Conservation Genetics of the Freshwater Mussel Margaritifera hembeli (Bivalvia: Margaritiferidae)

Principal Investigator: Kevin J. Roe
Student Investigator: n/a
Collaborators: n/a
Duration: September 2007 to March 2009
Funding Source(s): US Fish & Wildlife Service
Goals and Objectives:

The objective of the project is to document population genetic structure, the extent of gene flow, and historical connections between populations of the Louisiana Pearlshell (Margaritifera hembeli Conrad, 1838). This information could be used in identifying unique or genetically distinct populations of this threatened species and serve as guidelines for future conservation related actions, such as hatchery propagation and reintroduction or population augmentation aimed at reversing declines and preventing extinction of this species throughout its range.
Goals for this project have been separated into three phases as follows:

Phase I – Generate species-specific microsatellites for the M. hembeli. Obtain specimens from across the range of the species.
- A genomic DNA library will be constructed from a single individual of the sheepnose. The genomic library will be probed for stretches of nucleotide repeats, such as CA(n) or CGTT(n). These nucleotide repeats are the microsatellite markers. This phase will include primer design of potential microsatellite sites.

Phase II – Screen potential microsatellites
- Species-specific microsatellite primers will be tested in a subset of the individual M. hembeli specimens. The goal of this phase is to identify 20-25 microsatellite regions that have variation both within a population as well as between populations. Individuals will be screened with all available primer sets. Primer sets that amplify variable microsatellite regions will be used in Phase III.

Phase III – Determine genetic diversity of M. hembeli
- Populations will be surveyed with microsatellite primers. The number of individuals genotyped from each population will depend on the availability of samples. Microsatellite data will be analyzed for genetic variation and population structure.

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Progress:
To date, substantial progres has been made on the project. Samples for ~200 individual mussels have been obtained representing ~ 12 loaclities across the species range of M. hembeli, and DNA has been extracted from these samples. A species specific microsatellite library has been developed and ~8 polymorphic microsatellite markers have been identified. The Principal Investigator is currently in the process of generating microsatellite genotypes for all samples on hand for the markers mentioned above, and to date have genotypes all samples for two of the eight loci.

Future Plans:
As all mussel specimens of this species are on hand, expect the remaining genotyping and analysis of the resulting data to be completed by Winter/Spring of 2009.