

**Titles, mentors and abstracts for the summer 2009 AMNH Research Experiences
for Undergraduates program in Evolutionary Biology and Systematics**

Systematics of the lower termites

Dr. Jessica Ware & Dr. David Grimaldi

A thorough phylogenetic analysis of basal termite relationships is crucial to our understanding of the evolution of significant isopteran features such as social behavior and gut-symbiosis. The proposed REU project would involve termite morphology (photomicrography, SEM technique, and standard light microscopy) and molecular analysis (extraction, amplification and sequencing, as well as phylogenetic and divergence estimation analysis).

Population distribution of globally endangered sea turtles in protected feeding grounds and fisheries of the Western South Atlantic.

Dr. Eugenia Naro-Maciel

Conservation scientists across the globe agree that highly migratory animals protected in one area may face threats when moving to other localities during their migrations. Understanding the linkages between groups in protected areas and outside them is therefore key to effective conservation. In the case of highly migratory and endangered sea turtles, protected populations may be linked through migration to others in the region where threats are significant, or be affected by capture in fisheries. Accidental capture of sea turtles in the course of long-line, driftnet, and trawl fishery activities is among the greatest of threats to certain species of sea turtles today. By investigating the migratory connections of these turtles, this project will provide insight into population isolation and conservation priorities necessary to establish whether areas should be managed as independent units or as regional populations, and will clarify questions of scale in conservation and management, providing a scientific basis for conservation prioritization. Students working on this project will carry out all phases of laboratory research, from DNA extraction through sequencing, and data editing, analysis, and presentation.

Fine-scale dynamics in coral-reef communities: Implications for coral recruitment and reef resilience

Dr. Katherine Holmes & Dr. Dan Brumbaugh

Coral recruitment, a fundamental component of reef resilience (i.e., the ability of reefs to recover from disturbance), depends on a number of other ecological processes, including the maintenance of appropriate microhabitats for larval settlement and juvenile growth. Biogenic settlement and growth habitats, in turn, are produced and maintained through a dynamic balance of benthic colonization, competition, herbivory, and predation by a suite of diverse taxa. Many interactions among these processes and species remain poorly understood, especially in more pristine reefs with intact fish and benthic communities. To help fill this gap, we have conducted baseline study of coral-reef community succession, recruitment, and related processes on Palmyra Atoll in the northern Line Islands of the central Pacific. Due to its isolation and history free from substantial human populations (with the exception of occupation during World War II),

Palmyra Atoll supports fish communities that are considered to be relatively intact and pristine, with large numbers of apex predators such as shark, snappers, and jacks. Using digital images of terracotta settlement tiles, tracked for three years at three locations and three depth zones across back and fore reefs around Palmyra, REU interns will focus on computer-based image analysis of the assemblages of macroalgae and marine invertebrates on these tiles. Specific issues to be investigated include the role of site and depth in assemblage structure over time, how assemblage structure influences coral recruitment and growth, and the apparent role of grazing on colonization and community dynamics. In addition to introductory coursework in ecology and statistics, interest in and experience with marine biodiversity (especially algae and invertebrates), graphics software, and image analysis will be useful, though not required.

Putting Teeth into Bat Phylogeny

Dr. Nancy Simmons

Bats (Order Chiroptera) represent one of the remarkable success stories of mammalian evolution. Nearly worldwide in distribution, there are >1100 extant species and >390 extinct species of bats; among mammals they are second only to rodents in diversity. Although much is known about relationships of major extant lineages and a few of the better-preserved fossil genera, large numbers of fossil taxa cannot yet be placed into context in existing bat phylogenies for one simple reason: they are known only or mostly from dental remains scattered in museums around the world, and no character set exists for evaluating their relationships. As a result, our understanding of the "when," "what" and "where" of early bat evolution remains woefully incomplete. A long-term project is being developed to address these problems through creation of a Virtual Museum of Paleogene bat fossils and dental exemplars of extant bat families that will be openly accessible to researchers all over the world via MorphoBank (morphobank.geongrid.org), a web-based platform for morphological systematics. A new dataset of dental characters for bats will be developed in that platform that will facilitate placement of >100 fossil bat species into more comprehensive phylogenies based on morphology and gene sequence data. This summer, work will focus on gathering images and data from extant exemplars and developing a dental character set that will form the basis of this project.

How Many Bat Species Are There?

Dr. Nancy Simmons

Understanding biological diversity and its distribution on the planet requires knowledge of species limits and the extent of sympatric diversity of closely related taxa; it also requires a historical perspective. The most recent summary of bat diversity, completed just over 5 years ago, listed over 1100 extant bat species. This represented a 20% increase over the previous summary from ten years prior. There is no species-level summary of fossil bat diversity. New methods (most notably DNA sequencing and examination of echolocation call structure) and new data (collections from additional areas) have resulted in continued description of new species of bats, and the numbers continue to increase yearly. How many bat species are there, and how are they distributed geographically? What is the rate of discovery of new taxa, and how can we estimate how many new species await discovery? How does modern species diversity

compare to fossil diversity, and how complete is the bat fossil record? These questions will be addressed in a thorough review of bat species diversity that will involve mining and analyzing not only literature reports but also museum collections.-----

Molecular genetics as a conservation management tool for Scarlet macaws (*Ara macao*) in La Selva Maya

Kari Schmidt

The scarlet macaw is an iconic and charismatic species on the verge of extinction in Central America, where its once extensive range has been reduced to a few small, presumably isolated, populations. This project is aimed at assessing the impacts of fragmentation on the genetic structure and diversity of scarlet macaws in La Selva Maya, a tri-national system of protected areas in Belize, Guatemala and Mexico and the last remaining stronghold for the species in the region. Mitochondrial haplotypes and multilocus microsatellite genotypes will be used to assess the genetic variation within and extent of gene flow between focal breeding sites in each respective country. These results will complement current conservation activities in the area and provide an empirical framework for the design and implementation of intensive management activities (i.e. reintroductions or translocations).

DNA Barcoding of endangered species

Dr. George Amato

DNA barcoding has been proposed as an important advance in molecular biology for rapidly and cost-efficiently using a short reference sequence of DNA to help catalog and inventory biodiversity. It is designed to provide an agreed-upon framework for an applied approach to cataloging species and to making the information available to managers and decision makers as well as the scientific community. By combining well-established molecular biology techniques with emerging developments in bioinformatics, DNA barcoding offers the opportunity to transform the way in which society uses biodiversity information. DNA barcoding methods have wide-ranging applications to help protect biodiversity against such threats as human-caused (anthropogenic) changes in the environment and the pervasive illegal commercial trade in animals and animal products. Endangered species that could benefit from a DNA barcoding approach include commercially hunted wildlife, wildlife consumed for the traditional medicine trade, rare species collected for private living collections, and unsustainable harvesting for other wildlife products.

New evidence from the postcranial skeleton for higher placental mammal phylogeny and evolution

Dr. Michael J. Novacek

Mammals are comparatively well known from morphology, fossils, and more recently, genomic data. Nevertheless, the nature of the mammalian data set for phylogeny is skewed. In the area of morphology, most studies have emphasized the dentition and skull, whereas information on the postcranial skeleton is much more poorly known. It is important to improve this balance by expanding the database on postcranial skeletal features and applying the new information to selected problems in the higher

phylogeny of placental mammals. This study will involve the identification and organization of selected postcranial data with images and character descriptions using a powerful new interactive, web-based software program MorphoBank (morphobank.geongrid.org). Data will be collected for both living and fossil taxa relevant to an interesting and important problem in mammalian phyogenetics—that concerning the higher relationships of the traditionally recognized lipotyphlan insectivorans (shrews, hedgehogs, moles, solenodons, tenrecs, and golden moles as well as a variety of fossil taxa). Recent genomic studies break with tradition in removing tenrecs and golden moles from “core lipotyphlans” (Eulipotyphla) and grouping them with elephant shrews, proboscideans, hyraxes, sirenians and aardvarks in the clade Afrotheria. However, most recent morphological analyses continue to group tenrecs and golden moles with other insectivorans. Some postcranial skeletal characters have been cited as either supporting or rejecting Afrotheria, but further sampling of certain anatomical regions (for example, the ankle and foot) in some key taxa would offer an opportunity to better understand the relevance of postcranial data to the Afrotheria question.