

with luteolin, luteolin phosphorylated eNOS and stimulated NO release. These data indicate that, within arterial vasculature, luteolin: 1) induces vasorelaxation through an endothelium dependent mechanism; 2) produces a dose dependent and immediate decrease in α_1 AR induced contraction; 3) increases the phosphorylation of eNOS and subsequently improves NO production. Taken together, we suggest that luteolin induces vasorelaxation not by increased eNOS translation but rather by receptor-mediated stimulation of NO production by extant eNOS.

Natural History & Biodiversity

SMALL MAMMALS FROM THE CLOUD FOREST AT CERRO BOBI, SIERRA DE LOS CUCHUMATANES, GUATEMALA. Nicté Ordoñez¹, Walter Bulmer², Ralph P. Eckerlin², & John O. Matson³, ¹Dept. Biol. Sci., Texas Tech Univ., Lubbock, TX 79409, ²Div. of Nat. Sci., Northern VA Community Coll., Annandale, VA 22003, ³Dept. Biol. Sci., San Jose State Univ., San Jose, CA 95192. Very little is known about small mammal ecology and distribution in the highlands of Guatemala. Small mammals were removal trapped from the mixed hardwood/coniferous cloud forest at Cerro Bobi in the Sierra de los Cuchumatanes, Huehuetenango, Guatemala during July 2005 and December 2005/January 2006. The coniferous cloud forest is located at 5km SW San Mateo Ixtatan, NW side of Cerro Bobi (3110m). The habitat can be characterized as follows: overstory of fir (*Abies*), pines (*Pinus*), oaks (*Quercus*), and other broad-leaved trees. A heavy litter of moss, lycopsids, ferns, and fallen logs was on forest floor. A total of 131 individuals representing 10 species of small mammals (8 rodent and 2 shrew) was collected. The site was sampled during two distinct seasons (wet and dry). While there were small differences in the small mammal species composition and abundance between the 2 samples, this was attributed to small sample size and sampling error. *Peromyscus guatemalensis* was the most abundant species in both seasons. Especially important is the collection of the Maya mouse (*Peromyscus mayensis*), not formally reported since its original description in 1975.

IDENTIFICATION OF CRYPTIC CHLOROPHYTES THROUGH MOLECULAR SEQUENCE DATA. Matthew R. Semcheski, Todd A. Egerton & Harold G. Marshall, Department of Biological Sciences, Old Dominion University, Norfolk VA 23529. The phenomenon of phenotypic plasticity is evident in many organisms throughout the natural world and is a byproduct of the biotic and abiotic factors of the environment in which an individual or population inhabits. Plasticity is especially prominent among microscopic photosynthetic taxa, which produce a variety of ambiguous forms. We identified a number of morphologically variable specimens, all originating from a single monoculture of the chlorophyte *Scenedesmus* sp., which included single-cell spinous and non-spinous forms, along with multicellular spinous and non-spinous forms. In order to discern plasticity vs. genetic variation in a number of ecomorphs of *Scenedesmus* sp., the complete ITS-1, 5.8S, and ITS-2 region was sequenced. Phylogenetic analyses confirmed that all samples analyzed, while being morphologically distinct, do indeed belong to the *Scenedesmus* genus. Upon further investigation, it was determined that at the outset, with nutrients non-limiting and an absence of predators, *Scenedesmus* sp. grew rapidly in the single-cell non-spinous form.

Over time, a population of rotifers had contaminated the *Scenedesmus sp.* cultures, triggering the production of multicellular, spinous forms, a typical anti-predator strategy for this genus. It is then concluded that *Scenedesmus sp.* does exhibit phenotypic plasticity in response to biotic and abiotic changes in the surrounding environment. Additionally, some genetic variation was found in several other isolates from a pure *Scenedesmus sp.* culture, all of which, group within the *Scenedesmus-Desmodesmus* complex.

SALAMANDER DIVERSITY AT C. F. PHELPS WILDLIFE MANAGEMENT AREA, FAUQUIER AND CULPEPER COUNTIES, VIRGINIA. J. D. McGhee & M. D. Killian, Department of Biological Sciences, University of Mary Washington, Fredericksburg, VA 22407. Salamander guilds are important components of ecosystems, and may be declining in Virginia. Consequently baseline information on salamander diversity and abundance is needed. Our objective was to assess salamander diversity at a single site in the Rappahannock River watershed, C. F. Phelps Wildlife Management Area. We randomly selected stream and upland terrestrial sites to run 50-meter transects, for both quadrat and natural cover searches. We assessed diversity using a Shannon-Weiner index on all captures and non-larval captures, compared findings quantitatively to similar studies, and assessed diversity in on-site watersheds. We found 11 of 13 expected species, with $H' = 1.33 \pm 0.05$ SD, $J' = 0.55$, and for non-larval diversity $H' = 1.18 \pm 0.08$ SD, $J = 0.49$. The slope of captures per species was similar to other studies, $\beta_1 = -0.50 \pm 0.10$. A single watershed (Fishing Run stream) was considered more diverse than other watersheds on site. We conclude that C. F. Phelps Wildlife Management Area supports a relatively diverse salamander community, and may act as a baseline for the surrounding region. Management efforts should be focused to maintain stream structural diversity, and monitoring agricultural input.

GEOGRAPHIC INFORMATION SYSTEMS AUGMENT ECOLOGICAL MONITORING IN DAM REMOVAL PROJECT. Alan B. Griffith & Damon Lowery. Dept. of Biological Sciences, University of Mary Washington, Fredericksburg, Virginia, 22401. As dam removals have increased in frequency, due to dam deterioration and interest in ecosystem restoration, there is a growing need to determine the ecological effects of dam removal. Few studies have been conducted on dam removals and pre-dam removal data is particularly limited. We present here a case study that explores the use of Geographical Information Systems (GIS) to supplement vegetation sampling data on the ground. Our part of an interdisciplinary study aims to measure changes in distribution and abundance of vegetation after the removal of 2 earthen dams on a tributary of Holts Creek in New Kent County, VA. We previously reported results of plant distributions and abundances measured before the removal of these dams. Our sampling revealed that at least one invasive species, *Murdannia keisak* and *Microstegium vimineum* were broadly distributed and in high abundance within the dams' watershed. As dam removal proceeds, it will be essential to monitor the establishment of these invasive species and other species. Based on our current knowledge of GIS applications we 1) will visualize vegetation samples as spatially related information, 2) have gathered existing geo-referenced information for the

impacted watershed, and 3) have uncovered potentially useful spatially related information, for which no data exists. This process has led us to collect geo-referenced data that will improve our ability to monitor vegetation changes after dam deconstruction.

PHYTOPLANKTON DIVERSITY TRENDS IN THE RAPPAHANNOCK, YORK AND JAMES RIVERS. Todd A. Egerton & Harold G. Marshall. Dept. of Biological Sciences, Old Dominion University. Norfolk VA 23529. The examination of the causes and consequences of biodiversity is a central tenet in ecological research. In estuarine habitats, one factor which has been shown to have an effect on diversity is salinity. Remane (1934) described the change in community composition of benthic invertebrates along a salinity gradient and the accompanying change in species richness. He observed the greatest numbers of species in the freshwater and marine portions, and the lowest in the brackish mesohaline region. This study examines the long term diversity of phytoplankton species along the Rappahannock, York/Pamunkey, and James rivers, tidal tributaries to Chesapeake Bay. These three rivers have varying levels of algal productivity and diversity, and show the same general pattern as described by Remane, with reduced species richness in the mesohaline. Additionally, there is a significant positive correlation between phytoplankton diversity and productivity, but only in the upstream, low salinity stations. This may be attributed to the large seasonal fluctuations in phytoplankton abundance in the freshwater sites, and the relative constancy of the populations in the Chesapeake Bay. This study is based on the long-term phytoplankton monitoring data, gathered as a component of the Chesapeake Bay Program.

PHYLOGENY OF THE CARYOPHYLLALES (ANGIOSPERMS): EXPLORING THE EFFECTS OF GENE CHOICE AND MISSING DATA. Sunny S. Crawley, Shelli A Newman & Khidir W Hilu, Department of Biological Sciences, Virginia Tech, Blacksburg VA 24061. Previous work on reconstructing Caryophyllales phylogeny has relied on data from two to many genomic regions, totaling 3,000 to 46,000 base pairs of sequence information. Topology, resolution, and support for the internal structure of the order have varied, but improvement has been noted as the number of genes/characters increased. We explore here the impact of gene choice and degree of missing data on tree topology and support within Caryophyllales. We chose two rapidly evolving regions (*matK* and surrounding *trnK* intron), two slowly evolving regions (*atpB* and *rbcL*) and one with an intermediate rate of evolution (*ndhF*). We supplemented new *matK/trnK* sequences with complete and partial sequences from GenBank for all genomic regions. Maximum parsimony and maximum likelihood methods were used to analyze 130 species with six basal eudicot species as outgroup. Varying degrees of missing data were analyzed as several different data partitions. The phylogenetic structure of the order recovered with rapidly evolving regions was comparable to that obtained with the three other regions. Topology and support based on combined analysis of five regions was remarkably similar to those obtained using much larger numbers of genes/characters; this was achieved despite having about 46% missing data. Combining genes of different mode of evolution and inclusion of partial

sequences resulted in both increased taxon representation and improved overall phylogenetic structure.

SPECIES RICHNESS AND SPATIAL DISTRIBUTIONS OF FISHES AT NEARSHORE HABITATS, ST. JOHN VIRGIN ISLANDS. Eugene G. Maurakis^{1,2,3}.¹Science Museum of Virginia, 2500 W. Broad St., Richmond, VA 24542, ²University of Richmond, VA 23173, ³George Mason University, Fairfax, VA. Objectives were to identify species diversity and delineate distributions of species at sand- and boulder-shoreline beach habitats, and compare similarity of species and feeding type associations to establish a baseline at these two beach habitats. Fish species richness and spacial distributions, and habitat descriptions were surveyed by visual census using snorkel and mask at 1-m intervals from 1- 40 m from shore at 20 transects at Little Lameshur, Great Lameshur, and Francis Beach, St. John, U.S. Virgin Islands during daylight hours. A total of 69 taxa (67 species) representing 33 families of fishes were observed. Average number of species (32.7) at boulder beach habitats were significantly greater than that (24.3) at sand beach habitats. The most speciose functional feeding groups were mobile benthic invertivores (11 species at 9 m from boulder shore habitats), scrapers and piscivores (each 9 species at 6 m from boulder shore habitats), and macrocarnivores (6 species at 6 m from sand shore habitats). Total numbers of functional feeding groups (range=10-12) and species per functional feeding groups (range=29-46) at all distances from shore at boulder transects were consistently higher than those (functional group range=8-10; species=19-30) at sand transects.

A SURVEY OF STRUCTURES USED BY RAFINESQUE'S BIG-EARED BATS IN VIRGINIA (*Corynorhinus rafinesquii*). L.T. Pletcher, S. Murdock & J.D. Kleopfer, Virginia Department of Game and Inland Fisheries. The Rafinesque's Big-eared Bat, a Virginia state-endangered species, is categorized as a species of greatest conservation concern (Tier I). The objective of this study was to determine the distribution and abundance of this species by surveying man-made structures. This 2008 study continues previous inventory efforts begun by the VDGIF in 1993 which have identified individuals and colonies roosting in man-made structures, many of which had not been monitored since 2001. This study was conducted by revisiting previously documented structures and counting the number of individuals present, road cruising for potential new structures and using county GIS information to obtain landowner cooperation. Of the 94 previously documented structures, 23 were confirmed to be in good status and 15 of these had bats present. The fate of 21 structures is unknown, 14 structures have been destroyed since 2002, and 29 were known to be destroyed prior to 2001. There were 4 active maternity colonies, each containing 30 - 50 females and young. Eleven solitary roosts were documented. Approximately 200 individuals were observed, mostly in Southhampton and Sussex Counties and the City of Virginia Beach. No individuals were found in Charles City, Surry, and Prince George Counties, or the City of Petersburg. The overall population status in Virginia is unknown. Continued publicity and education are needed to enlist landowner cooperation and locate other bat roosts.

MITOCHONDRIAL DNA VARIATION IN THE EASTERN FOX SQUIRREL (*SCIURUS NIGER*). N. D. Moncrief, VA Museum of Natural History, 21 Starling Ave., Martinsville Virginia 24112 & R. A. Van Den Bussche, Department of Zoology, Oklahoma State University, Stillwater OK 74078. The eastern fox squirrel (*Sciurus niger*) occurs naturally over most of eastern North America. This species displays striking patterns of geographic variation in size and coat color. These patterns of morphologic variation are consistent with a hypothesis of southward range contraction and isolation in two refugia (in Texas and Florida) during the Last Glacial Maximum, followed by northward range expansion after the glaciers receded. Similar hypotheses have been proposed to explain the patterns in phylogeographic structure exhibited by many plants and animals in eastern North America. As part of a more comprehensive study of geographic variation in *Sciurus niger*, we analyzed a 402 bp segment of the cytochrome b (cyt b) mtDNA gene in populations throughout the species' range. Despite the broad geographic sampling in our study, there was no phylogeographic structure in our data. Unique haplotypes differed from high-frequency haplotypes by only one or two base pairs, producing a star-like phylogeny of haplotypes. Bootstrap analysis of neighbor-joining trees revealed a lack of phylogenetic structure among haplotypes. Variation within populations and within the species as a whole was characterized by high haplotype diversity and low nucleotide diversity. Taken together, our data indicate that the eastern fox squirrel underwent a rapid range expansion and rapid morphological divergence within the past 20,000 years.

Psychology

INTERHEMISPHERIC COLLABORATION: EFFECTS OF STIMULUS FORMAT AND TASK PROCESSING SIMILARITY. Urvi J. Patel, Dept. of Psych., Christopher Newport Univ., Newport News VA 23606. Observers were presented with a five stimuli array; two items above the point of fixation (one to each visual field), one item below the point of fixation (to one visual field), and two items directly above the other at the point of fixation (to both visual fields). During each experiment, observers engaged in three conditions: (1) responded to whether the bottom stimulus matched either of the top two stimuli (single primary task), (2) responded to whether the two center stimuli matched (single secondary task), and (3) responded to the primary stimuli OR to the secondary stimuli as prompted by a post-stimulus cue (dual task). While all letter stimuli were presented for Experiment 1, Experiment 2 displayed letter primary stimuli and picture secondary stimuli. Performance on the single and dual primary trials was of principal interest. The critical comparison involved trials on which the two matching stimuli projected to the same visual field (within-hemisphere trials) versus trials on which the two matching stimuli projected to opposite visual fields (across-hemisphere trials). While no difference between trials was found when the dual task involved stimuli of different format, an across hemisphere advantage was found when the dual task involved stimuli of the same format. Processing similarity of stimulus format may determine whether the benefits to spreading the processing load between the two hemispheres outweigh the costs.