

## Genetic Variation of Northern and Southern Populations of *Quadrula fragosa* (Conrad, 1835) using Microsatellites

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### Goals and Objectives:

- How diverse are the northern and the southern populations of *Q. fragosa*?
  - What is the degree of genetic difference between northern and southern populations?
  - What are the population dynamics between northern and southern locations?
  - How many females will be needed to generate the same level of genetic diversity in a founder population?
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### Progress:

The winged mapleleaf, *Quadrula fragosa*, historically occurred in the Mississippi, Tennessee, Ohio, and Cumberland river drainages, but has suffered severe population and range reductions. At the time that the species was federally listed as endangered, its range was thought to have been reduced to a stretch of the St. Croix River between northwestern Wisconsin and east-central Minnesota. Recently, morphologically "*Q. fragosa*-like" specimens were discovered at sites in Arkansas (Ouachita River) and Missouri (Bourbeuse River). These specimens were genetically determined to be *Q. fragosa* with mitochondrial DNA sequence, suggesting that two new populations of *Q. fragosa* exist outside the St. Croix River. Because these new southern populations may have a significant impact in the development of conservation management plans for the northern population of *Q. fragosa*, specific information about population structure and genetic diversity of *Q. fragosa* is needed.

Since the fall of 2005, specimens that will be used in the population genetic study have been collected from three southern populations. These populations include a new location (Little Red River, Oklahoma), which contain individuals genetically identified as *Q. fragosa* during this study. Subsequently, we have expanded our research scope to include this population. U.S. Fish and Wildlife Service provided fresh tissue from the St. Croix population (Minnesota) for genomic DNA library development. Two enriched microsatellite libraries were generated for di- (CA) and tri- (CAA) nucleotide repeats and these libraries were cloned into *E. coli* bacteria. Currently, we are screening clones that contain the repeat inserts of interest using chemoluminescence methods. Once positive clones are identified from this method, we will sequence the insert and develop microsatellite primers that will be used in the population genetics study.

### Future Plans:

Microsatellites developed from this project will be used to assess genetic differences within and among populations and will improve our understanding of the population dynamics of this federally endangered mussel. This information will be critical in developing conservation management plans for the species.