Genetic Structure of the Fatmucket Mussel (*Lampsilis siliquoidea*) in the St. Clair River Delta and Tributaries: Effects of the Dreissena Invasion?

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Introduction

Native Unionid mussels recently comprised the bulk of benthic biomass in Lake St. Clair. Despite these prodigious numbers, the invasion of invasive dreissenid mussels in the mid eighties caused a precipitous decline in unionid numbers throughout the lake by attaching to, and fouling, native mussel shells. This invasion caused their virtual extirpation from the open waters of the lake within ten years (Figure 2). In 1999, a refuge habitat was discovered in the St. Clair River Delta where unionid mussels, though having suffered 100-fold decrease in density, were managing to survive in the presence of dreissenid infestation. Because this refuge habitat is so essential to preserving endangered mussel species and because it has suffered such a severe demographic decline, it is critically important to understand the genetic health of unionids in this habitat in order to effectively manage the remnant unionid population. A common species within the St. Clair Delta and its tributaries, the Fatmucket mussel (*Lampsilis siliquoidea*), was investigated to provide an idea of the genetic structure and health of a species which represents a "best case scenario" and could provide some idea of the genetic health of less common and endangered species in Lake St. Clair.

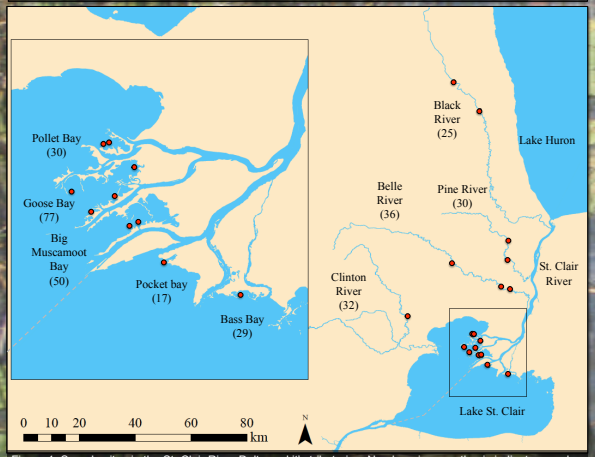

Figure 1. Sample sites in the St. Clair River Delta and it's tributaries. Numbers in parenthesis indicate sample size.

Questions

1) How much genetic diversity is present in the remnant populations of Fatmucket in the St. Clair delta?

2) What is the level of gene flow occurring between sampling locations in the St. Clair delta and surrounding watersheds? Are distinct populations present?

3) Is genetic differentiation related to geographic isolation within the St. Clair delta and its tributaries?

4) Is there any evidence of a recent genetic bottleneck in the Fatmucket populations of the St. Clair delta?

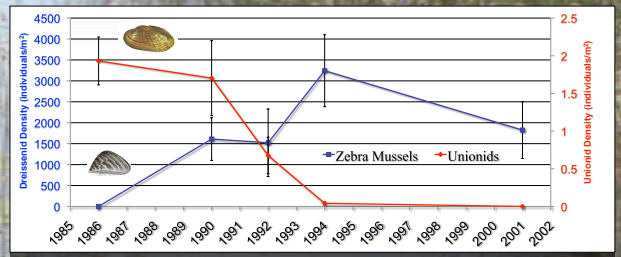

Figure 2. Density of Unionid and Dreissenid mussels in Lake St. Clair between 1985 and 2001. Data from Nalepa et al. (1988), Nalepa et al. (1996), and Hunter & Simmons (2004).

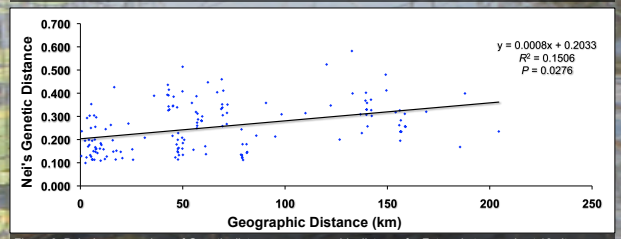

Figure 3. Pairwise comparison of Genetic distance vs. geographic distance for Fatmucket mussels at 18 sites within the St. Clair River Delta and its tributaries.

Methods

Sample Collection
- Sample sites were selected within each of major bays of the St. Clair River Delta and within each of the major tributaries to the St. Clair River (Sampling locations).
- Tissue samples were collected from 341 Fatmucket mussels at nine sampling locations throughout the study area (Figure 1).
- Sample sizes ranged from 17 to 77 individuals with an average sample size of 36 individuals per sampling location. (Figure 1).

Microsatellite amplification
- DNA was extracted from tissue samples using an alcohol extraction method.
- DNA was amplified using PCR at eight microsatellite loci with markers designed for the congener *Lampsilis abrupta*.
- Samples which amplified at >4 loci were scored using GENEMARKER v 1.80

Statistical analysis
- Genotyping errors (Stuttering, large allele dropout, Null alleles)
  - MICRO-CHECKER v 2.2.3
- Allelic richness
  - FSTAT v 2.9.3.2
- Population Structure
  - STRUCTURE v 2.3.3
  - BAPS v 5.2
- Genetic differentiation
  - F_{ST}/Nei's Geetic Distance
    - Genalex v 6.41
  - D_{est}
    - SMOGD v 1.2.5
- Isolation By Distance (Mantel Test)
  - Genepop v 4.0.10
- Genetic Bottleneck
  - BOTTLENECK v 1.2.02

Results

- 326 samples successfully amplified at 8 microsatellite loci.
- No genotyping errors due to stuttering or large allele dropout were detected. Five of eight loci were found to have a significant level of null alleles. Frequencies >.20 were found at two loci.
- Locus polymorphism was found to be comparable to other unionid populations unaffected by zebra mussels. No statistical difference in allelic richness was found among sampling locations.
- Both STRUCTURE and BAPS predicted one population as the most likely arrangement within the study area.
- Genetic differentiation was found to be low to moderate using both F_{ST} (0.004 - 0.099) and D_{est} (0.003 - 0.220).
- Genetic distance was found to be significantly correlated with geographic distance (P = 0.028) though the R^2 value was low (R^2 = 0.150) at this geographic scale (Figure 3).
- Wilcoxon tests using three models of evolution and a mode-shift test did not show significant evidence for a recent genetic bottleneck after Bonferroni correction (P = 0.002) at any sampling locations or when all sampling locations were combined.

Discussion/Conclusions

1) The study did not find evidence of unusually low genetic diversity within the St. Clair Delta or its tributaries. This indicates that the Fatmucket mussel in not currently in peril of suffering a severe loss of fitness due to inbreeding or genetic drift.

2) Individual based population structure analysis concluded that all of the sampling locations within the study made up one large interbreeding population. This finding indicates that any population fragmentation caused by dreissenid-related mortality is not so severe that gene flow has ceased to occur at the scale investigated. It also indicates that if translocation of individuals becomes necessary, inadvertent homogenization of dissimilar populations will not be a serious concern.

3) While genetic differentiation was significantly correlated with geographic distance, little differentiation was seen at the scale investigated by this study. This indicates that while gene flow is occurring among the most geographically distant sampling locations, close sampling locations are more genetically similar.

4) No evidence of a significant genetic bottleneck was detected in the St. Clair Delta or its tributaries. It is possible; however, that due to the long generation time and of unionid mussels, the uncertain future of unionid population density in Lake St. Clair, and the recent nature of the demographic bottleneck of unionids, it may be some time before a genetic bottleneck is detectable by the methods employed here.

The findings of this study indicate that for a common, host generalist species like the Fatmucket mussel; the drastic decline in unionid density in Lake St. Clair has not yet had a critical impact on genetic health or connectivity. Unfortunately, this finding is only applicable to the "best case scenario" presented by a relatively common and adaptable species. Further research and monitoring is needed to accurately asses the impacts that the dreissenid invasion may have had, or is currently having, on the sensitive and less common species of native mussels in the St. Clair Delta and its tributaries.

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