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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 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 three buildings: Juanita Greer White Hall (WHI), the Science and Engineering Building (SEB), and the Facilities Management Administration (FMA) building. 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, Microbiology, and Quantitative Biology. SoLS faculty are recruited from some of the best research institutions including Rockefeller, Birmingham, Alaska, Penn State, Indiana, Illinois, Washington University in St. Louis, Colorado, Washington State, UC Berkeley, Harvard, Wisconsin, Northern Arizona, Boston, Emory, New Mexico, Montana, and UC Riverside. Our faculty members also collaborate with faculty and researchers at many universities and government agencies throughout the nation and international institutions, providing expanded opportunities for our students.

The University of Nevada, Las Vegas (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.
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.
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: Biotechnology, Cell and Molecular Biology, Comprehensive Biology, Ecology and Evolutionary Biology, Education, 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 five 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 (QB). 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.
Doctor of Philosophy in Biological Sciences

The Doctor of Philosophy (Ph.D.) in Biological Sciences within the School of Life Sciences (SoLS) consists of five 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 (QB). 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 bio-modelling. 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/Ballgown. 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.
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 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**
- Santiago Bataller - Ph.D. student
  Advisor: Jeffery Shen
- Tammara Beeghly - Ph.D. student
  Advisor: Laurel Raftery
- Adrienne Bugayong - Ph.D. student
  Advisor: Nora Caberoy
- Mackenzie Burke - Ph.D. student
  Advisor: Andrew Andres
- Jennifer Clark - Ph.D. student
  Advisor: Andrew Andres
- Juan Duhart - Ph.D. student
  Advisor: Laurel Raftery
- Corey Geurink - Ph.D. student
  Advisor: Dennis Bazylinski
- Randolph Grell - Ph.D. student
  Advisor: Kelly Tseng
- Dylan Guerin - Ph.D. student
  Advisor: Kelly Tseng
- G.M. Jonaid - M.S. student
  Advisor: Mira Han
- Cindy Kha - Ph.D. student
  Advisor: Kelly Tseng
- Kathryn Lantz - Ph.D. student
  Advisor: Andrew Andres
- Sheila Mosallaei - Ph.D. student
  Advisor: Laurel Raftery
- Jacklyn Newsome - M.S. student
  Advisor: Martin Schiller
- Travis Parsons - Ph.D. student
  Advisor: Laurel Raftery
- Lorena Samentar - Ph.D. student
  Advisor: Nora Caberoy
- Surbhi Sharma - Ph.D. student
  Advisor: Martin Schiller
- Michael Treat - Ph.D. student
  Advisor: Frank van Breukelen
- Anne Villacastin - Ph.D. student
  Advisor: Jeffery Shen
- Jared Wilson - Ph.D. student
  Advisor: Frank van Breukelen

**Ecology and Evolutionary Biology**
- Lorenzo Apodaca - Ph.D. student
  Advisor: Dale Devitt
- Lynda Burns - Ph.D. student
  Advisor: Lloyd Stark
- Theresa Clark - Ph.D. student
  Advisor: Lloyd Stark
- Alicia Crespin - M.S. student
  Advisor: Dan Thompson
- Jordan Dowell - M.S. student
  Advisor: Dale Devitt
- Dominic Gentilcore - Ph.D. student
  Advisor: Scott Abella
- Ka-Voka (Simone) Jackson - M.S. student
  Advisor: Scott Abella
- Elizabeth (Wendy) Jones - Ph.D. student
  Advisor: Donald Price
- Andre Nguyen - M.S. student
  Advisor: Javier Rodriguez
- Tiffany Pereira - M.S. student
  Advisor: Scott Abella
- Audrey Rader - M.S. student
  Advisor: Scott Abella
- Tomoko Sakishima - Ph.D. student
  Advisor: Elizabeth Stacy
- Alaric Smith - Ph.D. student
  Advisor: Allen Gibbs
- Casey Stamereilers - Ph.D. student
  Advisor: Filippos Tzourkas
- Camille Traylor - M.S. student
  Advisor: Scott Abella
- Anthony Waddle - M.S. student
  Advisor: Frank van Breukelen
- Tamara Wynne - M.S. student
  Advisor: Dale Devitt

**Integrative Physiology**
- Alexis L. Crisp - Ph.D. student
  Advisor: David Lee
- Michael Isaacs - Ph.D. student
  Advisor: David Lee
- Kit Knight - Ph.D. student
  Advisor: David Lee
- Austin McKenna - Ph.D. student
  Advisor: Allen Gibbs

**Microbiology**
- Timothy Alba - Ph.D. student
  Advisor: Eduardo Robleto
- Tatiana Ermi - M.S. student
  Advisor: Eduardo Robleto
- Ariel Friel - Ph.D. student
  Advisor: Brian Hedlund
- Austin Ganje - Ph.D. student
  Advisor: Brian Hedlund
- Joy Immak - Ph.D. student
  Advisor: Helen Wing
- Bryan King - Ph.D. student
  Advisor: Dennis Bazylinski
- Holly Martin - Ph.D. student
  Advisor: Eduardo Robleto
- Chrisabelle Mefferd - Ph.D. student
  Advisor: Brian Hedlund
- Michael A. Picker - Ph.D. student
  Advisor: Helen Wing
- Joshua Sackett - Ph.D. student
  Advisor: Brian Hedlund
- Jillian Socea - Ph.D. student
  Advisor: Brian Hedlund
- Scott Thomas - Ph.D. student
  Advisor: Brian Hedlund
- Carmen Vallin - Ph.D. student
  Advisor: Eduardo Robleto
- Daniel Walsh - M.S. student
  Advisor: Brian Hedlund
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

Journal Articles
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)

**Selected Publications**

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

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.

**Selected Publications**


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.

Selected Publications


- 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.


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), metatranscriptomics 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 Publications**


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**


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


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 endo-parasites 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


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 ducreyi, 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.
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


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


Selected Awards

- 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
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)


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.
I have a long-running interest in the connections between Earth history and biotic diversity. These sorts of questions fall under the general purview of the field of Biogeography. More specifically, I have been using since graduate school the tools developed over the past 4 decades within the subdiscipline of Phylogeography.

I find the landscapes of western North America to provide an excellent system within which to explore such questions for several reasons. First, the history of large, regional arid biomes here is relatively recent – thus, taxa adapted to deserts, shrublands, and grasslands often have diversified within the most recent several millions of years, many having undergone rich adaptive radiations. Second, the landscapes themselves often have developed within a relatively recent timeframe (e.g., the Great Basin has developed over about the past 17 million years, and the Baja California Peninsula is even younger). Collectively, these, and other, attributes mean that one can often infer specific geological and climatic histories that underlie focal speciation histories. We have presented several such models that continue to generate interest in the research community, being tested with additional co-distributed species, with a new generation of molecular datasets, and with application of powerful statistical models.

I have a focal taxonomic interest in small mammals, some having experienced important diversification histories in western North American arid regions (e.g., heteromyid rodents). Along with students and colleagues, we also have addressed phylogeographic and biogeographic structure and history in a wide range of reptiles, amphibians, fishes, birds, plants, and even scorpions. The legacy of these studies lives in the exciting and innovative new research directions being explored by my former students, some now very productive colleagues. I likely will not be taking new graduate students, and seem to be doing as much or more writing on synthesis rather than new data sorts of papers. Maybe I need to realize that I might be getting old!

Selected Publications


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


Eduardo Robleto
Professor
Ph.D., University of Wisconsin, Madison

Research Interests
- Microbiology
- Microbial Genetics
- Mutagenesis
- Evolution
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**


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


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 Awards

- 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].

Selected Publications

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. Experimental topics include the DT of vegetative and reproductive phases, the physiology and timelines of hardening and dehardening phenomena, how different life phases of mosses (shoots, asexual propagules, antheridia, juvenile structures) exhibit variation in response to desiccation stress, and the length of time structures can tolerate continuous desiccation. Specifically, my laboratory is investigating how the four components 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.

Recent research highlights include an illustration that desert mosses were employing an inducible strategy of DT (2013), the first experimental assessment of dehardening in mosses and the implications for mechanistic studies in the field of DT (2014), the first demonstration that the model moss Physcomitrella patens was desiccation tolerant (2014), the first demonstration that different life phases of a single species exhibit different intrinsic strategies of DT (2016), the first study to show that mosses, specifically in the genus Syntrichia, are in fact not constitutively protected but exhibit a complex inducible strategy of DT (2017), the first demonstration that antheridia of mosses are DT (2016), and soon the first comprehensive assessment of the role of prehydration in surviving DT (2018).

Current funded projects include (1) an NSF grant exploring DT in the genus Syntrichia, (2) a U.S. 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


Selected Awards

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

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 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). 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 this endangered butterfly. Using genetic markers and phylogeographic analyses, we are also studying divergence, plasticity, habitat selection and reproductive isolation in Spring Mountains dark blue butterflies whose myrmecophile larvae feed on the flowers of host plants that bloom at different times. A potential example of allochrony and sympatric speciation.

Daniel Thompson
Associate Professor
Ph.D., University of Arizona
Research Interests
• Evolutionary Biology
• Ecology
• Phenotypic Plasticity

Selected Publications
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 organ disease, nerve degeneration, 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 pursue these studies using 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. **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. To address this question, we recently developed a new model to study vertebrate eye regrowth in *Xenopus*. We use a combination of cellular, molecular, and bioinformatic approaches to define mechanisms that regulate eye regrowth. Furthermore, we are working to identify and characterize the stem cells that drive this regrowth process and to define new stem cell markers. By comparing eye regeneration mechanisms with those for limb regeneration, we aim to identify commonalities in repair mechanisms in different vertebrate organs.

2. **Using Xenopus as a Model for Rapid Assessment of Environmental Toxicology**

Each year, approximately 1,000 new chemical substances enter commercial use with limited toxicity and environmental data. *Xenopus* has a strong history as a vertebrate model for environmental health studies, and their responses correlate well to mammalian findings. *Xenopus* embryos and tadpoles are highly sensitive to the environment, and their developmental processes are well studied. Our initial studies identified chemicals that disrupt normal biological processes in both frog embryos and tadpoles but which have not been implicated previously as toxicants. We are establishing assays to examine the effects of chemical toxicants on the injury response, a biological process that is not evaluated in toxicity protocols (Delos Santos et al., 2016). Our goal is to establish *Xenopus* as a suitable and accessible model for the rapid determination of chemical safety and to use it for determining the molecular mechanisms of animal toxicity.
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** (asterisk denotes equal contribution)


**Selected Awards**

- 2016: NIH NIAID K22 Career Transition Award
- 2012: Bill Costerton Award for Outstanding Interdisciplinary Biofilm Research
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

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 Tbs 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

I am a plant ecologist interested in the mechanisms that drive primary plant succession. Primary succession can be defined as directional changes in plant communities after severe disturbances that leave no soil layers intact. Ecologists have been studying succession for about 100 years but are still in disagreement about what causes it, and even if it exists! Attempts at general theories that will explain successional change are useful exercises but are not readily applicable to specific examples of succession. My approach to this dilemma is to examine many examples in different ecosystems, using similar methods, and then to look for similarities or differences between ecosystems. I utilize field observations and experiments, lab experiments, and conceptual models and interpret my results in the context of all temporal phenomena in ecology. I also examine disturbances (that lead to succession) and restoration (the purposeful manipulation of succession). Through my teaching of ecology and conservation biology, I convey my enthusiasm about and concern for the future of natural processes.

Selected Publications

Books

Journal Articles
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 and Secretary 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**
