

Inheritance of microsatellite loci and delineation of lake sturgeon
(*Acipenser fulvescens*) population genetic structure

by

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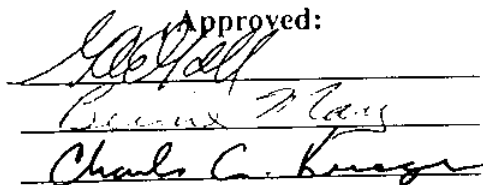
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Project summary

The lake sturgeon (*Acipenser fulvescens*) is a threatened species belonging to the family Acipenseridae and was historically found in the Mississippi, St. Lawrence, and Hudson drainage basins of North America. Overharvest, habitat alteration, and pollution have contributed to the decline of this ancient species. The biology of the species suggests that natural re-population of lake sturgeon will be slow, necessitating the need for active management. Key components of a successful management plan are the identification of existing lake sturgeon stocks and the protection of remaining genetic diversity. The objectives of this project were to 1) develop informative microsatellite loci to aid in examining population structure, 2) examine the inheritance patterns of microsatellite loci, and 3) compare genetic variation within and among seven populations of lake sturgeon.

Low levels of variation at traditional molecular markers have hampered genetic research within the family Acipenseridae. In an effort to develop a suite of polymorphic markers, 113 microsatellite markers were constructed from a shovelnose sturgeon (*Scaphirhynchus platorhynchus*) genomic library (Chapter 1). In order to identify loci that could be useful in lake sturgeon population genetics studies, these loci and those available from other studies were screened for polymorphism and quality of amplification. Four *S. platorhynchus* (*Spl* 120, *Spl* 106, *Spl* 101, *Spl* 35) loci, one Atlantic sturgeon (*Acipenser oxyrinchus*; *Aox* 27) locus, one lake sturgeon (*Afu* 68) locus, and one new locus derived from the amplification products of *Afu* 68 (*Afu* 68b) were chosen for optimization and further examination in lake sturgeon.

The complexity of the sturgeon genome mandates the confirmation of Mendelian inheritance in molecular markers in order for them to be used in population studies. Four loci conformed to a disomic model of inheritance (*Spl 120*, *Aox 27*, *Afu 68b*, and *Afu 68*). A specific inheritance model could not be tested for the duplicated loci (*Spl 106*, *Spl 101*, *Spl 35*) due to the small number of observations of each phenotype. However, banding patterns, gametic segregation patterns, and evidence of double reduction events support a tetrasomic mode of inheritance at these loci. The results indicate the lake sturgeon genome is evolving from tetrasomy to disomy (Chapter 2).

The seven microsatellite loci were used to examine genetic variation between and within seven populations of lake sturgeon (St. Lawrence River, Mattagami River, Menominee River, Des Prairies River, Niagara River, Wolf River, and Lake Erie). Multivariate factor analysis using Nei's genetic distance produced three distinct population groupings concordant with geographic location: 1) Mattagami (Northern Ontario), 2) Menominee/ Wolf (Wisconsin), and 3) St. Lawrence/ Des Prairies/ Niagara/ Erie (Great Lakes). However, population-pairwise comparisons were made using *G*-test, and significant differences were found between all populations, suggesting the existence of seven genetically differentiated populations and warranting these populations be managed as separate entities (Chapter 3).