

CURRENT WILDLIFE PROJECTS

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

**Principal Investigator:** Bonnie S. Bowen  
**Student Investigators:** Tiffanie Kuhn Johnson, Justin Church (undergraduate research assistants)  
**Duration:** September 2001 to April 2004  
**Funding Source(s):** U.S. Army Corps of Engineers

**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*.

**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 is needed to make scientifically sound decisions regarding the numbers, localities, and logistical concerns of proposed relocations.

Prior genetic research on *L. higginsii* by PI Bowen has demonstrated that this species contains a high level of mitochondrial DNA genetic variation within populations and that there is little evidence for genetic differences among the populations. Ongoing research in the current project has focused on surveying genetic variation at three mitochondrial DNA (mtDNA) genes from an extensive sample of individuals that are distributed throughout the range of the species. Statistical analyses of the mtDNA survey is being completed. The data 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.

During 2003 the project was expanded to include a survey of nuclear DNA microsatellite variation, using the genetic primers developed by Eackles and King for the congener *Lampsilis abrupta*. We are currently completing the survey of variation at ~10 loci for individuals from several localities and from individuals that have been used in the captive propagation project. Extensive genetic variation has been detected and we are optimistic that this technique will be useful for conservation genetic applications in *L. higginsii*.

**Future Plans:**

Plans for 2004 are to complete statistical analyses of mtDNA as well as laboratory and statistical analyses of microsatellite DNA. Results will be disseminated at a workshop in June 2004 on Conservation Genetics of Freshwater Mollusks and Fish, which is sponsored by the FMCS. Manuscripts will be prepared for publication in peer-reviewed journals.

## A landscape approach to grassland bird conservation in the Prairie Pothole Region of Iowa and Minnesota

**Principal Investigator:** Rolf R. Koford  
**Student Investigator:** Shane S. Patterson (M.S.)  
**Collaborators:** David Naugle and Frank Quamen, University of Montana  
 Rex Johnson, Diane Granfors, Ron Reynolds, Neal Niemuth, and  
 Mike Estey, USFWS Habitat and Population Evaluation Team  
**Duration:** August 2001 to May 2004  
**Funding Source(s):** Iowa and Minnesota DNR, U.S. Fish and Wildlife Service  
**Goals and Objectives:**

1. Assess local and landscape factors affecting grassland bird use in the Prairie Pothole Region (PPR) of MN and IA.
  2. Develop species-specific habitat models for grassland-bird species of conservation priority. These models will enable us to take information garnered from individual study sites and expand to a regional scale.
  3. Apply species-specific habitat models in a GIS context to identify priority grassland-bird landscapes throughout the PPR of IA and MN.
  4. Compare the efficacy of predictive models of abundance based on conducting a single count versus two counts (~2 weeks apart) in the region.
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### Progress:

In 2003, study sites were selected in the tallgrass portion of the Prairie Pothole Region (PPR) in Iowa and Minnesota. The rich glacial alluvial soils that characterize this area are ideal for row-crop agriculture, which now constitutes the region's most prevalent form of land use. As a result, the modern-day PPR is a highly fragmented remnant of what was once a vast network of prairies, lakes, ephemeral wetlands, riparian woods, and aspen parkland. Our study will aim to determine the best remaining segments of habitat for an array of declining obligate grassland-bird species in the PPR. An analogous study is being carried out in the mixed-grass segment of the PPR in Montana, North Dakota, and South Dakota by the collaborators at the University of Montana.

A stratified cluster sample was utilized to randomly allocate 439 point-count sites to specific grassland locations throughout the PPR of MN and IA. Strata were classified by grassland abundance in the surrounding landscape (ranging from 0-82% grass in the tallgrass region) and grassland type (grassland, hayland, and cropland). Points drawn from the cropland classification were limited to 10% of the total sample, since they have been shown to be a less-preferred habitat of obligate grassland birds. The remainder of points was equally divided between grassland and hayland categorizations.

At each site, we surveyed birds for 10 minutes within 100m fixed-radius point counts from sunrise to 10:00 during the interval of 20 May to 04 July. For each grassland bird detected within a count circle, we recorded time of detection, distance from bird to observer, land-cover type utilized, and sex when identifiable. Occurrence data were also collected for non-focal species and flyovers within the count radius and for focal species detected outside of the count circle.

To assess local habitat characteristics, we noted species composition of plants at 20 points throughout each count circle. We also measured litter depth, effective leaf height, and visual obstruction at 10 of the points for which vegetation was recorded. This site vegetation data will enable us to evaluate the interaction among local, landscape, and regional factors in relation to the abundance of priority grassland species.

A second round of counts was conducted at 110 sites that were randomly selected from our first group. Counts took place 10-15 days after the first count at each location and were completed during the interval of 13 June to 04 July. To allow for proper comparison, count and vegetation protocols were identical to those that were used for the first round of sampling.

### Future Plans:

Analysis and preparation of reports are planned for 2003-2004.