

## GENETIC VARIATION AND SPAWNING POPULATION STRUCTURE IN LAKE ERIE YELLOW PERCH, *Perca flavescens*: A COMPARISON WITH A MAINE POPULATION

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**Introduction.** Yellow perch, *Perca flavescens*, recolonized the newly formed Great Lakes system about 10,000 years ago from three proposed glacial refugia. Previous genetic investigations discerned differences among groups of Great Lakes fishes related to differential colonization from the glacial refugia – with Lake Erie populations largely comprising Mississippi refugium descendants (especially in the western and central basins) and some from the Atlantic refugium in the east. Allozyme and mtDNA RFLP genetic studies of yellow perch in Lake Erie found low genetic variability, which may be related to historically low variability in the Mississippi refugium populations (Todd and Hatcher 1993, Billington 1993).

Populations of yellow perch in Lake Erie have been rebounding after declining in the late 1980s. At the request of the Lake Erie Yellow Perch Task Force, the objective of the present study is to analyze the genetic stock structure and variability of yellow perch in Lake Erie. We also are comparing the data to several outgroup population areas of their range, including the other Great Lakes. This investigation analyzes the entire mtDNA control region (912 bp) of 118 yellow perch from spawning locations spanning Lake Erie (Fig.1), and makes comparisons with a native outgroup population from south-central Maine.

**Methods.** Fin clip tissue samples were collected from 16 spawning locations around Lake Erie (Fig. 1), including the western, central, and eastern basins.

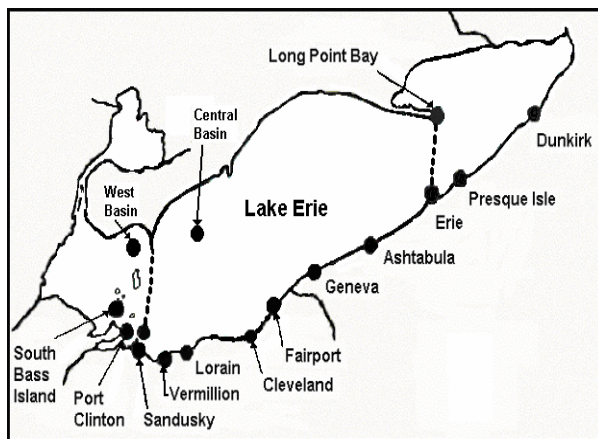


Figure 1. Lake Erie sample sites for yellow perch.

Maine samples were from Searsmont. 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.

The proportion of polymorphic nucleotides ( $p_n$ ), as well as haplotypic diversity ( $h$ ) and nucleotide diversity ( $\pi$ ) were calculated. Neighbor joining trees and maximum parsimony analysis of relationships among haplotypes, including comparison to the European yellow perch *P. fluviatilis* 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.** Ten mtDNA control region haplotypes were identified to date in Lake Erie, and three others in Maine (Fig. 2). Gene diversity in Maine was 0.57 +/- 0.12 s.e. and 0.37 +/- 0.06 in Lake Erie. Haplotypic diversity was 0.71 +/- 0.20 and 0.33 +/- 0.03, respectively. Nucleotide diversity was 0.67 +/- 0.03 for Maine and 0.39 +/- 0.03 for Lake Erie.

No haplotypes were shared between Lake Erie and Maine, and those from Maine formed a clade distinguished by 5 synapomorphies in the neighbor-joining (NJ) and maximum parsimony (MP) consensus tree. The data revealed a significant difference between the Maine and Lake Erie populations, equivalent to 62.8% of the variation in AMOVA (Analysis of Molecular Variance) comparisons in Arlequin and an  $F_{ST} = 0.66$ ,  $p < 0.00001$ , and a very great genetic divergence.

Haplotype #2 was located basally in the tree (Fig. 2) to all other *P. flavescens* haplotypes, including those from Maine, and was the sister type to all other *P. flavescens*. The frequency of #2 was greatest in western Lake Erie, and decreased from west to east. Two haplotypes were unique to the central basin and 5 to the eastern basin. The western basin was dominated by 3 shared haplotypes, but no unique ones to date. Haplotype #1 was widely distributed across Lake Erie, comprising about 80% of the samples. Haplotype #3 was relatively common in the west, less common in the central basin, and absent from the eastern basin.

AMOVA hierarchical  $F_{ST}$  analyses showed that

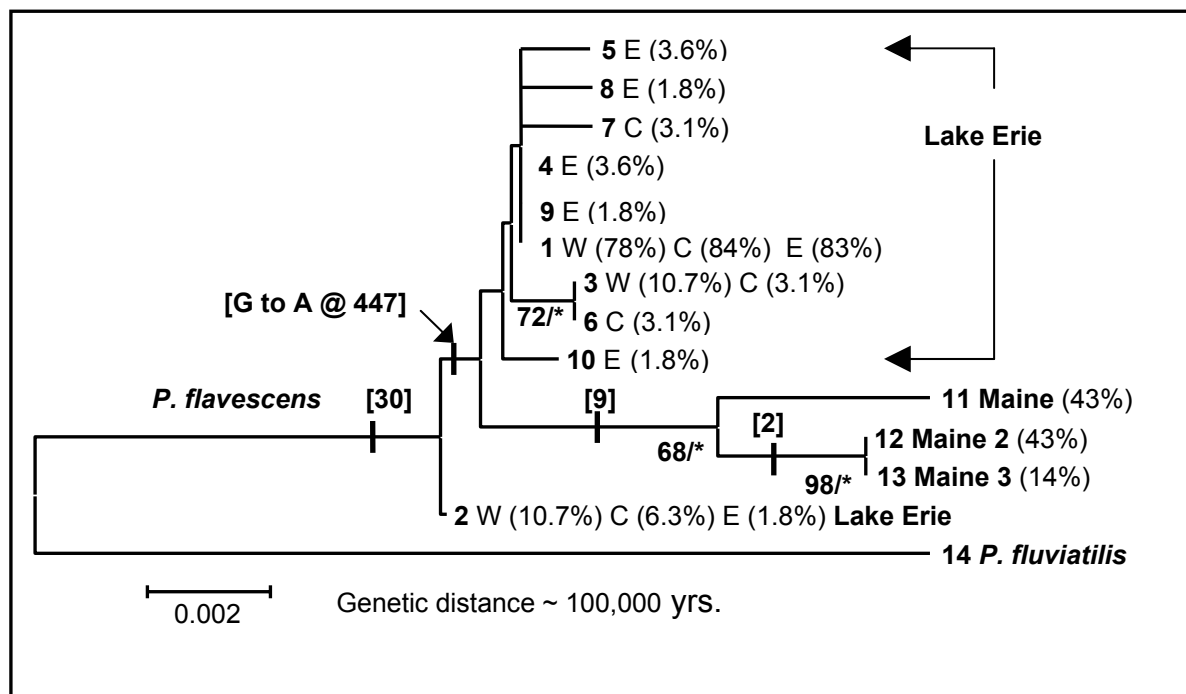


Figure 2. NJ (MEGA 2.0) tree of yellow perch mtDNA from Lake Erie and Maine with comparison to *P. fluviatilis*. Genetic distance is calibrated using 2%/my clock (Stepien and Faber 1998). Numbers in parentheses are haplotype frequencies. W = West Basin, C = Central Basin, and E = East Basin. Numbers with “/\*” are bootstrap values congruent with the most-parsimonious maximum parsimony consensus tree (PAUP\*).

pairwise divergences among some spawning site populations were significant (e.g., those with larger sample sizes at present), comprising about 3% of the variance overall.

**Discussion.** MtDNA control region sequence haplotypes revealed greater genetic diversity in Lake Erie than was found in analyses of allozymes (Todd and Hatcher 1993) and mtDNA RFLPs (Billington 1993). However, our data show that Lake Erie is dominated by a single mtDNA control region haplotype (#1), which comprises about 80% of the population in all basins. We discerned greater genetic variation within the Maine population.

Lake Erie populations of yellow perch have lower levels of genetic diversity overall than do walleye (Stepien and Faber 1998, Stepien and Taylor, in progress), which may be due to their “boom and bust” history in Lake Erie in comparison to the Maine population. However, since European yellow perch *P. fluviatilis* display similarly low levels of genetic diversity in allozymes and the mtDNA control region in comparison to *Stizostedion* - and both *Perca* are similar in levels to their sister genus *Gymnocephalus* (Stepien et al. 1998) - some of this low genetic diversity may reflect the phylogenetic history of these genera.

MtDNA control region sequences reveal higher genetic variation than was previously discerned, as well as significant population divergences among spawning sites for yellow perch in Lake Erie (e.g.,

those with larger sample sizes at present), which suggests spawning site philopatry and differential colonization patterns stemming from glacial refugia.

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