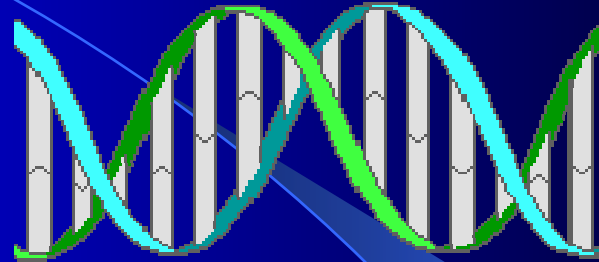# What DNA tells us about Walleye (& other fish) in the Great Lakes

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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, 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 and yellow perch.

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.

CACACACACACACACACA 10
CACACACACACACACACACA 11
CACACACACACACACACACACA 12
CACACACACACACACACACACACA 13
CACACACACACACACACACACACACA 14

Inheritance of Microsatellites
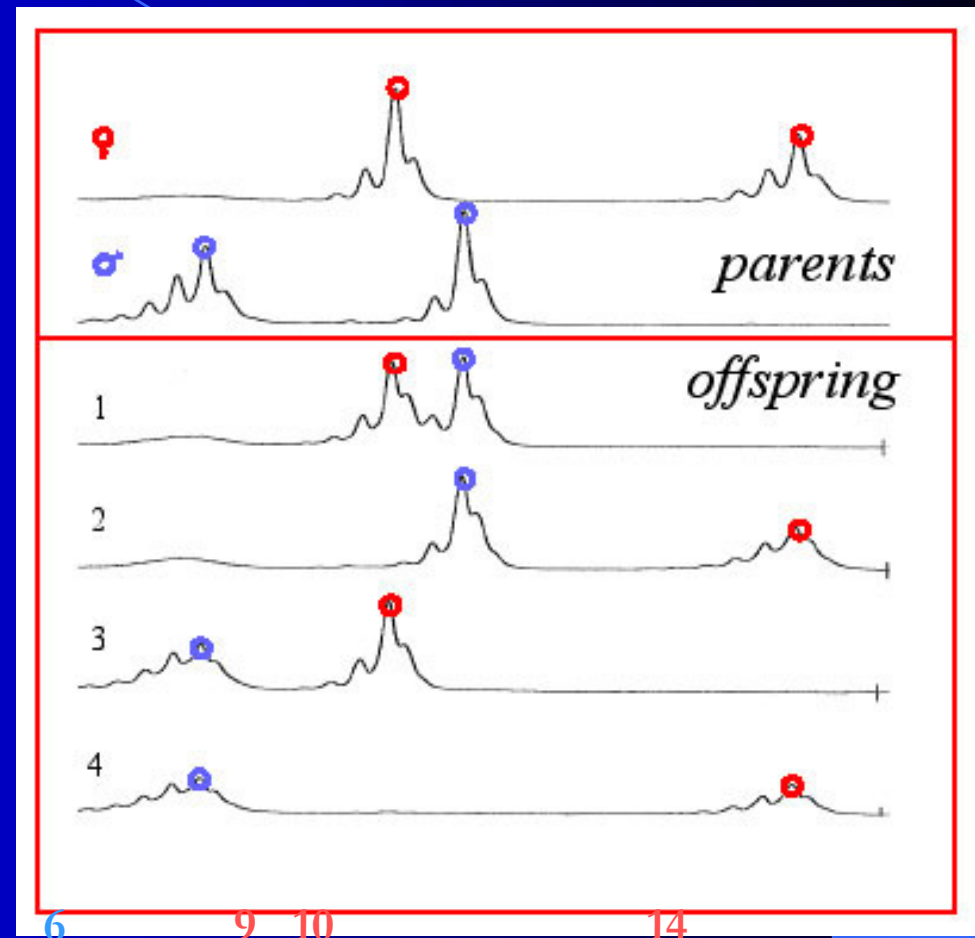
CACACACACACACACACA 9
CACACACACACACACACACACACACA 14

CACACACACACA 6
CACACACACACACACACACA 10

CACACACACACACACACA 9
CACACACACACACACACACA 10

CACACACACACACACACACACA 10
CACACACACACACACACACACACACACA 14

CACACACACACA 6
CACACACACACACACACACA 9

CACACACACACA 6
CACACACACACACACACACACACACACA 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**

Methods

- **Analyzed 10 (going to 15) nuclear microsatellite loci**
- **1000+ Walleye**
- **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)

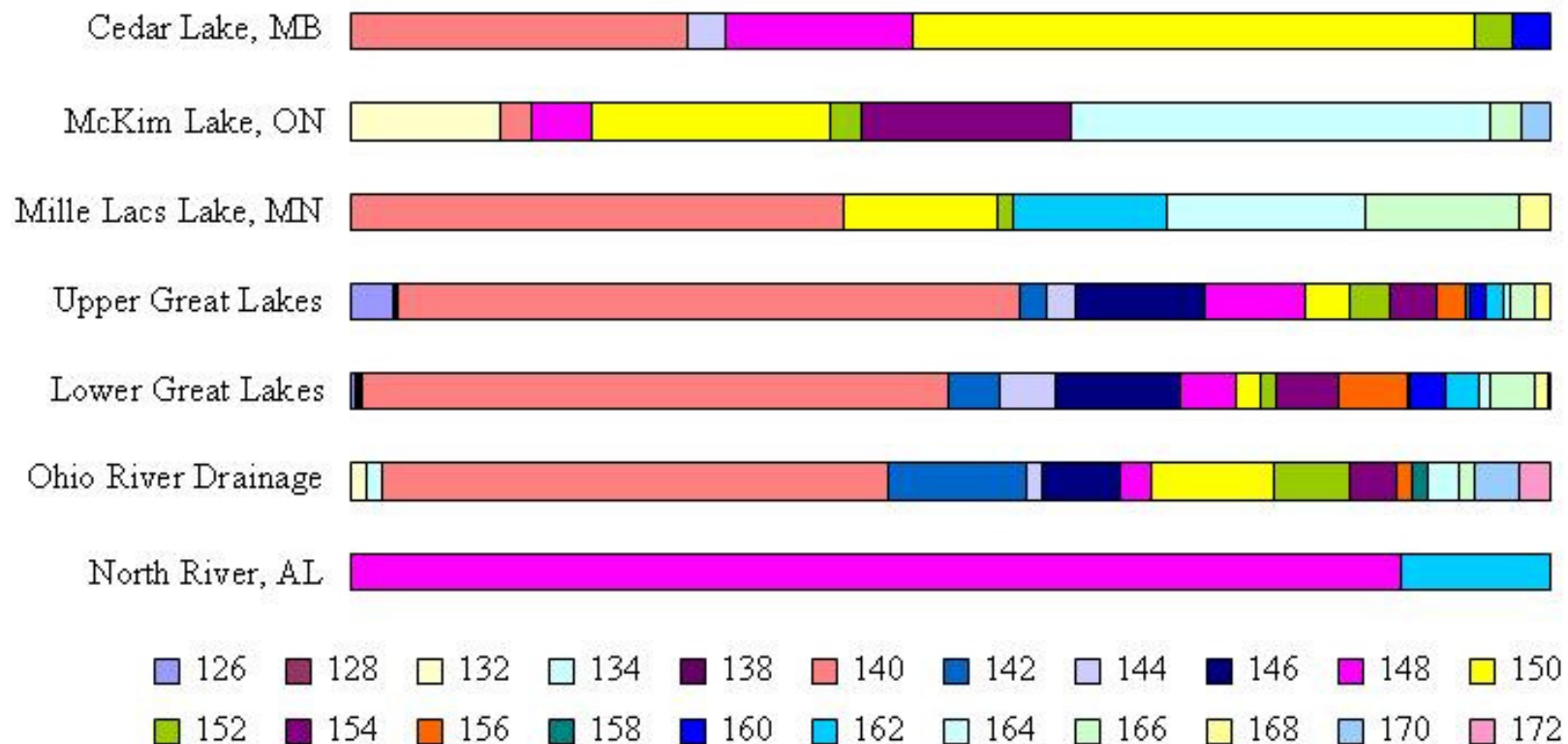# Walleye Population Study Sites
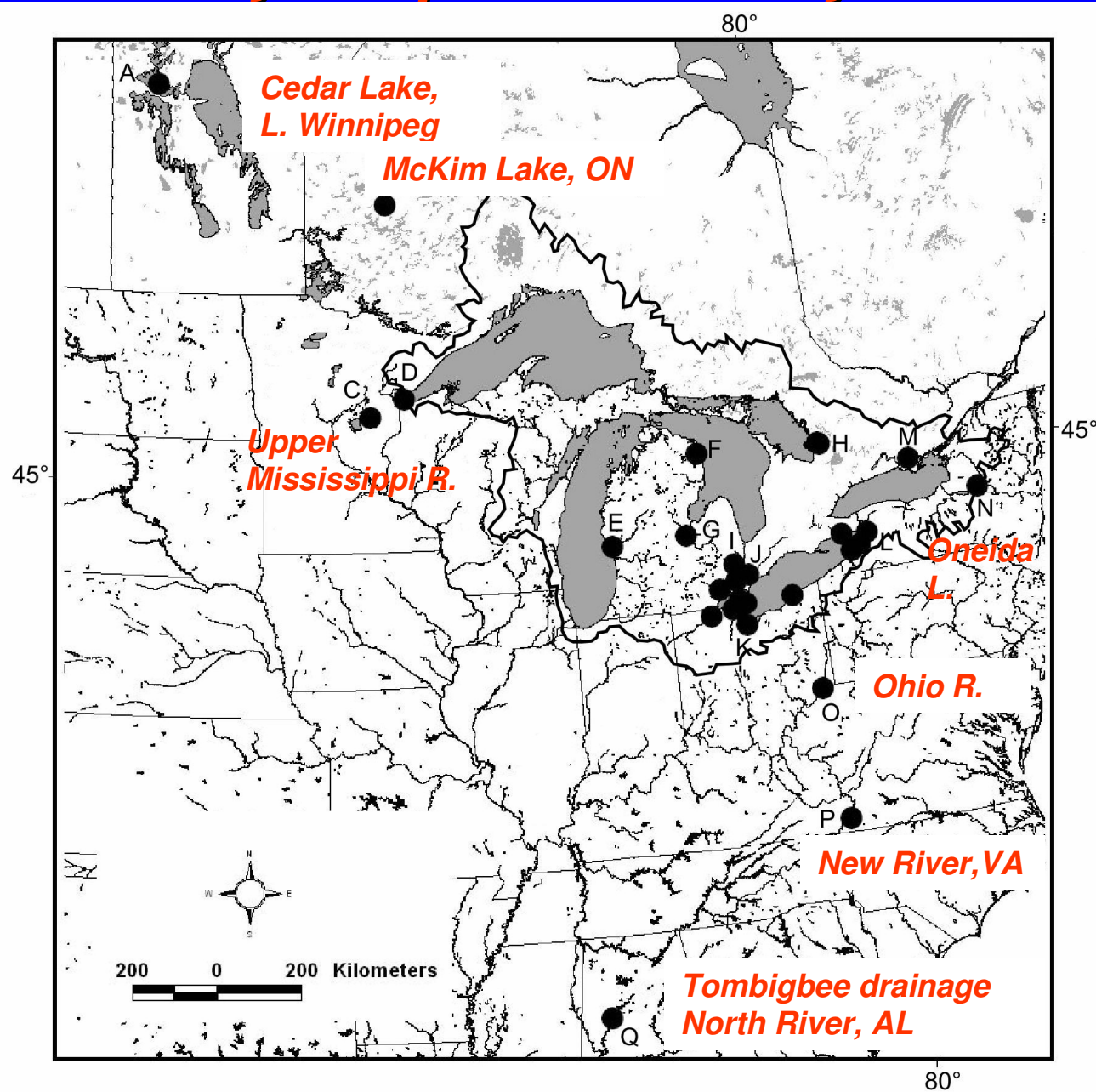
Genetic Diversity Comparisons

| Site	N	Heterozygosity	Proportion private alleles
Lake Winnipeg	16	.60	.02
Upper Mississippi River	39	.58	.05
Lake Superior	38	.62	.02
Lake Michigan	50	.69	.00
Lake Huron	125	.70	.03
Lake St. Clair	78	.73	.03
Western Lake Erie	319	.69	.03
Eastern Lake Erie	182	.72	.02
Lake Ontario watershed	70	.69	.00
Ohio River drainage	39	.68	.01
Tennessee River drainage	06	.50	.20
Total/Mean	972	.70	--

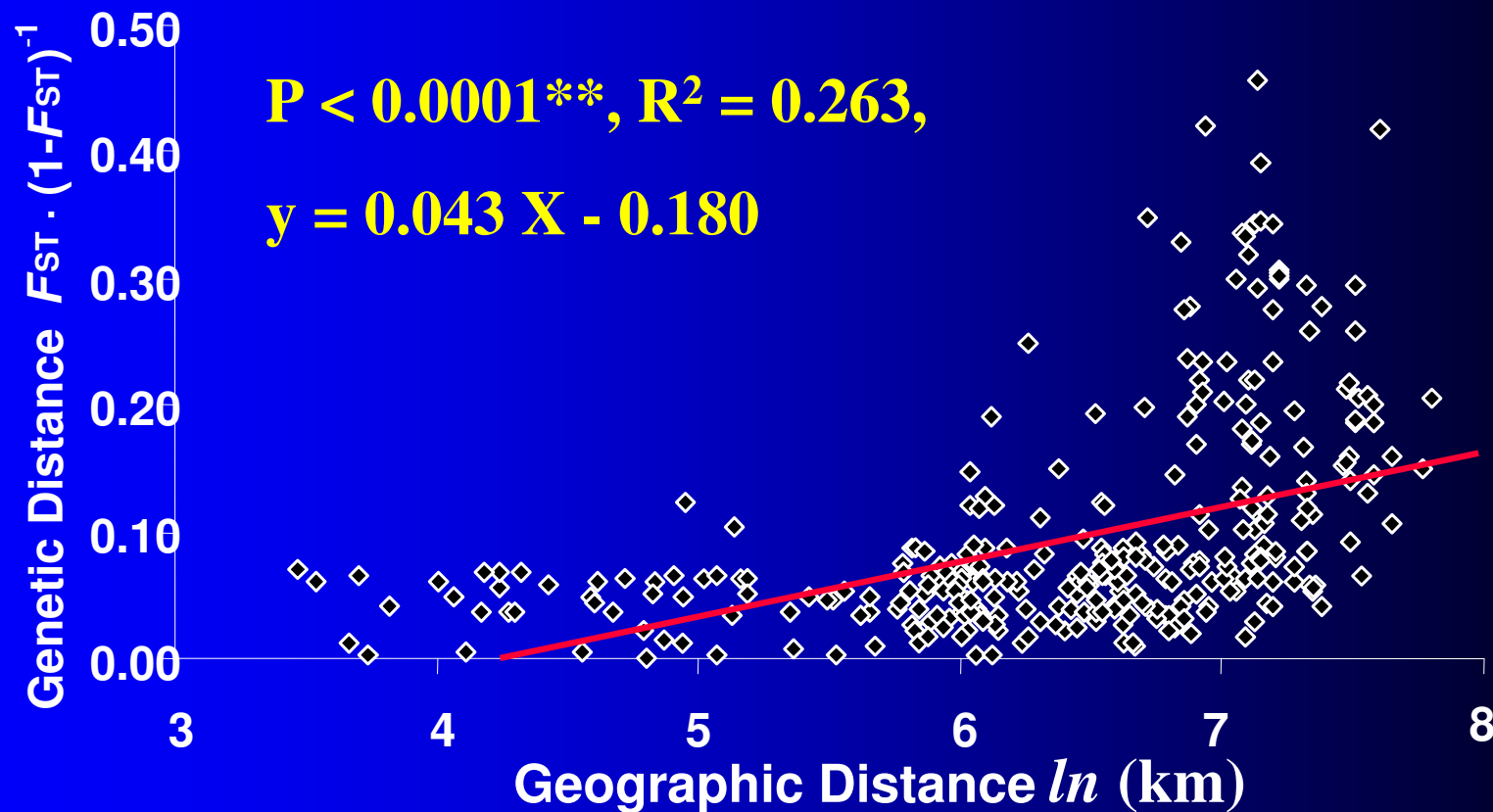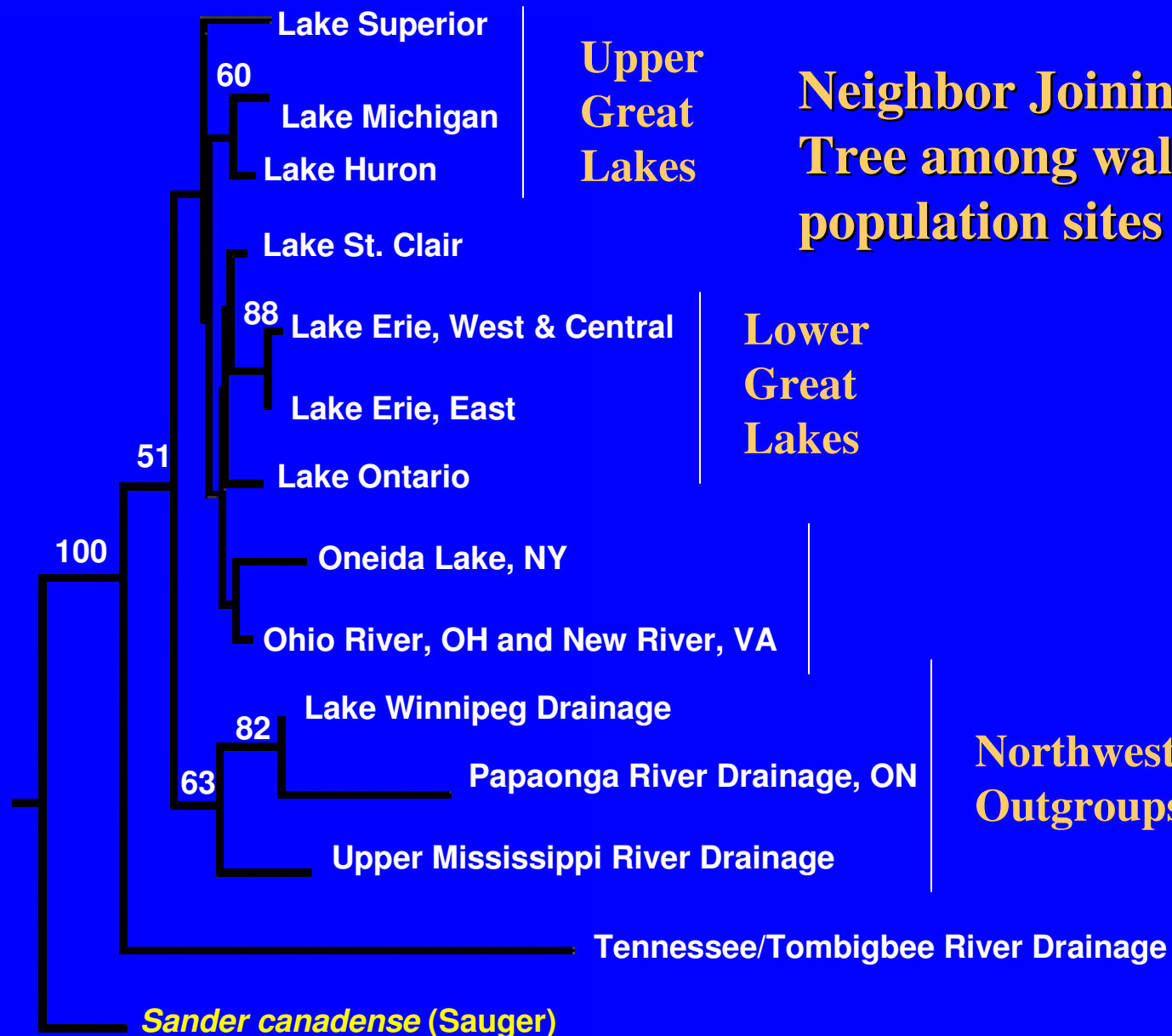# Example: Allelic variation among walleye population sites

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

Svi L7
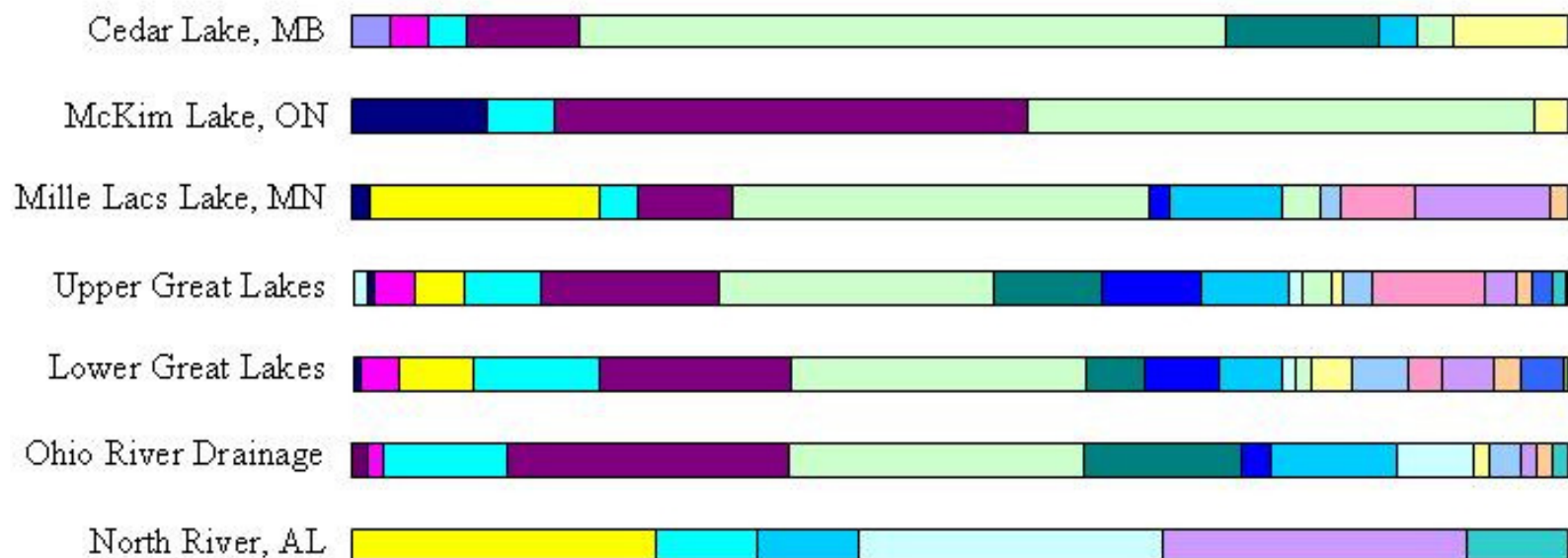
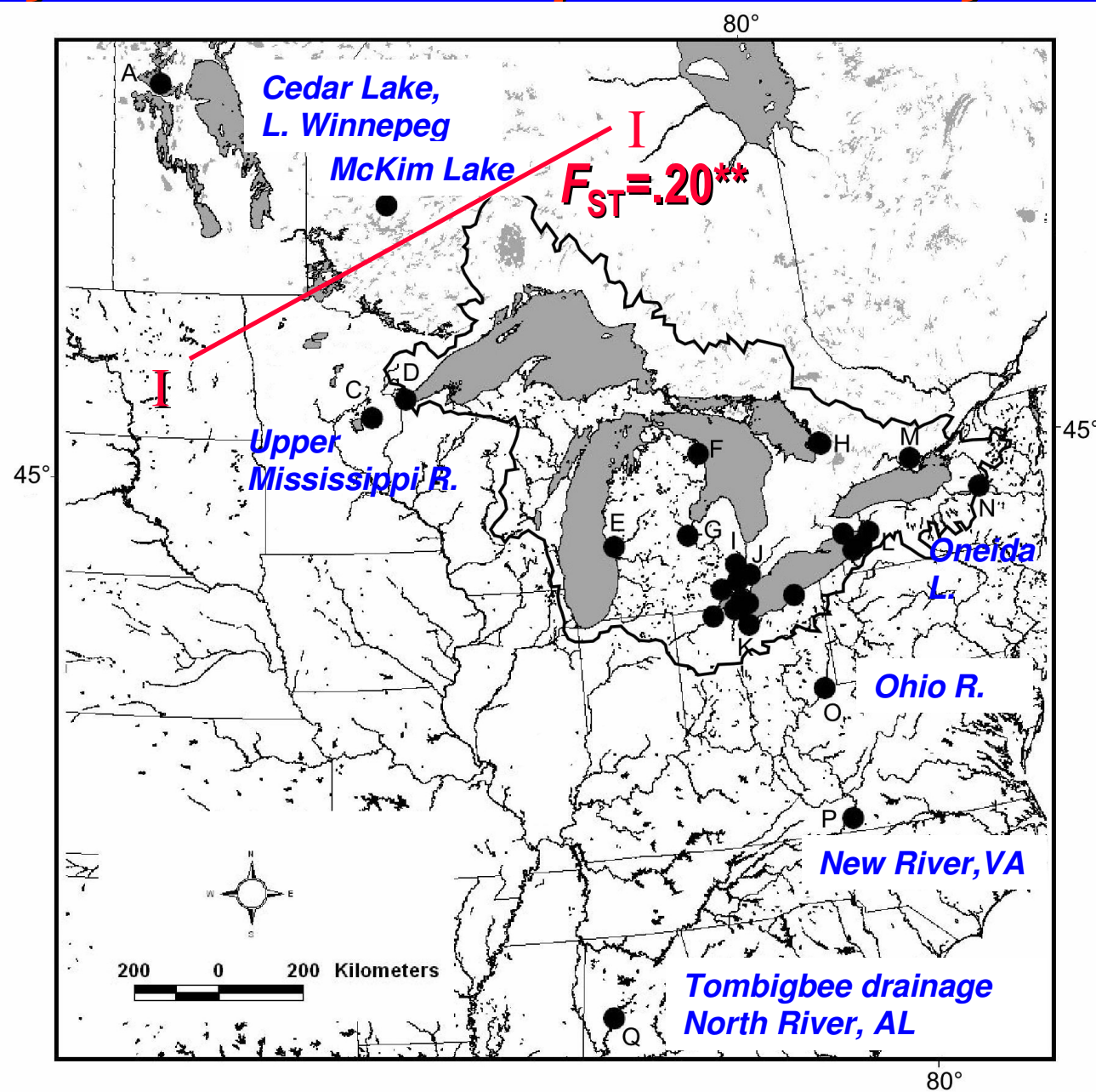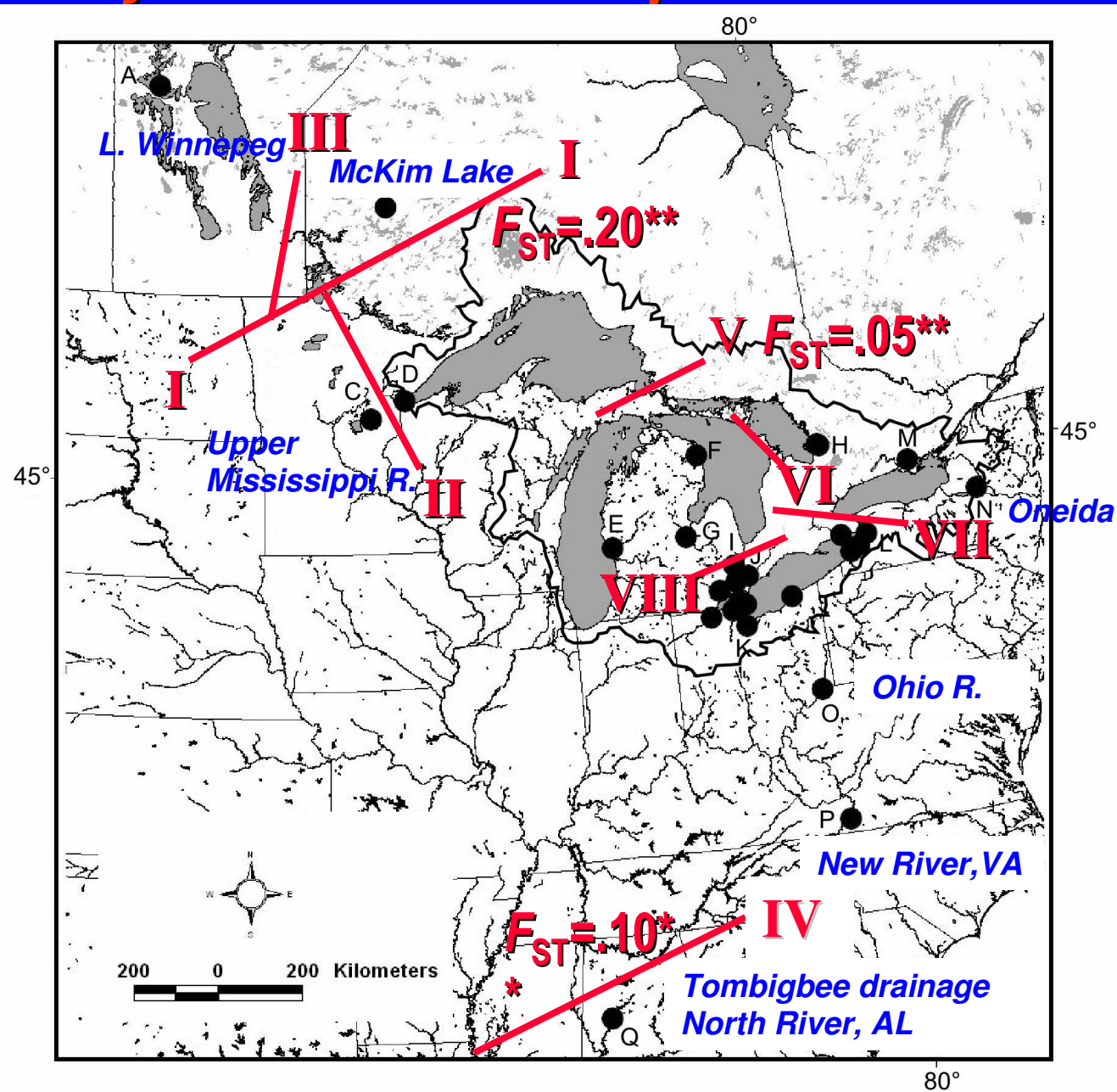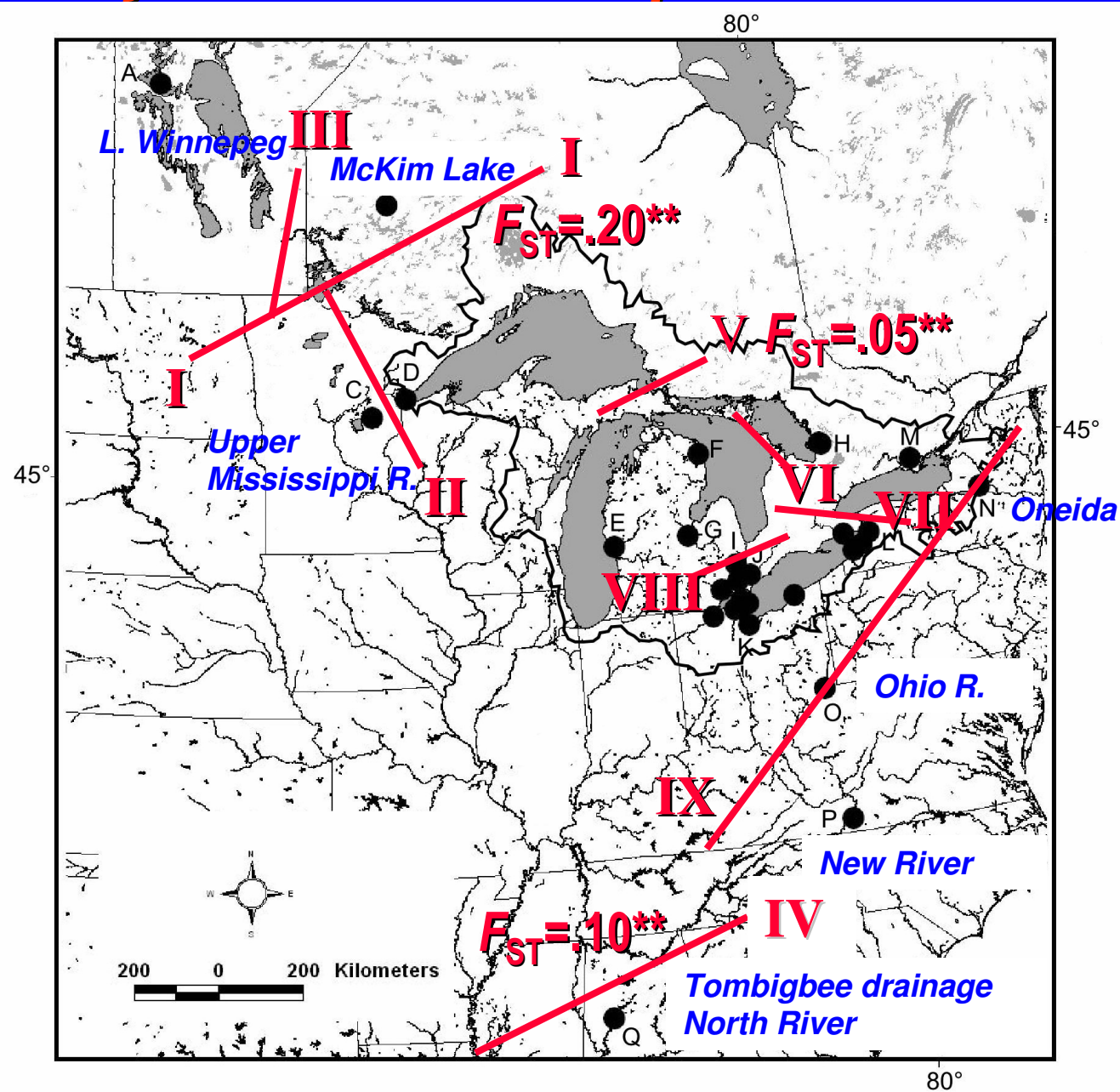# Mantel Test shows Broadscale Genetic Isolation by Geographic Distance

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

$y = 0.043 \, X - 0.180$

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

Geographic Distance ln (km)

Neighbor Joining Tree among walleye population sites

Lake Superior
60
Lake Michigan
Lake Huron

Upper Great Lakes

Lake St. Clair
88 Lake Erie, West & Central
Lake Erie, East
Lake Ontario

Lower Great Lakes

51
100
Oneida Lake, NY
Ohio River, OH and New River, VA

Lake Winnipeg Drainage
82
63
Papaonga River Drainage, ON
Upper Mississippi River Drainage

Northwest Outgroups

Tennessee/Tombigbee River Drainage

Sander canadense (Sauger)

0.01   Nei's (1972) Genetic Distance

Walleye Broadscale Population Study Barriers

Cedar Lake,
L. Winnepeg

McKim Lake

F_{ST}=.20**

Upper
Mississippi R.

Oneida
L.

Ohio R.

New River, VA

200   0   200 Kilometers

Tombigbee drainage
North River, AL

Walleye Broadscale Population Barriers

Walleye Broadscale Population Barriers

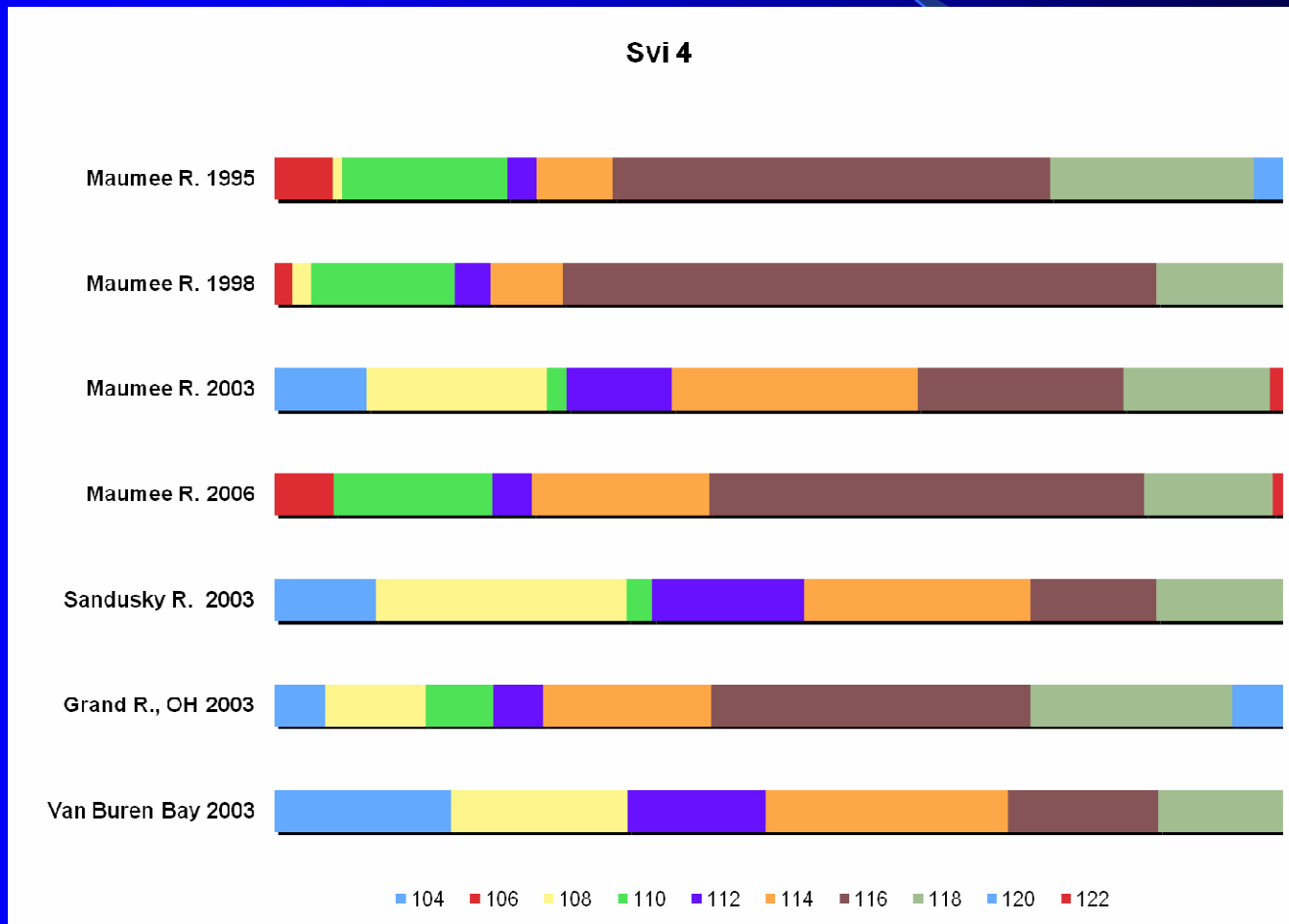# Bayesian Structure Analysis to Identify Population Groups
K=9, pp=0.98

F_{ST}=.050**

F_{ST}=.060**

II

III

III

I

III

II

I

= Gene Flow
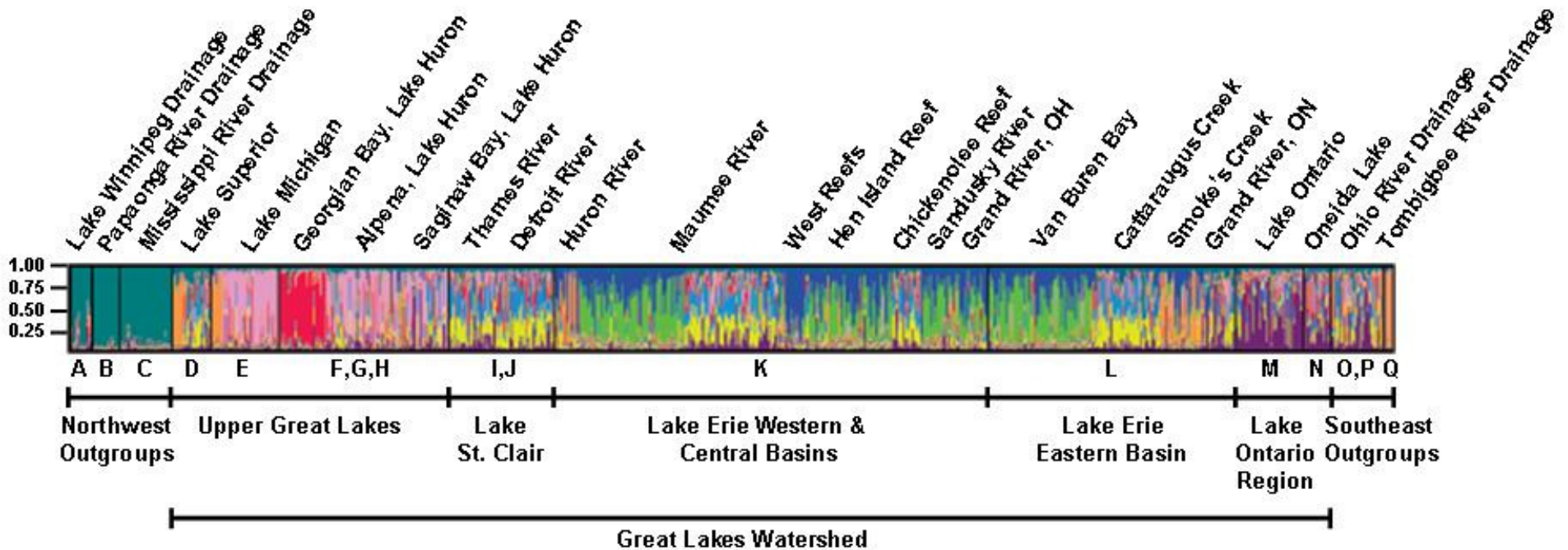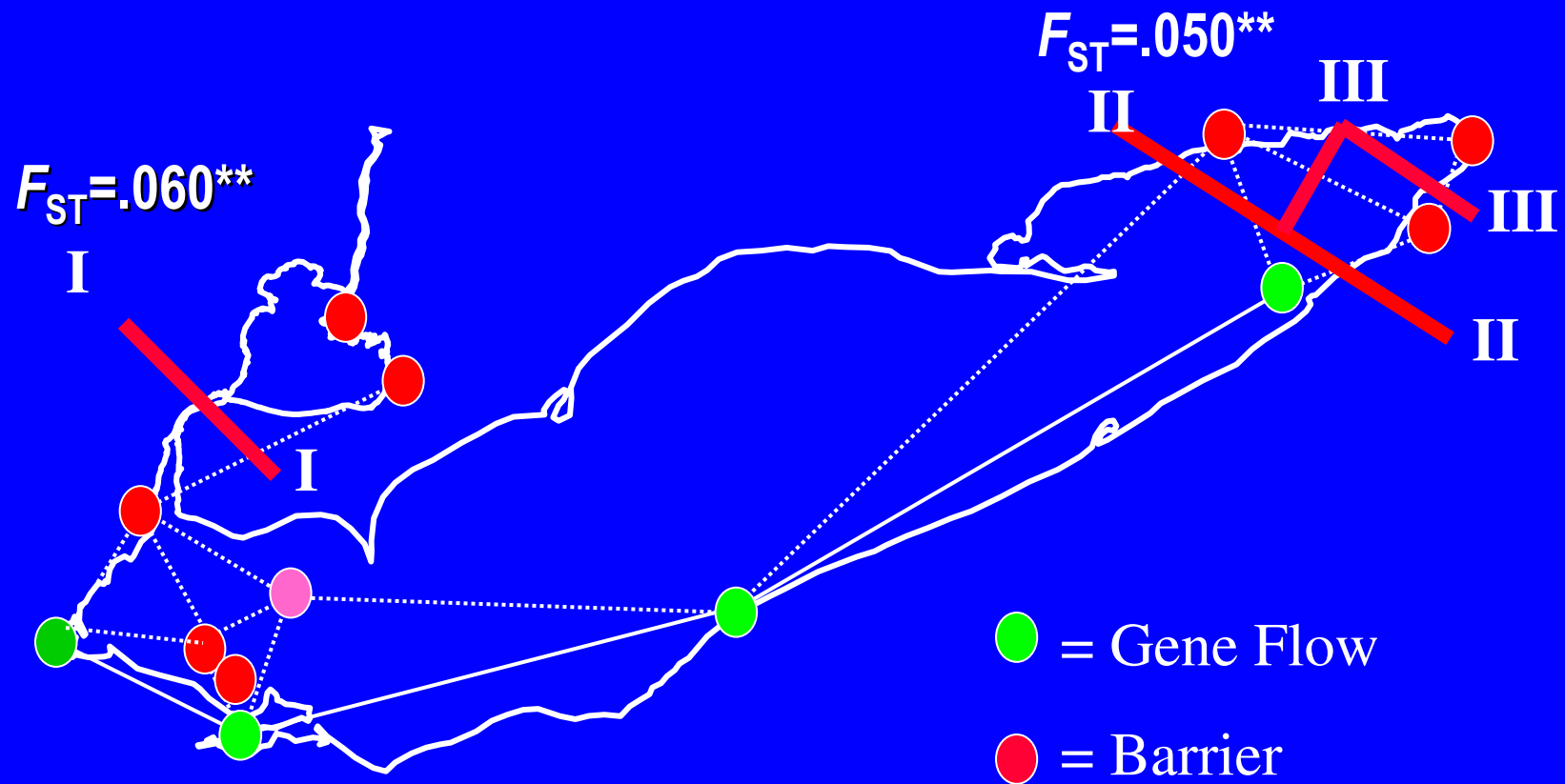
= Barrier

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

2003 fine-scale Walleye patterns along Lake Erie southern shore

Differences between Maumee River Walleye run years

	1.	2.	3.
1. Maumee R 1995	~		
2. Maumee R 1998	NS	~	
3. Maumee R 2003	**	**	~
4. Maumee R 2006	NS	NS	**

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 are temporally stable

-Some high gene flow years may be linked to higher
recruitment

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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Rex Strange