

Phylogenetic Systematics:

The Missing Ingredient in the Conservation of Freshwater Unionid Bivalves

By Charles Lydeard and Kevin J. Roe

Recently, a surge of research activities has focused on the captive care and propagation of North America's freshwater unionid bivalves (Mollusca: Bivalvia: Unionacea). These studies are vital and may ultimately save many species from extinction. However, phylogenetic systematics needs to be considered if we are to ultimately succeed in conserving North America's most imperiled group of organisms (Stein and Flack 1997).

Phylogenetic systematics is essentially reconstructing the genealogical relationships of organisms based on the distribution of attributes such as anatomical features or DNA sequences (Hillis and Moritz 1996). This enables investigators to graphically recognize and represent natural groups (i.e., species) in a branching diagram that depicts hypothesized evolutionary relationships among organisms. Recognition of natural units is important for the intelligent use of limited resources allotted for the conservation of threatened and endangered organisms.

The greatest diversity of the near-cosmopolitan freshwater unionacean mussels or clams occurs in North America, which has nearly 300 species. The vast majority of these are concentrated in the southeastern United States (Lydeard and Mayden 1995). Regrettably, nearly 75% of all mussels are considered extinct, endangered, threatened, or of special concern, making unionids the most imperiled group of animals in North America (Stein and Flack 1997). Although malacologists have been aware of the

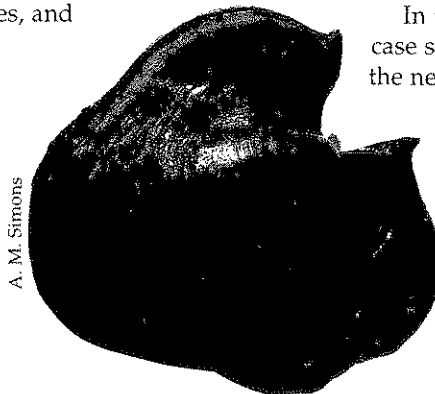
decline in numbers of species and the range contraction of many others since the early 1900s, they did not recognize the dire situation of mussels until recently. One widely cited paper that contributed greatly to our understanding of the conservation status and plight of freshwater unionids was published in *Fisheries* by Williams et al. (1993). In addition, The Nature Conservancy and other nonprofit organizations (e.g., Master 1990) have helped disseminate information about declining mussel populations due to habitat loss and degradation, sedimentation, and siltation from poor land-use practices, and introduction of exotic species such as the zebra mussel (*Dreissena polymorpha*).

Recognition of species among freshwater bivalves has been a contentious area because traditional classifications are largely conchologically based. Shell characters such as shape, dimensions, sculpture, and degree of inflation vary geographically and in response to environmental conditions. Investigators near the beginning of the twentieth century described virtually every specimen from a different geographical area as a new species. Subsequent taxonomists interpreted such differences as

phenotypic variation and synonymized many phenotypes into single species (Williams and Mulvey 1997). A taxonomist's view of a species is an hypothesis that needs to be tested with phylogenetic systematics. Unfortunately, few phylogenetic studies have been conducted on freshwater unionid mussels, and it is quite possible that many of the nominal species and genera do not represent natural units. Based on evidence available in the few phylogenetic systematic studies conducted, we should exercise caution treating conventional taxonomic species as real evolutionary species.

In this essay we give two case studies that underscore the need for phylogenetic systematics to help conserve freshwater mussels. The first involves the federally threatened inflated heelsplitter (*Potamilus inflatus*), which is known from the Amite River in Louisiana and the Black Warrior River of Alabama. These two disjunct populations are relicts of a formerly widespread distribution, and

they are virtually indistinguishable conchologically. We recently conducted a phylogenetic analysis of the genus *Potamilus* to determine if the two populations were genetically distinct (Roe and Lydeard 1997) because managers were interested in potentially augmenting the Louisiana population with specimens from the Black Warrior River. Our analysis revealed that not only are the populations distinct, but they are genetically more different than the congeners *P. purpuratus*



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Populations of the threatened inflated heelsplitter (*Potamilus inflatus*) from the Black Warrior River in Alabama are genetically different than populations from the Amite River in Louisiana.

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and *P. alatus*, which are morphologically distinct and unarguably different species. In other words, the Louisiana and Alabama populations are two distinct, cryptic species. Had this information not been obtained, and individuals from Alabama were introduced into Louisiana, the two forms likely would have hybridized, and the genetic integrity of the Louisiana species would have been lost forever.

When genetically distinct forms are brought together, gene complexes adapted to local conditions are disrupted by hybridization, which may lead to outbreeding depression and a decline of the population that was supposed to be augmented. Inadvertent genetic swamping of species via introgressive hybridization or loss of a population from outbreeding depression has often been documented in the literature (e.g., Avise and Hamrick 1996). Many cases were apparently due to accidental or purposeful introductions in which the genetic history of the population was not realized until after the harm had been done.

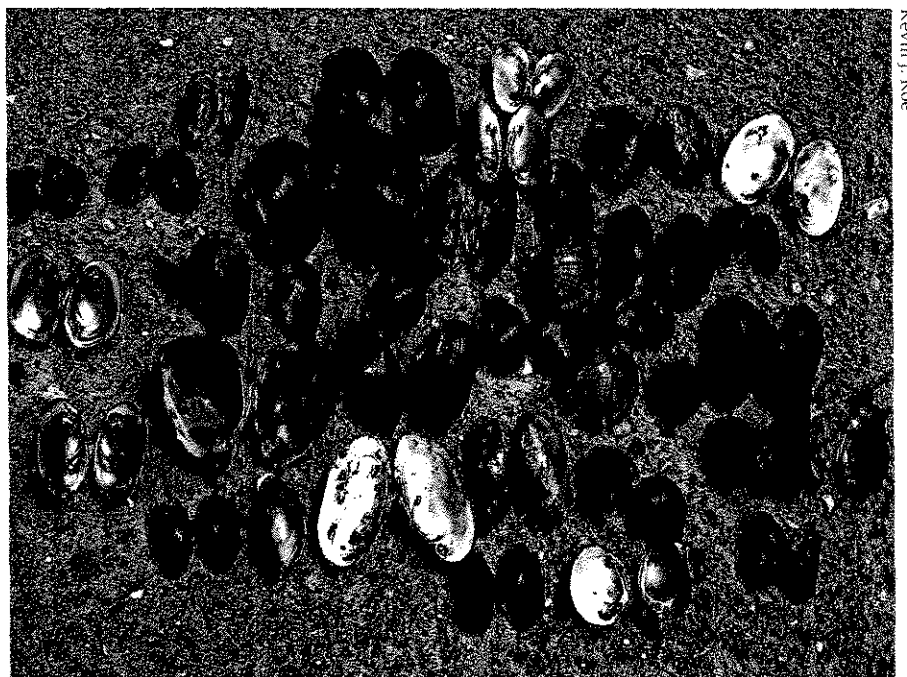
Another case study involves looking at phylogenetic relationships within the genus *Amblema* (Mulvey et al. 1997). Traditionally, *Amblema* has comprised *A. plicata plicata*, *A. plicata perplicata*, and *A. neislerii*. The question was whether the conchologically distinct *A. neislerii* was genetically distinct from *A. p. plicata* and *A. p. perplicata*, and whether the two subspecies were distinct from one another. Based on a phylogenetic analysis, Mulvey et al. (1997) concluded that *A. neislerii* was indeed a different species. In addition, *A. p. plicata* and *A. p. perplicata* were genetically indistinguishable. However, within the range of *A. plicata* a genetically distinct form was discovered that was hypothesized to be a unique species—*A. elliotii*, which is endemic to the Coosa River of Alabama. Superficially, *A. elliotii* looks similar to *A. plicata*, but it is genetically most closely related to *A. neislerii*. These examples are the only DNA-based phylogenetic studies on specific genera within unionid mussels, and both revealed unexpected patterns different from conventional classification. Regrettably, the

dearth of phylogenetic studies is largely due to the lack of taxonomists who choose to work on invertebrates. However, with the recent attention on freshwater mussels, perhaps more students will focus their efforts on systematic studies.

The information being gathered on transporting, feeding, maintaining, and propagating freshwater mussels for relocation and reintroduction efforts is important, and we laud these efforts. However, we recommend that specimens from different geographic areas within a given putative species be managed as separate entities until enough phylogenetic studies have been completed to ensure that no harm will come from mixing different populations. ➤

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Mussel species may look similar but actually be genetically more closely related to species that appear different. Here, a variety of mussels have been found in the Sipsy River, Alabama.

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