

**2007 FMCS SYMPOSIUM**  
**PLENARY SESSION: DIRECTIONS IN MOLLUSC CONSERVATION:**  
**MOLECULES TO ECOSYSTEMS**  
**ABSTRACTS**

**PE 01**

**FRESHWATER BIVALVE (UNIONIFORMES) DIVERSITY, SYSTEMATICS AND EVOLUTION: STATUS AND FUTURE DIRECTIONS**

Arthur E. Bogan<sup>1</sup> and Kevin J. Roe<sup>2</sup> North Carolina State Museum of Natural Sciences, Research Lab, 4301 Reedy Creek Road, Raleigh NC 27607, <sup>2</sup>Dept. of Natural Resource Ecology and Management, Iowa State University, Ames, IA 50011

Freshwater bivalves of the order Unioniformes represent the largest bivalve radiation in freshwater. This radiation is unique in the class Bivalvia in having an obligate parasitic larval stage on the gills or fins of fish. This diverse assemblage is divided into six families, 180 genera and roughly 800 species. These families are distributed across six of the seven continents and represent the most endangered group of freshwater animals alive today. Unioniform bivalves have been the subject of study and illustration since at least Martin Lister (1675). Over the past 250 years impressive gains have been made in our understanding of the evolutionary history and systematics of these animals. We briefly summarize the current state of unioniform systematics and evolution and suggest research themes for future research. Advancement in the areas of systematics and evolutionary relationships within the Unioniformes will require a resurgence of survey work and re-evaluation of all taxa, especially outside of North America and Western Europe. This will require collection of animals for shell morphology, comparative anatomy and molecular analyses. Along with re-examination of described taxa, we need a renewed emphasis on the natural history, host fish relationships, ecology and physiology of these animals. Traditional conchological and anatomical characters need to be reviewed and new character suites added. New morphometric methods need to be applied to the ontogenetic changes in shape during growth. The fossil record of freshwater bivalves needs to be carefully reviewed and a phylogeny of this group needs to be developed. However, evidence of rampant convergence in shell morphology needs to be factored out of the record. As our understanding of the systematics of these animals improves, it will result in a better understanding of the evolution of this expansive radiation in freshwater. New avenues are being opened in understanding the evolution of the unioniform bivalves. We need to expand our set of tools to include or develop additional markers such as single copy nuclear genes and microsatellites. Examination of double uniparental inheritance of mitochondrial DNA is providing new insights in to the evolution of this order. Gene order has been shown to differ among genera but is still to be explored. Expanding our understanding of the evolutionary relationships and history of unioniform bivalves will provide a solid foundation to study the zoogeography of these rather sessile, obligate freshwater organisms. The unique natural history of unioniform bivalves provides a fertile area for testing and developing evolutionary theories.

**PE 02**

**LIFE HISTORY STRATEGIES OF UNIONOID MUSSELS**

M.C. Barnhart<sup>1</sup>, G.T. Watters<sup>2</sup> <sup>1</sup>Missouri State University, Springfield, MO 65897; <sup>2</sup>Ohio State University, Columbus, OH 43212

The unique life history strategy of Unionoida is essential to understanding both the evolutionary success of the group and the present conservation crisis. The parasitic larval stage was a key adaptation of the Unionoid ancestor, permitting upstream dispersal in freshwater. Later evolutionary diversification was associated with the origin and exploitation of particular adaptations for parasitizing hosts. Examples of adaptations associated with clades include hooked glochidia (Unioninae), mantle lures and bradycticty (Lampsilini) and host capture behavior (*Epioblasma*). Such adaptations led to varying degrees of host specificity (use of particular host species), which in turn affected other aspects of life history and ecology as diverse as fecundity, reproductive season, habitat, and geographic distribution. Host specialists are more efficient than generalists at contacting particular host species, but are more constrained in host utilization and the related aspects of life history. Unionoids in general are long-lived as adults and many species require several years to reach reproductive maturity. This high somatic investment may allow mussel populations to persist when reproductive success is unpredictable. The age structure of populations is often strongly biased toward adults, suggesting that successful recruitment years are infrequent. These features of life history and population dynamics may reflect fluctuations in host availability. They are also likely to reflect vulnerabilities of the post-parasitic juvenile life stage to environmental factors, which are poorly known. Although recent studies by many workers have greatly improved our understanding of mussel life history, there are tremendous opportunities for future studies. In particular, sustained efforts to propagate endangered species and monitor their populations can provide critical data on the requirements of each life stage and on population dynamics.

### **PE 03**

#### **A STAGE-BASED MODEL TO INVESTIGATE LINKAGES BETWEEN DEMOGRAPHIC AND GENETIC FEATURES OF UNIONID POPULATIONS.**

David J. Berg<sup>1</sup>, James A. Stoeckel<sup>2</sup>, Todd D. Levine<sup>2</sup>, and K. Douglas Blodgett<sup>3</sup>. Department of Zoology, Miami University, <sup>1</sup>Hamilton, OH 45011 or <sup>2</sup>Oxford, OH 45056; <sup>3</sup>The Nature Conservancy, Illinois River Project Office at Emiquon, Lewiston, IL 61542

North American freshwater mussels are continuing to suffer dramatic declines in population size due to a number of anthropogenic stressors such as habitat destruction and commercial harvest. Within populations, neutral genetic variation is lost because of genetic drift. The intensity of drift is negatively correlated with population size. In turn, population size is dependent on demographic parameters such as mortality, migration, and recruitment rates. Thus, demographic and genetic features of populations should be tightly linked. We are developing a stage-based model to investigate the effects of variation in mortality on population size and genetic diversity. Demographic parameters for this model are derived from published data for species of mussels that exhibit considerable variation in population ecology, while our own research has provided measures of population genetic variation using a variety of molecular markers (allozymes, mtDNA sequences, microsatellites) for many species of mussels across a large portion of North America. Using STELLA™ software, our model incorporates a variety of demographic parameters (age-structure, age-specific mortality, recruitment) and population genetic parameters (haplotype frequency, heterozygosity). We will use this model to examine effects of constant and age-specific mortality on populations that have varying levels of genetic diversity. Results of this model will provide insight into interactions of demography and population genetics. For

example, we should be able to compare changes in population size and genetic diversity under contrasting scenarios of age-specific mortality due to harvest regulations and constant mortality due to habitat degradation. We will also examine the importance of migration by comparing isolated populations to populations within a tightly linked metapopulation. While changes in population demography are important for estimating extinction risk for populations in the short-term, survival over evolutionary time is dependent on maintenance of genetic variation. Models that incorporate both demographic and genetic features of populations should be of great utility for the development of effective conservation strategies.

#### **PE 04**

#### **COMMUNITY AND FOODWEB ECOLOGY OF FRESHWATER MUSSELS**

Caryn C. Vaughn<sup>1</sup>, S. Jerrine Nichols<sup>2</sup>, and Daniel E. Spooner<sup>1</sup>. <sup>1</sup>Oklahoma Biological Survey and Department of Zoology, University of Oklahoma, Norman, OK, 73019; <sup>2</sup>U.S. Geological Survey. Ann Arbor MI, 48105.

Freshwater mussels link the water column and bottom sediments through their feeding activities. All species use gill and/or foot cilia to generate water currents that bring in suspended food particles. While there are some species differences in cilia number, spacing, and size, in all species, water enters the shell through the posterior inhalant siphon and also along the anterior shell margin (pedal feeding). Thus, all mussel species can access food particles both suspended in the water column and in the sediment. Particles are sorted by the gill cilia and either ingested or biodeposited as mucus-coated pseudofeces. Research to date shows that mussel diets are remarkably similar regardless of age, size, species, or cilia number and size. Studies using tissue fatty acid profiles, stable isotope ratios, and mussel digestive enzyme production show that all species feed on particles <20 microns in size, particularly micro-algae and bacteria. In addition, direct assimilation of organic molecules such as glucose can occur. Based on these similarities, can we assume that all species perform the same role in foodwebs and communities?

We know that many ecosystem services performed by mussels (clearance of algae from the water column, nutrient excretion, biodeposition of organic matter) are linearly related to community biomass; thus, there is the potential for strong ecosystem effects when mussel biomass is high and hydrologic residence times are long. Multiple studies demonstrate that mussels provide biogenic structure and nutrients to other organisms; algal growth is higher on the shells of living mussels compared to shells alone, and macroinvertebrate richness and densities are higher on shells of living mussels and in mussel patches than in other streambed areas. Effects of mussel community composition vary with spatial and temporal scales and are regulated by factors such as temperature, with significant differences between species' physiological condition (metabolic rate, body condition) and ecological output (respiration and excretion rates) under different environmental conditions. At the scale of a mussel bed, experiments demonstrate potentially strong interactions between mussel species with dominant, driver species regulating factors such as periphyton biomass, but also increasing the body condition of co-occurring rarer mussel species. At the scale of whole rivers, species richness becomes important, with different species driving interactions and ecosystem services under different environmental conditions. Although more research is needed, information to date indicates that mussel feeding activities and community structure can have strong impacts on the entire foodweb, and that interactions

between mussel species are important. Thus, efforts to restore mussels should focus on restoring entire communities.

## **PE 05**

### **USING LANDSCAPE ECOLOGY TO UNDERSTAND FRESHWATER MUSSEL POPULATIONS**

Teresa J. Newton<sup>1</sup>, Daelyn A. Woolnough<sup>2</sup>, and David L. Strayer<sup>3</sup>. <sup>1</sup>USGS Upper Midwest Environmental Sciences Center, La Crosse, WI 54603; <sup>2</sup>Biology Department, Trent University, Peterborough, ON K9J 7B8 Canada; <sup>3</sup>Institute of Ecosystem Studies, Millbrook, NY 12545

Ecology has been transformed over the past 20 years by the development and application of the landscape ecology subdiscipline, i.e., the influence of spatial pattern on ecological processes. Mussel populations and the environments they inhabit are heterogeneous, raising the question: “To what extent can landscape ecology principles be applied to the scientific understanding and management of freshwater mussels?” We review three areas in which landscape ecology might be applied to freshwater mussels.

First, mussel ecologists are grappling with how to define and conceptualize patches of suitable mussel habitat. Recent progress with models and empirical data shows that hydraulics can be successfully used to delineate patches of mussel habitat. It is not yet clear whether hydraulics alone will ultimately provide a satisfactory definition of mussel habitat, or whether we will need to consider additional variables such as host fish, food, or predators. As in other applications of landscape ecology, we do not know whether mussel ecology will be best served by simple binary patch/matrix models, or if habitat quality should be viewed as a continuous variable, nor if we will need to model within-patch dynamics. Special problems associated with mussel populations include distinguishing “fossil” patches in which conditions were suitable for mussel recruitment in the past from “active” patches in which recruitment still occurs, and the possibility of strong source-sink dynamics resulting from Allee effects in sparse populations.

Second, mussel ecologists have begun to think about the importance of connectivity among habitat patches. We would like to know the conditions under which connectivity among patches is important, and which attributes of the environment, the mussel species, and its host, determine connectivity among mussel beds. Major challenges are determining whether connectivity can be estimated in the field, whether human activities that reduce connectivity (e.g., dams) have produced large extinction debts in mussel populations, and whether connectivity is strongly directional in running waters.

Third, recent studies have shown that characteristics of the watershed (especially land use) affect mussel populations. This work is still in an early stage, and needs to be critically tested. We also need to better understand the links between events on the watershed (e.g., timing and amounts of water, nutrient, and sediment inputs, condition of the riparian zone) and the quality, extent, location, and connections among patches of mussel habitat. In addition, it is critical to identify the locations on the watershed that have the strongest links to mussel populations.

Landscape ecology has the potential to improve scientific understanding and management of mussel populations, and in particular help define the best spatial scales for scientific studies and management activities. However, terrestrial paradigms will need to be used carefully.

## **PE 06**

### **FRESHWATER MUSSEL ECOSYSTEM ECOLOGY: THE INTEGRATED FUNCTIONAL ROLES OF WATER QUALITY, POLLUTION, AND PHYSICAL HABITAT IN SUPPORTING ADULT AND EARLY LIFE STAGES OF FRESHWATER MUSSELS AND THEIR ROLE IN NUTRIENT RECYCLING**

W.G. Cope<sup>1</sup>, A.D. Christian<sup>2</sup>, R.B. Bringolf<sup>1</sup>, N. Wang<sup>3</sup>, T.J. Newton<sup>4</sup>, J.L. Farris<sup>2</sup>, T. Augspurger<sup>5</sup>, F.J. Dwyer<sup>6</sup>, M.C. Barnhart<sup>7</sup>, R.J. Neves<sup>8</sup>, E. Hammer<sup>9</sup>, and C.G. Ingersoll<sup>3</sup>.

<sup>1</sup>North Carolina State University, Raleigh, NC 27695-7633; <sup>2</sup>Arkansas State University, State University, AR 72467; <sup>3</sup>U.S. Geological Survey, Columbia, MO 65201; <sup>4</sup>U.S. Geological Survey, La Crosse, WI 54603; <sup>5</sup>U.S. Fish and Wildlife Service, Raleigh, NC 27636-3726; <sup>6</sup>U.S. Fish and Wildlife Service, Columbia, MO 65201; <sup>7</sup>Missouri State University, Springfield, MO 65897; <sup>8</sup>Virginia Tech University, Blacksburg, VA 24061-0321; <sup>9</sup>U.S. Environmental Protection Agency, Chicago, IL 60604-3590.

A recent assessment of the published literature on the topics of water quality, pollution, and physical habitat and their roles in supporting adult and early life stages of freshwater mussels revealed two types of informational sources contributing to our current understanding of environmental health. Descriptive field-based studies showed that mussels have been adversely affected by poor water quality and associated pollutants, and loss and degradation of physical habitat. Noted site-specific effects, contaminant accumulation, as well as global declines were documented by these studies. Based on these observations and the development of ASTM International standard methods for conducting laboratory toxicity tests with early life stages of freshwater mussels, recent experimental-based studies have attempted to determine links, causal mechanisms, and establish rigorous testing and assessment methods. We evaluated the routes and pathways of exposure for all life stages (glochidia, encysted, juveniles, adults) of native freshwater mussels to environmental pollutants, in a life history and ecosystem ecology context, and found that each life stage has both common and unique characteristics that contribute to observed differences in sensitivity and exposure. For example, glochidia may be exposed only briefly (e.g., 1-12 days) through the water column, whereas juveniles and adults have sustained exposure through the water column, pore water, sediment and dietary routes. Juveniles and adults differ in their primary habitat and feeding mechanisms; thereby altering the importance of these routes in exposure, depending on life stage. This synthesis has shown that a combination of life history and ecosystem-level ecological information is needed to properly assess the risks of environmental exposure. Knowledge of differing habitat-based exposure routes on mussel life stages is critical to understanding the relation and applicability of recently developed ASTM International standard acute and chronic laboratory toxicity test methods for predicting toxicological risk and the ultimate protection and conservation of the mussel fauna. In terms of the role of freshwater mussels in ecosystem processes, a review of the literature has shown that mussels play an important role in nutrient recycling. Mussels feed on materials variable in C:N:P, use these nutrients for growth, and egest materials variable in C:N:P. Nutrients used for growth can be sequestered for long periods of time, whereas egested material may become

readily available for subsequent trophic interactions. Freshwater mussels perform vital functional roles in ecosystem processing.

## **PE 07**

### **DIRECTIONS AND INFORMATION NEEDS FOR FRESHWATER MUSSEL CONSERVATION**

Richard J. Neves<sup>1</sup> and Heidi Dunn<sup>2</sup>. <sup>1</sup>Virginia Cooperative Fish and Wildlife Research Unit, U.S. Geological Survey, Virginia Tech, Blacksburg, VA 24061; <sup>2</sup>Ecological Specialists, Inc., 1417 Hoff Industrial Court, O'Fallon, MO 63366

Conservation of freshwater biodiversity should be the highest priority in the U.S., based on global significance of our resident taxonomic groups and number of species susceptible to extinction over the next decade. Trends in demand for land, water, and energy indicate that means for conserving mussel resources while allowing for economic growth must be determined. Developing long-term plausible solutions will require coordination with other scientific disciplines, engineers, resource managers, developers, and higher levels of government. Current mussel conservation and management ranges from basic life history research to improvement of habitat conditions to facilitate mussel community maintenance and enhancement. In addition to actions presented as goals and strategies in the National Strategy for the Conservation of Native Freshwater Mussels about 10 years ago, information is needed to catapult our taxon-specific discipline to a more quantitative, scientifically defensible, and user friendly level. Our knowledge of mussel biology would increase greatly if sister disciplines include mussels as study animals in their areas of expertise, such as toxicology, population biology, veterinary medicine, physiology, biochemistry, biological engineering, and other such complementary sciences. We need field-level tools to determine baseline physical, cellular, and population-level conditions, and detect responses to physical and chemical stress on both the cellular and population level. Development of appropriate biomarkers would fill this gap. Greater knowledge of mussel habitat requirements and the effects of change on mussels are also needed in mussel conservation. Coordinating with personnel such as hydrologists, geomorphologists, and civil engineers can provide suitable techniques for measuring key habitat parameters. However, sustainable development and mussel conservation must have the support of governmental agencies, as field biologists often are inhibited by archaic policies and procedures. Higher levels of government must be educated on the importance of mussel conservation, and the need for policy changes to allow this effort to go forward. Additionally, engineers, developers, and resource managers must coordinate with mussel biologists on the front-end of private projects or government programs, such that mussel conservation needs are accommodated in the planning process rather than as an afterthought. Techniques such as mussel propagation for enhancing and restoring mussel populations, stream restoration to improve habitat, mussel toxicology to test water quality standards, and mussel sampling and monitoring to detect changes in mussel communities are being conducted. However, effectiveness of implementing these techniques in mussel conservation and management depends on our ability to better understand mussel biology and coordinate with outside disciplines. Although we have progressed in the last 10 years, mussel conservation needs are more acute, as most endangered populations continue to decline. A combination of mussel expertise, other biological expertise, regulatory agencies, and engineering disciplines will provide the toolbox of actions required to allay the currently projected extinction rate.

## **PE 08**

### **FRESHWATER GASTROPOD ECOLOGY AND CONSERVATION DIRECTIONS**

Kathryn E. Perez<sup>1</sup>, Russell L. Minton<sup>2</sup>, Kenneth M. Brown<sup>3</sup>, Jeffrey D. Sides<sup>4</sup>, Steven J. Lysne<sup>5</sup>.

<sup>1</sup>University of North Carolina at Chapel Hill & Department of Biology, Duke University, Durham, NC 27708. <sup>2</sup>Department of Biology, University of Louisiana at Monroe, Monroe, LA 71209. <sup>3</sup>Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803. <sup>4</sup>Department of Microbiology, University of Alabama at Birmingham, Birmingham, AL 35294. <sup>5</sup>U.S. Fish and Wildlife Service, Boise, ID 83709.

North American freshwater snails remain an understudied yet critically imperiled fauna. As part of a larger discussion on freshwater mollusks in general, we highlight five specific areas of concern regarding freshwater snails, and discuss how best to address those concerns in the context of conservation: ecology, taxonomy and systematics, the impact of invasives and other future threats, the needs of state and federal agencies for prioritization and implementation of management plans, and the role of the non-governmental groups and outreach for preservation of these natural treasures. We illustrate the how each of these topics relate to conservation efforts and present synthetic and prioritized research goals to improve our baseline knowledge of freshwater snail biology. For ecology, we review the literature on freshwater gastropods, identifying important trends and highlighting the importance of ecological data in studying these groups. A necessary precursor to conservation efforts is an adequate assessment of biological diversity. We present the current state of freshwater snail taxonomy, and show how modern methods such as population and molecular genetics have affected our understanding of natural evolutionary units and the identification of species. Invasive species have affected freshwater taxa across North America, through competition, habitat modification and parasitism to name a few. These alien species originate not only in other countries, but also in neighboring drainages and systems as native taxa become exotic through human-mediated introductions. We outline currently recognized and potential threats to native species and the impacts they are having and may have in the future. Finally, effective conservation strategies require the participation of people at all levels, from local communities to governmental agencies, for implementation and management. We summarize the status and efficacy of freshwater snail captive propagation, as well as partnerships with non-governmental organizations, federal agencies, and other stakeholders. Suggestions for the future direction of multi-partner cooperation in freshwater snail conservation are discussed.

## **PE 09**

### **A NEW NATIONAL FRESHWATER MOLLUSK CONSERVATION SOCIETY STRATEGY FOR CONSERVATION OF NATIVE FRESHWATER MOLLUSKS**

Rachel C. Muir<sup>1</sup> and Robert M. Anderson<sup>2</sup>. <sup>1</sup>U.S. Geological Survey, Biological Resources Division, Mailstop 131 National Center, Reston, VA 20102, <sup>2</sup>U.S. Fish and Wildlife Service, Pennsylvania Ecological Services Field Office, State College, PA, 16801.

The National Strategy for the Conservation of Native Freshwater Mollusks (Strategy) was developed a decade ago, prior to the establishment of the FMCS. Since the Strategy was published there have been significant changes in the conservation status of freshwater mollusks, the kind and degree of threats to aquatic ecosystems and mollusks, and in the state of our

knowledge of freshwater mollusks. A revised and current National Strategy can serve as a guidance document for the FMCS in its support of mollusk conservation, research and monitoring as well as FMCS policy and activities. The purpose of the session is to present a draft strategy to the Society and provide an opportunity for the exchange of ideas between the FMCS National Strategy subcommittee and the FMCS membership. The format will be a panel, with subcommittee members presenting specific recommendations for revision. These will include the topics addressed in the current National Strategy and new issues such as conservation genetics, propagation, adaptive management, expanded outreach, and coordination with other organizations and conservation efforts such as the National Fish Habitat Initiative. The resulting input will be incorporated into a document for FMSC board approval by June, 2007.



PL 01\*

**IDENTIFICATION AND GENETIC CHARACTERIZATION OF NEW POPULATIONS OF THE ENDANGERED WINGED MAPLELEAF, *QUADRULA FRAGOSA***

Amanda H. Hemmingsen and Jeanne M. Serb. Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA 50010

The winged mapleleaf, *Quadrula fragosa*, once occurred in the Mississippi, Tennessee, Ohio, and Cumberland River basins. Due to habitat degradation, the range of this species appeared to be reduced to a single population in the St. Croix River between east-central Minnesota and western Wisconsin border, resulting in the listing of this species as federally endangered. Recently, individuals that are morphologically similar to *Q. fragosa* have been found in Arkansas, Missouri, and Oklahoma. If these southern populations are true *Q. fragosa*, they will need to be included in conservation management plans. We conducted a phylogenetic analysis of mitochondrial ND1 gene sequences to genetically identify these “*fragosa*” morphotypes. Our results indicate that these southern populations indeed belong to *Q. fragosa*. We now are characterizing the genetic structure of all known *Q. fragosa* populations with newly developed microsatellite markers. These data will include genetic variation within and among populations of *Q. fragosa*, and identify gene flow. We will present our preliminary population dynamics results and discuss how this new information will aid in the conservation of this endangered species.

PL 02\*

**WHAT'S IN A NAME? A PRELIMINARY PHYLOGENETIC ANALYSIS OF THE GENUS *VILLOSA* USING MITOCHONDRIAL AND NUCLEAR DNA**

Kody F. Kuehn<sup>1</sup> and G. Thomas Watters<sup>2</sup>. <sup>1</sup>The Aquatic Ecology Lab and <sup>2</sup>Museum of Biological Diversity, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, 1315 Kinnear Road, Columbus, OH 43212.

The genus *Villosa* (Frierson 1927) is a small group of freshwater mussels in the subfamily Lampsilini (Family Unionidae). Currently, 17 species are recognized for the genus, of which, several are considered endangered, threatened, or species of special concern. As has been found with most unionids, the genus *Villosa* suffers from ambiguities in taxonomic position, due largely in part to a lack of reliable systematic characters. This has not only caused difficulties in assessing the relationships within the group, but may also be hindering conservation efforts as undetected cryptic species likely occur. As a result of this, a preliminary phylogenetic study was conducted to infer phylogenetic relationships among several of the species (15/17) within the genus *Villosa*. In addition, several other members of the subfamily Lampsilini are also included. The species of *Villosa* not present within this study include *V. amygdala* and *V. ortmanni*. Phylogenetic analyses were based on portions of mitochondrial (1417 bp) and nuclear (352 bp) DNA sequences. The results of this study corroborate previous studies on the genus *Villosa* indicating abundant polyphyly and several unique species groups. In addition, several species of *Villosa* were also found to be non-monophyletic. These results suggest traditional taxonomy as it currently exists is inadequate and as such should be reassessed based on both morphological and molecular data. Sequencing of the remaining species as well as other unique populations pertinent to the understanding of the phylogenetic relationships among the *Villosa* is ongoing.

**CRYPTIC BIODIVERSITY AND PHYLOGENETICS OF THE WIDE-RANGING FRESHWATER MUSSEL GENUS *ELLIPTIO* IN SOUTHEASTERN NORTH AMERICA**

Michael M. Gangloff<sup>1</sup>, Lynn M. Siefferman<sup>2</sup>, David C. Campbell<sup>3</sup>, and Kenneth M. Halanych<sup>4</sup>. <sup>1</sup>Auburn University Museum and Natural History Learning Center, 331 Funchess Hall, Auburn, AL 36849-5407. <sup>2</sup>Department of Biology, Jordan Hall, Indiana University, Bloomington, IN 47405. <sup>3</sup>Department of Biological Sciences, University of Alabama, Box 870345, Tuscaloosa AL 35487-0345. <sup>4</sup>Department of Biological Sciences, 101 Rouse Life Sciences, Auburn University, AL 36849-5407.

North America possess the world's greatest diversity of freshwater mussels (Bivalvia: Unionidae and Margaritiferidae) yet nearly 70% of its ~300 species are considered to be imperiled. Conservation of many cryptic taxa has been hampered by a high degree of taxonomic ambiguity resulting from few morphological characters and extreme phenotypic plasticity. For example, a recent list compiled by the American Fisheries Society recognized 36 taxa within *Elliptio*, making it the most species-rich unionid genus in North America. Although several *Elliptio* taxa are wide-ranging, >50% appear endemic to one or a very few river systems. However, due largely to taxonomic ambiguity, only 2 have received U.S. federal protection. We examined 2 mtDNA genes (CO1 and NAD1) from 21 putative *Elliptio* taxa. Phylogenetic analyses revealed that *Elliptio*, as currently recognized, is paraphyletic. Specifically, the Interior (Mississippi) Basin endemic *E. dilatata* appears to be only distantly related to *Elliptio* taxa occurring in smaller, Gulf and Atlantic slope drainages. Pairwise genetic distance comparisons indicate that some taxa (*E. arctata*, *E. complanata*, and *E. icterina*) appear to occur on both the Gulf and Atlantic slopes. However, we also saw evidence that cryptic taxa may exist within what is frequently referred to as the *E. complanata*-*E. icterina* species complex in eastern Gulf of Mexico drainages. Conversely, low genetic divergence rates suggest that several Atlantic Slope forms (e.g., *E. infulgens*, *E. viridula*) may be ecophenotypes of *E. complanata*. Phylogenetic relationships between some putative Gulf and Atlantic slope taxa were occluded by relatively short branch lengths and low bootstrap support. We are currently evaluating the ability of other mitochondrial and nuclear markers to elucidate phylogenetic and phylogeographic patterns with Gulf and Atlantic slope taxa as well as continuing extensive field surveys targeting rare forms in order to delimit conservation unit boundaries and/or re-assess status designations.

PL 04

**CENTRAL GULF *TOXOLASMA*: BIG DIVERSITY IN LITTLE MUSSELS**

David Campbell. Department of Biological Sciences, University of Alabama, Tuscaloosa, AL 35487.

The identity of *Toxolasma* species in the Gulf Coast drainages from the Apalachicola system to the Mobile has long been uncertain. Recent publications recognize at least one species in the Apalachicola, at least one in the Choctawhatchee, Yellow, and Escambia, and one in the Mobile system, but others have synonymized these with wide-ranging Tennessee-Ohio-Mississippi system species. Molecular data (primarily ITS and *cox1*) suggest that three species occur in the Apalachicola system, one of which occurs in the Chipola and eastern Choctawhatchee. Another species occurs in the Pea, Yellow, and Escambia, with slight differentiation of the Pea population. Two species are present in the Mobile system. *T. parvus* may be an invasive, as it is known to occur in fish ponds, or it may be native in the western Mobile system. Identity of Lea and Conrad names with type localities including the Mobile system require further investigation. The Escambia-Yellow-Pea and Choctawhatchee-Chipola species are undescribed. Multiple species names exist for Apalachicola system forms, but more investigation is needed to determine which names apply to which forms.

PL 05\*

**MOLECULAR PHYLOGENETICS OF *ELIMIA POTOSIENSIS*  
(CAENOGASTROPODA: PLEUROCERIDAE) FROM THE INTERIOR  
HIGHLANDS**

David M. Hayes<sup>1,2</sup>, Russell L. Minton<sup>3</sup>. <sup>1</sup>Department of Biological Sciences and  
<sup>2</sup>Environmental Sciences Program, Arkansas State University, State University, AR  
72467. <sup>3</sup>Department of Biology, University of Louisiana at Monroe, Monroe, LA 71209.

*Elimia potosiensis* (Lea 1841)(Caenogastropoda: Pleuroceridae) is a widespread freshwater snail endemic to the Interior Highlands. It is the only member of the genus in western drainages of the Mississippi River basin and has a center of distribution in Missouri and Arkansas with known western limits in southeast Kansas and Oklahoma counties bordering Missouri. In addition to *E. potosiensis potosiensis*, three subspecies have been described as probable ecophenotypes. Since pleurocerids tend to be unique by drainage and given the high instances of endemism in the Interior Highlands, it is possible that *E. potosiensis* represents multiple species. This study examines *E. potosiensis* and its subspecies in a molecular phylogenetic context using the mitochondrial gene, cytochrome oxidase *c* subunit I.

PL 06\*

**QUADRULA METANEVRA GLOCHIDIA METAMORPHOSE ON SELECT MINNOWS**

Andrea Crownhart<sup>1</sup>, Bernard Sietman<sup>1</sup>, Mark Hove<sup>2</sup> and Nissa Rudh<sup>2</sup>

<sup>1</sup>Minnesota Department of Natural Resources, 500 Lafayette Road, St. Paul, MN 55155.

<sup>2</sup>University of Minnesota, 1980 Folwell Avenue, St. Paul, MN 55108.

The monkeyface (*Quadrula metanevra*) is broadly distributed in medium and large rivers of the interior basin and highlands of eastern North America, and is classified as threatened in Minnesota and Wisconsin. Many life history details are unknown or poorly resolved; among these are the identities of glochidial hosts. The closely related rabbit's foot (*Quadrula cylindrica*), which is designated as endangered throughout its entire range, has been shown to metamorphose on various minnow species (Cyprinidae) in the laboratory. Based on these results, we tested the suitability of 18 minnow species in 11 genera, in addition to 28 non-minnow species in nine other families, as hosts for *Q. metanevra*. Glochidia of *Q. metanevra* metamorphosed on four cyprinid species in the laboratory: spotfin shiner (*Cyprinella spiloptera*), bluntnose minnow (*Pimephales notatus*), eastern blacknose dace (*Rhinichthys atratulus*), and creek chub (*Semotilus atromaculatus*). The genus *Quadrula* is composed of three monophyletic species groups: the *quadrula*, *metanevra*, and *pustulosa* species groups. The use of minnows as glochidial hosts by species in the *metanevra* group is in contrast to the *pustulosa* and *quadrula* species groups, which use catfish (Ictaluridae) as hosts. Future research will include testing host suitability of additional minnow species, and identifying juvenile mussels from naturally infested minnows.

PL 07\*

**HOST FISH DETERMINATION OF ENDANGERED SPECIES OF FRESHWATER MUSSELS IN SOUTHERN ONTARIO, CANADA**

K.M. McNichols, G.L. Mackie, and J.D. Ackerman. Department of Integrative Biology, University of Guelph, Guelph, ON, Canada, N1G 2W1.

There are approximately 54 species of freshwater mussels in Canada and 34 of these occur in Ontario. Currently nine species have been listed as endangered by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). Information about the life history of endangered mussels in Ontario is limited and is required to facilitate the recovery of these species. We identified and/or confirmed host fish for five endangered species of mussels in Ontario: northern riffleshell (*Epioblasma torulosa rangiana*), snuffbox (*Epioblasma triquetra*), kidneyshell (*Ptychobranhus fasciolaris*), round hickorynut (*Obovaria subrotunda*), and wavy-rayed lampmussel (*Lampsilis fasciola*). Four to seven fish species were tested with each mussel species. Northern riffleshell juveniles developed successfully on Iowa (5%) and Johnny (4%) darters and the mottled sculpin (87%). The logperch was confirmed as a host for the snuffbox (99%). Kidneyshell juveniles developed on Iowa (3%), Johnny (34%) and blackside darters (60%). Round hickorynut juveniles developed on the Iowa (49%) and the blackside (49%) darter. We confirmed three host fish species for the wavy-rayed lampmussel (smallmouth bass, largemouth bass, and mottled sculpin) and determined that the smallmouth bass produced a significantly higher number of juveniles (79%) than the largemouth bass (13%) and the mottled sculpin (8%). The identification and confirmation of the host fishes for these endangered species of mussels is vital to the recovery of these species. This information will also allow us to produce large numbers of juveniles in the laboratory which will lead to protection, augmentation of existing populations and reintroduction of extirpated populations in Ontario.

PL 08\*

**THE USE OF MICRO-SATELLITE ANALYSIS TO DETERMINE PATERNITY  
IN FRESHWATER MUSSELS**

Allison M. Asher<sup>1</sup>, Emy Monroe<sup>2</sup>, Jeannette Loutsch<sup>3</sup>, Dave Berg<sup>2</sup> and Alan D. Christian<sup>1,3</sup>. <sup>1</sup>Arkansas State University, Department of Environmental Science, State University, Arkansas 72467. <sup>2</sup>Department of Zoology, Miami University, Pearson Hall, Oxford, Ohio 45056. <sup>3</sup>Arkansas State University, Department of Biological Sciences, State University, Arkansas 72467.

While the mechanisms of release and uptake of sperm in freshwater mussels has been documented, the paternal contribution is unknown. The objective of this study was to determine whether single or multiple paternal contributions were exhibited within a *Villosa iris* female's brood. This study used a three step process of: 1) establishing the spatial patterns of individual male and female distributions in a stream reach, 2) non-destructively sampling male mantle tissue, collecting gravid females and harvesting glochidia from the females, and 3) determining paternal contribution to broods based on potential males in the population using micro-satellite loci. Twenty six *V. iris* were scattered throughout the 67.2 x 6.3 m surveyed bed. Within the bed, 10 males, 11 nongravid females, and 5 gravid females were observed. DNA was successfully extracted from glochidia using a modified Epicentre® Quick Extract™ solution protocol with DNA quantities ranging from 0.3 to 24.5 ng/μl. Adult DNA was extracted using a Qiagen® protocol with DNA quantities ranging from 35 to 400 ng/μl. Successful amplification of adult DNA has occurred with 8 out of 15 previously published micro-satellite primer sets, while successful amplification of glochidia occurred for 7 of these primers. Preliminary fragment analysis of gravid females and their glochidia alleles verified that mothers and their glochidia share alleles. The results of micro-satellite paternity analysis will provide a better understanding of reproductive events and will be useful for management and conservation planning.



PL 09\*

**AN EXAMINATION OF FEED QUANTITY REQUIREMENTS FOR  
RIFFLESHELL MUSSELS (*EPIOBLASMA* SPP.) HELD AT WHITE SULPHUR  
SPRINGS NATIONAL FISH HATCHERY, WEST VIRGINIA**

A. L. Bush<sup>1</sup>, R. J. Neves<sup>1</sup>, C. M. Gatenby<sup>2</sup>, and D. A. Kreeger<sup>3</sup>. <sup>1</sup>Department of Fisheries and Wildlife, Virginia Polytechnic Institute and State University, Mail Code 0321, Blacksburg, VA 24061. <sup>2</sup>White Sulphur Springs National Fish Hatchery, 400 East Main St., White Sulphur Springs, WV 24986. <sup>3</sup>Delaware Estuary Program, P.O. Box 7068, 25 State Police Drive, West Trenton, NJ 68628.

Knowledge of feed quantity requirements is essential to successful captive care of freshwater mussels. An optimum ration was determined for riffleshell mussels *Epioblasma* spp. held at White Sulphur Springs National Fish Hatchery, West Virginia. Cumberlandian combshell *E. brevidens*, oyster mussel *E. capsaeformis*, snuffbox *E. triquetra*, and northern riffleshell *E. torulosa rangiana*, along with the rainbow mussel *Villosa iris* were fed one of four rations (20,000 cells ml<sup>-1</sup>, 40,000 cells ml<sup>-1</sup>, 80,000 cells ml<sup>-1</sup>, or 120,000 cells ml<sup>-1</sup>) of the alga *Neochloris oleoabundans* for two-hour trials in June (15°C), August (18°C), and December (11°C), 2006. Measurements of filtration rate and absorption rate were used to determine milligrams of feed mussels absorbed per hour (net absorption rate). Optimum rations were based upon observed net absorption rates, and were compared among *Epioblasma* spp., *Epioblasma* vs. *Villosa*, between sexes, and among seasons. No differences were observed among *Epioblasma* spp. ( $P > .05$ ), nor between genera ( $P > .05$ ), or sexes ( $P > .05$ ). Net absorption rates in June were significantly lower than in August ( $P < .05$ ). Scheduled tests will determine net absorption rates of mussels in December. Optimum rations for *Epioblasma* spp. fed *N. oleoabundans* were 40,000-80,000 cells ml<sup>-1</sup> in June (15°C), and 80,000-120,000 cells ml<sup>-1</sup> in August (18°C).

PL 10\*

**CAN A GENERAL ORGANISMAL RESOURCE ALLOCATION THEORY  
EXPLAIN GROWTH IN FRESHWATER MUSSELS?**

Jeffrey J. Kovatch, Chris L. Burcher, and Geoffrey D. Smith. Department of Biological Sciences, Marshall University, 1 John Marshall Drive, Huntington, WV 25755.

Growth in animals has been proposed to follow general patterns across taxa over many orders of magnitude of mass. These general patterns are hypothesized to exist because incoming metabolizable energy is allocated to either tissue growth or maintenance. If average maintenance costs per cell and thus average cellular metabolic rates are constant throughout growth then total organism maintenance costs should be functions of the number of cells in the organism. Proportional allocation of energy to maintenance then becomes a function of organismal mass that will increase with age, and numerous data from many taxa support these assumptions. If sufficient data existed for changes in mussel wet-tissue mass with age then proportional allocation of energy to maintenance and growth of metabolically active tissue (i.e. wet tissue) could be estimated as a function of age. Influences of seasonal temperatures on energetic allocation patterns could also be estimated. Unfortunately, few studies have reported such data for freshwater mussels. Historically, metrics including total organism mass and shell length have commonly been reported and compared. These metrics are less useful for approximating differential energy allocation because shell mass and shell length can vary greatly within an age-class for a species; the difference may be due to concentrations of ambient minerals such as calcium. Although changes in shell size may serve as indicators of mussel health, patterns of rates of change in these shell metrics across environmental gradients are not consistent. What may be more important are rates of growth in soft tissue. Seasonal patterns of tissue growth and proportional energy allocation are demonstrated and discussed using data from the literature.

PL 11\*

## **MODELING FRESHWATER MUSSELS IN THE UPPER MISSISSIPPI RIVER**

Joseph A. Daraio<sup>1</sup>, Larry J. Weber<sup>1</sup>, and Teresa J. Newton<sup>2</sup>. <sup>1</sup>IIHR—Hydroscience and Engineering, Iowa City, IA 52242. <sup>2</sup>USGS, Upper Midwest Environmental Sciences Center, La Crosse, WI 54603.

Widespread extinctions and worldwide population declines of unionids have generated considerable research into their biology, ecology, and conservation needs. There is a need to better understand and explain the spatial distribution of mussels in rivers and streams, especially at smaller scales. A better understanding of the effects of flow hydraulics on dispersion and settlement of juvenile mussels is a vital first step in understanding the formation of mussel beds. In 2004, staff from IIHR and Delft Hydraulics developed a 2D mussel dynamics model that used an individual based approach to simulate feeding, growth, and reproduction. We expand on this previous model by creating a 3D hydrodynamics model (Freshwater Mussel Habitat Dynamics, FMHD) to address both research and management needs for freshwater mussels in the Upper Mississippi River. A 3D flow field is used in the FMHD model to simulate dispersion and settlement of juveniles with flow after release from their host fish. Preliminary results suggest that distribution patterns of juveniles are a function of flow hydraulics. These data are used in conjunction with a habitat suitability index model to determine physical features that may influence the establishment and maintenance of mussel beds. We also plan to create a sub-model that describes the spatial distribution of host fishes, and to investigate stochastic processes affecting mussels, turbulent effects on settling juveniles, and variation in the vertical locations of juveniles as they are released from the host fish.

PL 12\*

**SPATIAL DISTRIBUTION AND MICROHABITAT OF ADULT AND JUVENILE MUSSELS (BIVALVIA: UNIONIDAE) WITHIN A BED**

Eric J. Rahm<sup>1</sup> and James B. Layzer<sup>2</sup>. <sup>1</sup>Tennessee Cooperative Fishery Research Unit, Tennessee Technological University, Cookeville, TN 38501. <sup>2</sup>U.S. Geological Survey, Tennessee Cooperative Fishery Research Unit, Tennessee Technological University, Cookeville, TN 38501.

Specific environmental conditions needed for successful recruitment of freshwater mussels are poorly understood due to the difficulty in locating juvenile mussels. The objectives of our study were 1) to determine the spatial distribution of juvenile and adult mussels within the mussel bed, and 2) to determine if distributions of juveniles and adults were related to microhabitat variables. For our study we selected a 100-m long by 45-m wide section of the Green River in Kentucky. The site was divided into nine, 5 m wide strata running the length of the site. We measured mean water column velocity, near-bottom velocity, depth, and substrate roughness at 5 m intervals along transects placed at the center of each stratum. Shear stress was estimated at each habitat sampling point using 'Fleisswasserstammtisch' (FST) hemispheres. The complex hydrologic variables: Froude number, Reynolds number, and Reynolds roughness number were calculated for each habitat sampling point. A systematic sampling design with three random starts was used to determine quadrat sampling locations at the downstream boundary and 50 m upstream. A 50-m-long transect originated at each random start and a 0.25 m<sup>2</sup> quadrat sample was taken at 5 m intervals along each transect. Juveniles of *Actinonaias ligamentina*, *Elliptio dilatata*, and all mussels combined were negatively correlated with distance from the right descending bank. Density of adult *Elliptio dilatata* was negatively correlated with most habitat variables. Negative rank-order correlations were found between most habitat variables and the densities of juvenile and adult *Amblema plicata*.

PL 13\*

## **FUNCTIONAL CONNECTIVITY OF HOST FISH AMONG FRESHWATER MUSSEL COMMUNITIES**

Daelyn A. Woolnough<sup>1</sup>, Teresa J. Newton<sup>2</sup>, and John A. Downing<sup>3</sup>. <sup>1</sup>Biology Department, Trent University, Peterborough, ON K9J 7B8 Canada. <sup>2</sup>U.S. Geological Survey, Upper Midwest Environmental Sciences Center, La Crosse, WI 54603 USA. <sup>3</sup>Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA 50011 USA.

Life stages of obligate parasites, such as freshwater mussels, may be limited to certain areas. Therefore, in order for freshwater mussels to survive, their distribution must spatially and temporally overlap with their hosts. We demonstrate how the spatial patterns of freshwater mussel communities (15 species) and the host fish (35 species) for their larval stages influence connectivity between mussels and host fish across a 38 km reach of the Upper Mississippi River. Connections were measured with two methods—direct and functional connectivity. Direct connectivity is when a given mussel community is contained within the home range of its host fish; our results show that nine mussel species had large direct connectivity (>90% of communities contained within home range of hosts). Functional connectivity is a measure of the potential movement host fish provide among and between mussel communities while accounting for landscape heterogeneity. We found that mussel communities with greater functional connectivity had a better condition (i.e., high species richness, high abundance, large site size, and varied age distributions) and this relation was partially explained by the subfamilies of mussel species. These analyses suggest that host fish requirements of mussels may be partially responsible for the observed locations of native mussel populations in large rivers. Last, measures of connectivity may be used to predict the success of communities in fragmented environments.

PL 14\*

**EFFECTS OF POSITION AND ANATOMICAL STRUCTURE ON BURY TIME  
IN UNIONIDAE**

Daymon Hail, Blake Bextine, and Neil Ford. Department of Biology, University of Texas at Tyler, 3900 University Blvd., Tyler, Texas 75799.

Burial is an important part of the life cycle of bivalves. Once buried, the likelihood of survival is dramatically increased. Studies by Matteson 1955 and Smith 2001 show that even if water levels drop sharply, mussels that are buried can avoid predation, desiccation and over-heating for several days or even weeks. Therefore, this behavior was used as a baseline for mollusk survivability over a range of environmental conditions. In this experiment degree of burial, burial rates and body proportionalities were observed intra- and interspecifically for *Obliquaria reflexa*, *Truncilla truncata*, *Quadrula apiculata*, *Plectomerus dombeyanus*, *Tritogonia verrucosa*, *Quadrula mortoni*, *Lampsilis teres* and *Fusconaia askewi*. These variables were studied in their relation to the positions flat, anterior up and posterior up. With this data, a link could be established between the ability of an individual to bury itself and its species, position and body proportions. Some species, such as *Quadrula apiculata* and *Fusconaia askewi*, showed early success, being able to completely bury themselves in less than two hours. These species were, on the whole, placed in the Posterior Up position. In addition to this, they all have a body to foot ratio of approximately 2:1. This, according to observations, gives them a greater range of motion. The greater the range of motion the more likely an individual is to bury itself over a wider range of situations (positions). The results suggest that, while in captivity and when being replaced in the wild, all mussels should be oriented in the posterior up position. Although more research of this relationship is needed, this study suggests a causal relationship between position, proportion and burial.

PL 15\*

**THE ROLE OF DISTINCTIVE FRESHWATER BIVALVE COMMUNITIES  
AND THE EXOTIC ASIAN CLAM IN NUTRIENT RECYCLING ALONG THE  
CONTINUUM OF AN OZARK RIVER**

Mickey W. Matthews and Alan D. Christian. Arkansas State University, Department of Biological Sciences, State University, Arkansas, 72467.

The Buffalo River, of north Arkansas, is a 153 mile river flowing through the Ozarks to the White River. This is America's first National River with the National Park Service owning 11% of the watershed. During 2004 and 2005, 146 miles of the river were qualitatively and quantitatively surveyed. Detrended corresponded analysis of this survey data revealed 3 distinct community types: 1) *Ptychobranchnus occidentalis*, 2) *Actinonaias ligamentina*, and 3) *Cyclonaias tuberculata* that roughly represented species gradients along the river length, while *Lampsilis reeveiana* was distributed relatively evenly throughout the entire river. The objectives of this study were: 1) determine if nutrients were limiting along the river continuum 2) determine if the distinct community types recycled nutrients in similar nutrient ratios; and 3) to determine the relative role of the Asian clams in nutrient recycling. We hypothesized that nutrient recycling will differ among the community types along the river continuum. Nutrient recycling experiments, consisting of 1) 1 of the 3 community type species 2) *L. reeveiana*, and *C. fluminea*, were performed at 2 aggregates for each community type species for a total of 6 stations. *Lampsilis reeveiana* was used as a control for the river continuum effects and *C. fluminea* was compared to the native species. Nutrient limitation experiments, to determine primary producer nutrient limitation, were performed *In Situ* at all stations and were found to be co-limited for N and P ( $p \leq 0.05$ ). Data will be presented on C:N:P ratios of potential food sources, excretion, biodeposition, and body content for the 3 freshwater mussels and *Corbicula*.

PL 16\*

**A PHYSIOLOGICAL NULL APPROACH EXAMINING THE ROLE OF SPECIES INTERACTIONS ON ECOSYSTEM FUNCTION OF FRESHWATER MUSSEL COMMUNITIES**

Daniel E. Spooner and Caryn C. Vaughn. Oklahoma Biological Survey and Department of Zoology, University of Oklahoma, Norman, OK 73071.

Understanding the functional significance of communities under shifting environmental regimes is a critical research need. To date, we have shown that freshwater mussels exert strong effects on the benthic fauna by coupling energy from the water column to the sediment. The magnitude of their influence is dependent upon environmental context, with highest effects associated with low flow and warm water temperature. The physiological response of mussels to temperature is predictable and differs between species. Two species, *Actinonaias ligamentina* and *Amblema plicata* have opposing physiological and ecological responses to temperature and alternate in community dominance suggesting their relative contribution to ecological services may differ according to thermal regime. In addition, both species have also been identified as important predictors of mussel condition among species across mussel beds suggesting that species interactions (competition, facilitation) may also be important. We used recirculating streams to manipulate stream temperature (15°C, 25°C, and 35°C) and community composition to simultaneously test two hypotheses regarding the role of dominant species on ecosystem function. H<sub>1</sub>: Physiology governs performance and thus ecosystem services, H<sub>2</sub>: Species interactions govern performance and thus ecosystem services. We used laboratory derived physiology data to create performance null models predicting the ecological and physiological responses of the entire community, and relative contributions provided by each of the five component species. Our results suggest that in addition to temperature, community structure and species interactions are important factors governing energy capture, assimilation and subsequent services provided by mussel communities.



PL 17\*

**DEMOGRAPHY AND AGE-STRUCTURE OF AN ENDANGERED SPECIES:  
*POPENAIAS POPEII* IN NEW MEXICO**

Todd D. Levine<sup>1</sup>, Brian K. Lang<sup>2</sup>, and David J. Berg<sup>3</sup>. <sup>1</sup>Department of Zoology, Miami University, Oxford, OH 45056. <sup>2</sup>New Mexico Department of Game and Fish, Santa Fe, NM, 87507. <sup>3</sup>Department of Zoology, Miami University, Hamilton, OH 45011.

Long term data for freshwater mussel populations are rare, leaving substantial uncertainty about many demographic processes in these taxa. A ten-year dataset has been developed while monitoring a critically endangered species, the Texas hornshell (*Popenaias popeii*), in southeastern New Mexico. Using mark-and-recapture, we estimated survival and found it to be high (60-95%, annual apparent survival). Using program MARK, we evaluated competing models of survival and found a negative correlation of survival with water flow; 79% of mussels occupy habitat with velocities less than 0.05 m/sec that are protected by travertine shelves, root mats, and boulders. Using length as a proxy for age, we evaluated the age structure of the population. The length-frequency relationship was similar across years, with a modal length near 100 mm. Use of length-frequency distributions is predicated on a reliable relationship between age and length; therefore we created age-length curves using both annual length data from the M/R study and annual ring counts to explore this relationship. Using a VonBertalanffy growth curve, we estimated an asymptotic length near 100 mm, which corresponded to estimates derived from counted external annuli. Lengths substantially above estimated asymptotes indicate the potential for extreme longevity and indeterminate growth. Overall, these estimates and recent observations of small individuals (indicating recent recruitment) suggest that this population is currently stable. However, due to the restriction in *P. popeii*'s range, it remains vulnerable because there is little chance for recolonization in the event of an environmental catastrophe such as an exceptionally high discharge event.

PL 18\*

**CONDITION ASSESSMENT OF RELIC VALVES, AS ESTIMATORS OF TIME SINCE MORTALITY IN UNIONID BIVALVES**

Elizabeth A. Ashcraft, Jerry L. Farris, Brent L. Walker, and Jonathan D. Maul. Arkansas State University, State University, AR 72467.

Freshwater bivalve decomposition is a dynamic process requiring assessment of temporal, ecological, and environmental factors and interactions. Narrowing the range of uncertainty in estimating time since specimen death is key to utilization of relic bivalve shells as temporal indicators. By establishing a bivalve population with the same known time and method of mortality, progressive characteristics of decomposition were observed. Sequences of decompositional events were better defined than specific timelines. Bivalve decomposition was dependent upon species, sediment presence, and site-water flow. Tissue remained in association with valves following mortality, ranging from 3 to 12 days in *Corbicula fluminea*, 12 to 23 days for *Obliquaria reflexa*, and 26+ days for *Amblema plicata*. Microbial communities associated with bivalve tissue following mortality indicated an inverse relationship between distinction of microbial communities based on carbon source utilization and time since mortality. Drawings and digital photographs yielded a record of progressive changes in hinge deterioration, periostracum decomposition, and nacre condition one year following mortality. Preliminary studies on methods for evaluating long-term decomposition of internal nacre using image analysis of finely-polished thin sections provided CaCO<sub>3</sub> polymorph composition within valves. Total area percentages calculated with ESRI<sup>®</sup> ArcMap<sup>™</sup> for aragonite, drusy calcite, and silica were 38, 25, and 10%, respectively, with 27% of the thin section lost during fine polishing. X-ray diffraction identification of calcium carbonate polymorphs from various locations of nacre surface revealed aragonite, the dominant polymorph, along with calcite and vaterite. After establishing trends in bivalves with known time since mortality, reliable comparisons can be made with reference mussels to determine time since mortality for bivalves whose post-mortality time is unknown.

PL 19\*

**HIERARCHICAL ANALYSIS OF GENETIC VARIATION IN *LAMPSILIS CARDIUM*: EVALUATING GENE FLOW AND GENETIC DRIFT IN THE UPPER MISSISSIPPI RIVER**

Emy M. Monroe<sup>1</sup>, Teresa J. Newton<sup>2</sup>, and David J. Berg<sup>3</sup>. <sup>1</sup>Department of Zoology, Miami University, Oxford OH 45056. <sup>2</sup>USGS, Upper Midwest Environmental Sciences Center, La Crosse, WI 54601. <sup>3</sup>Department of Zoology, Miami University, Hamilton OH 45011.

The unique life-history of mussels and the linearity of riverine habitats provide a system in which to study the opposing effects of drift and gene flow on geographic variation in population genetic structure. Microsatellites are an ideal group of markers because they reveal fine-scale structure, and the Upper Mississippi River (UMR) provides a hierarchical system in which to work. We used *Lampsilis cardium* because it provides a relatively natural signal for an abundant and widespread species. Our objectives were to evaluate genetic structure at various spatial scales in the UMR and to infer the strength of drift and gene flow on this structure. Within the UMR, there is significant genetic variation present; heterozygosity averaged 0.82 and there were 130 alleles at 5 loci. However, this variation is not structured: analysis of molecular variance partitioned 99% of variation within populations, and  $F_{st}$  (a measure of inter-population differentiation) averaged 0.01. High gene flow was inferred from assignment tests; 82% of mussels were incorrectly assigned to their home population. Genetic distance was not correlated with geographic distance, indicating that the homogenizing effects of gene flow are greater than variation due to drift. These results suggest genetic variation is evenly distributed among populations and gene flow is amazingly high in this stretch of the UMR. Dispersal of this mussel could be due to wide-ranging, migratory fish hosts such as walleye, and the timing of glochidial release. *Lampsilis cardium* release larvae during spring floods, when fish dispersal is maximized in this large flood-plain river.

PL 20\*

**ASSESSMENT OF MITOCHONDRIA COI GENE FLOW IN *AMBLEMA PLICATA*  
IN THE OUACHITA HIGHLANDS OF SOUTHEASTERN OKLAHOMA**

Kathleen L. Reagan and Caryn C. Vaughn. Oklahoma Biological Survey and  
Department of Zoology, University of Oklahoma, Norman, OK 73019.

Appreciation of genetic diversity in unionids is essential to their preservation. Understanding how habitat perturbations, particularly those that fragment populations, affect this genetic diversity will provide information for better management of their natural habitats. We are examining genetic diversity and relatedness within a common mussel species, *Amblyma plicata*, from four rivers in the Ouachita Highlands of southeastern Oklahoma that are fragmented to varying degrees, by impoundments. We sampled *A. plicata* tissue from ten sites each in the Little, Glover, Mt. Fork and Blue Rivers. At each of ten sites, mussels were sampled from 15, randomly placed, 0.25m<sup>2</sup> quadrats. Tissue samples consisting of 20-40 µg of mantle tissue were clipped from a minimum of 30 individuals per site. A subsample of mussel individuals was taken from each site for shell thin-sectioning to determine age. The COI gene of the mitochondria will be used to examine both genetic diversity of *A. plicata* within and between sites. This will enable us to examine the impacts of impoundments on gene flow.

**POPULATION GENETIC ANALYSIS OF THE ENDANGERED CUMBERLAND COMBSHELL *EPIOBLASMA BREVIDENS*: IMPLICATIONS FOR SPECIES RECOVERY**

Nathan A. Johnson<sup>1</sup>, Jess W. Jones<sup>2</sup>, Paul J. Grobler<sup>1,3</sup>, Richard J. Neves<sup>4</sup> and Eric M. Hallerman<sup>1</sup>. <sup>1</sup>Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321. <sup>2</sup>U.S. Fish and Wildlife Service, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321. <sup>3</sup>Faculty of Natural and Agricultural Sciences, University of the Free State, Bloemfontein 9330, South Africa. <sup>4</sup>U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321.

A genetic characterization of two populations of the federally endangered Cumberlandian combshell (*Epioblasma brevidens*) was conducted in order to provide guidance for recovery planning. Twenty individuals were sampled from populations in the Clinch and Big South Fork Cumberland (BSF) rivers, TN. We sequenced a total of 1284 base-pairs (mitochondrial DNA, *ND-1* and *cytochrome-b*) and amplified 10 polymorphic microsatellite DNA loci. Analysis of molecular variance (AMOVA) for mtDNA indicated significant genetic differentiation between the two populations ( $p < 0.05$ ), with a majority of the variation residing between populations (69.27%), and less variation (30.73%) within populations. Only a single mtDNA haplotype was observed among individuals sampled from the BSF population, suggestive of a population bottleneck. Phylogenetic analysis of mtDNA sequences and population genetic analysis of DNA microsatellites ( $F_{st} = 0.10$ ,  $R_{st} = 0.11$ ) indicated that the populations were genetically diverged. Established molecular genetic criteria suggest that the investigated populations of *E. brevidens* in the Clinch and BSF rivers qualify as separate management units. Thus, we recommend that no inter-basin transfers of *E. brevidens* be made unless expressly warranted as conservation actions necessary to facilitate and ensure the stability of populations or recovery of the species. If future studies demonstrate that morphological and life history characteristics (including fish host specificity) between the two populations are inconsequential, then inter-basin transfers could be permitted.

PL 22\*

**THE ZOOGEOGRAPHIC AND MANAGEMENT IMPLICATIONS OF  
POPULATION STRUCTURE IN THE IMPERILED SNUFFBOX MUSSEL,  
*EPIOBLASMA TRIQUETRA* (BIVALVIA: UNIONIDAE)**

David Zanatta and Robert Murphy. Royal Ontario Museum, Department of Natural History, 100 Queen's Park, Toronto, ON M5S2C6, Canada.

Populations of the imperiled snuffbox mussel, *Epioblasma triquetra*, were sampled from seven localities across the central basin of North America. Samples were genotyped using a suite of 15 microsatellite DNA loci and maternal history was hypothesized using mitochondrial DNA sequences (COI). The Clinch and St. Francis Rivers' populations were quite distinct in their mtDNA. The St. Francis River's population had a unique, fixed haplotype. Among a suite of haplotypes, the population in the Clinch River had two unique haplotypes of common ancestry. The other populations were dominated by a common haplotype, which also occurred in the Clinch River's population. The microsatellite loci mirrored the results found with the mtDNA for the Clinch and St. Francis rivers. However, the microsatellites revealed much greater divergences and showed significant genetic structure between the populations in the formerly glaciated regions. Very little recent gene flow has occurred between any of populations as evidenced by high  $F_{ST}$  values and nearly perfect assignment tests. These results inferred the occurrence of three glacial refugia for *E. triquetra*: the Tennessee River (Clinch River), south of the Ozark Crest (St. Francis River), and the lower Ohio River drainage near the confluence with the Mississippi – possibly in the Meramec River drainage (Bourbeuse River). The population in the lower Ohio River was responsible for the post-glacial reinvasion into formerly glaciated regions, and likely also invaded into the upper Tennessee River drainage. The St. Francis River's population conforms to the definition of an evolutionary significant unit (ESU), and could possibly qualify as a distinct species. Artificial propagation, if necessary for this imperiled species, should not mix populations.

PL 23\*

## **DAMN THOSE DAMS – THEIR EFFECTS ON FRESHWATER MUSSELS**

Jeremy S. Tiemann, Hope R. Dodd<sup>1</sup>, Nick Owens, and David H. Wahl. Illinois Natural History Survey, 1816 S. Oak St., Champaign, IL 61820. <sup>1</sup>Current address: National Park Service, 901 S. National Ave., Springfield, MO 65804.

Five free-flowing and five impounded sites were sampled during July 2003 to test the effects of lowhead dams on habitat characteristics and freshwater mussel fauna of the Fox River in Illinois. Two habitat indices, the Qualitative Habitat Evaluation Index (QHEI) and the Stream Habitat Assessment Protocol (SHAP), were used to determine the effects of lowhead dams on habitat quality. Free-flowing sites had significantly higher scores of both QHEI and SHAP compared to impounded sites, indicating higher quality fish and invertebrate habitat. Three variables, catch-per-unit-effort (CPUE), extant species richness, and percent missing species, were calculated to establish the effects of lowhead dams on the freshwater mussel fauna. Free-flowing sites had significantly higher CPUE and extant species richness and lower percent missing species compared to impounded sites. Also examined were literature reviews and museum collection holdings to determine species distribution within the Fox River basin. These data suggest that six species (fragile papershell, *Leptodea fragilis*; pink heelsplitter, *Potamilus alatus*; pink papershell, *Potamilus ohioensis*; mapleleaf, *Quadrula quadrula*; pistolgrip, *Tritogonia verrucosa*; and fawnsfoot, *Truncilla donaciformis*) have dam-limited distributions in the basin. Our data are consistent with the hypothesis that lowhead dams can degrade riverine habitat and can have negative effects on the freshwater mussel fauna.

PL 24\*

**CONSERVATION VIA TRANSLOCATION OF FRESHWATER MUSSELS  
THREATENED BY HABITAT ALTERATION**

Jennifer Kurth<sup>1</sup>, Cynthia Loftin<sup>2</sup>, Joseph Zydlewski<sup>2</sup>, and Judith Rhymer<sup>1</sup>. <sup>1</sup>Department of Wildlife Ecology, 5755 Nutting Hall, University of Maine, Orono, ME 04469-5755. <sup>2</sup>USGS Maine Cooperative Fish and Wildlife Research Unit, 5755 Nutting Hall, University of Maine, Orono, ME 04469-5755.

Translocation of mussels from areas where habitat alterations are proposed can be an important conservation tool. The pending removal of the Fort Halifax dam on the Sebasticook River in Maine would potentially result in extensive mortality of two state-listed threatened species of mussels, the yellow lampmussel (*Lampsilis cariosa*) and the tidewater mucket (*Leptodea ochracea*) that occur in the impoundment above the dam. Our study determined the effects of within- and between-waterbody translocations on survival. In a 2004 pilot study, we translocated a co-occurring common species, the eastern lampmussel (*Lampsilis radiata radiata*), within the impoundment and to two other sites in the watershed, Unity Pond and Sandy Stream. As part of this effort, we used Passive Integrated Transponder (PIT) tags to track translocated mussels to assess the feasibility of this monitoring tool. Numbers of recaptured mussels differed among study sites; however, we found more tagged mussels with the PIT pack searches with visual confirmation (72-80%) than with visual searches alone (30-47%) at all sites. We repeated the experiment in 2005 with yellow lampmussels and tidewater muckets. We recaptured 57-90% of yellow lampmussels and 30-86% of tidewater muckets. PIT tags offer improved recapture of translocated mussels and increased accuracy of post-translocation monitoring.



**ASSESSMENT OF FRESHWATER MUSSEL RELOCATION AS A CONSERVATION STRATEGY**

Andrew J. Peck<sup>1</sup>, John L. Harris<sup>2</sup>, Jerry L. Farris<sup>1</sup>, and Alan D. Christian<sup>1,3</sup>. <sup>1</sup>Department of Environmental Sciences, Arkansas State University, State University, Arkansas 72467. <sup>2</sup>Environmental Division, Arkansas State Highway & Transportation Department, Little Rock, Arkansas. <sup>3</sup>Department of Biological Sciences, Arkansas State University, State University, Arkansas 72467.

Over the last 30 years, relocation of freshwater mussels has become an acceptable conservation strategy for impacts due to development projects such as bridge construction and dredging operations. Research has led to methodologies that effectively increased relocated mussel survivorship rates of target species from ~ 50% to ~ 90% under ideal circumstances. Previous examinations of this strategy's effectiveness have been limited to survivorship rates, but have not examined how relocation activities affect the fitness and behavioral traits of mussels. Further, recapture rates following relocations have been low for some species, making long-term assessment of this strategy difficult. Either mortality or movement may explain low recapture rates, but there is little empirical data to support either case. The Federal Highway Administration (FHWA) and Arkansas Highway and Transportation Department (AHTD) funded research to: 1) determine the success of mussel relocation efforts associated with highway construction projects by investigating survivorship, movements, mortality, fitness (i.e. condition factor), and fecundity of relocated and non-relocated adults and sub-adults; 2) determine success of mussel propagation efforts by investigating survivorship of juveniles returned to identified habitats and used for population enhancement; and 3) determine impacts at highway construction sites by comparing pre- and post-construction mussel assemblage abundance and composition, sediment deposition downstream of construction, and individual mussel fitness. This project seeks, in part, to use the data acquired to formulate a programmatic biological assessment/biological opinion streamlining initiative for that will be proposed to the USFWS by the AHTD and FHWA.

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**FACTORS POTENTIALLY AFFECTING THE REINTRODUCTION OF FRESHWATER MUSSELS (BIVALVIA: UNIONIDAE) INTO THE BUTTAHATCHEE RIVER SYSTEM, ALABAMA AND MISSISSIPPI**

Stuart W. McGregor, Marlon R. Cook, and Patrick E. O'Neil. Geological Survey of Alabama, Tuscaloosa, AL, 35486.

Forty-three species freshwater mussels have been reported from the Buttahatchee River system. Among the species reported are nine federally listed species, including the only currently known population of *Epioblasma penita*. This study summarizes efforts to document the factors that might influence the reintroduction of mussels into the system. Such information as presence of potential host fishes, sediment quality, and rates and sources of sediment loading in a reach of river devoid of mussels, based on limited synoptic data from selected sites, were determined. Information on host fishes was determined from literature and museum sources. A single sample of bed sediment from the lower reach of river in Alabama was evaluated, and no elevated levels of potential toxins were detected. Data collected from nine stations on the Buttahatchee River and selected tributaries indicated that sedimentation rates in the watershed are elevated and that much of the sediment originates in the upstream portion of the watershed. Mean suspended sediment rates varied from less than 1 ton per day to more than 2,000 tons per day. Bedload transport rates varied from less than 0.5 ton per day to 157 tons per day.

PL 27

**HOW MANY ENDANGERED AND/OR ENDEMIC MOLLUSK AND FISH SPECIES ARE REQUIRED TO PROTECT GLOBALLY RARE POPULATIONS IN THE CLINCH AND POWELL RIVER DRAINAGES OF SOUTHWESTERN VIRGINIA AND EASTERN TENNESSEE????**

Steven A. Ahlstedt, P.O. Box 460, Norris, TN 37828.

The conservation of North American freshwater mussel diversity is an increasing concern among state and federal resource managers whom are responsible for the protection and management of our natural resources. In the upper Tennessee River basin, many rare and endemic mussel species are currently extinct, extirpated, or exist as isolated populations separated by reservoir impoundments. Of concern are the Clinch and Powell rivers that contain some of the last vestiges of this unique faunal group. At present, 14 federally protected mussels and 4 fish are extant in the Clinch and Powell and some exist as single populations. Another 3 mussel species found here are candidates for federal listing. No other river system in North America contains 18 extant federally protected mussel and fish species. Their continued survival is critical as seed stock for recovering those species in other rivers following pollution abatement. Unfortunately, the headwater drainages of these rivers exist in the Appalachian coal fields of southwestern Virginia. The current high price of coal and the demand for cheap energy have resulted in an increase in permit applications for re-mining areas previously mined, and new coal mines. The market price of coal does not reflect the array of external costs to society and to ecosystems associated with mining. The continued listing of species under the Endangered Species Act and the continued downward trend in mussel species diversity and densities observed for those populations in the Clinch and Powell monitored over the last 25-years are testament to the failure of enforcing existing water quality regulations under the Clean Water Act.

PL 28\*

**CUMULATIVE WATERSHED EFFECTS IN THE SOUTH FORK SPRING RIVER: HABITAT, MUSSELS, MACROINVERTEBRATES, AND FISH RESPONSE VARIABLES**

Holly C. Martin<sup>1</sup>, John L. Harris<sup>2</sup>, and Alan D. Christian<sup>1,2</sup>. <sup>1</sup>Arkansas State University, Department of Environmental Sciences, State University, Arkansas 72467. <sup>2</sup>Arkansas State University, Department of Biological Sciences, State University, Arkansas 72467.

Changes in a watershed often influence biological communities. Among the most difficult tasks in characterizing a watershed are quantifying the stream habitat and determining cumulative impacts to streams and their biota. The South Fork Spring River (SFSR) originates in southeastern Missouri and flows through the Ozark and Salem plateaus of Arkansas. The objectives of this study are to: 1) qualitatively sample the entire SFSR for mussels; 2) quantitatively sample mussels at selected sites; 3) determine water quality by sampling fish and macroinvertebrate communities at selected sites; 3) characterize and assess habitat at selected sites; 4) determine cumulative watershed effects; 5) relate the biological and habitat data to the cumulative watershed effects; and 6) propose conservation actions in the watershed to minimize suspected effects. The entire SFSR was qualitatively surveyed for mussels. Based on the qualitative survey, three sites were selected from the upper, middle, and lower portions of the SFSR for a total of nine sites. Mussel aggregations were delineated and sampled to determine population densities, species richness, and size structure. Stream habitat characterization and assessment, fish community assessment, and macroinvertebrate community assessments also were conducted at each site. A total of 22 species of mussels were recorded from the SFSR with richness ranging 2 - 12 species per site. Of the 22 species, 16 have heritage conservation ranks of S1, S2, or S3. The remainder of the objectives for this project will provide a more complete picture of stream health for the SFSR.

PL 29\*

**SPECIES AND SIZE SELECTIVE PREDATION OF FRESHWATER MUSSELS ON THE BUFFALO NATIONAL RIVER, ARKANSAS**

Raven L. Lawson<sup>1</sup>, Mickey Matthews<sup>1</sup>, Faron Usery<sup>2</sup>, Shawn Hodges<sup>2</sup>, and Alan Christian<sup>1</sup>. <sup>1</sup>Department of Biology, Arkansas State University, State University, AR 72467. <sup>2</sup>Buffalo National River, National Parks Service, Harrison, AR 72601.

Predation of freshwater mussels has been hypothesized to be selective for both species and size. The objective of this study is to determine the relationship between the species and sizes of mussels represented in middens to those found in an adjacent mussel aggregate. This study was conducted at a mussel bed and middens found at one location on the Buffalo National River, Arkansas. The aggregate was quantitatively sampled in June of 2005 as part of a larger study. Both quantitatively sampled mussels and middens were identified to species and measured for length, width, and depth. Species composition and size distributions of mussels found in the aggregate were statistically compared to those found in the middens. A total of over 1500 mussels from 17 species were collected in the middens resulting in an estimated 15.52% of the bed being predated upon. Most of the species found in middens are listed as rare to uncommon in the state of Arkansas. It was observed, that in the beginning, predators were selecting for 1 or 2 particular species, while at the same time, selecting against 5 to 8 species. As time progressed, a trend of optimal foraging for all species began to develop. This selection shifted due to a possible depletion of resources. The same was also observed in the selection of certain size classes; within the 5 species most often observed in the middens, a distinct size class was selected for each sampling date; a shift from smaller individuals to larger individuals and vice versa occurred, but differed depending on the species of mussel predated upon. We concluded that predation can have an overall impact by predated on > 11% of the bed and on the composition and size structure of a mussel aggregate via species and size selection.

PL 30\*

**AN EVALUATION OF ESTIMATORS OF MUSSEL ABUNDANCE IN A LARGE  
LOWLAND RIVER IN THE SOUTHEASTERN U.S.**

Jason R. Meador and James T. Peterson. Georgia Cooperative Fish and Wildlife Research Unit, Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30602.

Accurate population estimates are crucial for the development and facilitation of effective freshwater mussel conservation strategies. Mark-recapture designs are commonly used to estimate population parameters, but design-specific assumptions must be met to obtain reliable estimates. We evaluated the efficacy of various sampling designs and estimators for estimating the abundance of three mussel species in the Altamaha River in Georgia. We found count based indices were substantially biased by incomplete detection and temporary emigration into the substrate. Temporary emigration also affected estimates from traditional mark recapture designs. Pollock's robust design, which allows for relaxation for certain assumptions, was found to be the best estimator. Our results emphasize the importance for estimating detection and emigration of mussels rather than relying solely on raw count data or traditional capture recapture methods. We also believe that this design is well suited for freshwater mussels not specific to the Altamaha River, and encourage implementation of the design in other systems.

PL 31\*

**CHANGES IN MUSSEL COMMUNITIES OVER TIME IN THE KIAMICHI RIVER, OKLAHOMA**

Heather S. Galbraith, Daniel E. Spooner, and Caryn C. Vaughn. Department of Zoology and Oklahoma Biological Survey, University of Oklahoma, Norman, OK 73071.

Long-term datasets documenting shifts in freshwater mussel community structure are rare. We quantitatively sampled 10, long-term monitoring sites in the Kiamichi River during the summers of 2003-2005, that were originally sampled in the early 1990s. We found significant declines in species richness across all of the beds. In addition, we found that densities of both rare and common species declined substantially. We also found shifts in community composition and species dominance in many beds. Many of these changes can be attributed to human perturbations, particularly siltation from gravel mining and removal of riparian habitat, and drought. Other studies in our lab group have found that ecosystem processes performed by mussels are linearly related to mussel biomass, and that species differ in their ecological performance based on community composition and environmental gradients. Thus, the changes that we observed likely will have strong influences on stream function.

**RELATIONSHIP OF PHYSIOGRAPHY, LANDSCAPE, AND DROUGHT TO SPECIES RICHNESS AND PRESENCE OF IMPERILED FRESHWATER UNIONIDS IN THE LOWER FLINT RIVER BASIN OF GEORGIA**

Jason M. Wisniewski<sup>1</sup> and James T. Peterson<sup>2</sup>. <sup>1</sup>Georgia Department of Natural Resources, Wildlife Resources Division, Nongame Wildlife-Natural Heritage Section, Social Circle, GA 30025. <sup>2</sup>U.S. Geological Survey, Georgia Cooperative Fish and Wildlife Research Unit, Warnell School of Forest Resources, University of Georgia, Athens, GA 30602.

Freshwater unionids in the Lower Flint River Basin have been subjected to a wide array of threats that have led to precipitous declines in their species richness and abundance. Physiography, landscape, and drought are all thought to be responsible for declining welfare of mussels in the basin. We generated statistical models relating unionid species presence and richness to physiography, land use, drought, downstream link magnitude (stream size), and isolation due to impoundment. We also estimated detection probabilities for three species of special concern. Species richness was most strongly and negatively related to drought and isolation. Presence of *Elliptio purpurella* was most strongly related to link magnitude and drought while *Hamiota subangulata* was negatively related to isolation and drought. *Pleurobema pyriforme* presence was negatively related to link magnitude, isolation, and percent urban land use. Species detection probabilities for these species ranged from 0.37 for *P. pyriforme* to 0.86 for *H. subangulata*. These models provide a useful tool that can be used to identify locations within the Lower Flint River Basin that have the highest probabilities of harboring populations of rare unionids and can be used to located sites for future reintroduction or augmentation.



**GUIDELINES FOR MAINTAINING EVOLUTIONARY POTENTIAL IN UNIONID BREEDING MANAGEMENT AND SUPPLEMENTATION**

Tim King and Cheryl Morrison. USGS-BRD, Leetown Science Center, Aquatic Ecology Branch, 11649 Leetown Road, Kearneysville, WV 25430.

Conservation efforts should strive to ensure that genetic diversity is preserved to maintain the potential for future evolutionary adaptation, and intervene as little as possible when managing the complex genomes of threatened species. Above all, resource managers must avoid the attempted creation of populations of unknown ecological and evolutionary potential. However, when supplementation is deemed appropriate, those involved should exercise vigilance to avoid the pitfalls of outbreeding depression resulting from mixing divergent evolutionary lineages. Moreover, supplementing population size of historically small populations can lead to the loss of critical adaptive features including the relationship established with the parasitized host(s). These consequences can be avoided if the appropriate phylogenetic, phylogeographic, and population genetic relationships are delineated for the targeted species. Once an appropriate donor population(s) has been identified for supplementation, every precaution should be taken to minimize the effects of gene drift and inbreeding depression by providing sufficiently large effective population sizes. The ability to generate unique multilocus genotypes through surveys of highly polymorphic genetic markers (e.g., microsatellite DNA), combined with statistical tools for determining inter-individual genetic distances, relatedness coefficients, kinship coefficients, and inbreeding coefficients, provides unprecedented resolution to identify and manage genetic diversity in captive-bred populations. For example, we propose that the genetic metric (i.e., distance, relatedness, kinship) that accounts for the highest level of variation among individuals in the source population (geographic vs. genetic metrics) would be the most appropriate metric for managing the genetic diversity of the captive population. This presentation will attempt to elucidate further on this landscape genetic approach and other recommendations designed to maintain evolutionary potential in highly managed unionid species.

**PROGRESS IN FRESHWATER MUSSEL CULTIVATION AND RECOVERY AT VIRGINIA'S AQUATIC WILDLIFE CONSERVATION CENTER**

Nathan L. Eckert<sup>1</sup>, Joseph J. Ferraro<sup>1</sup>, Michael J. Pinder<sup>2</sup> and Brian T. Watson<sup>3</sup>.

<sup>1</sup>Virginia Department of Game and Inland Fisheries, 1724 Buller Hatchery Rd, Marion, Virginia 24354. Virginia Department of Game and Inland Fisheries, 2206 South Main Street, Blacksburg, Virginia, 24060. <sup>3</sup>1132 Thomas Jefferson Rd, Forest, Virginia 24551.

The Virginia Department of Game and Inland Fisheries established the Aquatic Wildlife Conservation Center (AWCC) in 1998 to recover the high number of endangered freshwater mussels in the Upper Tennessee River System of Virginia. The facility is located along the South Fork Holston River (SFHR) near Marion, Virginia. The AWCC draws water from the SFHR that passes through a 5-acre pond to increase temperature and algal productivity. Adult mussels are held in circular fiberglass tanks that allow us to provide optimal habitat conditions for each species. Thirty-seven species of freshwater mussels have been held at AWCC with 23 spawning in captivity to provide viable glochidia. Seventeen species have been propagated producing over 900,000 juveniles. A portion of juveniles are held to grow-out in a flow through system supplied with filtered river water, six species have been raised to over one year of age in this system. To date, we have released over 265,000 mussels ranging in age from 1 week to 6 years. In addition to mussels, the state endangered spiny riversnail, *Io fluvialis*, is raised at AWCC with over 1,100 released ranging from 3 months to two year old. These species are released in 6 designated mussel restoration reaches in the Powell, Clinch, and North Fork Holston rivers of the upper Tennessee River System of Virginia.

**THE NEED TO MONITOR CONDITION OF FRESHWATER MUSSELS HELD IN CAPTIVITY**

Matthew A. Patterson, Julie L. Devers, and Catherine M. Gatenby. White Sulphur Springs National Fish Hatchery, United States Fish and Wildlife Service, 400 E. Main Street, White Sulphur Springs, WV 24986.

With some freshwater mussel species literally on the brink of extinction, several mussel culture facilities are conducting research on captive holding technologies designed to hold broodstock as well as provide refugia from acute (toxic spills, etc...) and chronic water quality problems. Technology developed at the White Sulphur Springs National Fish Hatchery was used to monitor survival and condition of adult *Actinonaias ligamentina* and *Elliptio dilatata* held in captivity for one year. Mussels were held in three treatments (100% spring water change 3 times per week, 50/50 spring and pond water change 3 times per week, and 100% pond water change 3 times per week) and fed a tri-algal diet (*Bracteacoccus grandis*, *Phaeodactylum tricornutum*, and *Oocystis polymorpha*) at a constant rate ( $2 \text{ mg dry weight} \cdot \text{L}^{-1}$ ) using an automated feeding system. Survival of *A. ligamentina* and *E. dilatata* at the end of one year was 100% in all treatments. However, only the *A. ligamentina* held in the 100% pond water treatment maintained condition throughout the year. The remaining treatments showed gradual declines in condition over time. This data suggest that survival alone is not a reliable indicator of mussel condition for any given captive holding system. Unfortunately, measuring condition index requires sacrifice of the animal. We strongly recommend that all facilities holding adult freshwater mussels either 1) hold surrogate common species that can be periodically sacrificed to assess the condition of mussels held in captivity or 2) develop reliable, non-lethal measures of condition that can be used on endangered species without compromising survival.

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**POND PROPAGATION OF PINK MUCKETS (*LAMPSILIS ABRUPTA*), LOW  
TECH CONSERVATION OF AN ENDANGERED SPECIES**

Don Hubbs. Tennessee Wildlife Resources Agency, P.O. Box 70, Camden, TN 38320.

Endangered mussel conservation can be enhanced through the development of less intensive propagation techniques that can be employed in natural systems. Laboratory and hatchery reared juvenile mussels require intensive feeding and maintenance inputs to achieve production. Development of effective propagation and rearing techniques requiring less manpower and fewer resources is important to under staffed, under funded state wildlife resource agencies. Small impoundments offer secure locations to conduct mussel propagation activities; however their effectiveness is yet to be demonstrated. In May 2006, two partially gravid female pink muckets were collected for propagation trials. Twenty hatchery reared fingerling largemouth bass (*Micropterus salmoides*) were used as host fish for pink mucket glochidia. LMB were exposed to the larvae, but not heavily infested with glochidia. Fish were placed 10 per cage, in a private farm pond, fish were fed and gills checked weekly. After juveniles had excysted, all fish were released on June 12. The cages were left in place for four months when they were removed on October 11, juvenile pink muckets (mussels were 18 to 27 mm), were recovered.

**ENVIRONMENTAL OCCURRENCE OF FLUOXETINE AND ITS EFFECTS ON FRESHWATER MUSSEL REPRODUCTION**

Robert Bringolf<sup>1</sup>, Rebecca M. Heltsley<sup>2</sup>, Chris Eads<sup>3</sup>, Teresa J. Newton<sup>4</sup>, Steve Fraley<sup>5</sup>, Damian Shea<sup>1</sup>, and W. Gregory Cope<sup>1</sup>. <sup>1</sup>Department of Environmental and Molecular Toxicology, North Carolina State University, Raleigh, NC 27695-7633. <sup>2</sup>National Institute of Standards and Technology, Hollings Marine Laboratory, Charleston, SC. <sup>3</sup>College of Veterinary Medicine, North Carolina State University, Raleigh, NC. <sup>4</sup>U.S. Geological Survey, La Crosse, WI. <sup>5</sup>North Carolina Wildlife Resources Commission, Clyde, NC.

Pharmaceuticals are designed with the intent of acting on a biochemical pathway in living organisms. Therefore, it is not surprising that heightened concern was raised when published reports documented the presence of pharmacologically active compounds in surface waters. Though most pharmaceuticals are not likely to accumulate to high concentrations in tissues, they are continually released at low levels and may be exerting effects on non-target aquatic organisms. Of particular concern are the anti-depressant drugs that exert their effects by manipulating levels of the neurotransmitter serotonin, an important modulator of reproduction in fish and bivalves. Previous studies have demonstrated that serotonin and anti-depressant drugs can be used to manipulate spawning in bivalves. The goals of this study were 1) to determine the reproductive effects of fluoxetine, a commonly prescribed antidepressant, on native mussels and 2) to couple laboratory results with measured environmental concentrations of fluoxetine in a municipal wastewater effluent. We exposed gravid female *Elliptio complanata* to a range of fluoxetine concentrations including low, environmentally-relevant levels. Endpoints were time to release of glochidia and viability of released glochidia. Additionally, effects of fluoxetine on mantle lure display behavior of gravid *Lampsilis cardium* and *L. fasciola* were determined. Display behaviors were categorized and recorded at intervals over 7 d. Finally, concentrations of fluoxetine and other anti-depressant drugs were measured by LC-MS-MS in water, passive sampling devices, sediment, and mussel tissue associated with a municipal wastewater effluent. A summary of the reproductive effects of fluoxetine on freshwater mussels and measured environmental concentrations will be presented.

**A COMPREHENSIVE ASSESSMENT OF THE HAZARDS OF CURRENT USE PESTICIDES TO NATIVE FRESHWATER MUSSELS**

Robert Bringolf<sup>1</sup>, Shad Mosher<sup>1</sup>, Peter Lazaro<sup>1</sup>, Chris Eads<sup>2</sup>, Chris Barnhart<sup>3</sup>, Damian Shea<sup>1</sup>, and Greg Cope<sup>1</sup>. <sup>1</sup>Department of Environmental and Molecular Toxicology, North Carolina State University, Raleigh, NC 27695. <sup>2</sup>College of Veterinary Medicine, North Carolina State University, Raleigh, NC 27606. <sup>3</sup>Department of Biology, Missouri State University, Springfield, MO 65804.

Native freshwater mussels (family Unionidae) are among the most imperiled faunal groups in North America. Numerous stressors, including pesticides, have been implicated in the widespread decline of freshwater mussels, yet the effects of pesticides on native mussels are largely unknown. Timing of pesticide application combined with the unique life history and reproductive strategy of mussels makes them susceptible to pesticide exposure at all life stages. Objectives of this study were to 1) determine the acute toxicity of technical grade pesticides to early life stages of freshwater mussels, 2) compare the acute and chronic toxicity of technical grade pesticides to early life stages of freshwater mussels with acute and chronic toxicity of pesticide formulations, and 3) determine the toxicity of pesticide formulations to adult mussels. We performed 73 standardized acute (glochidia, juveniles) and 15 chronic (juveniles, adults) toxicity tests with current use technical grade herbicides, insecticides, fungicides and commercial herbicide and insecticide formulations. Survival (acute and chronic tests) and growth (chronic tests) were assessed. Exposure concentrations of test chemicals were verified in water samples from at least 3 pesticide treatment levels in each toxicity test. A total of 7 species of glochidia, 4 species of juveniles, and 1 species of adults were tested; not all pesticides were tested with each species and life stage. A summary of toxicity test results will be presented.

**ASSESSING CONTAMINANT SENSITIVITY OF EARLY LIFE STAGES OF FRESHWATER MUSSELS**

Ning Wang<sup>1</sup>, Christopher G. Ingersoll<sup>1</sup>, F. James Dwyer<sup>2</sup>, Andy D. Roberts<sup>2</sup>, Tom Augspurger<sup>3</sup>, Cynthia M. Kane<sup>4</sup>, Richard J. Neves<sup>5</sup>, and M. Chris Barnhart<sup>6</sup>. <sup>1</sup>U.S. Geological Survey, Columbia, MO 65201. <sup>2</sup>U.S. Fish and Wildlife Service, Columbia, MO 65203. <sup>3</sup>U.S. Fish and Wildlife Service, Raleigh, NC 27636. <sup>4</sup>U.S. Fish and Wildlife Service, Gloucester, VA 23061. <sup>5</sup>U.S. Geological Survey, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061. <sup>6</sup>Department of Biology, Missouri State University, Springfield, MO 65897.

A series of acute and chronic early life stage toxicity tests were conducted with up to 11 mussel species and 6 toxicants to determine their relative sensitivity compared to commonly tested surrogate aquatic fish and invertebrates. All tests were conducted following methods described in the recently approved ASTM International *Standard Guide for Conducting Laboratory Toxicity Tests with Freshwater Mussels (E2455-06)*. Median effective concentrations (EC50s) for glochidia (24 or 48-h exposures) and newly-transformed juvenile mussels (96-h exposures) were generally lower than those for the surrogate fish, daphnids, or amphipods. The acute EC50s for mussels were above the current U.S. EPA ambient water quality criteria (WQC) for lead, zinc, cadmium, and chlorine, but were at or below the WQC for copper and ammonia. Chronic values (geometric mean of the no-observed-effect concentration and the lowest-observed-effect concentration) derived for survival and growth in 28-d chronic toxicity tests with 2-month-old mussels were above the chronic WQC for lead and cadmium, but were at or below the WQC for copper, zinc, and total ammonia. These studies demonstrate that (1) early life stages of mussels are acutely more sensitive to copper or ammonia compared to commonly tested organisms, and (2) the current WQC may adequately protect mussels from chlorine, lead, or cadmium exposures; however, the WQC may not be protective of mussels exposed to copper, ammonia, or zinc.

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**DETERMINATION OF PRIORITY SITES REQUIRING IMPROVED  
PROTECTIVE MEASURES FOR TRANSPORTATION-RELATED  
HAZARDOUS MATERIALS SPILLS**

Braven Beaty and Angela Watland. The Nature Conservancy, Clinch Valley Program, Abingdon, VA 24210.

Hazardous material spills due to transportation accidents have been detrimental to freshwater mussel populations, including federally-endangered species, in the Clinch and Powell river watersheds of Virginia and Tennessee. An analysis was necessary to identify key locations where transportation-related spills are most likely to occur in close proximity to mussel concentration sites and result in adverse impacts. Because such information can be used to direct strategies that reduce accident probabilities and/or minimize adverse impacts from spills, this assessment is of interest to several organizations, including the Virginia Hazardous Materials Response Program, local volunteer fire departments (first responders), and the Upper Tennessee River Roundtable (environmental organization). Using spatially-related traffic accident data, obtained from Virginia Department of Transportation, we conducted a GIS analysis to investigate the spatial correlation between vehicle accidents, particularly those involving trucks, and mussel concentration sites in the Clinch River basin. Specific road parameters were analyzed to further identify priority locations of accidental spill risk. Parameters investigated include: accident frequency, road class, slope analysis, distance to nearest surface stream, distance from mussel concentration site, and distance from appropriately equipped first responders. The results will be shared with first responders and regional hazardous materials response teams to better inform accidental spill response needs for both equipment and training. In addition, the results will be shared with Virginia Department of Transportation and other partners to encourage additional resources for implementation of protective measures at these key “high risk” locations.



**PHYLOGENETIC ANALYSES OF GENDER-ASSOCIATED MTDNA AND THE EVOLUTION OF MANTLE LURES IN AMBLEMINE BIVALVES (UNIONOIDEA: AMBLEMINEAE)**

J. M. Walker<sup>1</sup>, E. G. Chapman<sup>2</sup>, A. E. Bogan<sup>3</sup>, D. Campbell<sup>4</sup>, A. Christian<sup>5</sup>, J. Curole<sup>6</sup>, M. Davis<sup>7</sup>, J. Harris<sup>5</sup>, M. Hove<sup>8</sup>, B. Sietman<sup>7</sup>, G. T. Watters<sup>9</sup>, and W. R. Hoeh<sup>2</sup>.

<sup>1</sup>University of Southern Mississippi, Long Beach, MS 39560. <sup>2</sup>Kent State University, Kent, OH 44242. <sup>3</sup>North Carolina Museum of Natural Sciences, Raleigh, NC 27607.

<sup>4</sup>University of Alabama, Tuscaloosa, AL 35487. <sup>5</sup>Arkansas State University, State University, AR 72467. <sup>6</sup>University of Southern California, Los Angeles, CA 90089.

<sup>7</sup>Minnesota Department of Natural Resources, St. Paul, MN 55155. <sup>8</sup>University of Minnesota, St. Paul, MN 55108. <sup>9</sup>The Ohio State University Museum of Biological Diversity, Columbus, OH 43212.

Freshwater bivalves in the superfamily Unionoidea possess distinct male(M)- and female(F)-transmitted mtDNAs. The former evolves independently of and at a significantly faster rate than the latter. Thus, population genetic and phylogenetic analyses of M sequences facilitate the generation of independent estimates of genetic variation and evolutionary relationships which are often more robust than those provided by analyses of F sequences alone. This group of bivalves is highly imperiled with most members possessing larval stages that are obligate parasites on fish. We investigated the evolution of fish host attracting structures (mantle lures) using the cytochrome *c* oxidase I and II genes from both M- and F-transmitted mt genomes. Analyses of sequences representing 38 genera and 52 species indicated that there have been at least two losses of mantle lures within the group. Conservation of these bivalves can be facilitated with further knowledge of the fish hosts utilized by each species.

**PHYLOGEOGRAPHIC DISCONTINUITY IN THE ENDANGERED DWARF WEDGEMUSSEL (*ALASMIDONTA HETERODON*)**

Tim King<sup>1</sup>, Kristine Shaw<sup>2</sup>, Michael Eackles<sup>1</sup>, Cheryl Morrison<sup>1</sup>, and Susanna von Oettingen<sup>3</sup>. <sup>1</sup>USGS-BRD, Leetown Science Center, Aquatic Ecology Branch, 11649 Leetown Road, Kearneysville, WV 25430. <sup>2</sup>The Pennsylvania State University, 124 Life Sciences Building, University Park, PA, 16801. <sup>3</sup>U.S. Fish and Wildlife Service, 70 Commercial Street, Suite 300, Concord, NH.

Little information exists on the relatedness among dwarf wedgemussel (*Alasmidonta heterodon*) populations within or among major river drainages throughout the species' range, or the true taxonomic status of the species. We investigated the hierarchical structure of genetic variation in this endangered unionid to allow more informed management decisions that may preserve ecological and evolutionary integrity of the species. This presentation will focus on the results of studies designed to: 1) assess the population structure among *A. heterodon* inhabiting the Delaware and Connecticut rivers using variation at microsatellite DNA; 2) determine the phylogeographic structure among populations of *A. heterodon* surveyed from five river systems using sequence variation at two mtDNA regions (COI, ND1); and 3) position the observed DNA sequence variation from *A. heterodon* in the context of differentiation observed in the genus *Alasmidonta* and the subfamily Anodontinae. Microsatellite DNA variation at 13 loci was able to delineate significant population structuring among collections within and between the Delaware and Connecticut River systems. Sequence variation detected at the mtDNA COI and NDI regions was low but consistent with nuclear DNA patterns in suggesting that *A. heterodon* consists of a series of genetically distinct populations with definable phylogeographic structure. We suggest that *A. heterodon* inhabiting each major river system and which are reproductively isolated, be treated as separate management units. Finally, additional regions of DNA are needed to shed more light on the phylogenetics of the Anodontinae to validate our findings of notable polyphyly.

**POPULATION GENETIC STRUCTURE OF THE ENDANGERED FANSHELL PEARLYMUSSEL (*CYPROGENIA STEGARIA*) IN THE OHIO AND TENNESSEE RIVER DRAINAGES**

Paul J. Grobler<sup>1,2</sup>, Jess W. Jones<sup>1,3</sup>, Nathan A. Johnson<sup>1</sup>, Richard J. Neves<sup>1,4</sup> and Eric M. Hallerman<sup>1</sup>. <sup>1</sup>Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321. <sup>2</sup>Faculty of Natural and Agricultural Sciences, University of the Free State, Bloemfontein, 9330, South Africa. <sup>3</sup>U.S. Fish and Wildlife Service, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321. <sup>4</sup>U. S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Virginia Tech, Blacksburg, VA, 24061-0321.

The fanshell pearlymussel (*Cyprogenia stegaria*) is listed as federally endangered in the U.S. and as critically endangered in the IUCN Red List. Knowledge of any population genetic differentiation would facilitate implementation of the species recovery plan. We screened 96 specimens of *C. stegaria* from the Green, Rolling Fork, Licking and Clinch rivers using eight nuclear DNA microsatellites and a mitochondrial DNA (mtDNA) marker. *Cyprogenia aberti* from the St Francis and Verdigris rivers were sampled as a reference group. Nuclear markers suggested no differentiation among *C. stegaria* populations in evolutionarily recent times. Results from mtDNA suggest limited differentiation between *C. stegaria* from the Clinch River and other populations studied, and the existence of two distinct lineages, overlapping species boundaries with *C. aberti*. Genetic diversity within populations was closely comparable in three of the *C. stegaria* populations studied, but with a historical loss of genetic diversity in the Clinch population, evident at both nuclear DNA and mtDNA markers. No population can be regarded as a unique evolutionary unit from the available results, and exclusion of any population from an overall meta-population management strategy for *C. stegaria* is not justifiable. Our results also provide motivation for further study of the phylogenetic relationship between *C. stegaria* and *C. aberti*, which may have important taxonomic and conservation implications.

**HOST SPECIFICITY AND PHYLOGENETIC RELATIONSHIPS AMONG  
*UNIONICOLA* MITES PARASITIZING FRESHWATER MUSSELS**

Dale Edwards<sup>1</sup>, Brian Ernsting<sup>1</sup>, and Malcolm Vidrine<sup>2</sup>. <sup>1</sup>Department of Biology, University of Evansville, Evansville, IN 47722. <sup>2</sup>Division of Sciences, Louisiana State University at Eunice, Eunice, LA 70535.

North American water mites of the genus *Unionicola* occur in parasitic association with sponges or mollusks during one or more stages of their life cycle. More than half of the described species parasitize freshwater mussels, living on the gills or mantle and foot of their hosts. Although the taxonomy and host records of *Unionicola* mussel-mites have been reasonably documented, the phylogeny and host specificity for the group are less well known. The objectives of this study are two-fold: 1) reconstruct evolutionary relationships among subgenera of North America *Unionicola* that parasitize freshwater mussels using morphological and DNA sequence data; and 2) address patterns of host specificity among members of the group. Parsimony analysis of 29 morphological characters and 694 bp of the mitochondrial COI gene yielded a single tree with high bootstrap support. The topology of the tree indicated 2 major clades, with subgenera that occur in association with a host's mantle tissues forming one clade and subgenera that reside in a host's gills forming the other. An examination of host specificity among these mites indicated that they are highly host specific, with most species occurring in association with 1 or 2 species of hosts. When the average values of host specificity for *Unionicola* subgenera were mapped on the phylogenetic tree for these taxa, a clade comprised of gill mites appeared to be more host specific than a clade consisting of mantle mites. Differences in specificity between the 2 lineages may reflect the long evolutionary history that gill mites have had with mussels or the intense competition among gill mites for oviposition sites within unionid mussels.

**INTRASPECIFIC POLYMORPHISM IN HOST ATTRACTING STRUCTURES AND SIMULTANEOUS HERMAPHRODITISM IN *TOXOLASMA PARVUS* (BARNES, 1823) (UNIONIDAE): ADAPTATIONS FOR COLONIZATION**

G. T. Watters<sup>1</sup>, K. F. Kuehn<sup>1</sup>, R. J. Trdan<sup>2</sup>, J. M. Walker<sup>3</sup>, and W. R. Hoeh<sup>3</sup>.

<sup>1</sup>Department of Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, OH 43212. <sup>2</sup>Department of Biology, Saginaw Valley State University, University Center, MI 48710. <sup>3</sup>Evolutionary, Population, and Systematic Biology Group, Department of Biological Sciences, Kent State University, Kent, OH 44242.

Unionoid bivalves are typically dioecious with some taxa exhibiting shell and anatomical sexual dimorphism. Morphological adaptations such as mantle lures, which facilitate the transfer of parasitic larvae from brooding parent to host, are striking in some taxa (e.g., Lampsilini). *Toxolasma parvus* (Lampsilini) has been alternatively referred to as typically hermaphroditic and without shell sexual dimorphism or dioecious and exhibiting shell sexual dimorphism. This confusion and the recent discovery that some populations of *T. parvus* lack the diagnostic characteristic of the genus (= caruncle-type lure) elicited this study into the mantle lure morphologies and genetic divergences within *T. parvus*. This study examined the shell and mantle morphologies of living and preserved museum specimens of *T. parvus* and *cox1* sequence analyses on freshly collected specimens. No shell sexual dimorphism was observed in the *T. parvus* specimens examined. Ethanol-preserved *T. parvus* individuals displayed one of three distinct mantle lure morphologies: caruncles only, mantle flaps only, or caruncles + mantle flaps. Individuals with mantle flaps were genetically identical to caruncled individuals. The distribution of the observed variation in mantle lure morphology and lack of correlated DNA sequence differentiation suggest that this variation represents an intraspecific polymorphism. The variation in mantle lure morphology and the typically hermaphroditic mating system of *T. parvus* may facilitate the colonization of new habitats.

**A FISHERIES-BASED APPROACH TO POPULATION DEMOGRAPHY OF AN ENDANGERED FRESHWATER MUSSEL**

Karen Herrington<sup>1</sup>, Jerry Ziewitz<sup>1</sup>, and Steven Herrington<sup>2</sup>. <sup>1</sup>U.S. Fish and Wildlife Service, 1601 Balboa Ave, Panama City, FL. <sup>2</sup>The Nature Conservancy, Northwest Florida Program, P. O. Box 393, Bristol, FL 32321-0393.

Catch-curve regressions are a common tool of fisheries managers. Using length data and length-at-age relationships, catch-curves provide estimates of total annual mortality, survival, and year-class strength. Such demographic information is essential to understanding freshwater mussel populations as well; however, we could find no studies that have applied catch-curve analyses to this faunal group. As for many freshwater mussel species, little demographic information is available for the federally endangered fat threeridge (*Amblema neislerii*). To address this information need, we applied catch-curve regressions to data collected from a fat threeridge population in the Apalachicola River, FL. We collected freshly-dead shells of various sizes and aged them via examination of internal annuli by shell thin-sectioning. Ages ranged from three to 32 years. A von Bertalanffy growth equation fitted to the known length-at-age data was statistically significant ( $R^2 = 0.98$ ;  $p < 0.0001$ ) and was used to predict age from a larger length-only data set. Number-at-age data from several sample locations indicated that the fat threeridge exhibited a relatively stable age-structure. Weighted catch-curve analyses showed that the population's annual mortality rate was about 18%, with an average 82% survival rate between year classes. Strong and weak year classes were evident in roughly equal proportion, suggesting moderately variable recruitment over time. These traditional fisheries methods can be useful to malacologists and managers because only a single large sample of mussels is necessary. We believe catch-curves hold promise for much wider application in freshwater mussel research and management.

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**USE OF MICROHABITAT PATCHES BY FRESHWATER MUSSELS IN TWO TRIBUTARIES OF THE TENNESSEE RIVER SYSTEM AND RELEVANCE FOR TAILWATER MANAGEMENT**

Brett J. K. Ostby and Richard J. Neves. Freshwater Mollusk Conservation Center, Department of Fisheries and Wildlife Sciences, Virginia Tech University, Blacksburg, VA 24061.

During normal flow conditions in late spring and summer of 2003, 2004, and 2005, we measured several microhabitat-scale metrics and sampled mussels in six reaches of the unregulated Clinch River (Virginia and Tennessee). We observed that the occurrence of five species was positively associated with flow velocity, shear stress, and negatively associated with the degree of substrate embeddedness. These observations were used by the Tennessee Valley Authority (TVA) to assess whether minimum flow discharges in dam tailwaters replicate flow conditions known to support mussels in an unregulated system. We suspected that habitat use by mussels in the Clinch would not represent such use throughout the Tennessee River system; therefore, we conducted a similar study in two reaches of the Duck River, Tennessee in 2005 and 2006. Preliminary analysis demonstrated that the nature of relationships among habitat metrics and mussel occurrence differ between the rivers. For example, the Clinch population of *Epioblasma capsaeformis* is found in the faster flows, but the Duck population of this species (newly described as *E. ahlstedti*) is most abundant in intermediate flows. In the Duck River, we also observed at least one species (*Villosa taeniata*) that was more common in slower flows, whereas mussels were rare in slow flow habitats of the Clinch River. We discuss hypotheses for these differences and implications for management.

**QUANTIFYING BIOLOGICAL PARAMETERS OF NORTHERN RIFFLESHELL, *EPIOBLASMA TORULOSA RANGIANA*, IN FRENCH CREEK: ASSESSING VIABILITY AND SETTING RESTORATION BENCHMARKS FOR NEARBY WATERSHEDS**

Darran Crabtree<sup>1</sup> and Tamara Smith<sup>2</sup>. <sup>1</sup>The Nature Conservancy, French Creek Project, Allegheny College, Meadville, PA 16335. <sup>2</sup>Pennsylvania Natural Heritage Program, Northwest Field Station, Union City, PA 16438.

To understand the effects of actions taken to protect or enhance populations of rare mussels it is necessary to have baseline information on the current status of populations. We conducted quantitative, whole-river surveys in French Creek to establish the current viability of northern riffleshell (*Epioblasma torulosa rangiana*), a critically imperiled freshwater mussel, and our results may be used to set restoration goals for other rivers. Viability is a poorly understood concept for freshwater mussels so we use a multi-measure approach from both whole-river and site-level scales. At the whole-river scale, longitudinal distribution and population abundance are compared to the dominant species (*Actinonaias ligamentina*). At site-level scale, we used data from the 3 highest density sites to estimate age and sex distributions, mean annual survivorship, and instantaneous mortality. *E. t. rangiana* was distributed unevenly throughout the creek (bimodal pattern in 11 of 25 sites), and no animals were found in the upper third of the creek. At sites containing *E. t. rangiana*, site-specific densities ranged from 0.009 – 6.500 m<sup>-2</sup>. Maximum age of *E. t. rangiana* ranged from 7 – 10 years at three sites. Mean annual adult survivorships ranged from 0.514 to 0.698. Age distributions implied a high rate of mortality during early life followed by a late juvenile and adult stage with low mortality, and finally a senescence phase of high mortality. We believe that these biological attributes of riffleshell are important benchmarks for setting restoration goals in systems that share a similar biogeography to French Creek but whose fauna has been depleted.



**APPALACHIAN ELKTOE, *ALASMIDONTA RAVENELIANA* (LEA 1834):  
STATUS AND PROGRESS TOWARD RECOVERY OBJECTIVES**

Stephen J. Fraley<sup>1</sup> and John A. Fridell<sup>2</sup>. <sup>1</sup>North Carolina Wildlife Resources Commission, 50 Trillium Way, Clyde, NC 28721. <sup>2</sup>US Fish and Wildlife Service, 160 Zillicoa St., Asheville, NC 28801.

The endangered Appalachian elktoe is a Cumberlandian endemic species found only in the upper French Broad and Little Tennessee river systems in North Carolina and Tennessee. When federally listed in 1994, two populations were known. Five more populations were discovered in North Carolina in 1996-2002. Critical Habitat was designated in 2002 and includes the distribution of six populations as known at that time. Until recently, five populations were believed to be either stable (Little Tennessee, Tuckaseegee, Upper Pigeon) or expanding (upper Nolichucky, Little). The status of small populations in Cheoah and Mills rivers is unknown. Progress has been made toward recovery objectives. Recent studies have improved knowledge of life history and environmental toxicology. Captive propagation experiments are in progress with surrogate congeners (*A. varicosa*, *A. viridis*). A large parcel in the Little Tennessee River watershed was protected by a cooperative land acquisition in 2003, and habitat improvements are in progress as a result of two recent FERC hydropower relicensing agreements. However, there have been recent set-backs. Severe floods in 2004 affected populations range-wide. Since 2004, die-offs of undetermined cause have reduced CPUE at monitoring sites by as much as 80% in what was the most abundant population (Little Tennessee). Development is rapidly increasing across the species' range. A 2006 Five-Year Review assessed overall status as mixed and no change in listing was recommended. Priority recovery actions for the next five years include: determine cause(s) of declines, support improved water quality standards and habitat protection/restoration, range-wide population genetics study, and Cheoah R. augmentation plan.

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**ALASMIDONTA MARGINATA FROM THE SOUTH FORK OF THE ZUMBRO RIVER, ROCHESTER, MINNESOTA**

Marian E. Havlik. Malacological Consultants, La Crosse, WI 54601-4969.

Prior to construction of a new forcemain, six sites were surveyed in 2005 within two miles of the South Fork of the Zumbro River, downstream of Silver Lake Dam, Rochester, Minnesota. Each site was sampled from 30 m upstream to 61 m downstream of the proposed pipe centerlines. River widths ranged from 15-46 m, while depths were mostly 1m or less. The substrata were mostly cobble and gravel, with sand increasing as we moved downstream. Mussel translocations were done in 2006 at four sites chosen for forcemain crossings. Although densities were low at all sites, nearly 20.3% of the mussels were living *Alasmidonta marginata*, a state endangered species, likely the highest concentration in Minnesota. All living mussels were collected, including *Lasmigona costata* (2.0%) and *L. compressa* (1.8%), both Minnesota special concern species. There was modest reproduction of most of the nine living species. Minnesota listed mussels (24.1%) were externally aged, measured for length and height, and etched with unique numbers on both anterior valves, while common mussels were hash-marked on both anterior valves. Over 600 mussels were translocated upstream, between Site 1 and Silver Lake Dam: 388 (18.6% T & E mussels) from Site 1, the largest area; 136 (44.8% T & E mussels) from Site 2, while 46 (10.9% T & E mussels), and 32 mussels (21.9% T & E mussels) were found at Sites 3 and 4 respectively. At least nine fish species were identified from Site 1, the most productive mussel area. In September 2006 gravid *A. marginata* were collected for host fish studies. Follow-up studies are required for two years, to determine survival.

**USING LONG TERM MONITORING OF MUSSEL COMMUNITIES AS A TOOL FOR RESOURCE MANAGEMENT IN THE TENNESSEE RIVER: PART I**

Chad E. Lewis<sup>1</sup>, James B. Sickel<sup>2</sup>, and Richard N. Tippit<sup>3</sup>. <sup>1</sup>Mainstream Commercial Divers, Inc., Murray, KY 42071. <sup>2</sup>Department of Biological Sciences, Murray State University, Murray, KY 42071. <sup>3</sup>U.S. Army Engineer District, Nashville, P.O. Box 1070, Nashville, TN 37202.

**Comment [adc1]:** This is a two part talk, with Jim Sickel giving the second and asked to be back to back, but at least this have this one go first

In conjunction with the US Army Corps of Engineer's construction of a new navigation lock at Kentucky Dam in Livingston County, Kentucky, Tennessee River Mile 22.4, a long term mussel monitoring program was initiated in 2003. The purpose was to establish a baseline data set so that changes in the mussel community downstream from the dam could be monitored during construction and later operation of the new lock. Mussels were collected from four sites, including two experimental sites and two reference sites. Within each site, eighty 0.25 m<sup>2</sup> quadrats were sampled by excavation to a depth of 15 cm and screening of sediment. Substrate samples were washed through sieves down to 0.64 cm, and all mussels were identified, weighed (0.1g), measured (shell length to 0.1 mm), and aged (by ring count). A baseline of habitat conditions was documented by mapping the substrate topography using survey quality hydrographic equipment that was sufficient so that future scour or deposition could be defined in terms meaningful to the mussel community and the maintenance of high quality habitat. In addition to the hydrographic survey, six substrate samples were collected within each of the four mussel sampling sites to document the initial sediment composition in terms of grain size. The combination of the baseline mussel and habitat data will be used for future comparisons to document positive or negative changes in the mussel community and habitat conditions, whether the changes occur naturally or as a result of environmental disturbance.

**CONUNDRUMS OF MUSSEL MONITORING REVISITED – AGAIN:  
KENTUCKY DAM TAILWATER PROJECT**

James B. Sickel<sup>1</sup>, Chad E. Lewis<sup>2</sup>, and Richard N. Tippit<sup>3</sup>. <sup>1</sup>Department of Biological Sciences, Murray State University, Murray, KY 42071. <sup>2</sup>Mainstream Commercial Divers, Inc., Murray, KY 42071. <sup>3</sup>U.S. Army Engineer District, Nashville, P.O. Box 1070, Nashville, TN 37202.

Monitoring mussel communities to detect environmental impact provides opportunities to learn more about community interactions but is fraught with statistical conundrums. Much information is available on sampling methods and data analysis, yet no consensus exists regarding which methods are best to detect change in mussel communities or what change is even significant – ecologically or statistically. Data collected from four sites in 2003 and 2005, Tennessee River, examine community structure, and attempt to explain observed differences using both parametric and nonparametric statistics. Sites 1 and 2 are immediately downstream from Kentucky Dam and experienced the least change. Sites 3 and 4, the reference sites, are located far enough downstream to be unaffected by direct effects of the new lock. Site 3 showed extreme change, probably caused by loss of young *Fusconaia ebena* perhaps to fish predation. Site 4 was the least variable, but experienced statistically significant change that was probably not biologically significant. During these pre-operational surveys, we expect to define the natural fluctuations in the mussel community such that after lock completion we can detect any major changes that may occur. Discussion includes selection of sample sites, sample size, response variables, null model, model testing, data transformation, and parametric and nonparametric inference tests such as Monte Carlo ANOVA, Mann-Whitney, ANOSIM and MDS. Multidimensional scaling is useful for visualizing multivariate community data, while ANOSIM (Analysis of Similarities) can be used for inferential tests of community data and gives similar results to ANOVA but does not possess restrictions of normality and homoscedasticity.

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**DEVELOPMENT OF A GENERIC MUSSEL MONITORING PLAN FOR SITES  
IN THE TENNESSEE RIVER DOWNSTREAM FROM KENTUCKY DAM**

John J. Jenkinson. 305 Revere Avenue, Clinton, TN 37716.

The 22 miles of the Tennessee River downstream from Kentucky Dam still supports a diverse and abundant large river mussel fauna. That same river reach also is a critical loading and fleeting area for barges being moved on the Tennessee, Cumberland, Ohio, and Mississippi rivers. After years of consultation with the U.S. Fish and Wildlife Service and the Kentucky Department of Fish and Wildlife Resources, the U.S. Army Corps of Engineers and the Tennessee Valley Authority have agreed to include a mussel monitoring commitment in new barge loading and/or fleeting permits when activities at the proposed facility could affect extensive native mussel stocks. The specific purpose of this monitoring is to determine, with 95 percent confidence, if resident native mussel density at a facility experiences a 20 percent reduction over and above any reduction at pertinent reference sites. The size and depth of the river, along with the gravel/cobble nature of the substrate, dictate that divers must be used to perform these surveys; however, choices remain with regard to the survey design and the number of samples. Transect interval data from a well-sampled site in this reach formed the basis for simulated surveys using random sampling and various types to systematic sampling designs, each over a range of sample sizes. All of the sampling designs resulted in mean abundance values that varied from run to run, but including more samples did not necessarily result in better estimates of the actual mean. In contrast, repeated sampling at essentially the same sites, accompanied by paired T-test analysis of the data, yielded consistent and extremely accurate estimates of simulated changes in mussel abundance.

**QUANTITATIVE ASSESSMENT OF A FRESHWATER MUSSEL BED IN THE GREEN RIVER, KENTUCKY**

Monte A. McGregor<sup>1</sup>, Adam C. Shepard<sup>1</sup>, Thomas Barbour<sup>2</sup>, Jacob Culp<sup>1</sup>, and Leroy Koch<sup>3</sup>. <sup>1</sup>Kentucky Department of Fish and Wildlife Resources, Center for Mollusk Conservation, Frankfort Kentucky, 40601. <sup>2</sup>Kentucky Department of Natural Resources, Frankfort, Kentucky 40601. <sup>3</sup>USFWS, Kentucky Field Office, Frankfort, Kentucky 40601.

The Green River is a large tributary of the Ohio River located in South Central and Western Kentucky and portions of Tennessee. It has historically supported 71 species of freshwater mussels and is considered the most biologically rich branch remaining of the Ohio River system. We assessed the mussel population at one mussel bed in a 45 x 100m area with the use of 1m<sup>2</sup> quadrats in the summer 2004. We divided the defined boundary area into 10 segments, each 10m long and ~ 40m wide (i.e., stream width). We subdivided each segment into 5m wide x 10m long blocks for comparison of communities within the bed. We determined species presence, abundance, and distribution patterns for all species. The site was represented by 33 species (3,169 individuals) and was dominated by the mucket, *Actinonaias ligamentina* (59.6%), purple wartyback, *Cyclonaias tuberculata* (8.1%), threeridge, *Amblema plicata* (5.8%), washboard, *Megalonaias nervosa* (4.3%), and the mapleleaf, *Quadrula metanevra* (4.2%), collectively over 82% of the individuals. Mean densities by species ranged from 0.001 to 2.92/m<sup>2</sup> and 20 species were considered rare (each less than 1% of total abundance). Average mussel density for all samples (n=1,087) was 4.90/m<sup>2</sup> with maximum densities/m<sup>2</sup> ranging from 22 to 35/m<sup>2</sup>. Mussel densities per segment increased from downstream (2.06/m<sup>2</sup>) to upstream (9.61/m<sup>2</sup>) and from left descending bank (3.20/m<sup>2</sup>) to right bank (8.96/m<sup>2</sup>) within the bed. Species richness was similar throughout the bed with most segments having more than 20 species.

**THE USE OF MARK-RECAPTURE TO UNDERSTAND SEASONAL CHANGES  
IN A MUSSEL BED**

Chris B. Eads<sup>1</sup>, Arthur E. Bogan<sup>2</sup>, and Jay F. Levine<sup>1</sup>. <sup>1</sup>North Carolina State University, College of Veterinary Medicine, Raleigh, NC 27606. <sup>2</sup>North Carolina Museum of Natural Sciences, Raleigh, NC 27607.

Because of the vertical migration and burrowing behavior of freshwater mussels, excavation of substrate is the most reliable way to obtain complete population demographics for a mussel bed; however, these techniques require significant effort and can be destructive to the habitat. Consequently, visual and tactile surveys for mussels on the sediment surface remain common. The timing and cues related to vertical migration are poorly understood, but further study of this behavior would lead to better interpretation of survey results and better advanced planning for more effective surveys. We conducted visual surveys of the sediment surface to monitor a 15-meter x 9-meter grid in a relatively diverse mussel bed in a small piedmont stream in North Carolina. From May 2005 – September 2006, we surveyed the entire grid on 14 separate occasions using a double-pass method to find as many mussels on the sediment surface as possible. Detectability estimates indicated we found an average of 90% of the mussels visible on the sediment surface at a given time. All mussels were individually marked, and we monitored length, width, height, gravity and their location in the grid. Over the 14 surveys, we found and marked a total of 1,381 individuals representing 9 species, but individual surveys yielded only 308-762 mussels representing 4-8 species. While certain seasonal effects on vertical movement were evident in the data, there were also notable differences between surveys done at the same approximate time of year in 2005 and 2006.

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**IMPACTS OF PERIODIC DROUGHTS AND WATER USE ON STREAM FLOWS AND FRESHWATER MUSSELS IN THE LOWER FLINT RIVER BASIN OF SOUTHWESTERN GEORGIA**

S.W. Golladay, T.K. Muenz, and D.W. Hicks. J.W. Jones Ecological Research Center, Rte 2 Box 2324, Newton, GA 31770.

Freshwater mussel assemblages in the Flint River Basin of Southwest Georgia are among the richest in the Coastal Plain of the Southeastern U.S. Historically, 29 species including 7 endemics occurred in the Flint Basin. Recent droughts in combination with high rates of agricultural irrigation have raised concerns about the long term viability of mussels in the region. During the most recent drought (1999-2001), mussel abundance at sites where streams ceased flowing showed significant declines (median value 80% decrease) compared to flowing sites (median value 5% increase). Riffle preferring taxa often showed the greatest declines. Generally, greatest declines in mussel abundance occurred in the mid-reaches of the major tributaries of the lower Flint River. These reaches depend on a regional aquifer system, heavily used for irrigation, to maintain baseflows. Using long-term stream flow records, we evaluated changes in regional hydrology since the development of agricultural irrigation in the mid-1970's. Median 1-day minimum flows declined from 39-46% in the period of 1975 to 2004 compared to the period of 1940 to 1974. Greatest declines in monthly mean daily flows were observed from April through August. Total annual rainfall showed no trend from 1940 through 2004. However, seasonal patterns were slightly different with winters (January – March) being slightly wetter and summers (April – June) slightly drier. We attribute altered stream flows to increased regional water demand however; the demand for water is also exacerbated by long-term variations in climate and rainfall distribution. We conclude that periodic droughts in combination with increasing pressure on the regional aquifer system appear to be a significant threat to mussel populations in the region.



**THE USE OF COTTON SWABS FOR ACQUIRING DNA FOR GENETIC ANALYSES OF FRESHWATER MUSSELS**

Joe Carney<sup>1</sup>, Renee Fratpietro<sup>2</sup>, and Steve Fratpietro<sup>2</sup>. <sup>1</sup>Department of Biology, Lakehead University, Thunder Bay Ontario P7B 5E1. <sup>2</sup>Paleo-DNA Laboratory, Lakehead University, Thunder Bay Ontario P7B 5Z5.

Genetic studies are undoubtedly useful as a source of data to investigate questions relating to freshwater mussel species identity, population structure, phylogenetic relationships, conservation, phylogeography and evolution. Most contemporary studies into the genetics of freshwater mussels obtain material for genetic analyses using mantle biopsies. Buccal swabs using sterile cotton applicators is a common method for obtaining DNA in forensic investigations. We describe the development and application of this method for use in freshwater mussel genetic studies. Swabs of mantle tissue and/or the foot and visceral mass provide sufficient genetic material for PCR amplification and subsequent sequence analyses. The method is quick and efficient in the field and requires no specialized equipment other than sterile cotton swabs. Furthermore, the method causes no apparent damage to the individual, which may be an important consideration when the target species is imperiled. Although mantle biopsies have been shown not to impair survival of the biopsied individual we believe using swabs for acquiring freshwater mussel DNA samples is an improvement over existing methods and that it should be equally applicable to other mollusk taxa.

**UNIQUE WITHIN-POPULATION GENETIC VARIATION IN THE SPECTACLECASE MUSSEL, *CUMBERLANDIA MONODONTA*: ADDITIONAL INVESTIGATION USING THE INTERNALLY TRANSCRIBED SPACER (ITS) AND ALLOZYMES**

Curt L. Elderkin<sup>1</sup>, Perian Doko<sup>1</sup>, and David J. Berg<sup>2</sup>. <sup>1</sup>Department of Biology, The College of New Jersey, Ewing, NJ 08628. <sup>2</sup>Department of Zoology, Miami University, Hamilton, OH 45011.

*Cumberlandia monodonta* is a freshwater mussel found primarily in the Mississippi River watershed. It is a candidate for the Endangered Species Act and currently listed as having a high magnitude of threat. *C. monodonta* presently occupies 20 streams in 10 states as opposed to its original range which was known to include 45 streams in 15 states. The significant decline in the species' range has caused concern for the genetic diversity of remaining *C. monodonta* populations. A previous study analyzed both within-population and among-population variation at the mitochondrial (mtDNA) COI gene and 11 allozyme loci. Extant populations were sampled from the Clinch River TN, the Gasconade River MO, and the St. Croix River in MN. The results show mtDNA in *C. monodonta* to have two distinct phylogenetic lineages. Further, individuals that were significantly different at the mtDNA locus co-occurred in all populations. However, these differences were not supported by the data from allozyme loci, which revealed relatively low variation in allele frequencies. By analyzing a second nuclear marker, the Internally Transcribed Spacer (ITS-1), for these individuals, an explanation for the unique pattern found in the mtDNA may be established. The results of the ITS locus will be compared to mtDNA and allozyme data to determine if the evolutionary pattern found at a COI is also represented in a less conserved nuclear genetic marker. The data was obtained through the use of polymerase chain reactions (PCR) followed by DNA sequencing. Though amplification of the ITS-1 has been successful in other organisms including those of the same family, Margaritiferidae, this is the first attempt at *C. monodonta*.

**POPULATION GENETIC ANALYSIS OF THE ENDANGERED ROUGH PIGTOE PEARLYMUSSEL *PLEUROBEMA PLENUM* (BIVALVIA: UNIONIDAE)**

Jess W. Jones<sup>1,2</sup>, Nathan Johnson<sup>2</sup>, Paul Grobler<sup>2,3</sup>, Richard J. Neves<sup>2,4</sup> and Eric M. Hallerman<sup>2</sup>. <sup>1</sup>U.S. Fish and Wildlife Service, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321. <sup>2</sup>Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321. <sup>3</sup>Faculty of Natural and Agricultural Sciences, University of the Free State, Bloemfontein 9330, South Africa. <sup>4</sup>U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24061-0321.

A genetic characterization of extant populations of the endangered rough pigtoe pearlymussel *Pleurobema plenum* in the Clinch River, Tennessee, and Green River, Kentucky, U.S.A., was conducted to confirm taxonomic validity and to resolve conservation issues for recovery planning. Sampled individuals from these two populations were shown to be closely related based on phylogenetic analysis of mitochondrial DNA sequences, and on analysis of variation at 9 hypervariable nuclear DNA microsatellite loci. Individuals from both populations of *P. plenum* grouped together as one monophyletic clade. No discernable differences were observed in mitochondrial DNA sequences between populations of the Clinch and Green rivers. Microsatellite loci showed slightly diverged populations based on  $F_{ST}$  and  $R_{ST}$  values, which were 0.0238 and 0.0244, respectively. Therefore, based on established molecular criteria, these populations of *P. plenum* do not warrant designation as separate taxonomic units. Additional studies should be conducted on these populations to determine if possible differences exist in life history parameters. If such biological studies were to confirm the findings of this genetics study; namely, that the two populations are one taxon, then we see no reason to restrict inter-basin transfers or restrict the mixing of individuals from these two populations into other rivers to attempt recovery of the species.

**PHYLOGEOGRAPHY AND POPULATION GENETICS FOR ENHANCED  
CONSERVATION OF THE ENDANGERED CLUBSHELL MUSSEL,  
*PLEUROBEMA CLAVA***

Cheryl L. Morrison, Tim King, Michael S. Eackles, and Rita Villela. USGS Leetown Science Center, Leetown, WV 25430.

Historically, *P. clava* was abundant throughout the Ohio River drainage, occurring in 15 river basins, including the Allegheny River in PA, which now supports the largest reproducing populations. The status and genetic connectivity among the remaining, disjunct *P. clava* populations is uncertain and several face threats to their continued existence. The occurrence of two morphologically distinguishable forms of *P. clava* in the Allegheny River and its tributaries potentially complicates conservation measures since they may represent either ecophenotypic variation or cryptic species. The genetic structure among populations and morphotypes takes on additional importance as plans for artificial propagation and supplementation of *P. clava* from the Allegheny are being formulated. We assessed population genetic structure between four Allegheny River *P. clava* populations and compared levels of divergence between populations from five of the seven states where it occurs. Non-invasive tissue samples from approximately 200 *P. clava* were analyzed. Phylogeographic analyses of mtDNA COI and ND1 sequences reveal moderately divergent haplotypes from different watersheds, however, these divergent haplotypes also co-occur and may be the signature of incomplete lineage sorting of mitochondrial DNA haplotypes. *P. oviforme*, the Tennessee clubshell, is a morphologically similar species that co-occurs with *P. clava* in the Tennessee and Cumberland Rivers in KY and IN, and has haplotypes intermediate between the two *P. clava* haplotype groups. Population genetic analysis using 13 polymorphic microsatellite markers designed for *P. clava* show significant differentiation between watersheds. Estimates of effective population sizes for Allegheny River *P. clava* populations will be discussed, along with management implications from overall results.

**POPULATION BOTTLENECK AND SELECTION IN CONTROLLED ENVIRONMENTS ALTERS GENETIC STRUCTURE OF AN ENDANGERED ISOPOD: A CAUTIONARY “TALE” FOR PROPAGATION OF FRESHWATER MUSSELS**

Brian K. Lang<sup>1</sup>, Stephen M. Shuster<sup>2</sup>, Douglas A. Kelt<sup>3</sup>. <sup>1</sup>Conservation Services Division, New Mexico Department of Game and Fish, One Wildlife Way, Santa Fe, NM, 87507, USA. <sup>2</sup> Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011-5640. <sup>3</sup> Department of Wildlife, Fish, & Conservation Biology, University of California, One Shields Avenue, Davis, CA, 95616.

Within the last 16 years, artificial propagation and culture of freshwater mussels has served a critical role in the national strategy to conserve imperiled unionids. Federal recovery plans calling for propagation of endangered species (i.e., mussels) may be subject to the Department of Interior’s Policy Regarding Controlled Propagation of Species Listed Under the Endangered Species Act. Following guidelines set forth under this policy, we conclude after 10 years of captive propagation of the endangered Socorro isopod that the combined effects of population subdivision and selection have led to rapid and striking genetic and morphological divergence from the native isopod population. Furthermore, captive propagation appears to affect the social basis of this species’ mating system. These genotypic and phenotypic changes may reflect behavioral responses to selection on body size to avoid cannibalism, and possibly adjustments to spatially altered sex ratios in artificial environments. We emphasize these empirically-derived results in the context of current and future efforts to propagate, rear, and hold freshwater mussels. Advances in culture technology have improved propagation capacity and juvenile growth; resulting in the annual release of millions of juvenile mussels in native waters. While this practice indeed has merit, artificial propagation methods seldom consider selection pressures that could influence the fitness or genetic integrity of cultured mussels, such as ecologically relevant hosts, effective host specificity among genetically distinct mussel populations, or the immunological basis for host specificity at the molecular level. Future management of freshwater mussels may benefit from closer scrutiny of the effects of culture methods.

**IDENTIFICATION OF FISH HOSTS FOR WILD POPULATIONS OF  
FRESHWATER MUSSELS USING A MOLECULAR IDENTIFICATION KEY**

Stephen Kneeland and Judith M. Rhymer. Department of Wildlife Ecology, University of Maine, Orono, ME 04469.

The yellow lampmussel (*Lampsilis cariosa*) and tidewater mucket (*Leptodea ochracea*) are listed as Threatened in Maine, and are listed as Endangered, Threatened, or of Special Concern in several states and provinces throughout their range from Nova Scotia to Georgia. Based on laboratory trials, probable host fish for the yellow lampmussel are white perch (*Morone americana*) and yellow perch (*Perca flavescens*), and for the tidewater mucket, white perch. The goal of this research was to determine if these species act as host fish in natural conditions and also to assess additional species as possible hosts by sampling naturally parasitized fish in the wild. A species-specific DNA key utilizing restriction fragment length polymorphism (RFLP) patterns of the mitochondrial ND1 gene was developed to identify glochidia attached to wild-caught fish. Naturally parasitized fish were captured at thirteen localities throughout the range of *L. cariosa* and *L. ochracea* in Maine, and 687 glochidia from 230 fish were identified with the key. Fish hosts identified under laboratory conditions were confirmed from naturally parasitized fish, however, five additional fish species were also found to be potential hosts for *L. cariosa*, and one additional species for *L. ochracea*. For both mussel species, white perch was the most commonly and abundantly infested host fish, and several fish in multiple localities were found with heavy infestations of *L. cariosa* and/or *L. ochracea* glochidia. In contrast, only one individual of each of the other species of fish, including yellow perch, was found with *L. cariosa* or *L. ochracea* glochidia. These results are crucial for understanding the complex ecological interactions between mussels and their hosts and for conservation planning.

**MUSSEL SILOS: BERNOULLI FLOW DEVICES FOR CAGING JUVENILE MUSSELS IN RIVERS**

M.C. Barnhart<sup>1</sup>, T.B. Fobian<sup>1</sup>, D.W. Whites<sup>2</sup>, and C.G. Ingersoll<sup>2</sup>. <sup>1</sup>Missouri State University, Springfield, MO 65897, <sup>2</sup>U.S. Geological Survey, Columbia, MO 65201.

Field caging of juvenile mussels is potentially useful for evaluating habitat suitability and investigating pollution effects. However, it is challenging to cage tiny bivalves in rivers. Cages must prevent escape, provide adequate flow, survive floods, and be inconspicuous to avoid vandalism. Flow is a particular problem, because mesh small enough to retain juveniles presents considerable flow resistance. In the present design, flow is accomplished by the Bernoulli effect. Juveniles are contained within a cylindrical chamber capped at both ends with nylon screen. The chamber is held vertically within a portable dome-shaped housing of cast concrete. Water flow over the dome lowers pressure at the top and draws water through the chamber from below. Two pilot studies were carried out in 2006. In the first study, silos containing juvenile *Lampsilis reeveiana* were deployed in April and monitored for 8 months at one site. In the second study, silos containing *L. siliquioidea* and *L. rafinesqueana* were deployed in August and monitored for 2 months at 6 sites. Water quality variables were measured, including food availability (concentration of suspended particles 1-10 µm diameter). Juveniles were initially 3-6 mm long. In the 8 month study, overall survival was 94%. Rate of growth in shell length peaked in June at about 0.3 mm (2.3%) per day. Daily growth annuli were evident. In both studies, growth varied strongly among sites and was correlated with suspended particle concentration and flow. Of 30 silos, 2 were vandalized. Silos at 3 sites weathered a minor flood without mishap. The method shows promise for field investigations of factors affecting juvenile survival and growth.

**MAGNETIC RESONANCE IMAGING OF LIVE FRESHWATER MUSSELS  
(UNIONIDAE)**

F. Michael Holliman<sup>1,7</sup>, Denise Davis<sup>2</sup>, Arthur E. Bogan<sup>4</sup>, Thomas J. Kwak<sup>5,1,7</sup>, W. Gregory Cope<sup>6,7</sup>, Jay F. Levine<sup>3,7</sup>. <sup>1</sup>North Carolina Cooperative Fish and Wildlife Research Unit, Department of Zoology. <sup>2</sup>Magnetic Resonance Research Center, University of Pittsburgh Medical Center, 200 Lothrop Street, Pittsburgh, Pennsylvania 15213. <sup>3</sup>Department of Population Health and Pathobiology. <sup>4</sup>North Carolina Museum of Natural Sciences, 11 W. Jones Street, Raleigh, North Carolina 27601. <sup>5</sup>U.S. Geological Survey. <sup>6</sup>Department of Environmental and Molecular Toxicology. <sup>7</sup>North Carolina State University, Raleigh, NC 27695.

We examined the soft tissues Eastern *Elliptio complanata*, a mussel commonly found in freshwaters of the Atlantic slope of North America that often serves as surrogate for imperiled unionids. Data were collected on live mussels with a widely available, standard, (human) whole body, magnetic resonance imaging (MRI) system to examine the body plan, to evaluate tissue composition in the context of MRI, and to test for associations between estimated tissue volumes and a body condition index [BCI = mussel wet weight (g)/ maximum length (mm)]. Soft tissue features depicted in the profiles included the foot, stomach, intestine, anterior and posterior adductor muscles, and pericardial cavity. Body plans were consistent among the mussels. Noteworthy observations on soft tissue morphology include hemolymph filled fissures in the posterior adductor muscle, a relatively large hemolymph filled sinus located at the ventral-anterior aspect of the posterior adductor muscle, and we document segmentation of the intestine in Unionidae, a diagnostic description not reported previously. Contrast-to-noise ratios indicated good agreement among the mussels in the relaxation rates of various tissue types. Strong correlations were demonstrated between estimates of tissue volumes (mm<sup>3</sup>) taken from the images and BCI, showing promise as an index of well being. Relatively little is known of the basic biology and ecological physiology of freshwater mussels. Traditional approaches for discovering biology, tissue processes, and measuring sub-lethal physiological stress, are destructive, or invasive. Our study, the first to test scientific hypotheses related to the structure and function of freshwater mussel soft tissues using MRI, clarifies the body plan of unionid mussels and demonstrate that measures and shifts in tissue relaxation rates and organ/tissue volumes will provide insight into mussel well being.



**CAN HABITAT MAPS CREATED FROM TOW-BEHIND SONAR BE USED TO PREDICT MUSSEL POPULATIONS IN THE KANAWHA RIVER?**

Thomas G. Jones, Brian Richards, and Ralph Taylor. Department of Integrated Science and Technology, Marshall University, Huntington, WV 25755.

The study sites were located in Winfield and RC Bird pools of the Kanawha River between the confluence with the Ohio and Kanawha river mile 58. All sites were chosen using a random number generator which included 1/10 mile locations across both pools and right/left bank for the start of the 100 m transect. Any tenth mile site that included mooring facilities, Lock and Dam, etc were excluded as potential sampling sites due to safety reasons. Ten random sites were located using the total available 1/10 sites. The other ten best habitat sites were limited to those locations that had greater than 60% gravel composition based on US Army Corps substrate maps. All sites were sampled using a 100m transect anchored on the bank and extending perpendicularly into the channel. A diver would begin at the bank and search one meter wide area both upstream and downstream from the rope. Searches included disturbing the top 10cm of substrate. Each live mussel or dead shell was collected by 10 m interval. Divers also randomly sampled ten particles from each interval. The particles' intermediate axis was measured in millimeters. All live specimens were identified, imaged, and wet weighed. They were then returned to their approximate original location. The best habitat transects did not exhibit significant differences in number of species, number of individuals, or densities. The lower Kanawha River has suffered for years of extreme anthropogenic impact. The current populations of mussels are not utilizing the best available habitats but are highly fragmented across the lower river.

**EFFECTS OF TREMATODE INFESTATIONS ON GAMETOGENESIS IN FRESHWATER MUSSELS**

William F. Henley<sup>1</sup>, Julie L. Devers<sup>2</sup>, and Richard J. Neves<sup>3</sup>. <sup>1</sup>Freshwater Mollusk Conservation Center, Department of Fisheries and Wildlife Sciences, Virginia Tech, Blacksburg, VA 24060. <sup>2</sup>White Sulphur Springs National Fish Hatchery, White Sulphur Springs, WV 24986. <sup>3</sup>U. S. Geological Survey, Virginia Cooperative Fish & Wildlife Research Unit, Virginia Tech, Blacksburg, VA 24061.

Degree of trematode infestations in unionid mussels varies widely in aquatic systems of the southeastern United States, and heavy infestations have been tentatively linked to particular mussel die-offs. Recent histological evaluations have shown that 0 to 100% of mussels of multiple species were infested at sampling sites in the North Fork and Middle Fork Holston rivers, Clinch River, New River, Kentucky Lake (KL), Clear Creek, Whites Creek (WC), Duck River (DR), and Halleyville City Lake in Virginia, West Virginia, Tennessee, and Alabama. To determine the effects of infestations on gametogenesis in *Villosa iris*, *Lampsilis fasciola*, and *Quadrula pustulosa* from KL, DR, and WC, histological sections from infested (I) and non-infested (NI) mussels were evaluated using point-count volumetry to assess fractions of acinar tissues in gonads (FAT), acini containing mature or developing gametes (FAMD), and acini containing resorbing gametes (FAR). Mean FAT, FAMD, and FAR of I versus NI of *Q. pustulosa* from KL and DR were significantly different ( $p < 0.05$ ), with means for I and NI mussels of 0.25 and 0.56, 0.15 and 0.83, and 0.54 and 0.12, respectively. Mean FAT and FAMD of I versus NI specimens of *V. iris* and *L. fasciola* of WC were significantly different ( $p < 0.05$ ), with means for I and NI mussels of 0.14 and 0.41 and 0.03 and 0.48, respectively. Histological evaluations also indicate that atrophy of muscle, connective, and digestive tissues is common in infested mussels. Trematode infestations may have a significant adverse impact to local recruitment due to a reduction of gamete production and poor physiological condition in highly infested mussels.

**ZEBRA MUSSEL ERADICATION IN VIRGINIA: A 1<sup>st</sup> OPEN-WATER SUCCESS STORY**

Brian T. Watson<sup>1</sup> and Raymond T. Fernald<sup>2</sup>. <sup>1</sup>VA Dept. of Game & Inland Fisheries, 1132 Thomas Jefferson Road, Forest, Virginia, 24551. <sup>2</sup>VA Dept. of Game & Inland Fisheries, P.O. Box 11104, Richmond, Virginia 23230.

In September 2002, the Virginia Department of Game and Inland Fisheries (VDGIF) confirmed that a zebra mussel infestation was present in Millbrook Quarry, western Prince William County, documenting the first known population within the Commonwealth. Given the potential impacts if zebra mussels were to escape, VDGIF worked with federal, state, and local agencies; industry and conservation organizations; and individuals to pursue eradication. The 3½ year effort involved establishing an interagency workgroup to assess the feasibility of eradication; investigating the hydrologic, geochemical, and biological characteristics of the quarry and infestation; evaluating potential avenues for eradication; surveying nearby Broad Run, Lake Manassas, and other popular dive sites and reservoirs to ensure that zebra mussels had not escaped into other waters; issuing a Request for Proposals to eradicate the infestation; selecting a process and contractor to conduct the eradication; and surveying Broad Run for occurrence of species that might be impacted by chemical seepage from the quarry. Eradication was comprised of elevating potassium concentrations in the quarry through the introduction of potash – a commercial grade fertilizer. The quarry was injected with 174,000 gallons of potash solution (12% potassium) over a 3-week period, with a 100 ppm target concentration. Eradication was confirmed via visual confirmation by scuba divers, video documentation by robotic camera, and 100% mortality of eighty bioassays of 100 zebra mussels placed at various locations and depths throughout the quarry. In contrast, other aquatic wildlife continues to thrive in the quarry. This is the first successful eradication of a zebra mussel population from an open water body.

**UNIONID COMMUNITIES OF ONTARIO'S AUSABLE RIVER:  
RIFFLESHELLS, KIDNEYSHELLS AND SNUFFBOXES... OH MY!**

Daryl J. McGoldrick<sup>1</sup>, Shawn K. Staton<sup>2</sup>, Janice L. Metcalfe-Smith<sup>1</sup>, and Angela Baitz<sup>3</sup>.

<sup>1</sup>Environment Canada, Burlington, ON, L7R 4A6. <sup>2</sup>Fisheries and Oceans Canada, Burlington, ON, L7R 4A6. <sup>3</sup>Ausable Bayfield Conservation Authority, Exeter, ON, N0M 1S5.

The Ausable River is located in southwestern Ontario, which is the region that supports the richest unionid fauna in Canada. The nearby Sydenham River is home to 34 of Canada's 55 freshwater mussel species, including 7 species listed as Endangered under Canada's *Species at Risk Act*. Whereas the mussel community of the Sydenham River has been extensively surveyed, little historical information exists for the Ausable River. The only significant historical survey of the Ausable is that of J.D. Detweiler, who reported a mussel community of 8 species dominated by *Amblema plicata* in 1916. Two major water diversions in 1875 and 1892 completely reshaped the drainage pattern of the watershed for the purpose of improving the land for agriculture and significantly altered habitat once suitable to unionids. Impacts associated with intensive agricultural activities continue to threaten unionids. From 1998-2006, 25 sites throughout the watershed were surveyed for mussels using a combination of timed-searches and quantitative surveys with excavation. A total of 26 species were found alive or as shells during these surveys and 54% of the mussels collected were *A. plicata*. Mean unionid density was greater in the Ausable River (5.9 / m<sup>2</sup>) than the Sydenham River (4.8 / m<sup>2</sup>). The Ausable River was found to support a large reproducing population of *Ptychobranchus fasciolaris* and small but recruiting populations of *Epioblasma triquetra*, *E. torulosa rangiana* and *Lampsilis fasciola* (all listed as Endangered in Canada), with densities at some sites comparable to or greater than those found in the Sydenham River.

**A REASSESSMENT OF FRESHWATER MUSSELS IN THE ALLEGHENY RIVER: SOME SURPRISING RESULTS**

Rita Villella, USGS, Leetown Science Center, Leetown, WV 25430.

The clubshell (*Pleurobema clava*) and northern riffleshell (*Epioblasma torulosa rangiana*) were listed as endangered in 1993. According to the recovery plan, clubshell distribution in the Allegheny River was "a sparse, viable population with low numbers and a discontinuous distribution over 66+ miles." Northern riffleshell ranged "from viable to those with depressed vigor, with an overall known broken distribution of some 80 miles." These statements reflected the best available data at the time the recovery plan was written. However, with few exceptions mussel surveys have not included either adequate sampling coverage or quantitative assessments, making it difficult to draw inference about distribution or abundance. In 2002, we began a survey using two-phase sampling to estimate mussel distribution, density, and abundance within 123 river km. Of the 63 randomly-selected sites sampled to date, clubshell was found at 55 sites (87%) and northern riffleshell was found at all sites. Site-specific densities as high as 15.6 m<sup>-2</sup> and 19.5 m<sup>-2</sup> were estimated for clubshell and northern riffleshell, respectively. In the upper 52 river km, abundance estimates were 6.5 million northern riffleshell (90%CI: 4.03, 9.2 mil) and 1.1 million clubshell (90%CI: 0.05, 2.2 mil). Although the reassessment shows the Allegheny River supports a significant abundance of both species, there are no comparable quantitative assessments making interpretation tentative. While not all assessments should be re-evaluated, our results suggest some assessments of rare species should be revisited using rigorous sampling designs to estimate river-wide distribution and abundance. Though more expensive than the typical survey, a reasonable question is whether the added costs are worthwhile. We believe that for some high priority rivers rigorous sampling designs are worthwhile and, in fact, necessary to accurately assess freshwater mussel populations.

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**MUSSEL DISTRIBUTION AND STREAM HABITAT IN PATTERSON CREEK WATERSHED, GRANT AND MINERAL COUNTIES, WEST VIRGINIA**

James B. Spence. Integrated Science & Technology, Marshall University, Huntington, WV, 25755.

Three mussel species of special concern, as listed by the US Fish and Wildlife Service, have historically been found in Patterson Creek in Mineral County, West Virginia. However, environmental impacts have caused a severe decline in freshwater mussels in this stream over the past decades. This 2005 study included mussel surveys, Rosgen Level II analysis, and physical fish habitat (Hydraulic Channel Unit—HCU) mapping in order to determine if the availability of fish habitat in the upper reaches of Patterson Creek and its major tributaries influences the distribution and diversity of freshwater mussels in the main stem of Patterson Creek, and provided an update on mussel distribution and diversity. This study will be used to compare to other watersheds in a similar manner. It was determined the reaches in this study contained diverse fish habitat as demonstrated by the quality and type of HCUs. However, mussel populations continue to decline, although one live elktoe (*Alasmidonta marginata*) was found, believed to be the first observation of this species in Patterson Creek. Most of the tributaries were classified as “B” types using Rosgen (1996) and these streams appear to contain good habitat for fishes. The presence of impoundments on most of the major tributaries to Patterson Creek has likely contributed to the decline in mussel abundance and diversity. There is a need to develop hierarchical-type studies whereby particular systems or species are also viewed in terms of their hierarchical setting. This research was conducted in view of the n-dimensional hypervolume describing a species niche (Hutchinson 1957). By understanding the hierarchical setting of watersheds, better decisions can be made concerning the protection of freshwater mussel species.

**CONSERVATION AND TAXONOMIC STATUS OF FRESHWATER MUSSELS  
(FAMILY UNIONIDAE) FROM THE OGEECHEE RIVER DRAINAGE,  
GEORGIA**

J.D. Williams<sup>1</sup>, C.E. Skelton<sup>2</sup>, E.M. Schilling<sup>3</sup>, G.R. Dinkins<sup>4</sup>, and R.T. Bryant<sup>5</sup>. <sup>1</sup>4820 NW 15<sup>th</sup> Place, Gainesville, FL 32605. <sup>2</sup>Department of Biological and Environmental Sciences, Georgia College & State University, Milledgeville, GA 31061. <sup>3</sup>11931 Couch Mill Road, Knoxville, TN 37932. <sup>4</sup>Dinkins Biological Consulting, 716 West Beaver Creek Drive, Powell, TN 37849. <sup>5</sup>506 G Avenue, Carrizozo, NM 88301.

The Ogeechee River drainage is an independent Atlantic Coast drainage located entirely within the state of Georgia. Its watershed encompasses an area of approximately 13k sq. km (5k sq. miles) and flows directly into the Atlantic Ocean just south of Savannah. Approximately 95% of the drainage is developed on the Coastal Plain with the remaining 5% above the Fall Line in the Piedmont province. Between 2002 and 2004, freshwater mussels were sampled at 50 sites, including a variety of habitats, throughout the drainage. The mussel fauna of the Ogeechee River drainage appears to be represented by 16 taxa, however enumeration of the fauna is difficult due to differing taxonomic interpretations. The endangered Atlantic Pigtoe, *Fusconaia masoni* was not found during the survey. However, the Savannah Lilliput, *Toxolasma pullus*, not previously known from the Ogeechee River drainage, was collected from a single site in the river proper. Two species previously considered to be Altamaha River drainage “endemics”, the Altamaha Arcmussel, *Alasmidonta arcula* and Altamaha Slabshell, *Elliptio hopetonensis*, are recognized as occurring in Ogeechee River drainage for the first time. The mussel fauna of the Ogeechee River drainage is most similar to that of the Savannah River drainage to the north which is represented by approximately 20 species. Type specimens of the 21 nominal mussel taxa described during the 1800’s from the Ogeechee River drainage were examined and assigned to currently recognized species.

**MACROHABITAT USE BY ENDANGERED FRESHWATER MUSSELS IN THE APALACHICOLA AND LOWER CHIPOLA RIVERS IN FLORIDA AND IMPLICATIONS OF HYDROLOGIC MODIFICATIONS**

Gregory F. Zimmerman<sup>1</sup>, Michael M. Gangloff<sup>2</sup>, and James D. Williams<sup>3</sup>.

<sup>1</sup>EnviroScience, Inc. 6751 A-1 Taylor Rd. Blacklick, OH 43004. <sup>2</sup>Auburn University Museum and Natural History Learning Center, 331 Funchess Hall, Auburn University, Alabama 36849. <sup>3</sup>4820 NW 15th Place, Gainesville, FL 32605.

The Apalachicola River is the largest river in Florida and drains one of the largest basins in the Eastern Gulf Region. The Chattahoochee, Chipola, and Flint rivers in Alabama, Florida, and Georgia are all major tributaries of the Apalachicola River and all of these rivers, with the exception of the Chipola River, are regulated for water control and navigation. The Apalachicola River basin historically contained a diverse mussel (Unionidae) fauna of 34 species including 7 endemics. At least 3 of these endemics are believed to be extinct and 5 species (*Amblema neislerii* and *Pleurobema pyriforme*-Endangered, *Elliptoideus sloatianus*, *Elliptio chipolaensis*, and *Hamiota subangulata*-Threatened) are protected under the Endangered Species Act. During the fall of 2005 and 2006 we completed comprehensive surveys to assess the impacts of water level regulation under the U.S. Army Corps Interim Operating Agreement on endangered mussel populations. Unstable midchannel habitats supported few mussels. Unionids were most numerous in relatively stable, shallow habitats such as channel margins and sloughs. *Amblema neislerii* was most abundant at depths <1 m, often at densities > 5/m<sup>2</sup>. *E. sloatianus* previously occurred in similar habitats but is now limited to stable, deeper habitats. The majority of shallow, stable habitats are now dewatered during low flow periods due to geomorphic alterations of the river channel associated with dam operations. The 2006 drought resulted in mass stranding and mortality of *A. neislerii* and *E. sloatianus* along channel margins and within side channels. These results suggest that channel margin and tributary habitats are critically important to the survival of threatened and endangered mussels in the Apalachicola and lower Chipola Rivers. These populations remain highly vulnerable to river level fluctuations and habitat modification under current dam operating procedures. This system offers a challenge for cooperative adaptive management of water resources and habitat restoration between stakeholders.



**FRESHWATER MUSSELS (BIVALVIA:UNIONIDAE) OF THE SOUTH FORK  
HOLSTON RIVER, VIRGINIA: A TALE OF TRAGITY AND HOPE**

Michael J. Pinder<sup>1</sup> and Joe J. Ferraro<sup>2</sup> <sup>1</sup>2206 South Main Street, Suite C, Blacksburg,  
Virginia, 24060, <sup>2</sup>Rt. 3, Box 391, Marion, Virginia 24354

The Holston River originates in southwestern Virginia from three tributaries, the South, Middle, and North Forks. The South Fork differs from the Middle and North Forks by having low calcium-bearing geologies and reduced mussel diversity. In the South Fork Holston River (SFHR), baseline mussel data from two limited surveys in the early 1900's found 13 species including the federally endangered *Epioblasma walkeri* (Wilson and Clark, 1914). Over the proceeding 40 years, logging, industry, and mining caused drastic alterations in the watershed. As many activities ended, the Tennessee Valley Authority (TVA) completed construction of the South Fork Holston Reservoir near the Virginia/Tennessee border. Its impounded waters extended into the South Fork's confluence with the Middle Fork, blocking a potential source of mussel recolonization. Throughout the 1960's and 1970's, the TVA and the U.S. Forest Service restored abandoned mine lands in the upper watershed. By the time Stansbery and Clench (1977) conducted the first comprehensive mussel survey in 1968, most impacts were abated and water quality improved. Even so, their survey found a degraded fauna containing 60 individuals of 9 species. One species, the federally endangered *Pegias fabula* (Lea, 1838), was a new record for the drainage. We resurveyed the same sites in 2001 finding 7 species totaling 66 specimens. Little recruitment was present in the mainly senescent mussel community. To restore the fauna, the Aquatic Wildlife Conservation Center (AWCC) in Marion, Virginia has begun augmenting mussels through release of propagated juveniles and translocating adults. The AWCC has been successfully holding, propagating, and raising Tennessee River System mussels using SFHR water since 1998.

**JAMES SPINYMUSSSEL CONSERVATION PARTNERING IN VIRGINIA**

Cindy Kane, Willard Smith, John Schmerfeld, Bridgett Costanzo, Sumalee Hoskin, and Jessica Rhodes. US Fish and Wildlife Service, 6669 Short Lane, Gloucester, Virginia 23061.

Grassroots support has been critical to the success of localized freshwater mussel conservation and recovery efforts. In Virginia, conservation efforts focusing on the federally endangered James spiny mussel (*Pleurobema collina*) have moved onto private and public lands at a grassroots level. Following in the footsteps of a time proven technique of the Tennessee Valley Authority for aquatic resource surveys, the U.S. Fish and Wildlife Service, Virginia Field Office, created the James spiny mussel Recovery Action Team and set in motion coordination and partnership efforts that have paid off big in terms of species range knowledge and on the ground conservation. Working with partners, we have surveyed to determine population trends, worked to improve riparian habitat, and have augmented at least one population. Our work has expanded knowledge about the James spiny mussel range within two rivers and we have discovered three new populations within its known range. We have also learned that several populations have declined or have been extirpated, and that a few others have increased in density. We would not have this basic demographic information if not for the partnerships with other groups over the past three years. Most federally listed mussel species lack an active recovery team. Despite inadequate funding and lack of a formal team, major recovery tasks have been accomplished because of voluntary support and partnerships in on-the-ground activities. We have also conducted reviews of major developments, hydropower and transportation projects with potentially significant impacts. Confirmatory genetic work on the species throughout its range has also been completed. Our partners include other Federal and State regulatory and natural resource agencies, students, academicians, NGOs, citizens, landowners, and watershed groups.

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**TEXAS MUSSEL WATCH, A CITIZEN BASED VOLUNTEER MONITORING PROGRAM**

Marsha Elizabeth May and Lee Ann Linam. Wildlife Science, Research and Diversity Program, Texas Parks and Wildlife Department, 3000 S. IH 35, Suite 100, Austin, Texas 78704.

In 1998, Texas Mussel Watch (TMW), a Texas Parks and Wildlife Department (TPWD), Texas Nature Trackers Program, first trained a group of 20 volunteers to help TPWD document the presence or absence of freshwater mussel species in the rivers, lakes, streams, and ponds of Texas. Over 200 volunteers have participated in TMW workshops since the inception of the project, logged over 950 volunteer hours, covered over 150 sites in 18 Texas river systems in 53 counties, and recorded the presence 39 unionid species. During TMW workshops, participants are presented with information on the distribution, biology, and identification of unionids in Texas, as well as information on non-native species such as Asian clams (*Corbicula fluminea*) and zebra mussels (*Dreissena polymorpha*). Highlights include the discovery of the rare golden orb (*Quadrula aurea*) in the San Marcos River, Central Texas; the discovery of two species that had not previously been found in Austin County, the Texas lilliput (*Toxolasma texasensis*) and tapered pondhorn (*Uniomerus declivis*); and seven live Texas fawnsfoot (*Truncilla macrodon*) in the Brazos River in Washington County. TMW is reaching out to more Texas citizens through partnerships with Texas Master Naturalist Chapters and Nature Centers.

**PRIORITY WATERSHEDS FOR FRESHWATER MOLLUSKS IN THE  
SOUTHEASTERN UNITED STATES: RESULTS OF A WORKSHOP  
INCLUDING CRITERIA AND METHODS FOR PRIORITIZATION**

Rachel Muir<sup>1</sup>, Paul Johnson<sup>2</sup>, and Rita Villella Bumgardner<sup>3</sup>. <sup>1</sup>U.S. Geological Survey, 12201 Sunrise Valley Drive, Mailstop 131, Reston, VA 20192. <sup>2</sup>Alabama Department of Conservation, Route 3, Box 86, Marion, AL 36756. <sup>3</sup>Leetown Science Center, 11649 Leetown Road, Kearneysville, WV 25430.

In April, 2006 the United States Geological Survey, the Southeastern Aquatic Resources Partnership (SARP) and the Alabama Department of Conservation sponsored a workshop entitled “*Aquatic Species Recovery: Identifying Priority Watersheds of the Southeast Today for Species Restoration Tomorrow*”. Invited participants included scientists from southeastern State natural resource agencies, the USGS and other federal research and management agencies, non-government conservation organizations and industry. Workshop participants were experts in freshwater resources research and monitoring, conservation and taxonomy of southeastern aquatic fauna, and aquatic resource management. The goals of the workshop were to update distribution and trends data for key taxa, including freshwater mussels and snails, establish a repeatable methodology for identifying priority watersheds, and to identify research needed to achieve effective conservation of freshwater fauna and freshwater aquatic ecosystems of the southeastern United States. Subsequent to the Workshop we compared our results with priority species addressed in State Wildlife Action Plans (SWAPs) for the southeastern States and national and regional habitat planning for the National Fish Habitat initiative (NFHI). Using criteria established from the workshop priority watersheds were preliminarily identified for each of the southeastern States and for the region. The target users for the Priority Watersheds Workshop results are Federal, State and private agencies and organizations that plan and implement conservation actions and agencies that conduct research. Results from the workshop can serve the goals of State, Federal and private multi-jurisdictional conservation efforts and plans, including the FMCS revised national strategy.

**INVENTORY OF FRESHWATER MOLLUSKS IN THE SAVANNAH RIVER BASIN, SOUTH CAROLINA AND GEORGIA**

Lora Zimmerman<sup>1</sup>, Jim Williams<sup>2</sup>, Art Bogan<sup>3</sup>, Tim Savidge<sup>4</sup>, Tom Dickinson<sup>4</sup>, and Chris Sheats<sup>4</sup>. <sup>1</sup>USFWS, Charleston, South Carolina 29407. <sup>2</sup>USGS, Biological Resources Division, Gainesville, FL 32606. <sup>3</sup>North Carolina Museum of Natural Sciences, Raleigh, NC 27607. <sup>4</sup>The Catena Group, Hillsborough, NC 27278.

The Savannah River Basin contains the most diverse unionid fauna of all Atlantic Slope river systems in North America. Although hydrologically modified and partially channelized for navigation, there are at least six high priority species of concern in the Savannah River Basin. Most information regarding mussel occurrence in the river originates from work conducted at the Savannah River Site. Though useful, this data is limited in scope, covering only 22 of the almost 180 river miles between Augusta Shoals and the Savannah River Estuary. In 2006, the Charleston Field Office in cooperation with the Georgia Department of Natural Resources, the South Carolina Department of Natural Resources, International Paper, The Nature Conservancy, the North Carolina Museum of Natural Sciences, and volunteers completed mussel surveys of the lower and middle Savannah River. Survey objectives included documenting mussel distribution and habitat usage that will be used for prioritizing habitat and flow restoration projects. A total of 76 sites were surveyed between J. Strom Thurmond Reservoir, near Augusta, and the Savannah River Estuary. Significant findings from this effort include Brother spike (*Elliptio fraterna*), a species thought to be extirpated from most of its range and not found in the Savannah since 1972, and Altamaha arc mussel (*Alasmidonta arcula*), a declining species previously thought to be endemic to the Altamaha River Basin, Georgia. DNA verification of these and other extraordinary findings were completed by the North Carolina Museum of Natural Sciences.

**STATUS OF TEXAS UNIONIDS, INCLUDING SPECIES OF CONCERN, NEW REGULATIONS AND SANCTUARIES**

Robert G. Howells. BioStudies, 160 Bearskin Trail, Kerrville, Texas 78028.

Surveys of freshwater mussels in Texas conducted by Texas Parks and Wildlife Department from 1992 through early 2004 were updated 2004-2006 to clarify the current status of noteworthy assemblages and particularly of rare species. State Wildlife Grant funding supported field work by several academic institutions; volunteers provided input as well. Current status of mussel assemblages was mixed. Some remain in reasonably good condition, a number have been reduced in abundance and diversity or completely eliminated, and survivors were found at one site thought lost. In eastern Texas: *Fusconaia askewi*, *F. lananensis*, *Pleurobema riddellii*, *Lampsilis satura*, and *Potamilus amphichaenus* were found to be more abundant than previously thought, but *Obovaria jacksoniana* was not found in 2004-2006. In Central Texas, *L. bracteata* was present at four sites (lost from two others), *Quadrula aurea* survives at five locations, *Q. petrina* is probably present at three sites (lost from two others), *Q. houstonensis* seems nearly lost in the Colorado but living specimens were found in the central Brazos in 2006, *Truncilla monodon* was found only in limited numbers in the central Brazos, and two recently dead specimens (in 2000) of *Quincuncina mitchelli* are the only evidence of survival since 1978. In the Rio Grande, *Popenaias popeii* survives in small numbers near Laredo and between Big Bend and the Pecos River, *Potamilus metnecktayi* was found alive near the mouth of the Pecos River, a few *T. cognate* also persist near Laredo, but *Q. couchiana* has not been found alive since the 1890s and *Quincuncina mitchelli* may have vanished here even earlier. These data supported creation of new harvest regulations in 2006, including redefining no-harvest sanctuaries.

**FRESHWATER MUSSELS OF THE LOWER MISSISSIPPI RIVER**

Paul Hartfield. U.S. Fish and Wildlife Service, Jackson, MS, 39041.

Although alluvial plain tributaries of the lower Mississippi River support a rich assemblage of freshwater mussel species, the river channel proper has historically been considered relatively depauperate. High bedload, channel erosion and instability, pollution, and river engineering have been identified as possible limiting factors to the fauna by various authors. Over the past three years, an almost 300 mile reach of the main channel between Mississippi River Mile 425-705 was searched for freshwater mussels. Searches were confined to the bankful channel, but conducted during low flow periods. Areas searched included the main channel, and secondary channels associated with islands and dike fields, but did not include borrow pits, oxbows or other aquatic habitats associated with higher elevation batture lands between the mainline levees. A total of 16 species of unionid mussels were collected; 10 species were found alive, including the endangered *Potamilus capax*; four others were collected fresh dead; and two were represented only by weathered dead shells. *Corbicula fluminea* and *Dreissena polymorpha* were also collected alive. Highest diversity and density of freshwater mussels was associated with secondary channels, dike fields, and areas maintained by bank stored water during low flow events.

**PRELIMINARY REEVALUATION OF THE FRESHWATER MUSSELS  
(BIVALVIA: UNIONOIDA) OF THE CONGO REGION, AFRICA**

Daniel L. Graf<sup>1</sup> and Kevin S. Cummings<sup>2</sup>. <sup>1</sup>Academy of Natural Sciences, Philadelphia PA 19103 USA. <sup>2</sup>Illinois Natural History Survey, Champaign IL 61820 USA.

Based upon the range limits of freshwater mussel (Unionoidea) species, we consider the Congo Region of Africa to extend from Gabon south to Angola and Zambia, east to Lake Tanganyika, including the entire Congo Basin. As part of an on-going project to revise the Gondwanan freshwater mussels, we have examined African material in fourteen major collections on three continents. Specimen lots, including associated labels, were digitally photographed, textual data were captured on-site or later from the images, and everything was combined with appropriate taxonomic data and incorporated into the MUSSEL Project Database. Those data, including images, are served via our web site (<http://www.mussel-project.net/>). In addition to museum work, we have made two collecting expeditions to the Congo River Basin: the Upper Congo in Zambia in 2005 and the Lower Congo in the Republic of Congo in 2006. We survived both trips. At least 34 species of freshwater mussels in three families (Unionidae, Iridinidae and Etheriidae) are known from the Congo Region; most of those species (26, 76%) are endemic to the region (or some portion thereof). We discuss the patterns of diversity of the Congo Region freshwater mussels in the context of continent-wide diversity patterns and areas of endemism within the region. This research was funded by the National Science Foundation.



PL81\*

**ASSESSING DNA DAMAGE IN HEMOCYTES OF THE FRESHWATER MUSSEL *ELLIPTIO COMPLANATA* WITH THE COMET ASSAY: IMPLICATIONS FOR ESTABLISHING A NON-LETHAL SCREENING TOOL**

Sharon T. Prochazka<sup>1</sup>, W. Gregory Cope<sup>1</sup>, Robert B. Bringolf<sup>1</sup>, and Leslie Recio<sup>2</sup>. <sup>1</sup>North Carolina State University, Department of Environmental & Molecular Toxicology, Box 7633, Raleigh, NC 27695; <sup>2</sup>Integrated Laboratory Systems, Inc., P.O. Box 13501, Research Triangle Park, NC 27709.

The single cell gel electrophoresis (SCGE) or Comet assay is widely used to detect DNA damage resulting from exposure to genotoxic compounds. In this study, DNA damage was quantified in hemocytes from Eastern elliptio (*Elliptio complanata*) freshwater mussels following the exposure of isolated hemolymph (*in vitro*) and whole organism (*in vivo*). The primary objective of this study was to assess whether genotoxicity resulting from *in vitro* exposure is representative of genotoxicity from *in vivo* exposure to potential and known genotoxic agents. To discriminate between genotoxicity and cytotoxicity, the Bradford protein assay and an ATP bioluminescence assay were performed in conjunction with the Comet assay. Results obtained from *in vivo* and *in vitro* tests with current use pesticides and hydrogen peroxide, a known genotoxic agent, indicate that *in vitro* tests show promise as a genotoxicity screening tool for unionids. All hemolymph used in this study was collected using non-lethal sampling techniques, which are highly desired for imperiled faunal groups such as unionids.

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**A Preliminary Survey of Abundance and Species Diversity of Freshwater Mussels (Unionidae) in Three Reserve Areas on the Sabine River in Northeast Texas**

Jessica M. Gullett and Neil B. Ford. Department of Biology, University of Texas at Tyler, Tyler, TX 75799

Native populations of United States freshwater mussels (Unionidae) are declining for a variety of reasons such as water pollution and encroachment of nonnative species. In many regions, such as the Sabine River in Northeast Texas, areas are being designated as “no take” zones to protect the native mussel populations. However, these reserves were not surveyed when they were established. This study compares the abundance and species diversity of mussel fauna in three reserves, as well as within each reserve, to determine whether these habitats are high quality sites for mussels. Within each reserve, six different sites were chosen based on substrate composition. Six timed hand searches were completed along with three density surveys in order to assess abundance and diversity. Data from six sites within one reserve have been collected thus far from the Sabine River, and a total of 862 individuals and 14 species were collected. Within this reserve, abundances decreased noticeably at sites further downstream possibly due to changes in substrate composition. The same methods will be used to evaluate the remaining two reserves next spring. Ultimately, results of this study aim to show the importance of choosing appropriate habitats for mussels before declaring specific areas as reserves.