

## AN ANALYSIS OF GENETIC RISK TO A NATIVE SPAWNING STOCK OF WALLEYE *Sander vitreus* DUE TO STOCKING IN CATTARAUGUS CREEK

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**Introduction.** Prior to the last 3 years, a substantial native spring spawning run of walleye *Sander vitreus* (*Stizostedion vitreum*) was unknown in Cattaraugus Creek – an eastern Lake Erie basin tributary whose mouth is near a native walleye spawning ground in Van Buren Bay – due to the remote location of these grounds belonging to the Seneca Nation. Believing that there was no native walleye run but that the habitat was suitable, the New York Department of Environmental Conservation (NYDEC) stocked Cattaraugus Creek with about 2.2 million 1-3 day-old fry and 44,000 fingerlings from Maumee River (western Lake Erie) run origin hatchery fish per year from 1995-2000. Genetic data from our laboratory showed that walleye spawning in Lake Erie tributaries and reefs are genetically divergent, suggesting spawning site philopatry- i.e., return to natal areas (Stepien and Faber 1998). The NYDEC then discovered a substantial native stock return in Cattaraugus Creek, estimated as 2000-4000 individuals. The present study tests the degree of genetic diversity and divergence of the original spawning stock, using older walleye in comparison to the nearby spawning group in Van Buren Bay. We then compared the genetic composition of the older fish with younger individuals (age 2-4), which are unknowns that may represent either stocked individuals and/or the offspring of the original individuals.

**Methods.** Fin clips from spring spawning run walleye were collected by Ohio Division of Wildlife from the Maumee River (the source for the hatchery stock), the Sandusky River. NYDEC collected spawning run walleye from Cattaraugus Creek in the eastern basin of Lake Erie (including older individuals, ranging from 7 to 20 years old by otolith rings) and younger individuals. We compared 25 old (pre-stocking) versus 20 young (stocked and non-stocked individuals). We also compared a nearby population (Van Buren Bay) and the stocking source population (Maumee River).

We analyzed sequence from entire 1200 bp of the mtDNA control region in comparison with our data base of 400 walleye from the Great Lakes. DNA was extracted and purified with a Quiaquick kit. The entire mtDNA control region was PCR amplified following Stepien and Faber (1998). PCR products were purified using an Exosap kit and sequenced separately in both directions for verification on a

Beckman CEQ 8000 capillary autosequencer. We analyzed sequence from entire 1200 bp of the mtDNA control region in comparison with our data base of 400 walleye from the Great Lakes.

Neighbor joining trees and maximum parsimony analysis of relationships among haplotypes, including comparison to sauger *S. canadense* were constructed with MEGA2 and PAUP\*, and support for relationships was compared with 1000 bootstrap replications. Hierarchical analysis of variance using AMOVA in Arlequin examined divergence among spawning sites and population groups.

**Results.** AMOVA hierarchical  $F_{ST}$  analyses showed significant differences among all spawning sites tested in Lake Erie (including those shown in Table 2 and Fig. 1). Results revealed that the original spawning population in Cattaraugus Creek is very genetically diverse, with many unique haplotypes and significantly diverged from the other spawning sites tested (Fig. 1 and Table 1). However, there was no significant difference between the genetic compositions of Cattaraugus Creek older versus younger individuals.

**Discussion.** The native Cattaraugus Creek spawning stock is very genetically diverse and should be maintained. It is likely that the history of exploitation pressure in this spawning habitat area has been light, leading to the preservation of high genetic variability to date. The genetic composition of the native Cattaraugus Creek population is very different from the nearby population spawning in Van Buren Bay. Recent spring returns in Catt Creek are not significantly genetically divergent from the older returns. There is no indication that stocking efforts significantly influenced the native Cattaraugus Creek walleye group.

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### Reference

Stepien, C.A. and J.E. Faber. 1998. Population genetic structure, phylogeography, and spawning philopatry in walleye (*Stizostedion vitreum*) from mtDNA control region sequences. *Mol. Ecol.* 7:1757-69.

## Neighbor-Joining Tree of relationships among mtDNA control region haplotypes (MEGA 2003)

St= Lake St. Clair, MI  
M=Maumee River, OH  
S=Sandusky River, OH  
G=Grand River, OH  
V=Van Buren Bay, NY  
O=Grand River, Ontario  
C=Cattaraugus Creek, NY

*Note: Many unique Cattaraugus Creek haplotypes, widely distributed throughout the tree. This spawning population is very genetically diverse.*

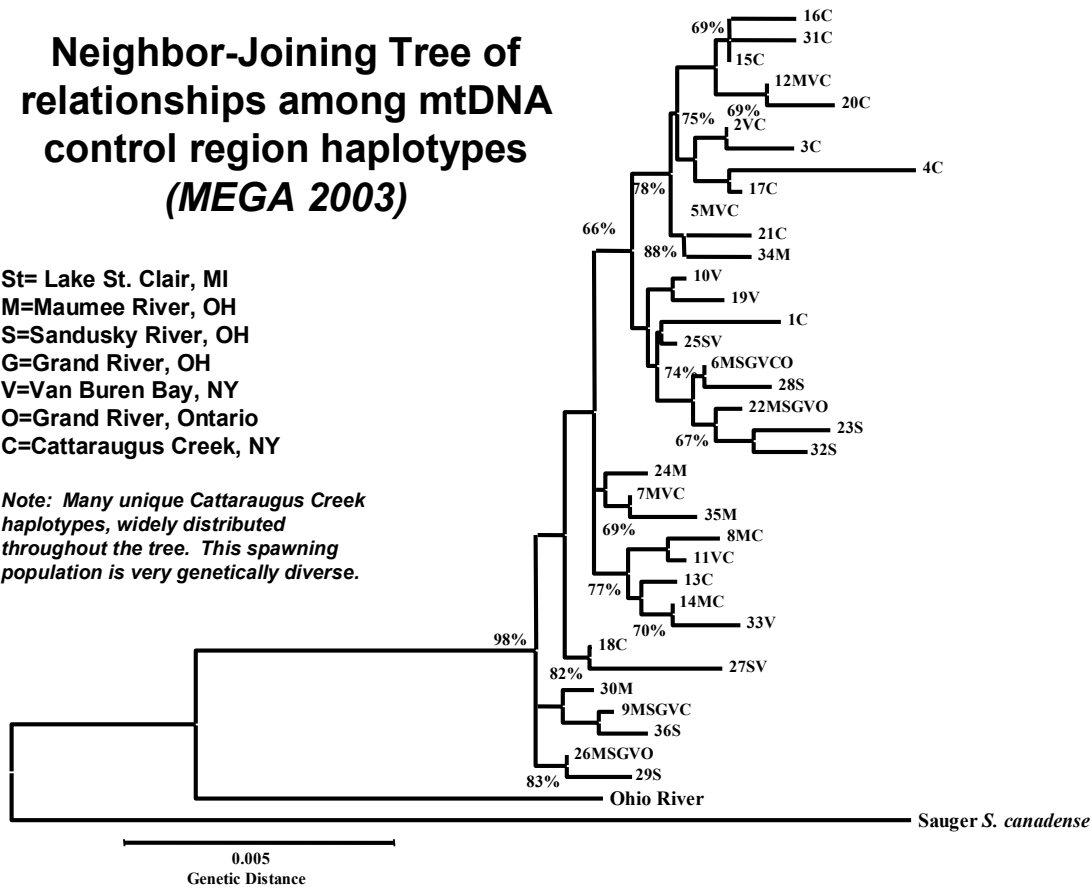


Fig. 1. (above). Neighbor-Joining tree of relationships among mtDNA control region haplotypes of walleye from spawning sites in Lake Erie based on 400 individuals analyzed (Mega 2.1). Numbers at nodes represent support from 1000 bootstrap replications. A unique type from the Ohio River (Stepien and Faber 1998) and its sister species, the sauger *S. canadense* are shown at the base of the tree, for comparison. Nodes with relatively high bootstrap support also were supported by maximum parsimony analyses in PAUP\*.

Table 1. (below) Distribution of mtDNA control region haplotypes among Lake Erie spawning sites examined.

Haplotype	2	5	6	7	8	9	12	14	11	22	26	Unique Catt. Creek	Unique Van Buren	Unique Maumee River
Catt. Creek Old	3 14.2%	1 4.8%	2 9.5%	1 4.8%	1 4.8%	2 9.5%	1 4.8%	1 4.8%	---	---	---	9 42.7%	---	---
Catt. Creek Young	1 5.6%	4 22.2%	---	2 11.1%	2 11.1%	1 5.6%	1 5.6%	---	4 22.2%	---	---	3 16.6%	---	---
Van Buren Bay	1 1.7%	4 6.7%	20 33.3%	2 3.3%	---	7 11.6%	---	---	3 5%	4 6.7%	13 21.6%	---	6 10.0%	---
Maumee River	---	14 23%	12 19.6%	3 4.9%	1 1.6%	4 6.6%	1 1.6%	2 3.3%	---	8 13.1%	11 18.1%	---	---	5 8.2%