

FINAL REPORT

“SHARE WITH WILDLIFE” GRANT: Genetic and Species Diversity in *Popenaias* (Bivalvia: Unionoida: Unionidae: Lampsilini) populations from New Mexico and Texas.

Principal Responsible Party: Dr. Walter R. Hoeh, Associate Professor,
Department of Biological Sciences, Kent State University, Kent, Ohio, 44242
Phone: (440)-840-3480 **Email:** whoeh@kent.edu

Statement Of The Objectives, Goals, And Tasks

Program Summary: Unionoid bivalves (freshwater mussels) exhibit a relatively high degree of inter-individual variation in shell morphology such that species diversity and species limits are, typically, inadequately understood for this group of organisms.

The proposed study will generate estimates of genetic and species diversity for *Popenaias* bivalve populations in New Mexico and Texas, and include these data in a larger systematic analysis of North American lampsiline freshwater mussels. Estimates of genetic differentiation will be based on DNA sequence data obtained from two independent genetic loci, the female (F)- and male (M)-transmitted mitochondrial DNA genomes. These relatively fast evolving and independent loci will allow for multiple evaluations of genetic and species diversity.

These evaluations will provide resource management professionals with the information required to make informed conservation decisions regarding the Texas hornshell (*Popenaias popeii*), a state endangered mussel (NMDGF 2006a) and a federal candidate for listing (priority 2) under the Endangered Species Act (Federal Register 2001). Genetic study of this species is called for under the state recovery plan (NMDGF 2007: 46) and the “*Comprehensive Wildlife Conservation Strategy for New Mexico*” (NMDGF 2006b: 335).

Project Objectives:

- 1) Analyze tissues from individuals of the Texas hornshell mussel (*Popenaias popeii*) from New Mexico and Texas. The tissues required for the proposed genetic comparisons are already housed in Hoeh’s lab at KSU. A maximum of 100 *P. popeii* tissue samples will be analyzed.
- 2) Extract DNA from mantle (and testes [when available]) tissue samples to access F and M mitochondrial DNA genomes from the sampled individuals.
- 3) Perform polymerase chain reaction (PCR) amplifications and automated DNA sequencing of F and M mtDNA fragments containing cytochrome *c* oxidase subunit I (*COI*) gene sequences.

- 4) Quantify the distribution of F and M *COI* sequence variation within and among populations of the Texas hornshell mussel (*Popenaias popeii*).
- 5) Use species-specific DNA sequences, representing geographically extralimital populations of other lampsiline bivalves (for comparative purposes), to estimate the contextual genetic relationships among *P. popeii* individuals and populations using Bayesian inference, maximum likelihood and maximum parsimony tree-building techniques.
- 6) Use the phylogenetic species concept in conjunction with levels of among- and within-population differentiation in F and M *COI* sequences to evaluate the genetic and species diversity in the Texas hornshell mussel (*Popenaias popeii*).
- 7) Submit a detailed final report to the NMDGF containing the findings of the research project.

Results:

- 1) *Popenaias popeii* (from NM) FCOI (EF033257) and MCOI (EF033294) mtDNA sequences were generated in my lab and are now available on GenBank.
- 2) The foundational research necessary for estimating the contextual genetic relationships among *P. popeii* populations and those of lampsiline bivalve species, which made use of both FCOI and MCOI sequences, has been published in the journal *Malacologia* (2008; Vol. 50: 303-318).
- 3) Mantle tissues from 18 *P. popeii* specimens from TX (collected by Tom Miller) have been processed in my lab and 13 FCOI and five MCOI sequences have been obtained.
- 4) Mantle tissues from nine *P. popeii* specimens from NM (collected by Brian Lang) have been processed in my lab and eight FCOI and two MCOI sequences have been obtained.
- 5) Genetic analysis of the 18 TX *P. popeii* *COI* sequences, with the 10 NM *P. popeii* *COI* sequences used for comparison, indicated extreme DNA sequence divergence (~30%) between FCOI and MCOI sequences (as expected) but relatively slight intra-FCOI and intra-MCOI sequence variation (<1.35%; Table 1). Thus, the relatively low levels of *COI* divergence among all specimens analyzed to date is consistent with the TX and NM *P. popeii* specimens being members of one species.
- 6) A maximum likelihood bootstrap majority-rule tree (Figure 1) indicates (1) significant support for the monophyly of the MCOI vs. FCOI sequences (BSP = 100%) as expected and (2) no statistical support for the genetic distinctiveness of NM vs. TX *P. popeii* specimens in either the FCOI or MCOI clades (Figure 1). Again, this supports the hypothesis that the TX and NM *P. popeii* specimens represent one species.

Majority rule

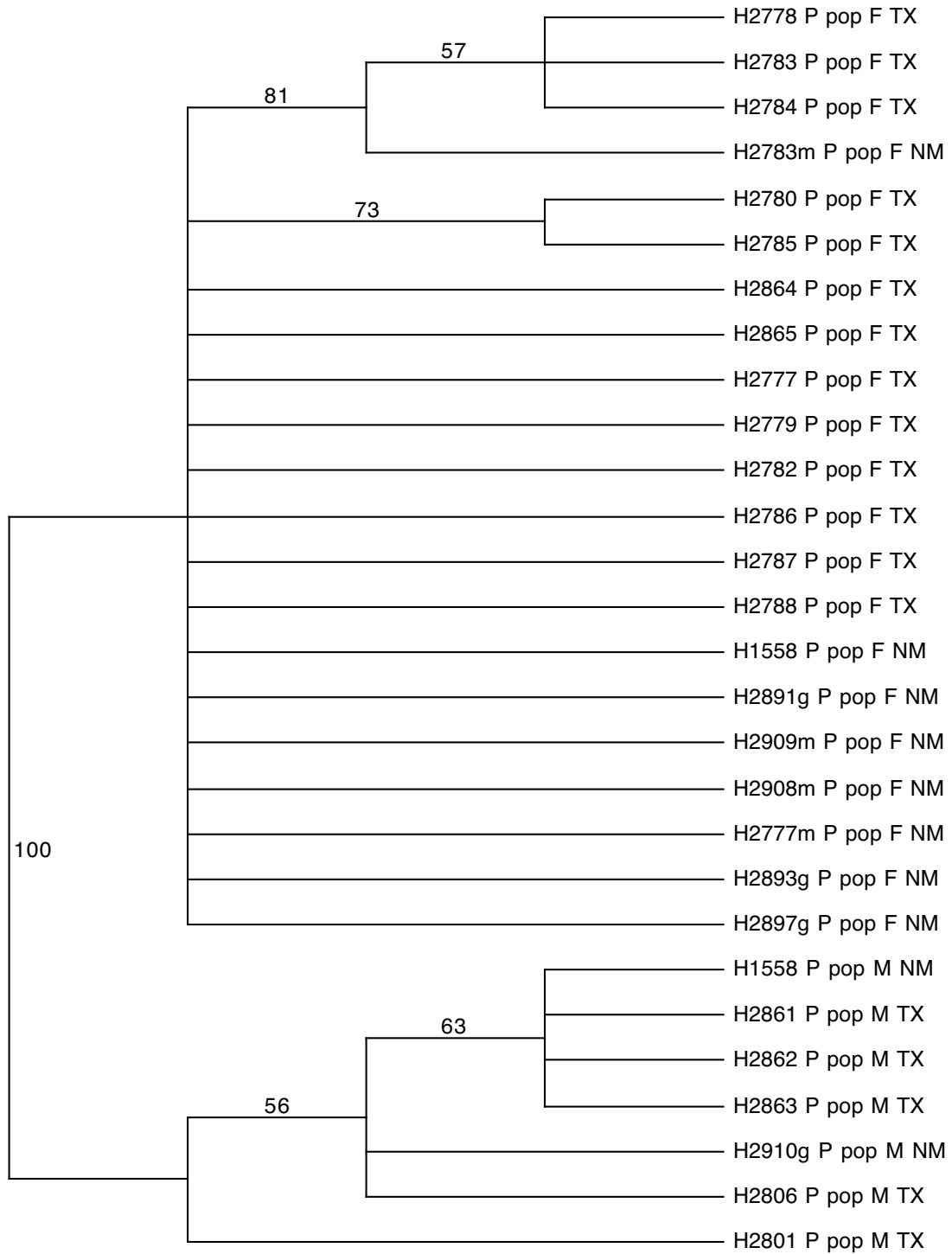


Figure 1. 50% majority-rule consensus Maximum Likelihood bootstrap tree (500 replicates).

