RESEARCH EXPERIENCES FOR UNDERGRADUATES
IN
INTEGRATIVE AND EVOLUTIONARY BIOLOGY

Sponsored by the National Science Foundation

Summer 2008 (June 9 to August 15)

Department of Biology

University of Massachusetts Boston

http://www.bio.umb.edu

The Program: The University of Massachusetts Boston, located on Boston Harbor, has been offering a ten-week Research Experiences for Undergraduates (REU) program for 15 years. The program provides opportunities to 10 undergraduate participants each summer to engage in research and other enrichment activities. Each student carries out an independent research project under the close guidance of a faculty advisor. (Available advisors and their research programs are described below—student-faculty matches are made based on mutual interest.) The program's theme of Integrative and Evolutionary Biology stresses the integration of diverse fields within biology, demonstrating common themes across the biological sciences and especially the connections between cell and molecular biology on the one hand, and ecology and conservation biology on the other. Student research projects span a wide array of problems in biology. The projects are designed to help students develop independence in making research decisions, skill in experimental design, and insight into their broad field of research. In addition to these individual research projects, all students participate in enrichment activities that promote a sense of community, teach communication skills, enhance understanding of issues surrounding modern biology, and prepare students for advanced work in science. These experiences occur during weekly discussions and workshops that focus on practical, personal, and ethical aspects of research. The program also features field trips in and around Boston Harbor and final research presentations. The program serves a culturally and ethnically diverse student population. Close mentoring relationships, as well as collegial interactions among student participants, are key components of the experience. The program is designed to stimulate and support interest in biological research and to begin to equip students with the skills and experiences they will need to pursue research careers.

Stipend: Participants receive a stipend of $4,200 for the ten-week period, plus a room and board allowance of $2,500. Students can also apply for reimbursement for travel expenses.

Program Dates: June 9 to August 15. (In certain cases, individuals may adjust starting or ending times by prior arrangement.)

The Campus: The University of Massachusetts Boston is located south of downtown Boston on a peninsula extending into scenic Boston Harbor. The 12,000-student campus shares the peninsula with the John F. Kennedy Library. The Biology Department consists of 24 full-time faculty and 75 graduate students working toward MS degrees in Biology or Biotechnology, or PhDs in Environmental Biology or Molecular, Cellular, and Organismic Biology. The resources of the Biology Department, as well as the University's recreational facilities, library, computer facilities, and Campus Center, are available to participants.

Eligibility: Applicants must be citizens or permanent residents of the United States and must be enrolled in college for the fall of 2008. Students who will graduate by June 2008 are not eligible to apply. Applicants should have completed at least one upper-level biology course as well as mathematics through college algebra. The program is full-time.

For more information and applications:

Visit our web site: http://www.bio.umb.edu (click on Research Experiences for Undergraduates)

Or contact: Marcia Kazmierczak/REU Program Assistant
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Minorities underrepresented in science are especially encouraged to apply.

To Apply: Download the application, or call or e-mail us for a hard copy. Send a completed application form along with the following: a resume; a letter describing your background, career goals, and interests in biology; preferences among listed research topics; current undergraduate transcript; and letters from two faculty members familiar with your academic performance.

Deadline: Completed applications are due March 1, 2008.

Housing: While there is no on-campus housing, apartments and rooms are widely available near the campus. Participants are responsible for making their own housing arrangements, but assistance in finding housing is available through the UMB Housing Referral Service (617-287-6011) or through the REU Program Assistant.

The following research opportunities are available:

i) Mechanisms of gene regulation: Steven Ackerman. My lab investigates gene regulation in plants and animals, specifically the initiation event of RNA synthesis. Our work addresses the biochemistry of transcription and the regulatory mechanisms governing this process. We purify wheat transcription proteins and use model in vitro transcription systems from plants and animals to characterize plant general transcription proteins. The plant components are substituted with their congeneric human protein in a homologous human transcription system, forming a

heterologous wheat/human system. The gene(s) for proteins of interest are molecularly cloned for further studies. We also investigate transcription mechanisms in vivo using transgenic wheat. Our biochemical studies also include wheat chromatin remodeling and its effects on transcription, how activator proteins affect transcription initiation via their interaction with wheat TAFs, and transcript families for the general transcription factors of wheat.

ii) Population ecology and demography: Solange Brault. My area of interest is the ecology of populations, applied to questions of conservation. I use quantitative models as the framework for my research, which enable me to bring together very different aspects of knowledge about a given population—for example, its life history and social structure, the effects of human interactions, and the effects of diseases or environmental disturbances. REU students will participate in a study of the population dynamics of the St-Laurent beluga whale. This population was reduced by hunting in the early 20th century and has failed to recover to its earlier numbers. Our aim is to understand the causes of this failure, by means of a demographic model connecting data from multiple studies of this population.

iii) Growth control in plants: Adán Colón-Carmona. Land plants are sessile organisms. Because they cannot move to avoid harsh environmental conditions, plants have evolved highly regulated cellular mechanisms, primarily cell division and elongation, to modify growth patterns of root and shoot organs. Our studies use cellular, molecular, and genetic tools to understand the contribution of cell division to the regulation of organ growth during seedling development. We are also studying the role of the motor proteins kinesins during organ formation by analyzing "knock-out" and gain-of-function mutations in kinesin genes. Finally, we are utilizing molecular methods to search for genes that can be utilized in the bioengineering of plants that biodegrade petroleum-based pollutants. Additional information can be found at our lab website: http://www.acc.umb.edu/

iv) Community and ecosystem responses to climate change and/or invasion: Jeff Dukes. My laboratory is interested in understanding how invasive plant species become established in or excluded from communities, and how global environmental changes affect ecosystems. In Massachusetts, we are examining how climate change affects old-field ecosystems. Will changes in precipitation patterns affect plant growth? How will global warming alter competition among plant species? What are the implications for people and for the environment? REU students will help collect data and carry out short-term field experiments as part of a team that is conducting a major climate change experiment in the Boston area. More information on the project is available at: <http://www.ecosystems.umb.edu> and http://globalecology.stanford.edu/DGE/Dukes/Dukes.html

v) Evolution in the deep sea: Ron Etter and Michael Rex. We are exploring fundamental questions about the evolutionary origins, radiation and geographic spread of deep-sea organisms. The deep sea is a vast and complex ecosystem that supports a surprisingly rich and highly endemic fauna, yet virtually nothing is known about how evolution unfolds in this remote environment. We use molecular genetic techniques to quantify geographic and bathymetric patterns of genetic variation, and to test hypotheses about gene flow, dispersal, population differentiation, speciation and the nature and scale of isolating mechanisms. We also use geographically referenced phylogenetic analyses to test hypotheses about how the deep ocean

was colonized. For example, we are exploring whether the deep-sea molluscan fauna evolved from numerous independent colonizations from coastal progenitors, or from in situ radiation. Students could be involved in exploring basic evolutionary questions at different geographic, bathymetric and taxonomic scales. Students will have the opportunity to participate in an oceanographic research cruise in the North Atlantic, June 4-21, 2008.

vi) Pollutants in aquatic systems: William Hagar. My laboratory group is interested in maintaining the quality of our environment and understanding interactions within aquatic ecosystems. Naturally-occurring stable isotopes are used to evaluate food webs and their structure in sensitive water systems. We are particularly interested in the effects of anthropogenic inputs on the quality of aquatic systems. We have developed computer-based, on-site, remote sensing devices for monitoring water systems. These devices continually gather on-site environmental information and transfer these data back to the laboratory. The focus of our current work is the effect of acidic precipitation on aquatic biota. The experiments, which include monitoring water systems and aquatic organisms, are a continuation of our over ten-year acid rain study. Students focus on the relationship between acid rain, transient pH changes, and pond biota.

vii) Control of cellular organization: Linda Huang. Although most cells contain the same basic set of organelles, the internal architecture of a particular cell type is characteristic and reflects the specific properties of the cell. The work in my laboratory seeks to answer questions of how signal transduction processes are used for spatial and temporal regulation of cellular organization. Our studies utilize molecular, genetic, and biochemical methods to understand the regulation of cellular architecture in the budding yeast *Saccharomyces cerevisiae*. We are specifically examining how evolutionarily conserved signal transduction pathways are utilized to control the complex cell morphological changes that occur during spore morphogenesis in S. cerevisiae.

viii) Genetic basis of biodiversity: Rick Kesseli. Our studies combine components of field work, greenhouse experiments, and molecular biology to examine the genetic basis of biodiversity. At the genomic level, we study the evolution of suites of selectively critical interacting genes that affect the genetic structure and fitness of species. In plants, genes responsible for shifts from outbreeding to inbreeding or from hermaphroditic to dioecious are one focus. The genes that bestow resistance to pathogens and the genetic bases of host-pathogen interactions are another. At the population level, we examine the genetic structure and dynamics of endangered and invasive plant species. Molecular markers serve to solve systematic ambiguities and to quantify genetic diversity, gene flow, or breeding systems.

ix) Gene Expression: Kenneth Kleene. Research in my laboratory focuses on two interrelated topics, the mechanisms of translational regulation and the evolutionary basis of the atypical patterns of gene expression in spermatogenic cells in mice. Currently, my lab is engaged in three projects. First, we are using transgenic mice and RNA electrophoretic mobility shift assays to delineate the functions of the 5' UTR, 3'UTR and RNA-binding proteins in regulating the developmental timing of translation of the sperm-mitochondria cysteine-rich protein mRNA in haploid spermatogenic cells. Second, we are studying the mechanisms of expression of cancer-testis genes, a huge group of genes that evolved originally to enhance male reproductive success

and is activated abnormally in malignant cells. Third, the theoretical basis of both projects is shaped by our conviction that differences in the selective pressures on somatic cells and spermatogenic cells, natural selection vs. sexual selection, are responsible for the atypical patterns of gene expression in spermatogenic cells. The atypical selective pressures on spermatogenic cells result in novel regulatory mechanisms and intriguing evolutionary phenomena. Our work uses comparative genomics to identify examples of novel selective pressures and regulatory mechanisms.

x) Neuropharmacology of the rat basal ganglia: Alexia Pollack. The basal ganglia are a group of subcortical structures that regulate voluntary motor behavior. My laboratory uses rats to examine the role of the neurotransmitters dopamine, glutamate and adenosine in modulating voluntary motor activity and gene expression in basal ganglia structures. The aim of this research is to correlate neurotransmitter-mediated effects on motor behavior with specific changes in the expression of transcription factors and neuropeptides in basal ganglia structures in order to uncover cellular/molecular mechanisms underlying motor behavior. REU students can participate in all aspects of this research from *in vivo* pharmacology and behavioral assessment to processing rat brains for analysis of changes in gene expression.

xi) Molecular microbial ecology: Michael Shiaris. My laboratory group studies genetic diversity and the roles of bacteria in the environment. We focus on soil archaea, pathogens in coastal waters, and rhizosphere bacteria. Students will examine the abundance, distribution, and/or dynamics of specific bacteria in coastal waters, sediments, or on plant roots. They will design experiments for the laboratory or field to answer questions about genetic diversity and bacterial function in the environment. Students will use microbiological and molecular methods including DNA fingerprinting tools to address these problems in microbial ecology.

xii) Bacterial toxins and virulence plasmids: Rachel Skvirsky. The native microflora of the mammalian gastrointestinal system consists of a diverse array of microbes existing in dynamic relationship with each other and with the host. Whether a bacterial strain can colonize and whether it establishes a commensal or pathogenic relationship with the host depend on complex interactions between bacteria and host and among the bacteria. Our recent work is aimed at identifying plasmid-encoded factors that help *E. coli* to colonize and establish either commensal or pathogenic interactions. We are focusing on the role of a specific bacterial plasmid and the anti-bacterial toxin it encodes. We are using two approaches. The first is to model the interactions between toxin-producing and non-producing *E. coli* through *in vitro* competition experiments, and the second is to analyze the effects of the plasmid on the interaction of *E. coli* with mammalian host cells.

xiii) Ecoinformatics and the Electronic Field Guide: Rob Stevenson. Informatics technologies are now being applied to a wide range of environmental sciences, including taxonomy, biodiversity, and ecological and ecosystem studies. Our lab is currently engaged in a project whose goal is to enable scientists and naturalists to make their own digital field guides and related products. The Electronic Field Guide project (see < http://www.electronicfieldguide.org>) will be of interest to students who want to pursue research in any of the following areas: ecology and natural history (especially of plants, shells, ants, spiders, worms, butterflies, and aquatic insects), photography, computer science, and GIS.

xiv) Evolutionary bioinformatics: Ying Tan. The rapid progress of genome sequencing projects and PCR technology has led to an explosion in the amount of DNA sequence data available. Our lab uses this data to address evolutionary and functional questions. One project focuses on the evolutionary bioinformatics of disease-related genes, such as Alzheimer's genes and breast cancer genes. This work carries out comparative analyses of available mammalian sequence data in order to gain insights into the functionality of particular disease genes. Another project studies the molecular evolution of circadian rhythm related genes; here we try to address the evolution of diurnality/nocturnality in ancestral primates and make functional predictions for circadian clock-related genes based on comparative studies. Students will pursue these projects using nucleotide substitution estimation, substitution pattern analyses, and molecular phylogenetic analyses.

xv) Cell Signaling in *Drosophila*: Alexey Veraksa. My laboratory is studying the regulation of intercellular communication, or cell signaling. We are using a model genetic organism, the fruit fly *Drosophila melanogaster*, to investigate the mechanisms of cell signaling during development. Students in my lab will participate in genetic or molecular biology experiments to characterize the functions of different protein complexes that participate in signaling events. The intensive nature of the REU program will allow a student to carry out a meaningful project, using such techniques as polymerase chain reaction (PCR), DNA cloning, DNA and protein electrophoresis, Western blotting, *Drosophila* embryo microinjection, and whole-embryo fluorescent immunolocalization.