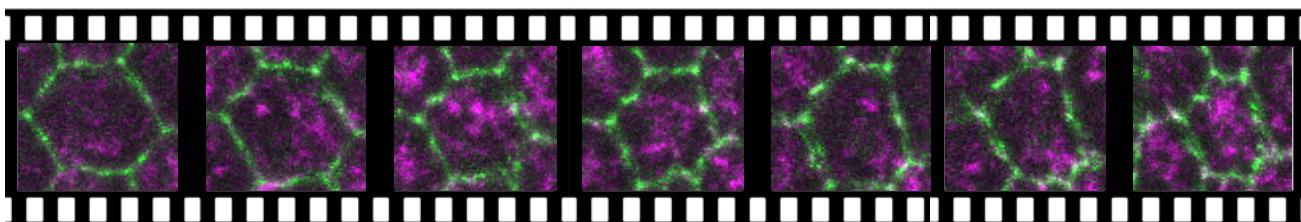
Research Interests

- Morphogenesis
- Mechanobiology
- Epithelial-Mesenchymal Transition



Selected Awards

- 2016-Present: NIH Pathway to Independent Award (K99/R00)
- 2013-2015: NJCCR Postdoctoral Fellowship



Helen Wing

Professor
Ph.D., University of Birmingham, UK

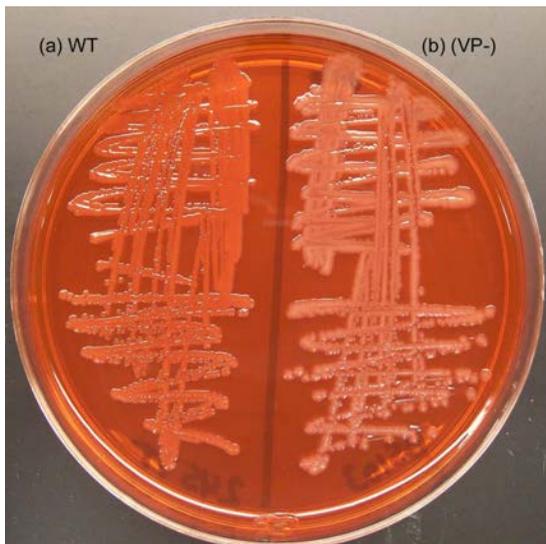
Research Interests

- Molecular Microbiology
- Bacterial Pathogenesis
- Bacterial Gene Regulation



My research program focuses on the molecular mechanisms that control virulence gene expression in bacterial pathogens. My team and I primarily study these events in *Shigella species*, the causal agents of bacillary dysentery in humans. We are interested in the environmental cues, timing and molecular events that trigger virulence gene expression. Most recently, we have become interested in the complex interplay between nucleoid structuring proteins, proteins that facilitate the packaging of DNA into tiny cells, and the transcriptional regulators of virulence in *Shigella*. Since *Shigella* species are fast becoming resistant to many commonly used antibiotics, there is a pressing need to improve our understanding of events underpinning the pathogenesis of these bacteria, so that new drug targets and ultimately new antibiotics can be found. This is the goal of our research.

I received a B.S. (Hons.) from the University of Nottingham and a doctorate from the University of Birmingham in the UK. I then completed a post-doctoral fellowship at Harvard Medical School and Massachusetts General Hospital in the Infectious Disease unit, before joining the faculty at the University of Nevada, Las Vegas in 2005. I have published over 20 peer-reviewed publications in high quality research journals, some of which have been cited more than 100 times. My publications commonly list UNLV graduate and undergraduate authors that have been actively engaged in the research presented. I have secured over 2 million dollars in research funding since arriving at UNLV, this includes 1.3 million from the National Institutes of Health (representing 9 years of continual support). My research has also been supported by the USDA, NSF and NASA. I sit on the editorial board of the on-line peer-reviewed journal *Genes*, I am the long-standing Treasurer of the Arizona and Southern Nevada branch of the American Society for Microbiology and I am an Executive Board member of the International Wind River Conference on Prokaryotic Biology.



Selected Publications

- Karney MMA, McKenna JA, Weatherspoon-Griffin N, Karabachev AD, Millar ME, Potochek EA and Wing HJ. 2019. Investigating the DNA-binding site for VirB, a key transcriptional regulator of *Shigella* virulence genes using an *in vivo* binding tool. *Genes* (Basel). 10 (2): 149, 1-12.
- Weatherspoon-Griffin N, Picker MA, Pew KL, Park HS, Ginete DR, Karney MK, Usufzy P, Castellanos MI, Duhart JC, Harrison DJ, Socea JN, Karabachev AD, Hensley CT, Howerton AJ, Ojeda-Daulo R, Immak JA and Wing HJ. 2018. Insights into transcriptional silencing and anti-silencing in *Shigella flexneri*: a detailed molecular analysis of the *icsP* locus. *Mol. Microbiol.* 108: 505-518.
- Weatherspoon-Griffin N, Wing HJ. Characterization of SlyA in *Shigella flexneri* Identifies a Novel Role in Virulence. *Infect Immun.* 2016;84(4):1073-82. PubMed Central PMCID: PMC4807491.
- Africa LA, Murphy ER, Egan NR, Wigley AF, Wing HJ. The iron-responsive Fur/RyhB regulatory cascade modulates the *Shigella* outer membrane protease IcsP. *Infect Immun.* 2011;79(11):4543-9. PubMed Central PMCID: PMC3257904.

Selected Awards

- Student nominated CSUN Faculty of Excellence Award (2009).
- R15 AI090573 "Understanding transcriptional silencing & anti-silencing mechanisms in *Shigella*." 04/01/10-12/31/20 (**Total: 1.3 million**) Role: PI.
- USDA-NIFA Award. "New treatment strategies for American Foulbrood; using the microbe's biology" against it" 11/01/10-10/31/13 (**Total: \$335,417**) Role: Co-PI.



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