

Genetic Identification of Walleye & Yellow Perch Stocks along the HEC: Preliminary Findings Pre- & Post-habitat Augmentation

Carol A. Stepien, Amanda E. Haponski & Timothy J. Sullivan
Great Lakes Genetics Laboratory
Lake Erie Center & Dept. Environmental Sciences
University of Toledo



Walleye & yellow perch

- Popular sport and commercial fishes in the Midwest:
Center of native distributions
- **Fluctuations of Great Lakes populations, especially in last decades**
- Exploitation, ephemeral recruitment & degradation of key spawning and nursery habitats
- **A genetic stock is a population subunit that freely interbreeds in a given geographic area, shares a common gene pool, and significantly differs from other such subunits (Hallerman et al. 2003)**



Genetic connectivity

- **Genetic connectivity = measure of the relative degree of gene flow & divergence among spawning populations (stocks)**
- **Limiting factors for genetic connectivity**
 - **Behavior**
 - **Spawning site philopatry**
 - **Natal homing**
 - **Habitat fragmentation**
 - **Causes increased isolation among sub-populations (stocks)**
- **What is the degree of genetic connectivity among fish spawning groups (stocks) along the HEC?**
- **Has genetic connectivity changed with restoration efforts along the HEC?**

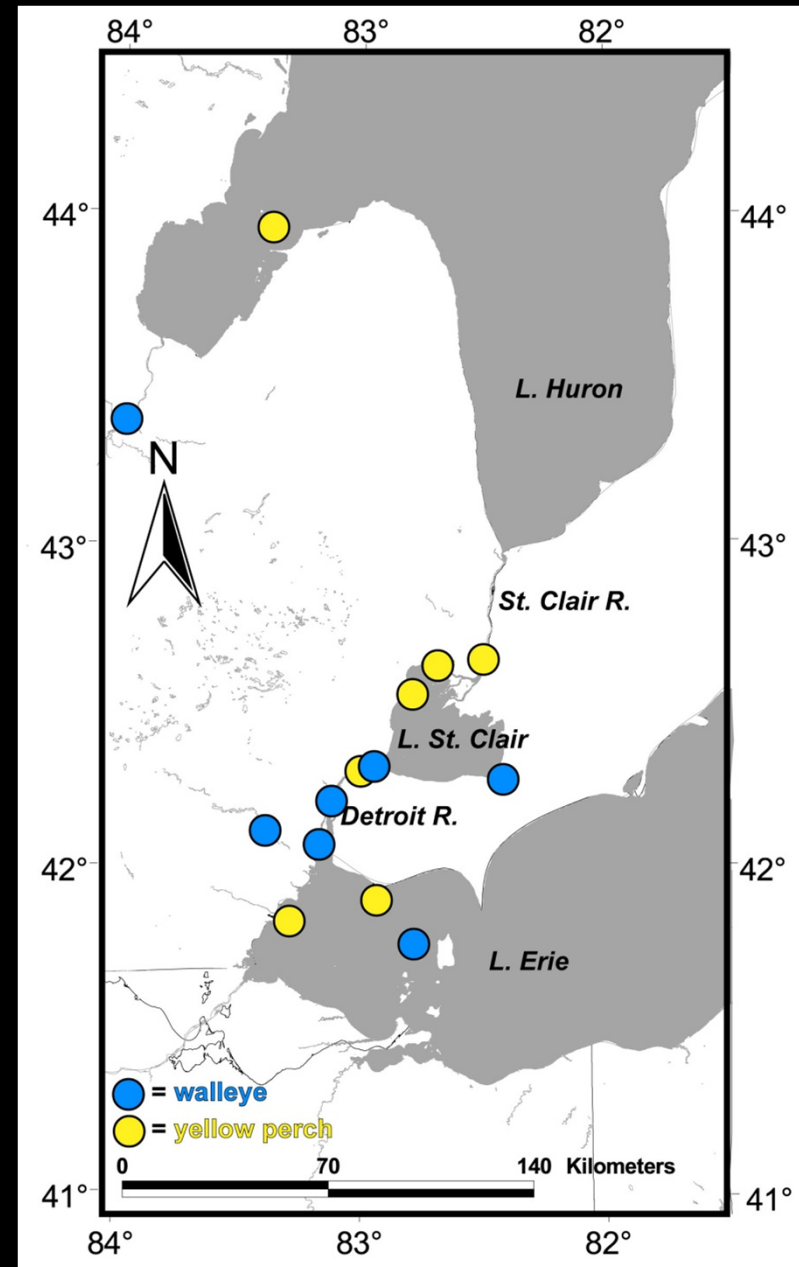
Study objectives

1. To compare the levels of genetic diversity of walleye & yellow perch spawning groups (stocks) along the HEC
2. To evaluate the patterns of genetic connectivity or divergence among them
3. Assess the impacts of habitat fragmentation & recent spawning habitat restoration at Belle Isle & Fighting Island



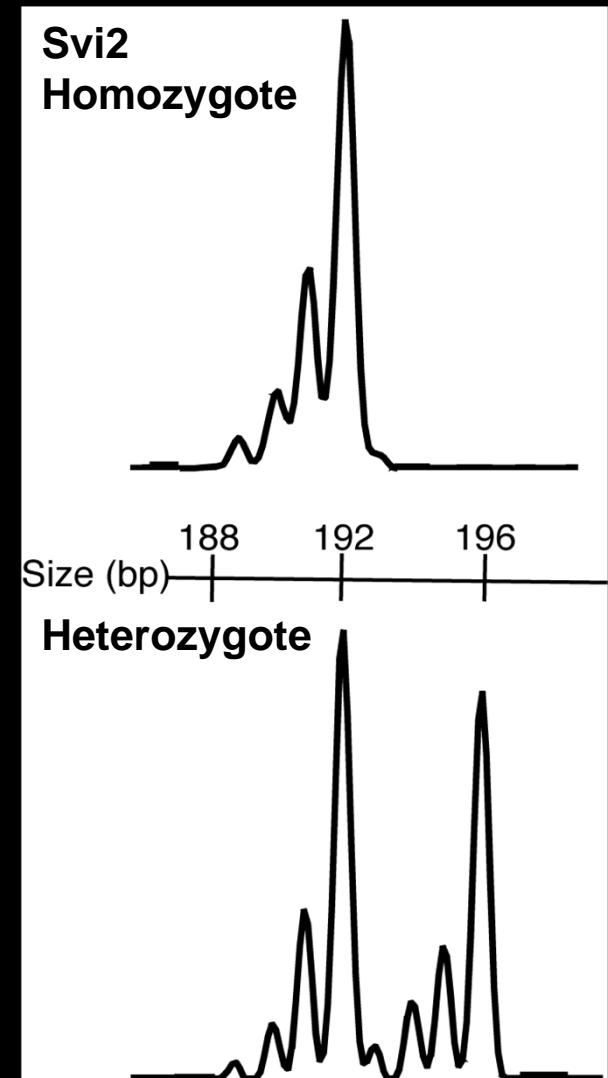
Sampling design & methods

- 291 walleye
- 7 spawning sites
- 9 nuclear microsatellite loci
- 248 yellow perch
- 7 spawning sites
- 15 nuclear microsatellite loci
- Analyses:
 - Diversity values (Genepop; Rousset 2008)
 - Pairwise comparisons (Arlequin & Genepop; Weir & Cockerham 1984; Raymond & Rousset 1995)
 - Effective # of migrants (Slatkin 1991)
 - Barrier tests (Manni et al. 2004)
 - Isolation by distance (Genepop; Rousset 1997)



Nuclear DNA microsatellite loci

- **Microsatellites (=VNTRs, variable number of tandem repeats) – short repeated DNA sequences**
e.g., CACACACA
- **Generally non-coding, most regarded as selectively neutral**
- **Mutate rapidly, gaining or losing repeats**
- **Populations (stocks) that are genetically isolated (i.e., low connectivity) accumulate changes that differentiate them from others**



1) Genetic diversity among sites along the HEC

Walleye

H_O = Observed Heterozygosity, A_R = Allelic Richness

Yellow Perch

Site	$H_O \pm S.E.$	$A_R \pm S.E.$	Site	$H_O \pm S.E.$	$A_R \pm S.E.$
A. Flint R. MI (N=44)	0.76 ± 0.05	7.2 ± 0.9	A. Saginaw Bay MI (N=56)	0.68 ± 0.06	8.6 ± 1.3
B. Thames R. ON (N=39)	0.74 ± 0.04	7.7 ± 0.9	B. Algonac MI (N=23)	0.69 ± 0.07	9.2 ± 1.6
C. Belle Isle MI (N=40)	0.73 ± 0.03	7.8 ± 1.0	C. Anchor Bay MI (N=47)	0.62 ± 0.07	8.5 ± 1.5
D. Fighting Is. MI (N=28)	0.69 ± 0.04	7.2 ± 1.0	D. Lanse Creuse Bay MI (N=23)	0.63 ± 0.07	8.7 ± 1.5
E. Grosse Isle MI (N=35)	0.73 ± 0.05	8.1 ± 1.1	E. Belle Isle MI (N=48)	0.70 ± 0.06	10.4 ± 1.6
F. Huron R. MI (N=40)	0.73 ± 0.03	7.8 ± 1.0	F. Monroe MI (N=30)	0.57 ± 0.07	7.0 ± 1.1
G. Hen Is. ON (N=65)	0.68 ± 0.03	7.1 ± 0.8	G. Sturgeon Creek ON (N=21)	0.58 ± 0.08	7.8 ± 1.5
Mean	0.72 ± 0.04	7.6 ± 1.0	Mean	0.64 ± 0.07	8.6 ± 1.4

Interpretation:

- 1) The HEC contains high levels of genetic diversity as well as unique variability
- 2) Relative diversity patterns are similar between both species

2) Genetic divergence among sites along the HEC

F_{ST} & X^2 comparisons

Walleye

Interpretation:

HEC walleye spawning groups show a mixture of divergence & connectivity

Sites	A	B	C	D	E	F
A) Flint R. MI	-----					
B) Thames R. ON	**	-----				
C) Belle Isle MI	**	NS	-----			
D) Fighting Is. MI	**	NS	**	-----		
E) Grosse Isle MI	**	NS	NS	NS	-----	
F) Huron R. MI	**	NS	NS	NS	NS	-----
G) Hen Is. ON	**	NS	**	**	NS	NS

Yellow Perch

Interpretation:

HEC yellow perch spawning groups show a lack of genetic connectivity among all sites

Sites	A	B	C	D	E	F
A) Saginaw Bay, MI	-----					
B) Algonac MI	**	-----				
C) Anchor Bay, MI	**	**	-----			
D) Lanse Creuse Bay MI	**	**	**	-----		
E) Belle Isle	**	**	**	**	-----	
F) Monroe MI	**	**	**	**	**	-----
G) Sturgeon Ck ON	**	**	**	**	**	**

2) Genetic exchange among sites along the HEC

N_M (=genetic migration) comparisons

Walleye

Sites	A	B	C	D	E	F
A) Flint R. MI	-----					
B) Thames R. ON	14	-----				
C) Belle Isle MI	9	195	-----			
D) Fighting Is. MI	6	33	45	-----		
E) Grosse Isle MI	7	307	158	150	-----	
F) Huron R. MI	12	Inf	214	32	114	-----
G) Hen Is. ON	7	65	47	47	76	61

Interpretation:

HEC walleye spawning groups show higher #s of migrants

Yellow Perch

Sites	A	B	C	D	E	F
A) Saginaw Bay, MI	-----					
B) Algonac MI	25	-----				
C) Anchor Bay, MI	16	84	-----			
D) Lanse Creuse Bay MI	22	50	44	-----		
E) Belle Isle MI	10	22	14	12	-----	
F) Monroe MI	12	26	34	22	12	-----
G) Sturgeon Ck ON	9	26	34	20	12	18

Interpretation:

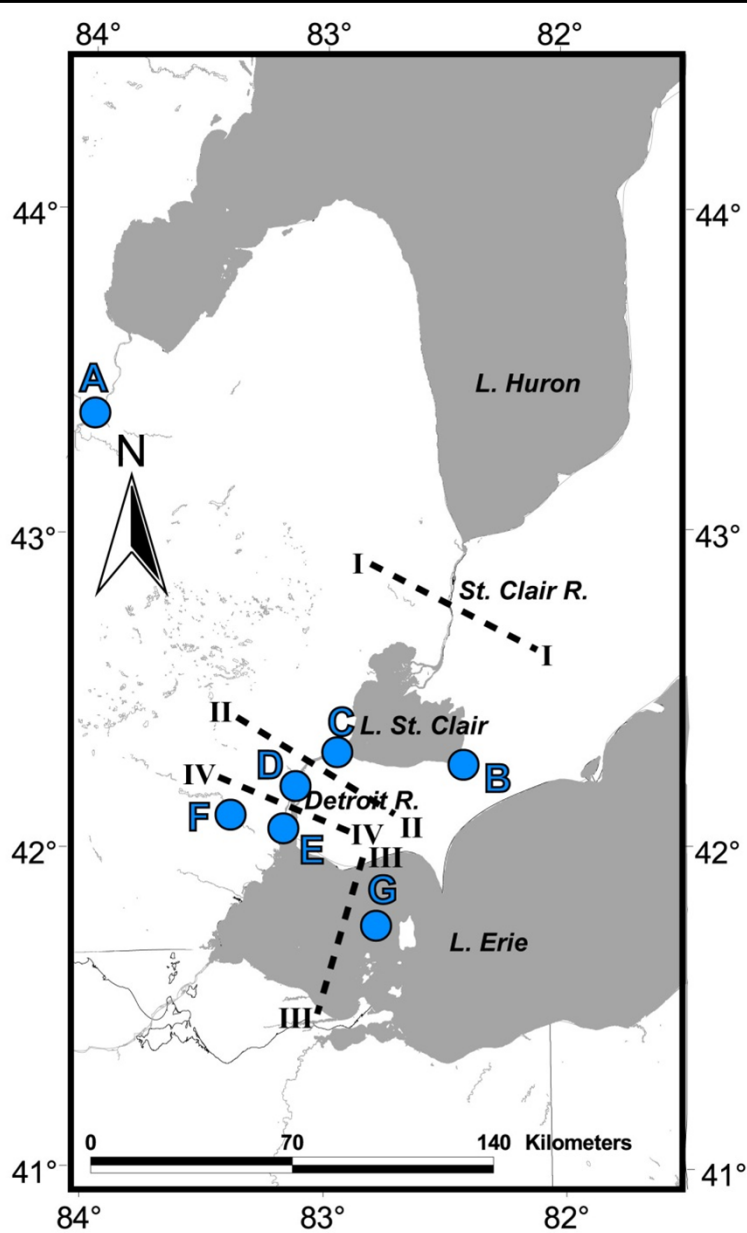
HEC yellow perch spawning groups show lower #s of migrants

2) Genetic divergence among sites along the HEC

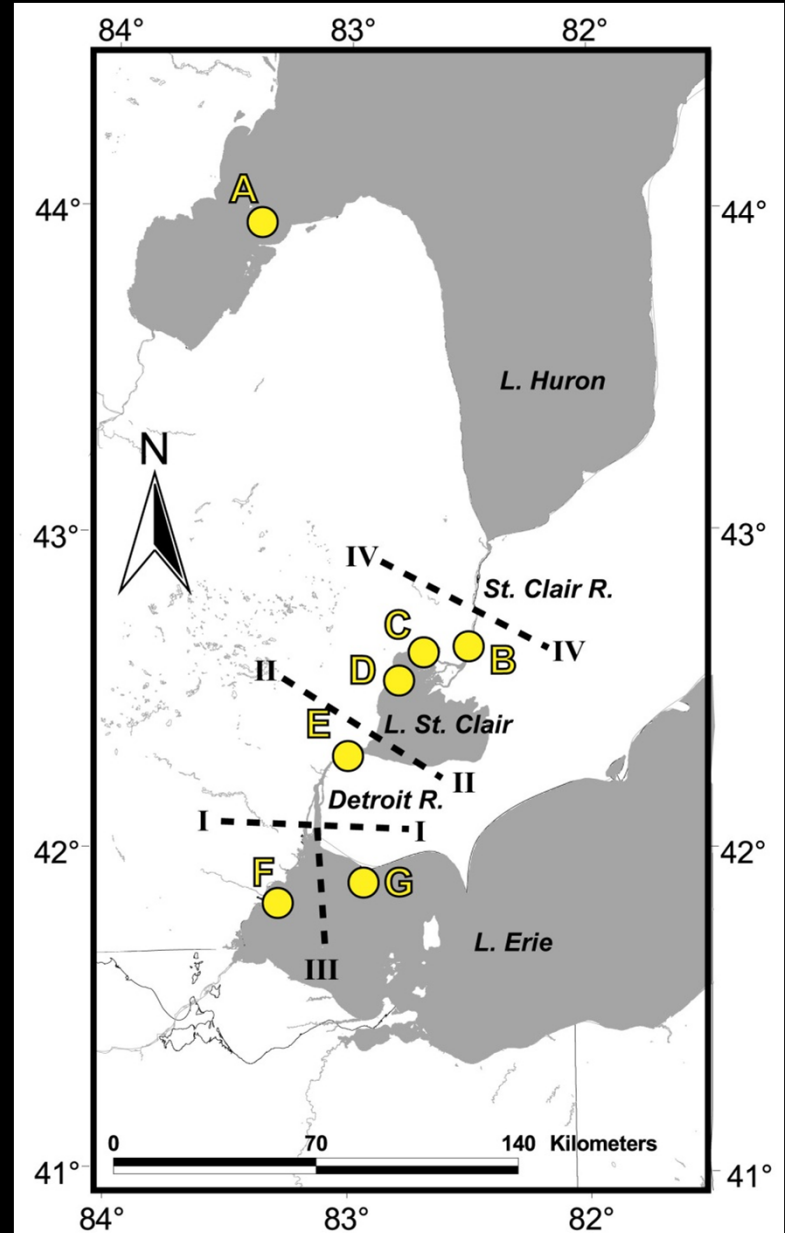
Walleye

Barrier analysis

Yellow Perch



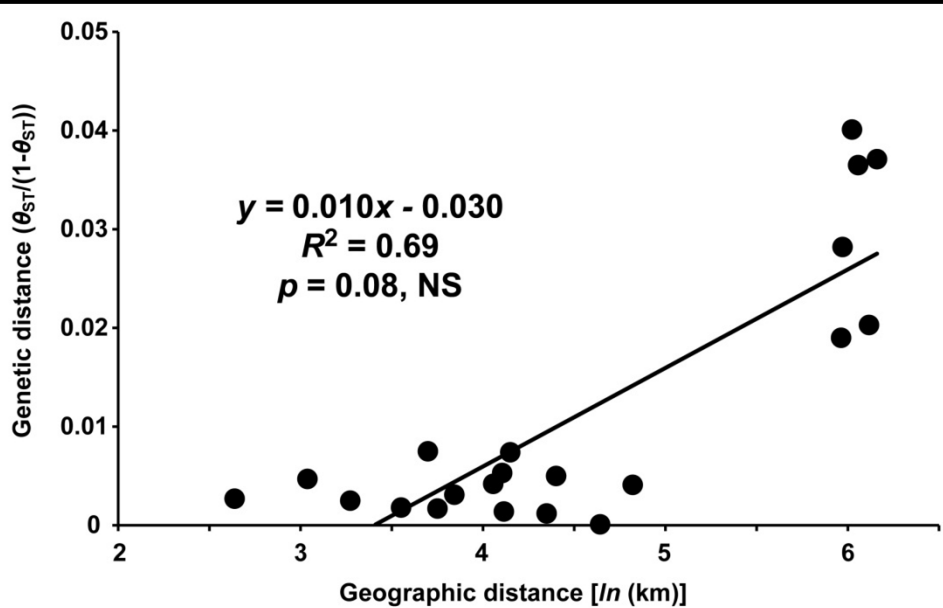
Ranking:
I = most significant
(supported by bootstrap & N loci)
IV = significant



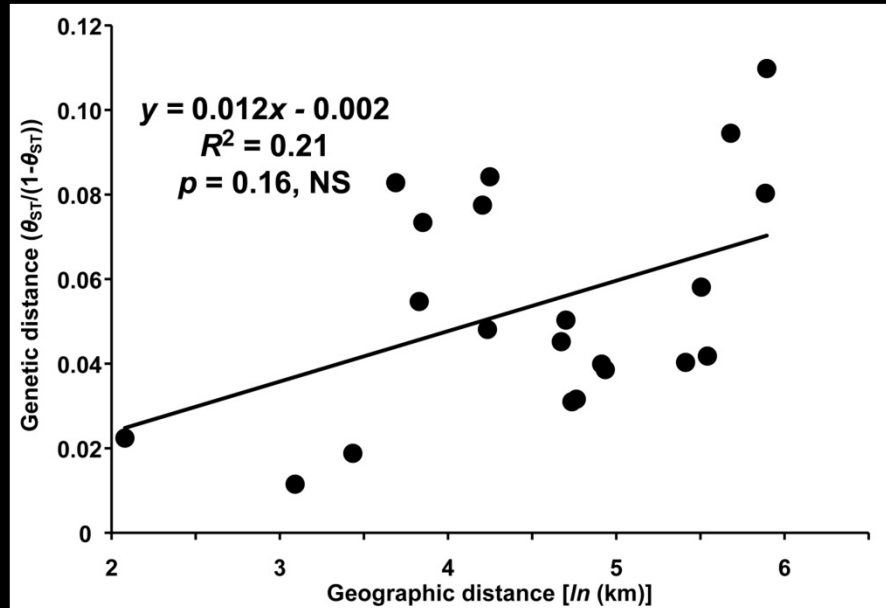
2) Genetic divergence among sites along the HEC

Genetic isolation by geographic distance

Walleye



Yellow Perch



Interpretation: Across the HEC relationships do not follow a genetic isolation by geographic distance pattern. **Factors other than geographic distance regulate the genetic connectivity among HEC spawning groups**

3) Changes in walleye genetic composition pre- vs. post-habitat augmentation at Fighting Island

Diversity comparisons

N =sample size

H_O =observed heterozygosity (diversity)

N_A =number of alleles

A_R =allelic richness (standardized)

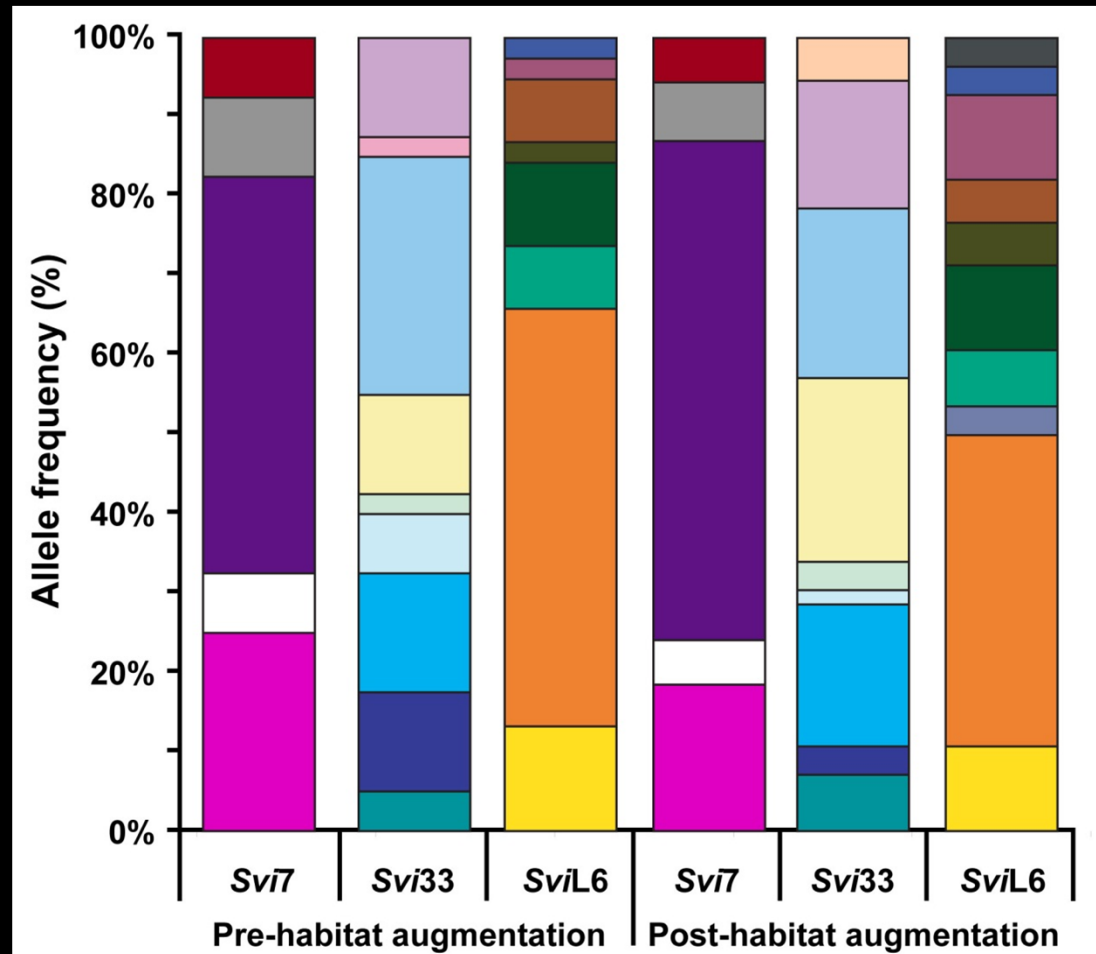
N_{PA} =number of private alleles (unique to a site)

P_{PA} =proportion of private alleles

	Pre-	Post-
N	20	28
H_O	0.72 ± 0.04	0.69 ± 0.04
N_A	67	70
A_R	7.3 ± 1.3	7.2 ± 1.0
N_{PA}	1	1
P_{PA}	0.01	0.01

Interpretation: Similar diversity levels from pre- to post-habitat augmentation (but sample sizes were low)

3) Fighting Island walleye – pre & post-habitat augmentation



Exact test =
32.7, $p=0.02^{**}$

3/9 loci shown

Interpretation: Genetic composition pre- vs. post-habitat augmentation significantly differed

3) Changes in walleye genetic composition pre- vs. post-habitat augmentation N_M (=genetic migration) comparisons

Site	B) Thames R.	C) Belle Isle	D) Pre	E) Grosse Isle	F) Huron R.	G) Hen Is.
Pre	43	30	---	187	35	45
Post	33	45	37	150	32	47

- Some return of individuals from pre- to post-habitat augmentation
- Genetic migration across the corridor with most migrating from Grosse Isle (E)

Summary & conclusions

- 1) High genetic diversity of walleye & yellow perch spawning groups across HEC, despite over a century of habitat degradation

- 2) Mixture of genetic connectivity & divergence among spawning groups
 - Walleye show more genetic connectivity
 - Fighting Is. spawners showing more divergence from other sites
 - Yellow perch spawning groups have high genetic divergence among sites

- 3) Genetic composition of Fighting Is. walleye significantly differed from pre- to post-habitat augmentation according to present sample sizes
 - Diversity levels were similar
 - Major contribution to spawning population appears to be from Grosse Isle

Acknowledgments

Grants:

Great Lakes Restoration Initiative
Project #70
USEPA
NOAA Ohio Sea Grant
NSF GK-12

Scholarships:

IAGLR
Norman S. Baldwin Fishery Science

Agencies:

ODNR
MDNR
OMNR
USGS
USFWS

Collectors:

M. Bagley	T. Hartman
J. Boase	T. Johnson
A. Bowen	K. Kayle
J. Chiotti	P. Kocovsky
A. Cook	R. Kuhaneck
S. DeWitt	B. Manny
J. Diemond	J. McFee
D. Fielder	E. Roseman
K. Glomski	M. Thomas
R. Haas	M. Werda

