

Genetic variability and geographic structure of *Lampsilis higginsii* mussels in the upper Mississippi River and tributaries

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Goals and Objectives:

1. Assess the genetic variability and geographic structure within and among five populations of *Lampsilis higginsii* in the Upper Mississippi, St. Croix, and Wisconsin Rivers using three segments of the mitochondrial DNA genome from 30 animals per population.
 2. Make management recommendations regarding relocations of individuals among populations, specifically with regard to (a) numbers of animals to be relocated and (b) appropriate geographical sites for relocations.
 3. Assess the level of genetic variability (number of alleles and percent heterozygosity) of microsatellites in a sample of *Lampsilis higginsii*.
 4. Provide recommendations on utility of microsatellites for identification of individual females and determination of multiple paternity in *L. higginsii*.
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Progress:

The Higgins' Eye Pearlymussel, *Lampsilis higginsii*, is a Federally endangered species, which is in jeopardy of extinction throughout its range, the Upper Mississippi River (UMR) and several associated tributaries. Plans for recovery of this species include a Relocation Plan submitted by the St. Paul District (MVP), Army Corps of Engineers (COE), to augment and/or create *L. higginsii* populations throughout its range. The Relocation Plan includes relocation of adult individuals and a propagation program. Information on the genetic characteristics of *L. higginsii* populations was obtained to make scientifically sound decisions regarding the numbers, localities, and logistical concerns of proposed relocations. The current project focused on surveying genetic variation at three mtDNA genes (1027 nucleotides) of *cytochrome-b*, *cytochrome c oxidase I*, and *16S rRNA* from an extensive sample of individuals (130) that are distributed throughout the range of the species. We also surveyed nuclear DNA microsatellite variation in 41 individuals, using the genetic primers developed by Eackles and King for the congener *Lampsilis abrupta*. Both the mtDNA and microsatellite analyses were completed in 2004.

Conclusions and Recommendations:

We found a surprisingly high level of genetic variation within populations of *L. higginsii*, using both mtDNA and microsatellite DNA markers. Using mtDNA, we detected 24 genetic forms (haplotypes), which clustered into four groups (clades). Statistical analyses of the mtDNA survey indicate that *Lampsilis higginsii* does not contain genetically distinct populations in the portions of the St. Croix and Mississippi Rivers that we studied. The level of genetic variation is high in *L. higginsii*, compared with other endangered species. We found that a small number of individuals sampled contained the mtDNA form typically found in *Lampsilis siliquoidea*, a common and widespread congener that occurs in the Midwest. Similar observations have been made in other animal groups. Additional research is required to determine the cause of this finding and the implications it has for conservation of *L. higginsii*. Our survey of nuclear DNA using microsatellites included DNA of 41 individuals from several localities and from individuals that have been used in the captive propagation project. We detected between 6 and 25 alleles per locus. This high level of genetic variation at nuclear loci is consistent with the mtDNA findings. A significant deficiency of heterozygotes at most microsatellite loci appears to be due to null alleles, which would limit the utility of these microsatellite primers for studies of paternity and maternity in *L. higginsii*.

The high level of genetic variation that we detected in *L. higginsii* represents a valuable genetic resource that should be preserved in this endangered species. We recommend that when relocations occur, a large number of individuals should be used in order to preserve as much genetic variation as possible and that more than 100 females should be used in the propagation program. Even though we did not find evidence of differentiation among populations, we recommend that animals used for relocations to new populations should come from nearby sources.

Papers presented at Professional Meetings:

“The endangered *Lampsilis higginsii*: using mitochondrial and microsatellite DNA data for developing propagation and recovery plans.” Invited presentation at the Conservation Genetics Workshop on Imperiled Freshwater Mollusks and Fishes, sponsored by Freshwater Mollusk Conservation Society, National Conservation Training Center, Shepherdstown, West Virginia, June 2004.