Dear Prospective Student:

Thank you for your inquiry concerning graduate study in Biology at New Mexico State University. I am pleased that you are considering our department as a place to continue your education and am looking forward to reviewing your application. The selection of a graduate program that meets your specific needs and career objectives is an important decision and one that I know you are giving careful consideration. The department offers research training leading to the M.S. and Ph.D. degrees. Non-thesis M.S. degrees are also offered, including a one-year program for students seeking biotechnology careers. Along with the necessary application materials, I have enclosed information about our programs, faculty, and the university that should help you reach an informed decision. We also have a web site you can visit (http://bio.nmsu.edu).

For students who wish to do research for their graduate degrees, probably the most important element in ensuring a successful course of graduate study is the selection of a research mentor whose area of expertise is compatible with your interests. For this reason, please carefully consider the research interests of our faculty. You will find leading scientists in many areas of biology represented in our faculty and, I hope, several with research interests compatible with your own. You are especially encouraged to directly contact these faculty before applying to find out what opportunities for graduate study exist in their labs. When applying you may list up to three potential advisors that you feel would be a suitable research mentor for your studies. Applicants to our general non-thesis Masters program should also identify potential mentors who can guide their course of study on their application form. Please note if you are applying to any of these program will not be accepted by the Biology Department as a graduate student until a faculty member has agreed to act as your advisor.

If you are applying for the one-year non-thesis Masters in Biotechnology, you do not need to list potential advisors on your application as you will be advised in your course of study by the committee in charge of this program. You can find more information on this program at the Biology Department’s website or by contacting the program director at biotechMS@mvar.nmsu.edu.

I realize that, for most applicants for graduate study, the possibilities for financial support are also an important consideration in your decision. Almost all of our approximately 85 research-oriented graduate students have some type of financial support. This support includes teaching assistantships and fellowships funded by the university, and research assistantships funded by research grants to our faculty from many of the federal and state research funding agencies. You will also wish to investigate fellowship programs such as the National Science Foundation Graduate Research Fellowships. Non-thesis Masters students are generally not eligible for these forms of support from the department.
To ensure that your application for admission and NMSU financial aid are given the most complete consideration, please apply as early as possible. If you wish to be considered for support through the Department of Biology, applications should be complete by October 4 for Spring semester and by January 15 for the following Fall semester. Your application will be reviewed most quickly if you proceed as follows.

ALL APPLICANTS SHOULD:

Send to the Graduate Coordinator, Biology Department, MSC 3AF, NMSU, Las Cruces, NM 88003:
1) a one-page statement of your educational objectives and research interests.
2) the Graduate Advisor form (enclosed).
3) the Application for Financial Support (enclosed), if you wish to be considered for a graduate assistantship.
4) an unofficial transcript from all colleges or universities you have attended.
5) three personal references (forms enclosed), each with a supporting letter attached.
6) unofficial scores on the Graduate Record Examination, if you have taken them.*

*The Biology Department does not require GRE scores for admission; however, individual professors may require GRE scores prior to acceptance. Check with your proposed mentors about providing GRE scores.

IF YOU ARE A U.S. CITIZEN OR PERMANENT RESIDENT:

The NMSU Graduate Schools handles admission for prospective graduate students. For more information, contact the NMSU Graduate School at (575) 646-2736, web site http://prospective.nmsu.edu/graduate/programs.html e-mail at gradinfo@nmsu.edu or in writing at

Graduate Student Services
MSC 3G
New Mexico State University
Las Cruces, NM 88003-8001

IF YOU ARE NOT A U.S. CITIZEN, APPLICATION SHOULD BE MADE THROUGH INTERNATIONAL STUDENT & SCHOLAR SERVICES:

For more information, contact the International Student & Scholar Services at (575) 646-3199, e-mail cip@nmsu.edu visit web site http://prospective.nmsu.edu/international/index.html or in writing at

International Student & Scholar Services
MSC 3G
New Mexico State University
PO Box 30001
Las Cruces, NM 88003-8001

Again, I am pleased that you are considering graduate study in Biology at New Mexico State University. If I can provide you with more information about our university, our department, or its faculty, please let me know. I wish you great success in your graduate studies and in your future career, and hope that you will decide that New Mexico State University offers the place and the people that will best meet your needs.

Sincerely,
Ralph Preszler, Ph.D.
Department Head
APPLICATION FOR FINANCIAL SUPPORT

Your application will not be processed until this form is completed and returned. The review process for assistantships will begin January 15 for Fall and October 4 for Spring support. ONLY completed Graduate School applications will be considered.

GENERAL INFORMATION

(Mr.) (Ms.) ____________________________________________
(last) (first) (middle)

Present Address ____________________________________________

Permanent Address ____________________________________________

(Until what date?) ________________________________

Phone No.(s): ________________________________

EDUCATION

List all Colleges and Universities attended and degrees awarded or expected:

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EXPERIENCE

List or explain any research or teaching experience you have had (use separate page if necessary).

REFERENCES

List the names, addresses and telephone numbers of three (3) references who will provide personal reference letter

Signature of Applicant: ________________________________ Date: ________________________________
GRADUATE ADVISOR FORM

Your application will not be processed until this form is completed and returned.
The review process for assistantships will begin January 15 for Fall and October 4 for Spring.

PROGRAM(S) OF INTEREST

- I am interested in a one-year non-thesis Master of Science degree in Biotechnology
- I am interested in a two-year non-thesis Master of Science degree in Biology
- I am interested in a thesis Master of Science degree in Biology
- I am interested in a Ph.D. in Biology

If you are applying for any program other than the one-year non-thesis Master of Science in Biotechnology, then you should list, in order of preference, professors under whom you would prefer to work. This decision should be based upon the information found in the “Faculty Research Interests” brochure. If you have no specific preference at this time, please indicate a general area of interest (e.g., Microbiology, Ecology, animal Physiology, Plant Biology, etc). Please understand that it is the policy of the Department of Biology to admit to its graduate program only those applicants who are accepted by a faculty member within the department.

RESEARCH MENTOR/ADVISOR PREFERENCE

Professor/Interest Area:

1) 

2) 

3) 

PLEASE ATTACH A STATEMENT THAT OUTLINES YOUR RESEARCH EXPERIENCES, INTERESTS AND CAREER GOALS

Please print your name, address, phone number and e-mail below:

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Table below for office use only

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<th>FACULTY: PLEASE INDICATE YOUR DECISION HERE</th>
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Revised 11/14/2009
GRADUATE COORDINATOR
DEPARTMENT OF BIOLOGY
BOX 30001/MSC 3AF
LAS CRUCES, NM  88003-0001
Telephone: (505) 646-3611
Fax: (505) 646-5665

PERSONAL REFERENCE

Applicant: Please complete this section before giving this form to an instructor or former professor acquainted with your educational and academic abilities.

☐ I waive my right to have access to this Personal Reference
☐ I do not waive my right to have access to this Personal Reference

Printed Name:_______________________________    Signature:_____________________________

ENDORSER: PLEASE ATTACH A LETTER EVALUATING THE SPECIAL STRENGTHS OR WEAKNESSES OF THIS STUDENT THAT WOULD AFFECT HIS/HER SUITABILITY AS A GRADUATE STUDENT: Please mail this form with your letter to the address above
We are particularly interested in the ability of the applicant to:
☑ Pursue graduate study
☑ Perform research
☑ Serve as a teaching assistant
☑ Serve in a professional capacity in the chosen field.

We are also interested in the general character of the applicant and special indications bearing on the applicant’s qualifications. For non-U.S. citizens: Please indicate degree of English proficiency for teaching duties.

*******************************************************************************/

In comparison with other graduate students you have known rate items A through I by a numeric score of 1-5. Base your ratings on the level of accomplishments you have come to expect from the applicant pool. (Ratings are: 1- Truly outstanding [top 10%]; 2- Superior; 3- Above average; 4- Average; 5- Below average; x-inadequate knowledge to rate)

( ) A. Intellectual ability
( ) B. Mastery of fundamental knowledge in his/her general field
( ) C. Motivation and drive
( ) D. Scholarship
( ) E. Ability in written expression
( ) F. Ability in oral expression
( ) G. Adequacy of ability for research
( ) H. Emotional maturity and stability
( ) I. Self-reliance and independence

*******************************************************************************/

How far do you think this applicant will progress? (Check one)
( ) Will probably complete a doctorate
( ) Will probably complete a master’s degree
( ) Is not likely to complete a graduate degree without excessive help
( ) Is not likely to complete any graduate degree

*******************************************************************************/

I have been acquainted with the applicant during the period of:___________ to ____________
as:______________________________________________________(teacher, advisor, supervisor, other)
NAME (print or type):________________________________________POSITION:________________________
INSTITUTION:________________________________________SIGNATURE:________________________
DATE:________________________________PHONE:_______________________________________

Revised 11/14/2009
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DONOVAN BAILEY

*Plant Systematics*

As a systematic botanist, I am particularly interested in addressing questions regarding the evolutionary relationships of plant taxa and the evolution of specific traits. Research in the lab primarily addresses these questions on North American members of the mustard and legume plant families (Brassicaceae and Fabaceae, respectively). These families are well represented in the western US and Mexican floras and they include numerous crop species as well as threatened/endangered species. The molecular biology techniques employed in the lab primarily include DNA based sequence approaches to phylogenomics and population genetics (including 454 sequencing). Data assembled from these methodologies are analyzed in a phylogenetic and/or population genetic context and the results are used to discuss the implications of the inferred evolutionary relationships, to develop new classifications, and to understand the origin of species (particularly hybrids and polyploids).

*Publications that represent the work I do:*


MARVIN H. BERNSTEIN

*Animal Physiology*

Oxygen deprivation (hypoxia) is a frequent fact of life for many animals, such as those that live at or visit high altitudes. Some champion bird species fly at altitudes where the oxygen supply is only one-fourth as high as at sea level and where daytime temperatures are often 50 degrees below freezing. The enormous oxygen requirement for flight (20 to 40 times higher than for resting) makes the feats of high-flying birds even more remarkable. For comparison, mammals including humans come down with mountain sickness at much lower altitudes, especially if they try to exercise. To understand physiological adaptations for flight and high-altitude tolerance in birds, my students and I study temperature regulation, energetics, cardiac and respiratory mechanics, oxygen and carbon-dioxide transport, and body-fluid volume regulation. We also investigate adaptations to hypoxia at the tissue and cell levels, especially in skeletal muscle, eye, and brain. For example, we have recently discovered a mechanism for supplementing the oxygen supply to the brain and retina of birds exposed to
hypoxia. As part of an experiment on tissue hypoxia, we have found that the body tissues store huge quantities of body fluids, and birds therefore never suffer from shock. We do experiments on animals at rest, during flight in a wind tunnel, or during exposure to cold and artificial high altitude. To investigate why mammals do not tolerate hypoxia as well as birds, we also study the effects of hypoxia on the brains of rats, using changes in learning ability and memory, as well as histological and biochemical changes, as indicators. The long-term goal is to understand both the mechanism and the evolution of hypoxia tolerance. I welcome opportunities to work with students interested in animal adaptations to environmental stresses at the systems, tissue, and cell levels.

Publications that represent the work I do:


WILLIAM J. BOECKLEN

Population and Community Ecology, Biogeography and Conservation Biology

My primary research interests are in ecological and evolutionary aspects of insect-plant interactions. In particular, I am interested in patterns of herbivory in dioecious plants and in the effects of host plant hybridization on the structure and dynamics of herbivore communities.

Sex-biased herbivory has been largely overlooked in the development of contemporary theories of insect-plant interactions. I have demonstrated previously that plant sex is a significant source of variation in densities of sawflies that attack arroyo willow (Salix lasiolepis). Male willows typically support higher densities of sawflies than do female plants. Currently, I am examining sex-biased herbivory in the desert shrub, Ephedra trifurca. These data will contribute to a general theory of herbivory in dioecious plants by relating intersexual variation in insect attack to sexual dimorphism of host plants in habitat utilization and resource allocation.

Evolutionary biologists have long recognized that hybrid zones can provide unparalleled insights into evolutionary processes, yet plant-insect ecologists have been slow to use plant hybrid zones to investigate evolutionary mechanisms thought to underlie plant-parasite interactions. I am investigating patterns of density and species diversity of gall-forming wasps (Hymenoptera:Cynipidae) and leaf-mining moths (lepidoptera:Gracilariidae and Nepticulidae) in oak hybrid zones. I am testing the null hypothesis of no differences among host taxa against three mutually exclusive and evolutionarily consistent alternative hypotheses: 1) hybrid oaks support greater numbers of individuals and species than do parental oak; 2) hybrids support fewer parasite species and individuals; and 3) hybrids are intermediate to parental hosts.

Publications that represent the work I do:


MARIA CASTILLO

Invertebrate Immunology

Our laboratory focuses on the study of the immunological aspects of the relationship between the Hawaiian bobtail squid, Euprymna scolopes and its beneficial partner, the luminous bacteria Vibrio fischeri (1). The interaction between these two organisms is very specific and limited to a specialized light organ located in the ventral cavity of the squid. The bacteria find within the host shelter and nutrients, while the squid utilizes the light produced by the bacteria as counterillumination to avoid predation during its nocturnal activities (2).

Our research investigates the presence, diversity, and function of complement-like proteins in the squid E. scolopes and their potential role in beneficial symbiosis. The complement system consists of a group of proteins that play an important role in immune processes such as cytolysis, opsonization, inflammation, and linking the innate and adaptive immune systems. Orthologs of several vertebrate complement components were recently identified in deuterostomes, ecdysozoans, and lophotrochozoans including tunicates, horseshoe crab, and squid respectively. The finding of complement molecules in invertebrates suggests a more primitive origin of these immune components than previously thought and presents an opportunity to study the changes of the immune system through evolution.

In addition, the specific association between E. scolopes and V. fischeri is a unique model system that allows us to study various aspects of immune interactions between organisms of different species in a context that differs from pathogenesis.


Publications that represent the work I do:


M. G. Castillo, X. J. Wu, N. Dinguirard, and T. P. Yoshino. 2008. HSP60 expressed on the surface membrane of
B. glabrata embryonic cells is involved in binding to Schistosoma mansoni primary sporocysts tegumental molecules. In preparation


JENNIFER CURTISS

Molecular Genetics of Eye Development

During development, the cells of a multicellular organism differentiate into thousands of distinct cell types. For instance humans develop skin heart and brain cells, among others. There are two essential aspects to this process that are of particular interest to my work:

1) Cells must be specified so that they know what tissue and organ type to become. In part, specification is controlled by “selector genes,” which encode transcription factors that regulate tissue-specific gene expression.

2) Different organs must develop in a regulated manner so that each organ’s size and position fits into the context of the entire organism. This requires that cells in different tissues and organs communicate with one another via signal transduction pathways, in order to integrate growth and pattern.

Remarkably, both selector genes and signaling genes are well conserved in all metazoans. For instance, a selector gene called Pax6 is of critical importance for human eye development: mutations in Pax6 cause a birth defect called aniridia, in which the iris of the eye fails to form, resulting in blindness. Homologs of the Pax6 gene are present in all metazoans, from jellyfish to insects to mammals, and seem to specify eye fate in all of them. Because of this, we can use organisms besides humans to study how selector genes are signaling pathways cooperate in development. My approach utilizes the powerful genetic and molecular tools available in the fruit fly Drosophila melanogaster.

In the Drosophila head the eye and antenna develop right next to one another. One focus in the lab is to understand how the eye and antennal selector genes are controlled. For instance, the eye selector genes must be expressed only in the eye precursors. If eye selector genes are expressed in antennal precursors they change their fate and develop into an eye instead. Likewise, the antennal selector genes must be expressed only in the antennal precursors, because they will cause eye precursors to change their fate and develop into an antenna. We know that cell communication through some kind of signaling pathway ensures that eye and antennal selector gene expression is kept separate. We are using genetics and histological techniques to find out what these signaling genes are and how they work.

The other focus in the lab involves two genes called dan and danr, which act like eye selector genes in that they are required to make an eye and are able to convert antennal precursors to an eye fate. Surprisingly however, they are also required for antennal development, and are able to convert leg precursors to an antennal fate. Thus, these two genes appear to “select” both eye and antennal fate. We are using genetics and molecular biology to explore how these genes function, and how they interact with other eye and antennal selector genes to control both eye and antennal development.

I welcome students who are interested in how an eye gets made, and how different cell types become different from one another. We will work together to design a project that utilizes both genetic and molecular
techniques to address current and relevant questions about cell specification.

Publications that represent the work I do:


ANGUS DAWE

Molecular Mycology

My lab is interested in the molecular biology of fungi, and in particular the signaling pathways that mediate fungal behavior. We work principally with Cryphontectria parasitica, a plant pathogen and causative agent of chestnut blight. Back when the eastern parts of the United States were first settled by European colonists, the American chestnut tree was the dominant species of hardwood throughout the Appalachian region from Georgia to Maine. However, during the late 1800s species of chestnut were imported into the US from Asia and they brought with them the chestnut blight. By the 1950s, the disease had spread throughout the natural range of the American chestnut trees, effectively wiping out a vast natural resource and altering forever the makeup of the eastern woodlands.

In the laboratory C. parasitica can be easily cultured and manipulated which allows us to ask genetic questions about its behavior and development. Also, C. parasitica can itself be infected by an RNA virus. An infected strain exhibits a number of changes from an uninfected one, the most striking of which is a loss of ability to cause significant damage to chestnut. Because of the reduction in fungal virulence, we call this virus a "hypovirus". Since we can genetically modify both the hypovirus and the fungus, we have a system that permits us to explore the interactions of an RNA virus and its host. Also, the hypovirus provides a tool to investigate molecular mechanisms of plant pathogenesis as well as other behavior and developmental pathways in C. parasitica. Research opportunities in my laboratory cover all aspects of molecular biology, genetics and genomics.

Publications that represent the work I do:


**KATHYRN A. HANLEY**

*Biology Arthropod-Borne Viruses; Evolutionary Ecology of Host-Pathogen Interactions*

Members of the Hanley lab study the biology of emerging RNA viruses. While most lab members focus on arthropod-borne viruses (arboviruses), a growing focus in the lab is the study of avian influenza virus in New Mexican waterfowl.

Arboviruses constitute one of the most significant emerging disease challenges to global public health. The escalating pandemic of dengue virus, the recent invasion of West Nile virus into the Americas, and the persistence of yellow fever virus in the tropics all attest to the threat posed by arboviruses. Yet relatively little is known about the ecological and evolutionary factors that drive arbovirus introduction and spread. My laboratory investigates the evolution, ecology, genetics and control of arboviruses in the genus *Flavivirus*, focusing on mosquito-borne dengue virus, the agent of dengue fever.

Dengue virus is comprised of four serotypes (Dengue1-Dengue4), each of which encompasses multiple genotypes. In recent decades the range of all four serotypes has expanded across the tropical and subtropical has expanded across the tropical and subtropical regions of the world, leading to extensive geographic overlap among the serotypes. One topic under study in the laboratory is how different serotypes and genotypes interact during co-infection of the mosquito vector. Characterizing these interactions is important because competition for vector transmission may also affect the evolution of dengue virus replication, and consequently virulence, in humans.

As the geographic range of dengue virus has expanded, the severity of dengue disease has also increased dramatically. Consequently dengue virus has been listed as a target for control by the World Health Organization. However, effective control efforts require a more detailed understanding of the forces that affect dengue evolution than is currently available. Identification of genomic regions that affect the specificity and efficiency with which the virus infects its mosquito vector is particularly important, since changes in rates of transmission may affect epidemic potential. A second area of research in the lab is to identify potential targets of vector-driven selection in the dengue virus genome using phylogenetic inference and then to experimentally evaluate the effect of targeted mutations in these regions on the ability of the virus to infect and be transmitted by its mosquito vectors.

Finally, the dengue virus serotypes circulating in humans are closely related to sylvatic dengue viruses isolated in the forest canopy in Asia and Africa. At present, these sylvatic strains do not appear to circulate in humans. The third focus of investigation in the lab is to identify what barriers, if any, prevent sylvatic dengue viruses from infecting humans and to determine the genetic basis and stability of such barriers.

Together these studies will identify some of the targets of vector-driven selection in dengue virus and the impact of vector-driven selection on dengue virus emergence. This research will enhance our understanding of dengue virus evolutionary ecology and will guide the refinement of existing strategies and the development of
new technologies to control the dengue virus pandemic.

I encourage students with an interest in the evolutionary ecology of pathogen-host interaction to consider joining the lab.

Publications that represent the work I do:


IMMO A. HANSEN

Mosquito Molecular Biology

The Hansen lab is interested in the molecular mechanisms by which cells and tissues sense nutrients and in response activate signal transduction pathways which regulate expression and/or deactivation of certain genes. We use the yellow fever mosquito Aedes aegypti as a model invertebrate. Specific research projects include the characterization of the mosquito transportome (membrane receptors and channels) in the fat body before and after a blood meal and the role of forkhead box (Fox) transcription factors in the fat body.

Why we study mosquitoes? - Mosquitoes transmit some of the most devastating human diseases: malaria, dengue fever, yellow fever and filariasis. During the 1950s and 1960s mosquito-borne diseases were thought to have been brought under control through reduction of mosquito populations by large-scale vector control programs. However, a resurgence of the diseases began during the late 1970s and continues to this day due to a complex array of factors such as pesticide resistance, lack of effective vaccines, parasite drug resistance, and political mismanagement (Krogstad, 1996).
Human malaria afflicts 300 to 500 million people every year and is responsible for an estimated one to three million deaths per year. Approximately 40% of the world’s population is currently at risk of malaria, mostly those living in poor countries in tropical and sub-tropical regions of the world (WHO, 2005).

The reproductive biology of mosquitoes is tightly linked to their ability to transmit disease pathogens. Therefore, a detailed understanding of reproductive processes on a molecular level may reveal new ways to disrupt the process of disease transmission. Many aspects of reproduction of these disease vectors could be important targets for the development of new disease-control strategies.

Publications that represent the work I do:


PETER HOUDE
Avian Systematics
http://biology-web.nmsu.edu/houde/phoude.htm

My interests lie in the very broad areas of the evolutionary biology of birds, and of other vertebrates to a lesser degree. My research covers several areas. 1) Phylogeny reconstruction - the genealogical relationships of organisms to one another. I concentrate on deciphering interfamilial and interordinal relationships. Recently, we discovered molecular genetic evidence that neoavian birds are comprised of two major groups that have evolved in parallel, much like marsupial and placental mammals. These data imply that at least five traditionally recognized orders of birds are polyphyletic, with member families in each of the two groups, and mistaken to be related on the basis of convergent morphologies. 2) Biogeography - the correlation of patterns of phyletic divergence and the origins of new taxa to the geographic distribution of species and the formation of geophysical barriers through time. Some researchers conjecture that groups of birds with modern endemism to southern continents must have originated there during the Cretaceous when those continents were united. However, among the orders of fossil birds I have described are the sister group to modern ratites, Lithornithiformes, and a primitive ostrich, Palaeotis, whose Northern Hemisphere distributions are quite inconsistent with those of their modern southern relatives. Similarly, our molecular genetic data show that various "gruiform" birds with southern disjunct endemism (e.g., kagu-sunbittern, or the pantropical finfoot family) are too closely related to have diverged in the Cretaceous. Indeed, fossils suggest that these dispersed through the Northern Hemisphere
during the Cenozoic, instead. 3) Macroevolution - the plasticity and polarity of morphological evolution within lineages. This is best understood by exploring pattern in the distribution of morphological characters that are superimposed onto a phylogenetic "tree" inferred independently from molecular genetic analysis. 4) Evolutionary rate - how rates of genetic and morphological evolution differ within and between taxa. I address these diverse problems through the combined study of fossil vertebrates, comparative anatomy (particularly osteology), DNA sequencing, and DNA hybridization.

In 2009 my lab acquired a "NextGen" DNA sequencer, the 454 - FLX along with supporting apparatus and staff, as the cornerstone of a new Genome Sequencing Facility at NMSU. My colleagues and I are using this technology, among other things, to develop new applications for the rapid characterization of thousands of novel loci for use in phylogenetic and population genetic studies of non-model organisms.

I welcome inquiries from prospective graduate students who are interested in integrating diverse classical and modern disciplines to address the systematics and macroevolution of any taxonomic group of organisms. I have separate laboratories devoted to paleontological and molecular studies. Among our department's natural history museums are comparative vertebrate collections for use in research and education.

Publications that represent the work I do (pdf's available from web page):


KAREN MABRY
Behavioral and Landscape Ecology

Research in my laboratory is summed up by the idea of the “behavioral ecology of ecological landscapes.” More broadly, I am interested in how ecological and mechanistic factors interact to produce behavioral variation within species, and in the consequences of such behavioral variation for ecological and evolutionary processes. Current research focuses on how ecological variation across landscapes affects the dispersal and habitat selection behavior of small mammals. For example, in a species that inhabits multiple habitat types, dispersing juveniles prefer to settle in the same type of habitat in which they were reared. I am applying a landscape genetics approach to understand how the habitat preferences of dispersers might affect the distribution of genetic variation across complex landscapes. I approach questions about the behavior and ecology of small mammals in the field using a variety of techniques, including live-trapping and radio-telemetry to monitor population dynamics and movements of individual animals in the field, and molecular genetic tools to reconstruct the genetic relationships among individuals.

Publications that represent the work I do:


Mabry, K.E. and J.A. Stamps. 2008. Searching for a new home: decision making by dispersing brush mice. The


**BROOK MILLIGAN**

*Evolutionary Genetics and Conservation Biology*

Research in my laboratory focuses on the interface between population genetics, ecology, and evolutionary biology. Specifically, we are interested in quantifying the rates at which evolution proceeds and in elucidating the rules governing evolutionary change of ecological and molecular traits. Ongoing population studies address such questions as 1) at what rate does neutral evolutionary change proceed and how does that determine the balances between genetic drift, migration, and natural selection, and 2) how do population size, mating system, and the demographic characteristics of populations interact to determine the rate of evolution? At a larger evolutionary scale we are concerned with such questions as 1) at what rate do large-scale evolutionary changes occur, and 2) are changes in one trait influenced by changes in others? One common theme in our research is the interest in quantifying the demographic properties of natural populations-population size, mating system, and migration rate, for example-that determine the rate of evolutionary change. A second major theme is the interest in using quantitative models of evolution to test alternative evolutionary or biogeographic hypotheses. Finally, we are interested in applying our research to practical concerns such as those arising in conservation biology.

Our approach to answering these questions combines both empirical and theoretical aspects. Genetic information from both nuclear and chloroplast DNA is collected from natural populations using modern molecular techniques including DNA sequencing and the polymerase chain reaction. Concurrently, we develop enhanced means of analyzing the genetic data, often relying on genealogical information for genes in natural populations. The genealogical approach to studying demographic properties of populations articulates directly with our studies of broader scale evolutionary patterns using phylogenies. Models of genetics, mating systems, and evolution coupled with demographic ecological models are central to our analysis of populations, while at broader evolutionary scales explicit models of character evolution play a central role. Finally, we are using populations of bacteriophage to simulate the processes we study in natural populations as a means of testing empirically the models used in our data analysis.

While much of our research is directed toward developing a fundamental understanding of the processes occurring in natural populations, we are specifically interested in the role our genetic data and models can play in conservation biology. As a result, we are currently studying a group of plants in the genus *Aquilegia* that occur in small, isolated populations and therefore model the situation encountered with many rare plants. We are also expanding our research focus to apply the techniques developed for *Aquilegia* to other rare plant species. In this way we hope to integrate our studies of basic evolutionary and ecological processes with the immediate need for information concerning the demographic properties of rare or endangered populations.

*Publications that represent the work I do:*


MICHELE K. NISHIGUCHI

Evolutionary Biology & Marine Symbiosis

Understanding the evolution of animal and bacterial associations has been an underlying theme in establishing the development and specificity of symbiotic relationships. There is a need to develop better systems to resolve interactions among symbiotic species where population dynamics and environmental processes clearly play an important role in the evolution of the association. These model systems should promote integrated approaches that take into account the response within as well as between various symbiotic populations and their host partners. My laboratory studies the mutualistic association between sepiolid squids (Mollusca: Cephalopoda) and their Vibrio symbionts, which provides a versatile and experimentally tractable model system to study the population dynamics and cospeciation between bacterial species and their diversity among host squids.

Since the symbiotic bacteria are environmentally transmitted to new hosts with every generation, this system is ideal for the study of specificity amongst the wide variety of bacteria that reside in the water column. Moreover, it provides a system to resolve whether the ecology of the free-living symbiont is as important as the ecology of the mutualism in the architecture of bacterial-host interactions. My laboratory examines the mechanisms that drive host-symbiont recognition, and assesses whether environmental factors or inherent genetic characters affect speciation and diversity among Vibrio bacteria. Researchers in my laboratory focus on aspects of molecular signaling, population genetics of Vibrio bacteria, molecular specificity of symbiosis genes, competitive exclusion of non-native symbionts, phylogenetic relationships among squids in the family Sepiolidae, as well as modeling certain aspects of the ecology of the association.

Publications that represent the work I do:


**RALPH W. PRESZLER**

*Curriculum Design & Biological Literacy*

The primary goal of my research is to develop educational theory and applications that promote the development of students' biological literacy. Such literacy is characterized by the ability to access, critically evaluate, and apply biological literacy to personal and societal issues. This goal has led me to interdisciplinary projects aimed at improving students' understanding of scientific process; as well as developing their more general critical thinking, language, and quantitative-reasoning skills. I am interested in the development and assessment of a wide variety of tools which students use as they learn biology at the university level. These tools include inquiry-based laboratory exercises, concept maps, case studies, and modification of the structure of lecture courses to incorporate activities which promote active student learning.

The successful implementation of theories and applications emerging from science education projects will require a dramatic shift in methods used by instructors at colleges and universities. This paradigm shift will involve a change in perspective from instructors simply disseminating information to instructors facilitating student discovery of the relevance of biological information. A major branch of my teaching and research responsibilities is the development of instructor-training programs which promote and catalyze this revision of approaches used by people teaching at the college level. A major thrust of my effort in this field is the development of training programs which encourage instructors to develop approaches to the scholarship of science teaching which will enable them to develop novel teaching methods, effectively assess the utility of these methods at both formative and summative levels, and disseminate their knowledge of teaching to the academic community.

Lastly, I am involved in projects which aim to integrate K-12 science instructors, and their students, into the university community. Hopefully, these K-12 science education projects will produce students who have a more developed understanding of the nature of science, and who have realized that they are welcome to participate and contribute to science.

I am interested in working with graduate students who would like to make theoretical and practical contributions to the advancement of science education in the development of student-centered, active-learning projects, instructor training programs, and outreach programs between the university and surrounding schools.

*Publications that represent the work I do:*


ELBA SERRANO

Neuroscience, Biophysics & Nanobiotechnology

Lab URL: http://biology-web.nmsu.edu/serrano/neurolab/neurolab.html

The primary research activity of the Serrano laboratory lab focuses on the nervous system, with an emphasis on the sensory organ systems responsible for hearing and balance and on the role of neuroglial membrane transporters in neuroprotection and cancer. Our approach integrates many methods including molecular biology, anatomy, genetics, informatics, biophotonics, tissue culture, bioimaging, electrophysiology, and flow cytometry. In a new line of investigation we are assessing nanocrystal quantum dots (NQDs) for biocompatibility with the ultimate goal of using NQDs as probes to query molecular processes in neurons, mechanosensory cells, and neuroglia. Our laboratory has emerging research interests in the development of technologies for live cell and organ imaging such as multi-photon microscopy and optical coherence tomography and in tissue engineering. Our research efforts are furthered through collaborations with colleagues in the Cell Decisions Processes Center (MIT, MA), Southwest Sciences Inc. (Santa Fe, NM), and the Center for Integrated Nanotechnology (LANL, NM). Our research is supported by NIH, NSF, and CINT.

Selected publications that represent the work we do:


CHARLES BRADLEY SHUSTER

Cell and Developmental Biology

My research interests focus on cell cycle regulation of the cytoskeleton during early development. In particular, I am focused on understanding the spatial and temporal regulation of cytokinesis, the final phase of cell division. Successful timing and execution of cytokinesis is an absolute requirement for the maintenance of chromosomal ploidy and thus proper development and survival of the organism. And while great progress has been made into our understanding of cell cycle regulation and mitotic spindle assembly, we still know little regarding how cells coordinate sister chromatid segregation with cytokinesis. Toward these ends, we have undertaken a multidisciplinary approach that uses molecular, biochemical, and live cell analyses to examine contractile ring formation in the sea urchin early embryo.

Another area of interest is focused on understanding the function of mammalian homologs of the Mitotic Exit Network (MEN), which coordinates mitosis and cytokinesis in yeast. Although orthologs of the individual MEN components have been identified in animal cells, data from both Drosophila and mammalian cells suggest that this network (termed the Salvador-Warts-Hippo pathway) appears to function by limiting cell proliferation in response to cell-cell contact. We are actively studying the mitotic roles for one component of the network (Mob1), as well as a potential role for the SWH pathway in mediating cell cycle arrest following mitotic failure.

Publications that represent the work I do:


MICHELE SHUSTER

Science Education

I am interested in developing and assessing approaches to science education that promote deeper understanding and durable interest in biological content. I have projects at a variety of levels, including K-8, undergraduate and training in scientific teaching for graduate students and postdoctoral fellows. The content areas that I am particularly interested in include cancer biology, molecular processes (e.g. protein targeting and localization) and bioinformatics. I am also interested in developing socioscientific approaches to address these content areas.
Publications that represent the work I do:


GEOFFREY B. SMITH

Environmental Microbiology, Molecular Probe Techniques

Contamination of the United States' groundwater with industrial wastes is a serious problem, particularly considering that the nation's ground water provides drinking water to an estimated 56% of U.S. households. New Mexico obtains 90% of its drinking water from groundwater sources. I am researching the bacteria, enzymes and genes involved in the microbial biodegradation of environmental contaminants such as benzene, the chlorofluoro carbons (CFCs) and the trihalomethane compounds such as chloroform. The environments that I am interested in carrying out these studies are in the groundwater of contaminated aquifers and in wastewaters. Biodegradation activity (as monitored by gas chromatography) is being studied under anaerobic conditions.

I am using DNA and RNA nucleic acid probes of interest in natural samples such as aquifers. I have developed a gene probe specific for the bacteria which reduce nitrate to nitrogen gas (denitrifying bacteria); the gene codes for the heme-type nitrite reductase enzyme. Other genes specific for pollutant biodegradation pathways such as those of the toluene-degradation (TOL) plasmid have been obtained for use in this work. The gene probes are used to analyze the genetic potential for biodegradation in samples such as the aquifer columns mentioned above. Additionally, the probes can be used to indicate the changes in microbial populations due to experimental perturbations such as the imposition of anaerobic conditions. A major advantage of DNA probe use is that the technique does not rely on the microorganism's ability to grow in laboratory media, and thus the technique has access to microbes previously undetected by other methods. A related research interest is the improvement of techniques to extract high-purity DNA from natural samples such as aquifers and soils.

Publications that represent the work I do:


HEATHER THROOP

**Ecosystem Ecology**

I am broadly interested in understanding the nature of ecological linkages between organismal-level processes and ecosystem-level processes. In particular, my research explores a) the patterns and mechanisms by which organisms respond to perturbations in environmental conditions and carbon and nitrogen cycles and b) the patterns and mechanisms by which individual organisms affect carbon and nitrogen cycles. I am fascinated with these biogeochemical cycles because of their biological importance and complexity, and also due to the tremendous extent to which they are currently being affected by human activities. My research integrates manipulative field experiments with modeling techniques. I use a broad a range of experimental techniques, spanning from the physiological level to the ecosystem level, allowing me to explore links among different levels of ecological organization. My work is highly interdisciplinary and I have current projects with collaborators who specialize in a diverse array of fields, including microbial ecology, physiological ecology, biogeochemistry, soil science, atmospheric science, hydrology, and restoration ecology.

Much of the current work in my lab focuses on organism-ecosystem links in arid and semi-arid environments throughout the world. We are particularly interested in exploring how woody encroachment, an increase in woody plants that has occurred globally over the past century, is affecting carbon sequestration in soils and decomposition of organic matter.

*Publications that represent the work I do:*


A fundamental question in developmental biology is how intrinsic and extrinsic factors influence the phenotype expressed by individual cells. This issue is particularly pertinent to excitable cells like muscle fibers which express an extreme diversity of biochemical, morphological, and physiological characteristics.

Currently, I am working on the electromotor system of electric fish. In all electric fish, some skeletal muscle fibers lose their contractile apparatus and convert their phenotype into non-contractile electrocytes, i.e., electrogenic cells of the electric organ (EO). How the genes coding for a select number of muscle-specific proteins are down-regulated while others are maintained and novel genes are up-regulated, is an intriguing problem in the control of muscle and EO phenotype. Interestingly, EOs are formed from a large variety of skeletal muscles including extraocular, brachial, pectoral, axial, and tail muscles in fish representing at least six independently evolved groups. The mechanisms by which only certain skeletal muscles undergo such phenotypic conversion remain to be determined. Furthermore, electrocytes are innervated by specialized electromotoneurons (EMNs) that derive from spinal and cranial motoneurons. How electrocytes and EMNs have evolved from their precursor cells to form a functional electromotor system is unknown.

Ultimately, my goal is to understand the mechanisms underlying the differentiation and maintenance of phenotypic fates among muscle-derived cells and motoneuronal cell types of the electromotor system in a variety of distantly related species. I plan to use a multi-disciplinary approach that combines a range of molecular, anatomical, microscopical, and in vitro techniques to address these research goals. Together, this research will: 1) reveal new insights on the mechanisms regulating the expression of genes coding for a select number of muscle-specific proteins; 2) determine the molecular and cellular interactions between muscles and their nerves; 3) have broad relevance including identification of mechanisms of tissue transdifferentiation, and clinical importance to pathological conditions caused by disease or injury where muscle development or maintenance is compromised; and 4) shed light on an evolutionary process: how neurons and their targets co-evolve.

Publications that represent the work I do:


TIMOTHY F. WRIGHT

Animal Behavior and Evolution

My research focuses on the function and evolution of vocal communication in parrots. Across the animal kingdom, the ability to learn vocal signals is restricted to a few evolutionarily distinct groups (songbirds, hummingbirds and parrots among birds; humans, bats and whales among mammals). Parrots are renowned for their vocal mimicry abilities in captivity, but less is known about how learning is used in the wild. Thus they present opportunities for understanding how learning shapes communication behavior, how the use of learned vocalizations differs between species, and why this ability evolved in the first place. These core interests have expanded through the years to a variety of related questions regarding the systematics of parrots, the evolution of their impressive longevity, and how best to conserve endangered parrot species that I approach collaboratively with other researchers and organizations.

We tackle these questions through a broad range of approaches including field observations, sound analysis, telemetry, captive studies, playback experiments, psychoacoustics and molecular population genetics and phylogenetics. Students in my lab make use of these techniques or invent new ones as appropriate to investigate their own questions in behavior and evolution.

Publications that represent the work we do:


JIANNONG XU

Functional Genomics & Mosquito-Malaria Interactions

Malaria is a mosquito-borne parasitic disease. Malaria infects 350-500 million people each year, killing more than one million, most are children under the age of 5 in Africa. Malaria involves the complex interplay of three involved genomes: human, Plasmodium parasite and vector mosquito. Biological control of vector mosquitoes is based on the deep and thorough understanding of the mosquito-Plasmodium interactions. Throughout coevolution, mosquito defense architecture has been shaped by the reciprocal interactions with malaria. Anopheles gambiae, the most competent vector mosquitoes, is genetically capable of limiting malaria infection to a tolerable level. The anti-malaria defense involves a complex immune network that consists of recognition, signal transduction and an array of mechanisms killing the Plasmodium. The system is genetically heterogeneous among individual mosquitoes in nature. The areas of work in my laboratory are (1) comparative and functional genomics on identifying immune pathways and involved genes that are required for fighting malaria; (2) population genomics studies on genetic diversity of immune genes in the natural populations; (3)
identification of genetic variants that influence the mosquito susceptibility/resistance to malaria by genetic association study using single nucleotide polymorphism (SNP) markers.

Publications that represent the work we do:


