Walleye spawning stocks in Lake Erie, the Huron-Erie Corridor, and across the Great Lakes
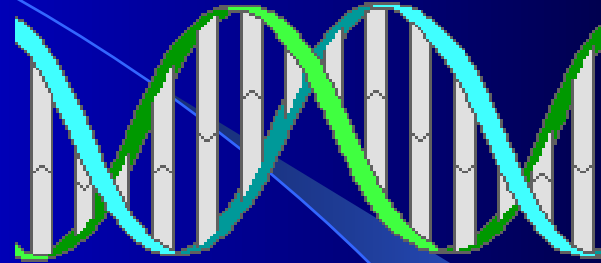
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What do we use DNA data for?

- 1. Delineate stocks
- 2. Determine which spawning groups/locations are the most critical
- 3. Measure changes in genetic diversity over time and space, in the face of exploitation and irregular year classes and recruitment
- 4. Predict where individuals originated (spawning group)
- 5. Match up eggs, larvae with adult life history stages
- 6. Identify unknowns (i.e., fish fillets, parents of fry, etc.)

Objectives of Our Study

To develop, test, analyze, and implement a high-resolution, low cost, and widely applicable DNA data base for analyzing fish stock structure in the Great Lakes for walleye.

Types of DNA data we are collecting: A Dual approach

Mitochondrial DNA Sequences:

Maternally-inherited

Can see clear geographic and historical patterns, and relation to other species

More expensive

Single locus

Nuclear DNA Microsatellite variation:

Biparentally-inherited

Less expensive, high through-put

Increased resolution power due to multiple loci

Couples well with mtDNA to address a variety of questions

Microsatellite DNA

Microsatellites (or VNTRs = variable number of tandem repeats) are short segments of DNA that have a repeated sequence such as CACACACA, which occur in non-coding DNA.

Microsatellites mutate rapidly and have no known function = "junk DNA".

These mutations are in the form of losses or gains of repeats.

Individuals in a population typically possess microsatellite alleles of different numbers of repeat copies, having variable lengths.

CACACACACACACACACACA 10
CACACACACACACACACACACA   11
CACACACACACACACACACACACA   12
CACACACACACACACACACACACACA   13
CACACACACACACACACACACACACACA   14

Inheritance of Microsatellites

CACACACACACACACACA 9
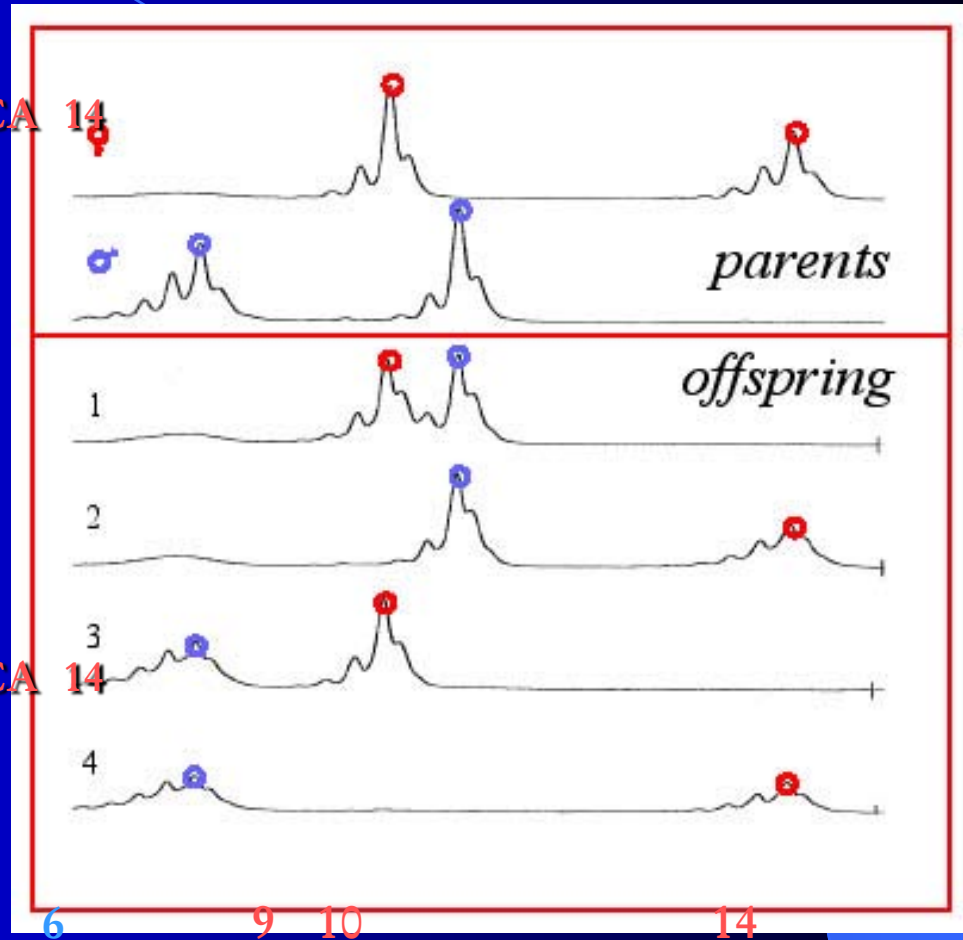CACACACACACACACACACACACACACA 14

CACACACACACA   6
CACACACACACACACACACA 10

CACACACACACACACACA 9
CACACACACACACACACACA 10

CACACACACACACACACACA 10
CACACACACACACACACACACACACACA 14

CACACACACACA   6
CACACACACACACACACA 9

CACACACACACA   6
CACACACACACACACACACACACACACACACA 14

Diploid organisms (such as walleye and humans) each have 2 copies.

Populations (stocks) that are isolated diverge in microsatellite frequency lengths over time

	Pop A:	Pop B:
9	10%	1%
10	80%	35%
11	8%	47%
12	2%	17%

We assay several different microsatellite loci to test this hypothesis independently and statistically.

Application of the Study

Our studies build upon the past studies to better understand fine-scale stock structure, allow unknowns to be genetically typed, and to produce a large interactive data base at low cost for use by fishery scientists and managers.

Genetics of the Walleye
Sander vitreus

- Our work to date, as well as tagging data & ecological data, indicates that there are significant differences in genetic composition among spawning groups

- These data appear to support spawning site philopatry (i.e., natal homing)

- Differences among populations in the Great Lakes have been maintained by this behavior since their founding after the Ice Ages
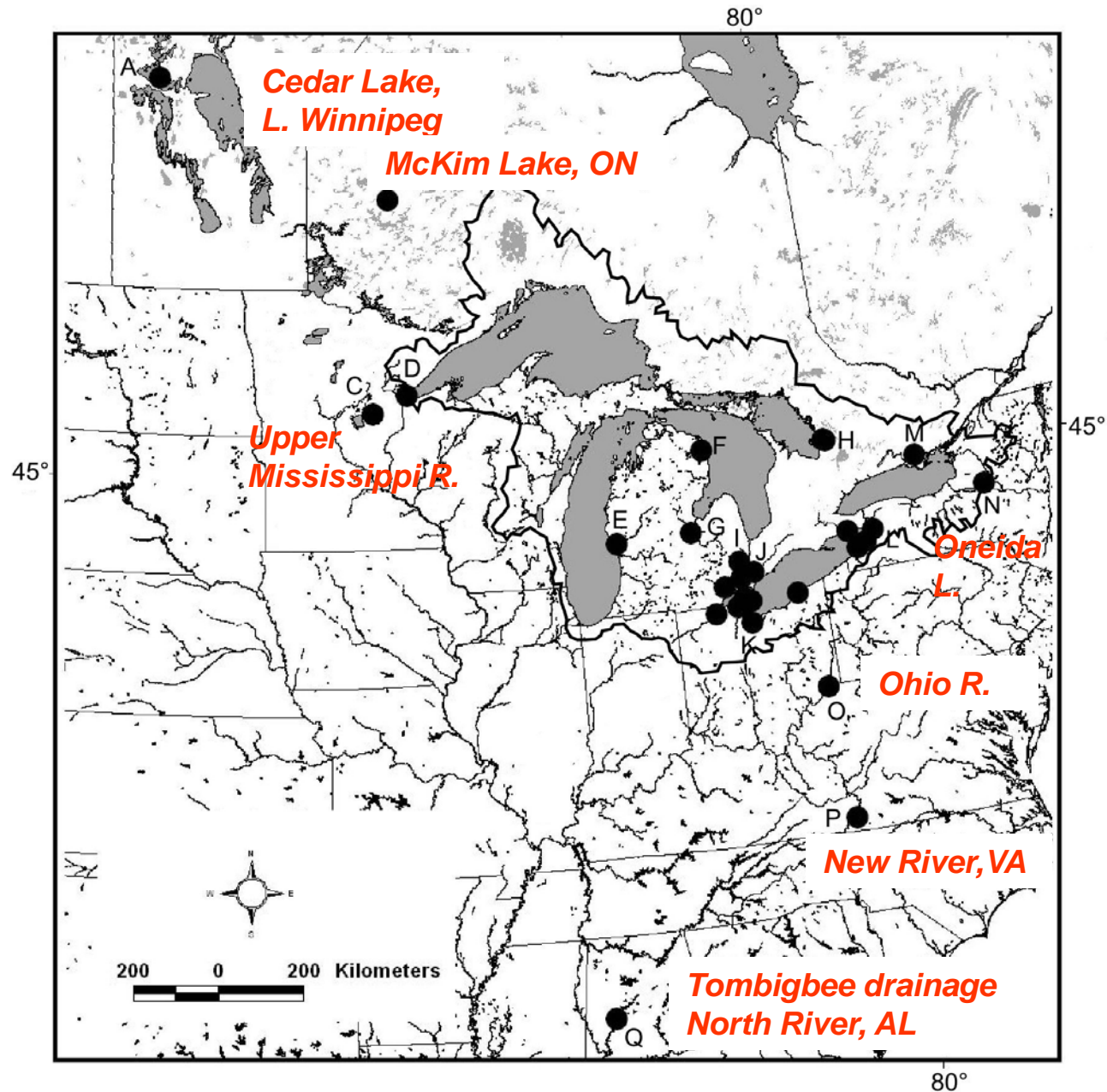
Our recent papers on walleye genetics

- Signatures of vicariance, postglacial dispersal, and spawning philopatry: Population genetics and biogeography of the walleye *Sander vitreus*. *Molecular Ecology, 2009. 18: 3411–3428. Stepien, Murphy*, Lohner, Sepulveda-Villet & Haponski*

- Status and delineation of walleye genetic stock structure across the Great Lakes, *Great Lakes Fisheries Commission Special Report, 2010: In Press. Stepien, Murphy, Lohner, Haponski & Sepulveda-Villet*

Methods

- **Analyzed 10-15 nuclear microsatellite loci 1876 Walleye, 1518 Great Lakes, 1266 Lake Erie**

- **28 spawning sites**

  -Great Lakes (Lakes Superior, Michigan, Huron, St. Clair, Erie*, Ontario)

  -Northwest outlying populations:
  - Lake Winnipeg area – Cedar Lake
  - Southwest Ontario -McKim Lake/Papaonga R.
  - upper Mississippi River drainage - Mille Lacs

  -Southeast outlying populations:
  - Ohio River drainage
  - Tennessee/Tombigbee R. drainage to Mobile Bay, Gulf of Mexico (North River)
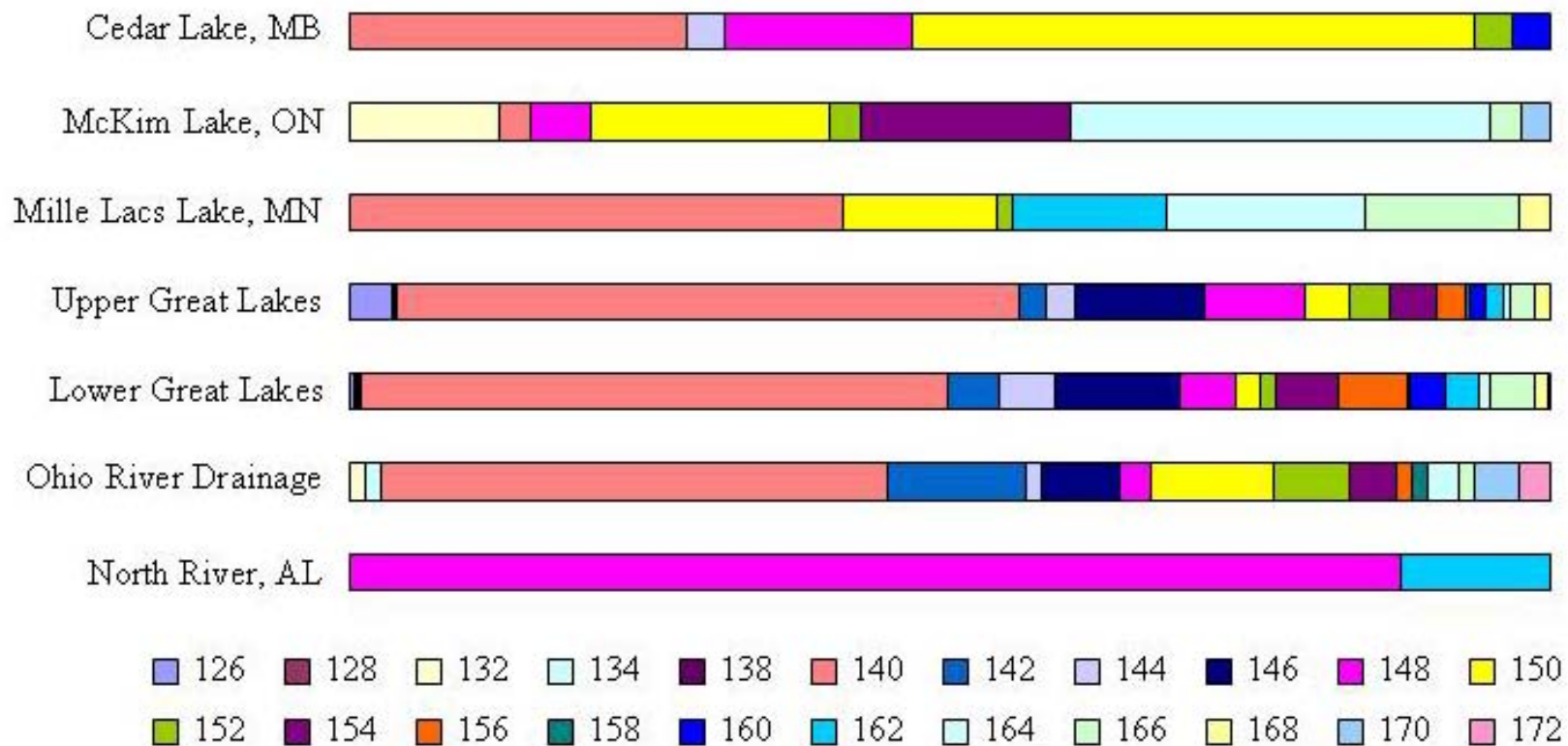
Walleye Population Study Sites

Cedar Lake, L. Winnipeg

McKim Lake, ON

Upper Mississippi R.

Oneida L.

Ohio R.

New River, VA

Tombigbee drainage North River, AL

200   0   200 Kilometers

Genetic Diversity Comparisons

Site	N	Heterozygosity	Proportion private alleles
Lake Winnipeg	16	.59	.00
Upper Mississippi River	39	.59	.04
Lake Superior	38	.68	.03
Lake Michigan	50	.72	.00
Lake Huron	125	.71	.02
Lake St. Clair	78	.73	.03
Western Lake Erie	268	.69	.03
Eastern Lake Erie	182	.73	.01
Lake Ontario watershed	70	.69	.00
Ohio River drainage	39	.68	.01
Tennessee River drainage	06	.54	.23
Total/Mean	921	.70	--

Example: Allelic variation among walleye population sites

Svi 6

Cedar Lake, MB
McKim Lake, ON
Mille Lacs Lake, MN
Upper Great Lakes
Lower Great Lakes
Ohio River Drainage
North River, AL

□ 126 ■ 128 □ 132 □ 134 ■ 138 ■ 140 ■ 142 □ 144 ■ 146 ■ 148 □ 150
□ 152 ■ 154 ■ 156 ■ 158 ■ 160 ■ 162 □ 164 □ 166 □ 168 □ 170 □ 172

Example: Allelic variation among walleye population sites at *Svi* L7 locus

Svi L7

Cedar Lake, MB
McKim Lake, ON
Mille Lacs Lake, MN
Upper Great Lakes
Lower Great Lakes
Ohio River Drainage
North River, AL

☐ 174	■ 176	☐ 178	☐ 180	■ 182	■ 184
■ 186	☐ 188	■ 190	■ 192		
■ 194	■ 196	■ 198	☐ 200	■ 202	■ 204
■ 206	☐ 208	☐ 210	☐ 212		
☐ 214	■ 216	■ 218	■ 220	■ 222	■ 224
■ 226					
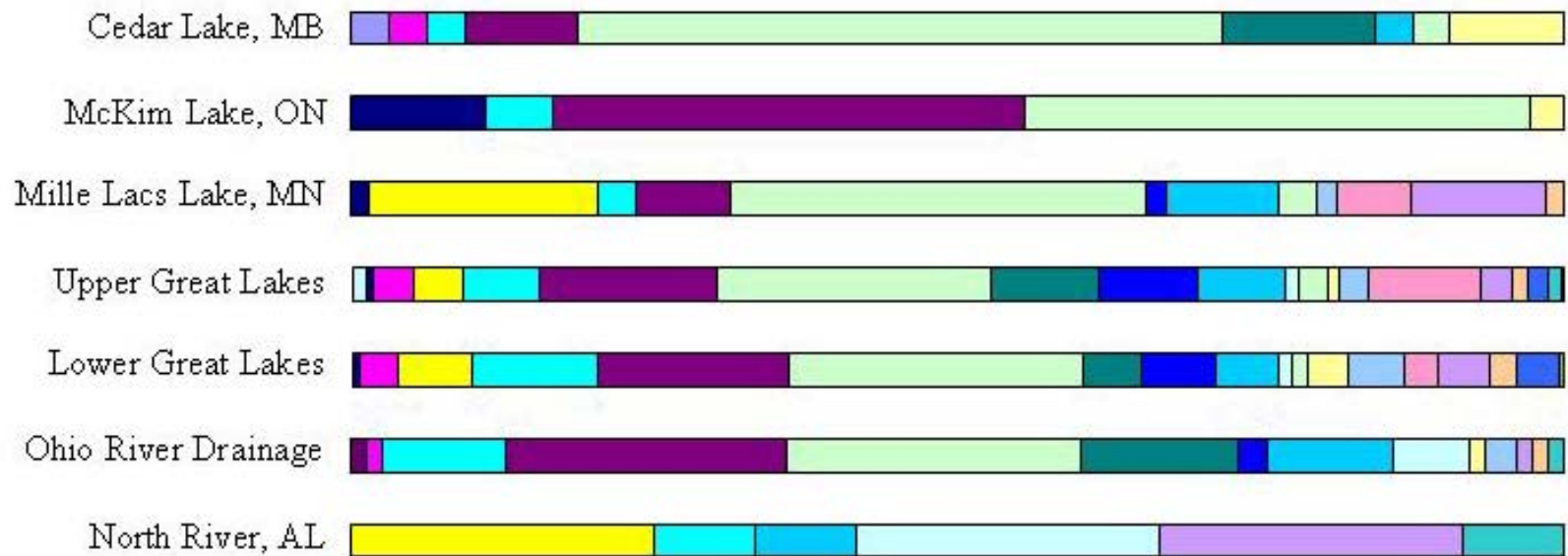
Mantel Test shows Broadscale Genetic Isolation by Geographic Distance

$P < 0.0001^{**}$, $R^2 = 0.263$,

$y = 0.043 \, X - 0.180$

Genetic Distance $F_{ST} \cdot (1 - F_{ST})^{-1}$

Geographic Distance ln (km)
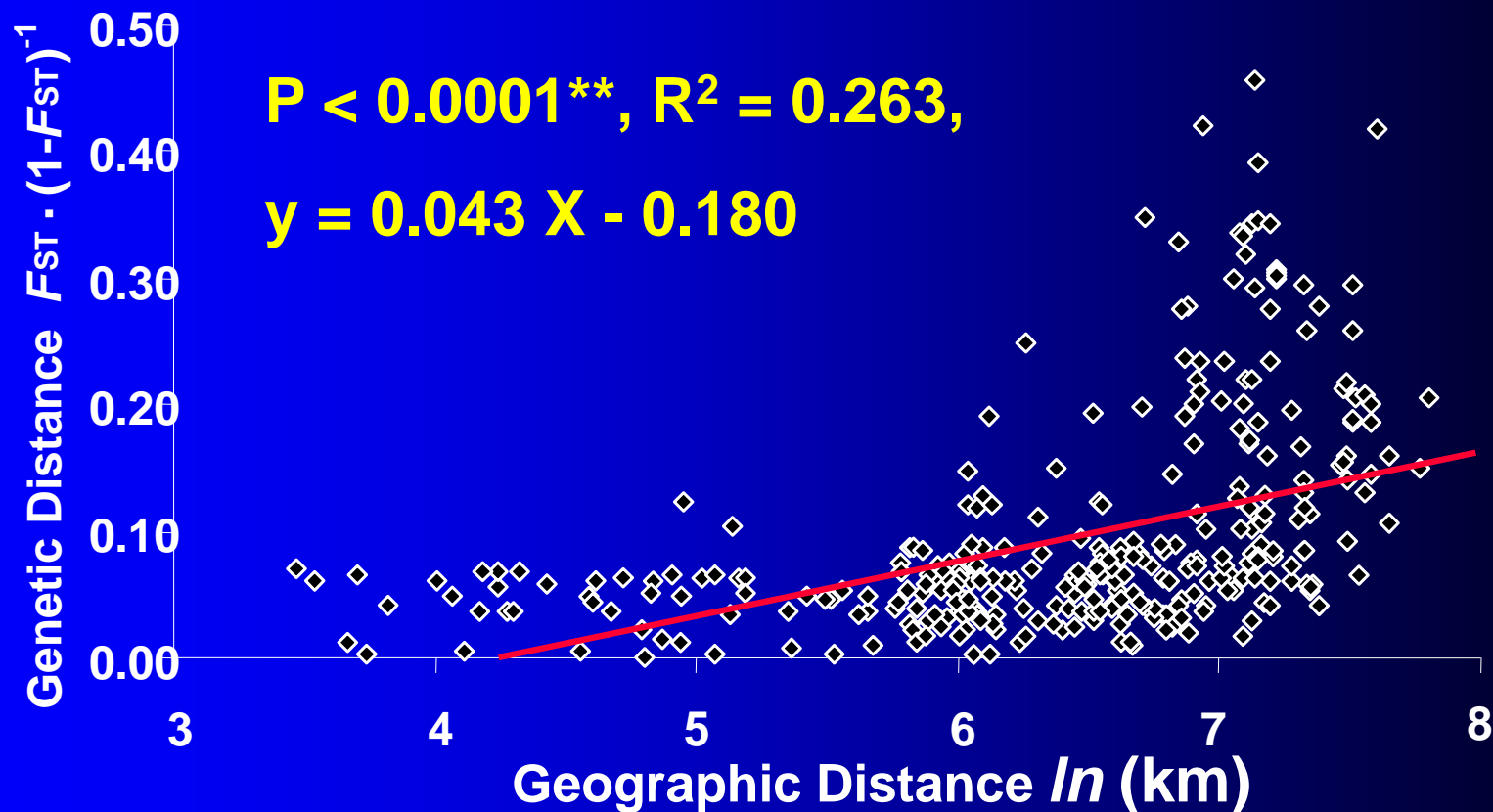
Genetic Structure of Walleye Across North America
(Stepien et al. 2009, Molecular Ecology)

$F_{ST}=.05**$

$F_{ST}=.04**$

$F_{ST}=.06**$

I

II

III

III

I

II
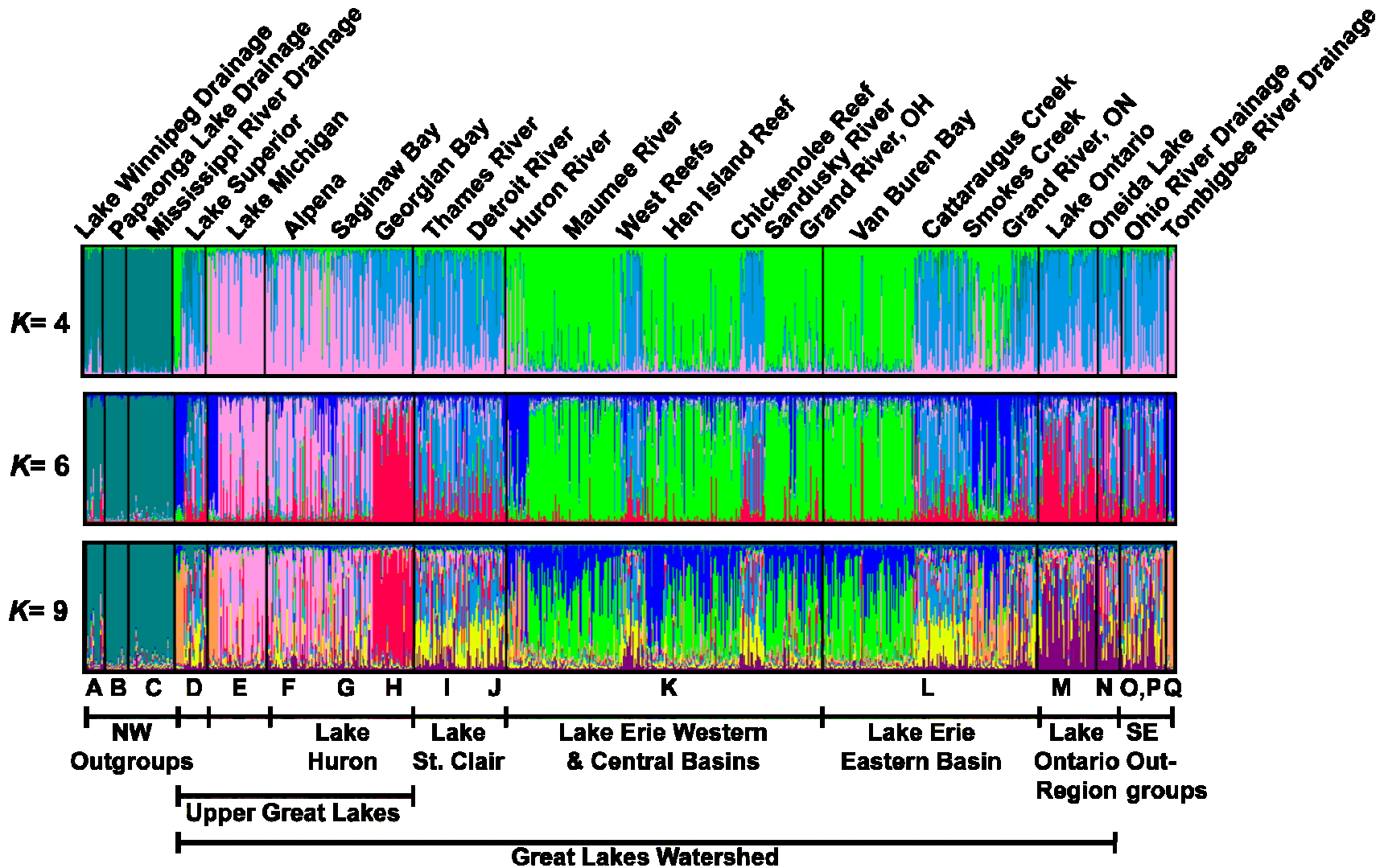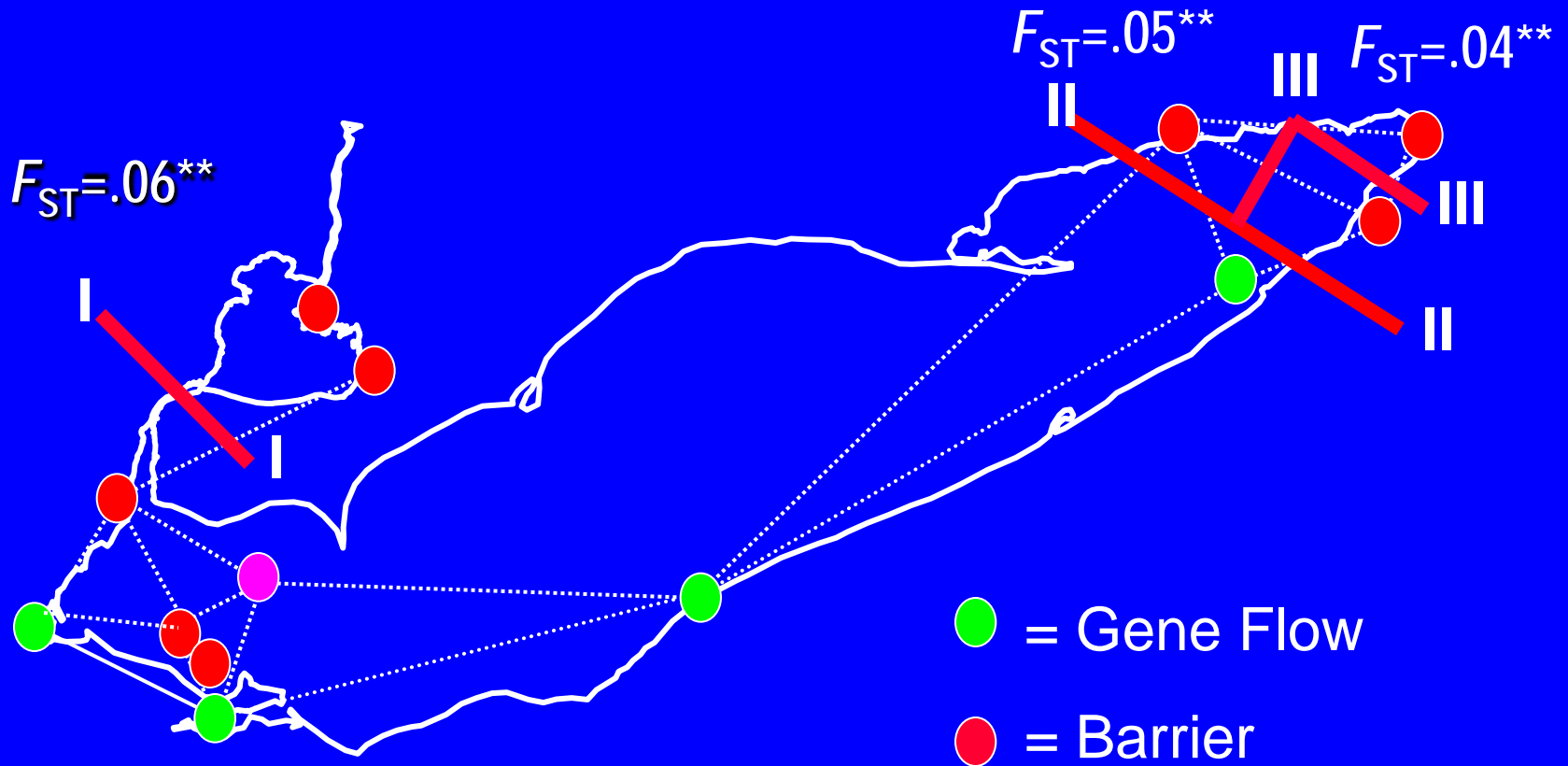
= Gene Flow

= Barrier

Walleye Finescale Population Barriers in Lake Erie N=501, 12 Sites

Gene flow among sites per year

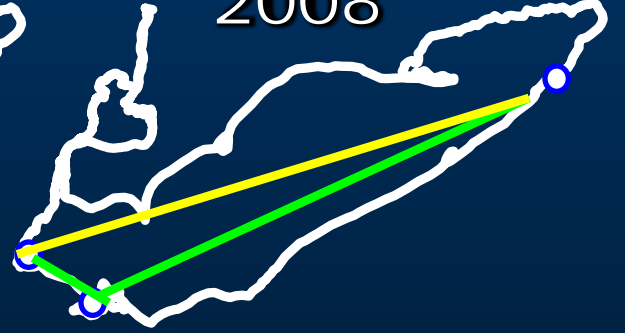**1995**

1998

2003

2005

2007

2008

High gene flow (NS)
Fst .000-.005

Some gene flow *
Fst .004-.008

No gene flow **
Fst .008-.033

Conclusions & Summary

1) *Does genetic diversity change across the range of walleye?*
Somewhat, .50-.74; highest in Great Lakes
Is it higher in nonglaciated areas?
No, highest in areas where glacial refugia meet in G. Lakes

2) *How many primary walleye population groups occur across the native range?* =9

3) *What/where are the primary genetic barriers?*
-NW region in Canada (Missouri refugium)
-Mobile Bay drainage, L. Superior, Georgian Bay (L. Huron), -L. Ontario, L. St. Clair, Ohio R. drainage
-In L. Erie: eastern river sites

4) *Do their genetic patterns fit an isolation by geographic distance hypothesis?* Yes broadscale
No finescale (Lake Erie)

5) *What fine scale patterns are discerned?*
-E Lake Erie walleye very different from W
-Spawning groups mostly appear temporally stable
-Spawning groups mostly are genetically differentiated, except along southern shore in some years
-Some years have more genetic mixing than others

Thank You!

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- NOAA Ohio Sea Grant
- USEPA
- Lake Erie Protection Fund

Collections:
- *Michigan DNR*
- *Minnesota DNR*
- *NY Dept. of Environmental Conservation*
- *Pennsylvania Fish and Boat Commission*
- *Ohio DNR Division of Wildlife*
- *Ontario Ministry of Natural Resources*
- *Wisconsin DNR*
- *US Fish & Wildlife Service*
- *US Geological Survey*

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