Waterscape genetics of the yellow perch (*Perca flavescens*): Patterns across large connected ecosystems and isolated relict populations

Osvaldo J. Sepulveda Villet

THE UNIVERSITY OF TOLEDO 1872

Great Lakes Genetics Laboratory
Lake Erie Center • University of Toledo

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Presentation outline

- Introduction
  - The study organism
  - Landscape Genetics
  - Objectives
- Broad-scale phylogeographic patterns in North America
  - Sampling locations
  - Divergence patterns and testing for isolation by distance (IBD)
  - Phylogenetic relationships among groups
  - Genetic structure across the sampled groups
  - Testing the influence of glacial refugia
  - Conclusions

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The case for yellow perch

- **Popular sport and food fish in the Midwest: Center of native distribution**
- **Fluctuations of Great Lakes populations, especially in last decades**
- **Exploitation & unstable recruitment**
- **Analysis of genetic structure as a management tool**

Landscape Genetics

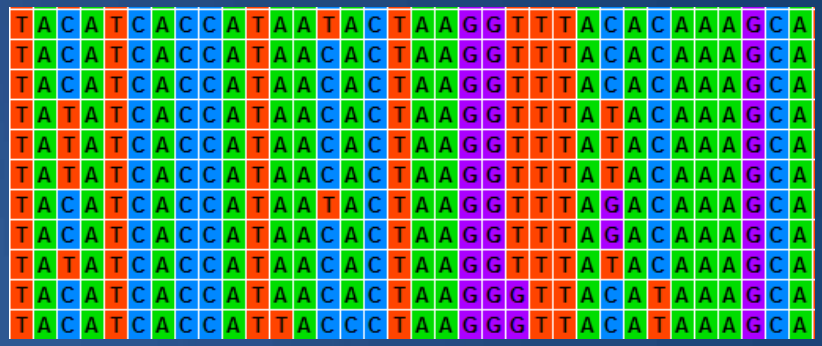
- **Merging population genetics with landscape ecology**
- **Test the influence of environmental factors on the genetic makeup and distribution of populations**
- **Determine barriers to genetic continuity**
- **Implications for stock and fishery management practices**

Objectives for this study

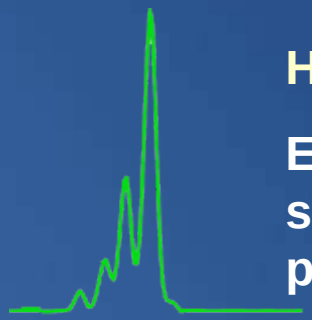
- Analyze genetic diversity and divergence patterns using two markers:
  - 15 nuclear microsatellite loci
  - Mitochondrial DNA control region sequences
- Detect phylogeographic patterns & possible barriers for dispersal across the native North American range
- Test contributions of glacial refugia to present-day populations
- Compare Lake Erie MUs with genetic structure of spawning groups

Molecular markers used in the study

- **Mitochondrial DNA**
  - Uniparentally inherited
  - ¼ effective population size
  - Appropriate to test long-standing divergences

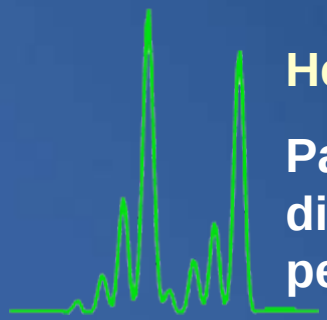


- **Nuclear microsatellites**
  - Non-coding repetitive regions
  - Biparentally inherited
  - Rapid loss or gain of repeats
  - Isolation allows accumulation of changes
  - Use of multiple microsatellites provides higher “resolution”



Homozygote

Each parent contributed same allele, only one peak visible



Heterozygote

Parents contributed different alleles, two peaks visible

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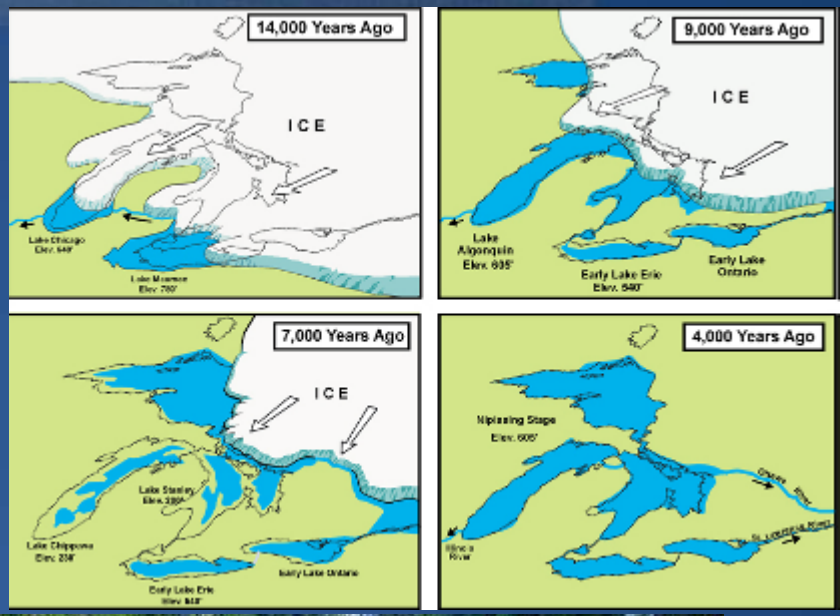
Why study the phylogenetics of yellow perch?

- Great Lakes are a “young” ecoregion
- Different theories on origin of present- day populations
- Broader questions regarding how species disperse into new habitats
- Aquatic organisms have additional challenges on dispersal
- Yellow perch can act as proxy for other fish and aquatic species

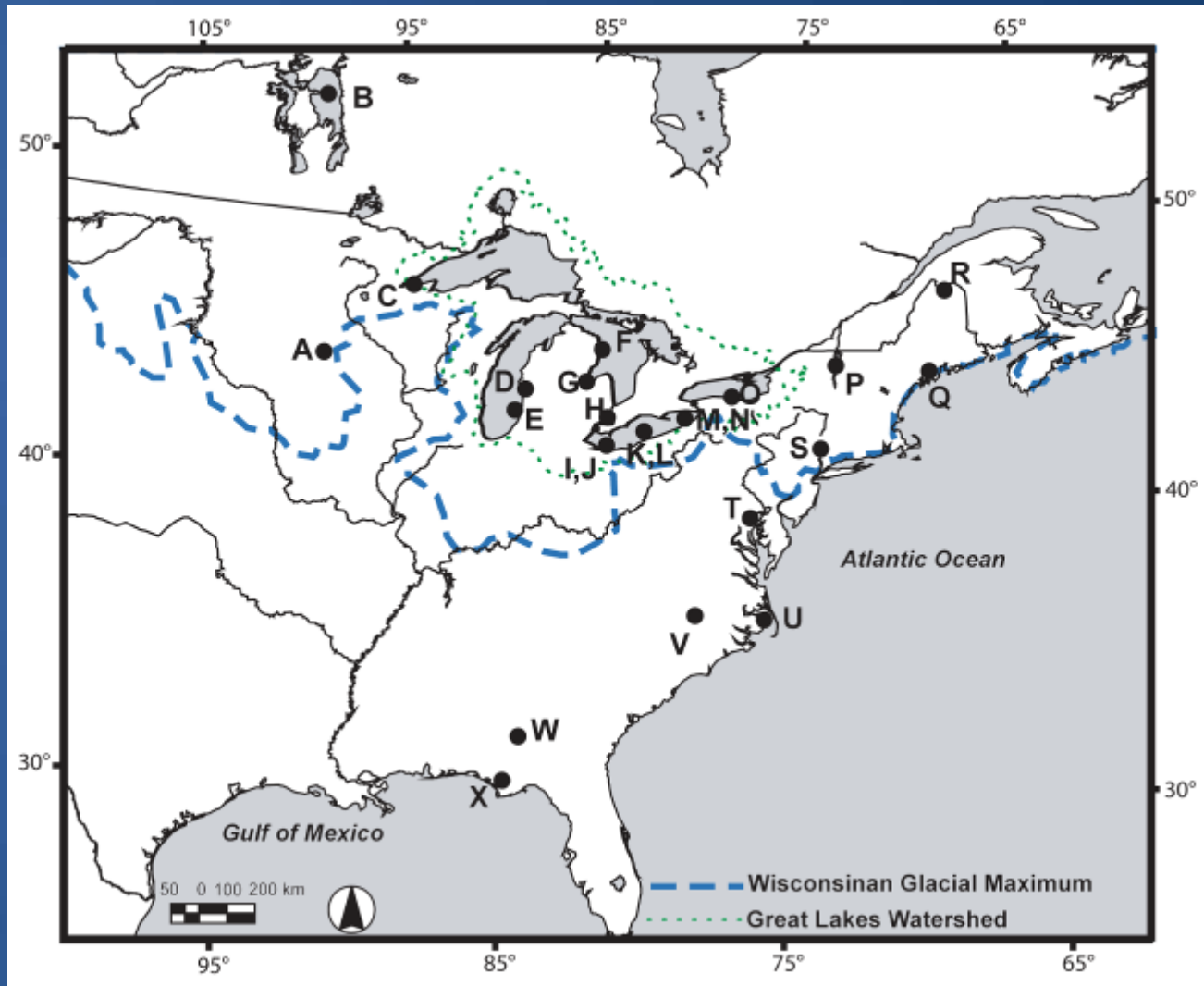


Hypotheses tested in broad-scale study
(Sepulveda-Villet & Stepien, in review, Mol. Ecol.)

- **1- Genetic diversity and divergence patterns are comparable in connected versus isolated population sites.**
- **2- Population relationships do not reflect a pattern of genetic isolation with geographic distance in connected versus unconnected sites.**
- **3- Relationships among northern populations do not show genetic patterns consistent with colonization from various hypothesized glacial refugia.**
- **4- Genetic diversity and divergence are comparable in unglaciated regions than in those that were glaciated.**

Locations sampled

- All representative native regions analyzed
- Samples north and south of Glacial Maximum
- Southern relict populations are rare and scarce
- Great Lakes center of native distribution



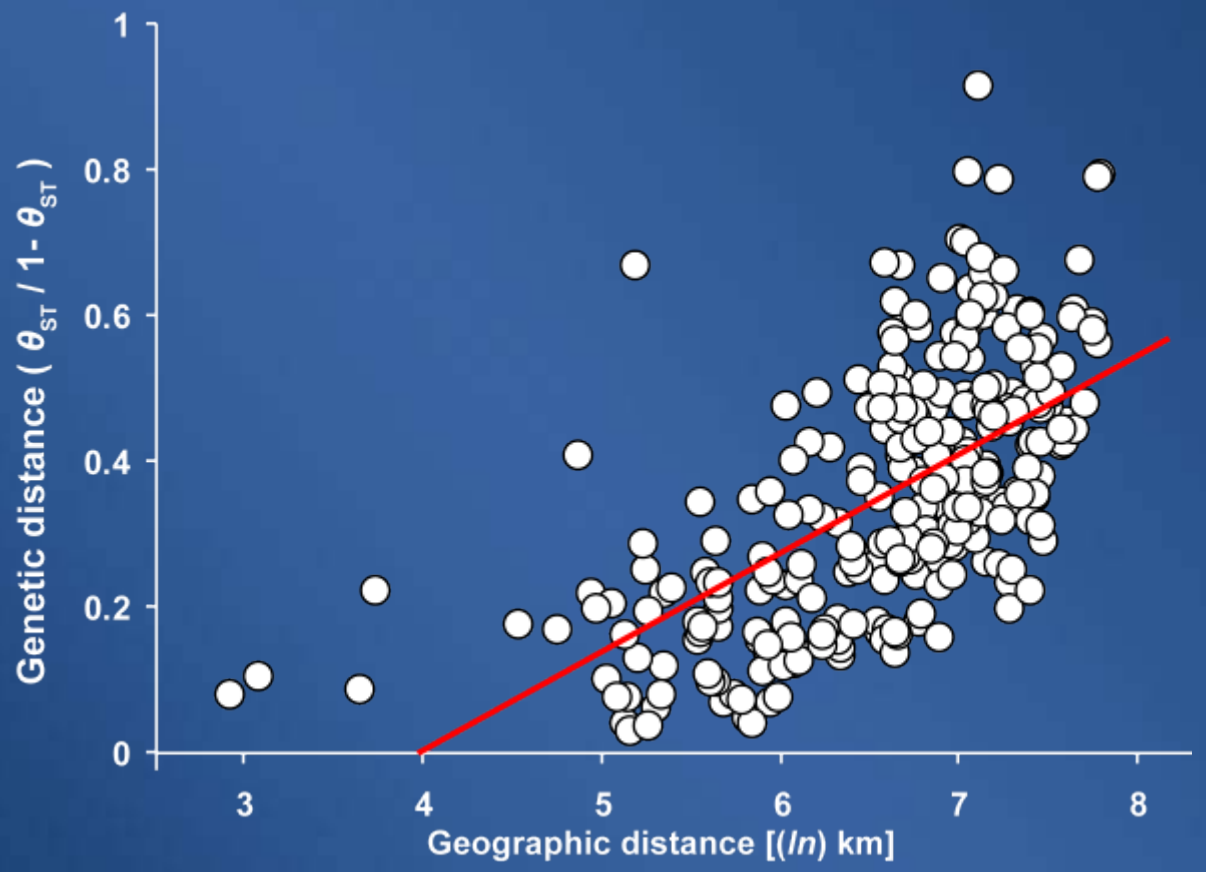
Pairwise comparisons across regions: Quantifying divergences

- **Interpretation: All regions sampled significantly divergent from each other when msats analyzed; one comparison not divergent with mtDNA due to low resolution.**

	Northwest Lake Plains	Great Lakes region	Lake Champlain	North Atlantic coastal	South Atlantic coastal	Gulf coastal
Northwest Lake Plains	-----	0.007	0.240	0.685	0.592	0.929
Great Lakes region	0.140	------	0.410	0.762	0.787	0.827
Lake Champlain	0.228	0.188	------	0.327	0.290	0.287
North Atlantic coastal	0.227	0.172	0.136	------	0.422	0.404
South Atlantic coastal	0.236	0.219	0.196	0.119	------	0.436
Gulf coastal	0.285	0.260	0.258	0.189	0.186	------

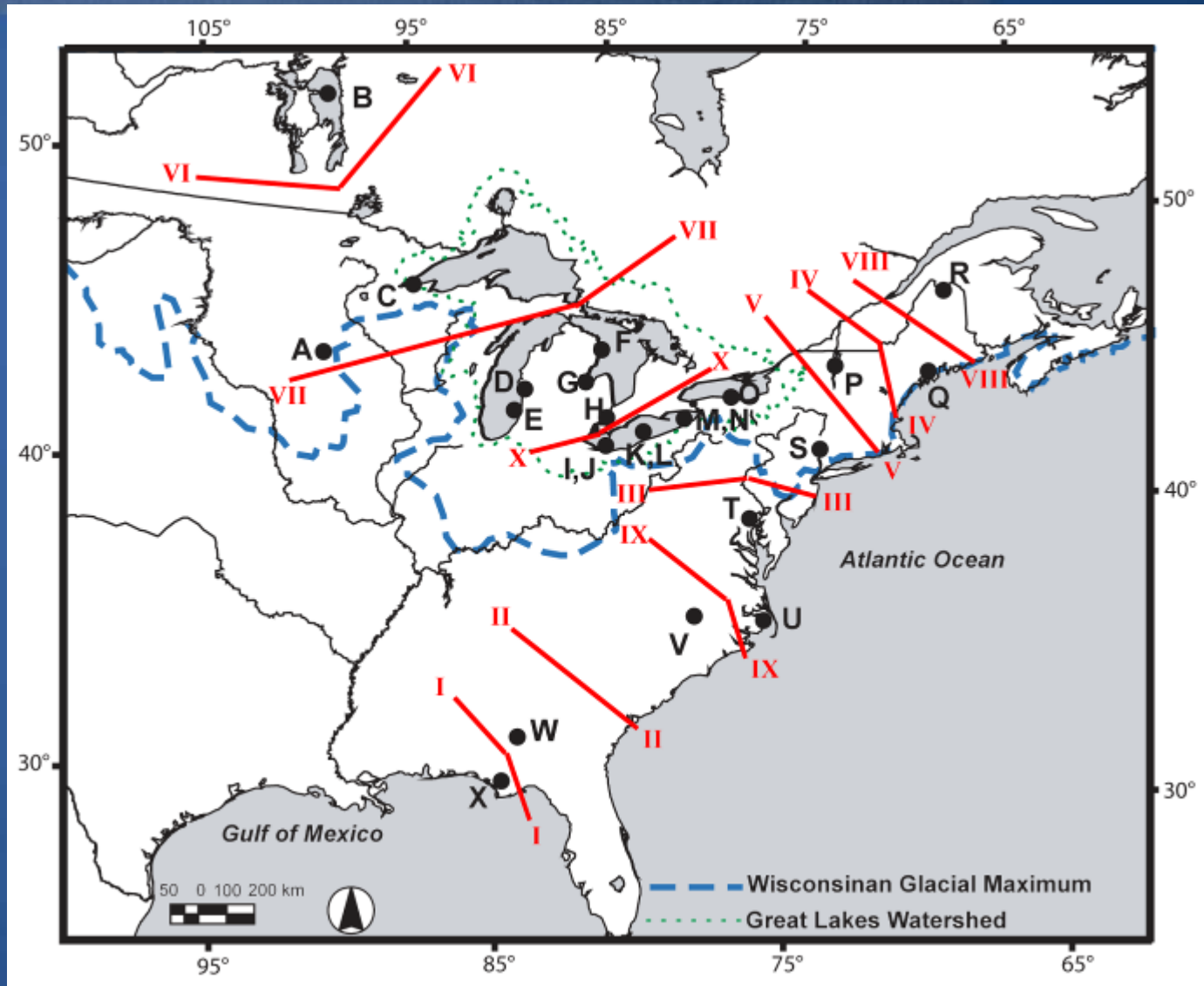
Testing isolation by distance

- **Interpretation: At large scales, geographic distance significantly correlates to genetic distance.**



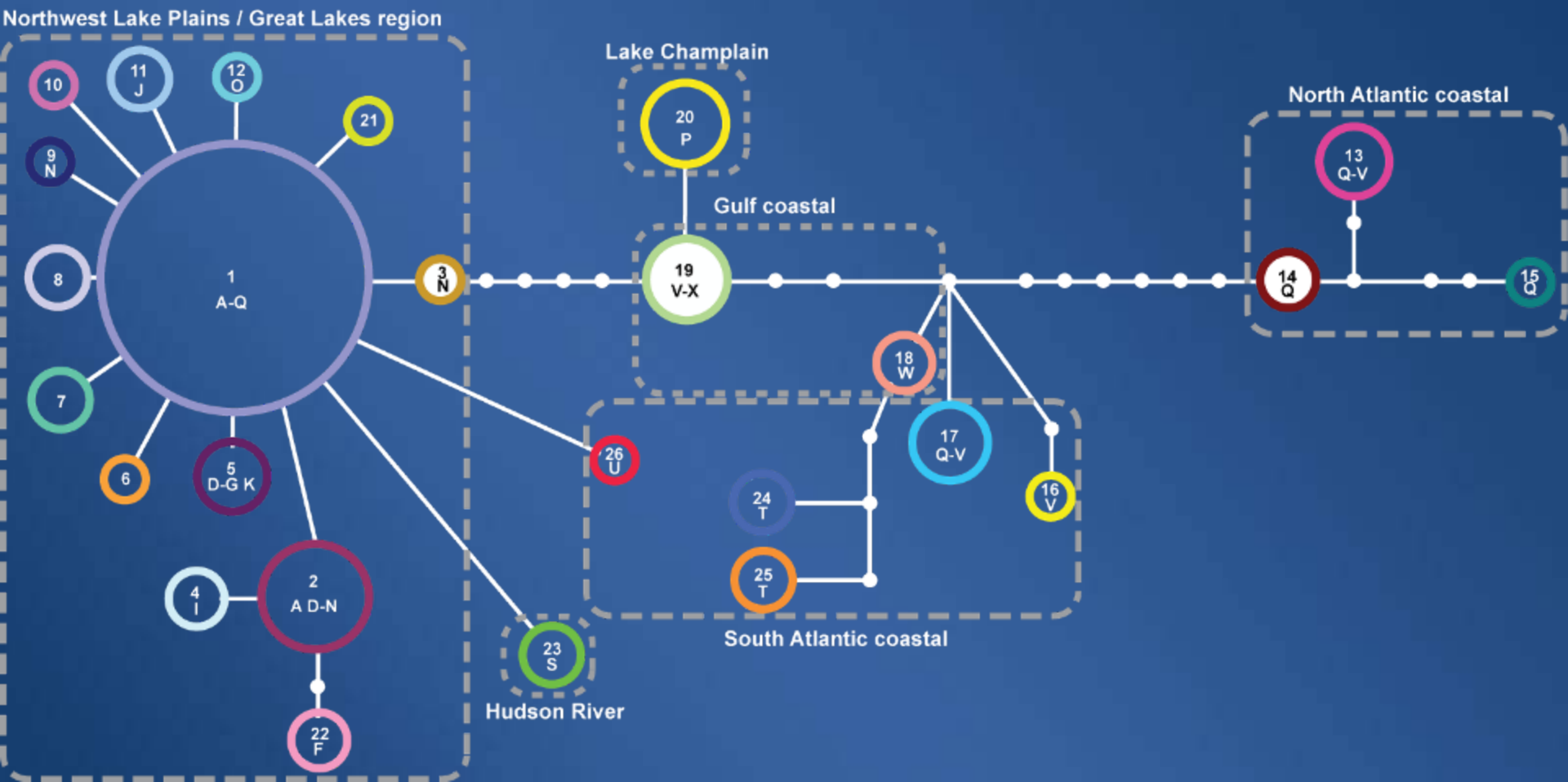
Barriers to genetic continuity

- Primary barriers separate Gulf coastal relicts
- Atlantic coastal sites then separate
- Northwest Lake Plains follow
- Little difference in Great Lakes at large scale



Relationships among haplotypes

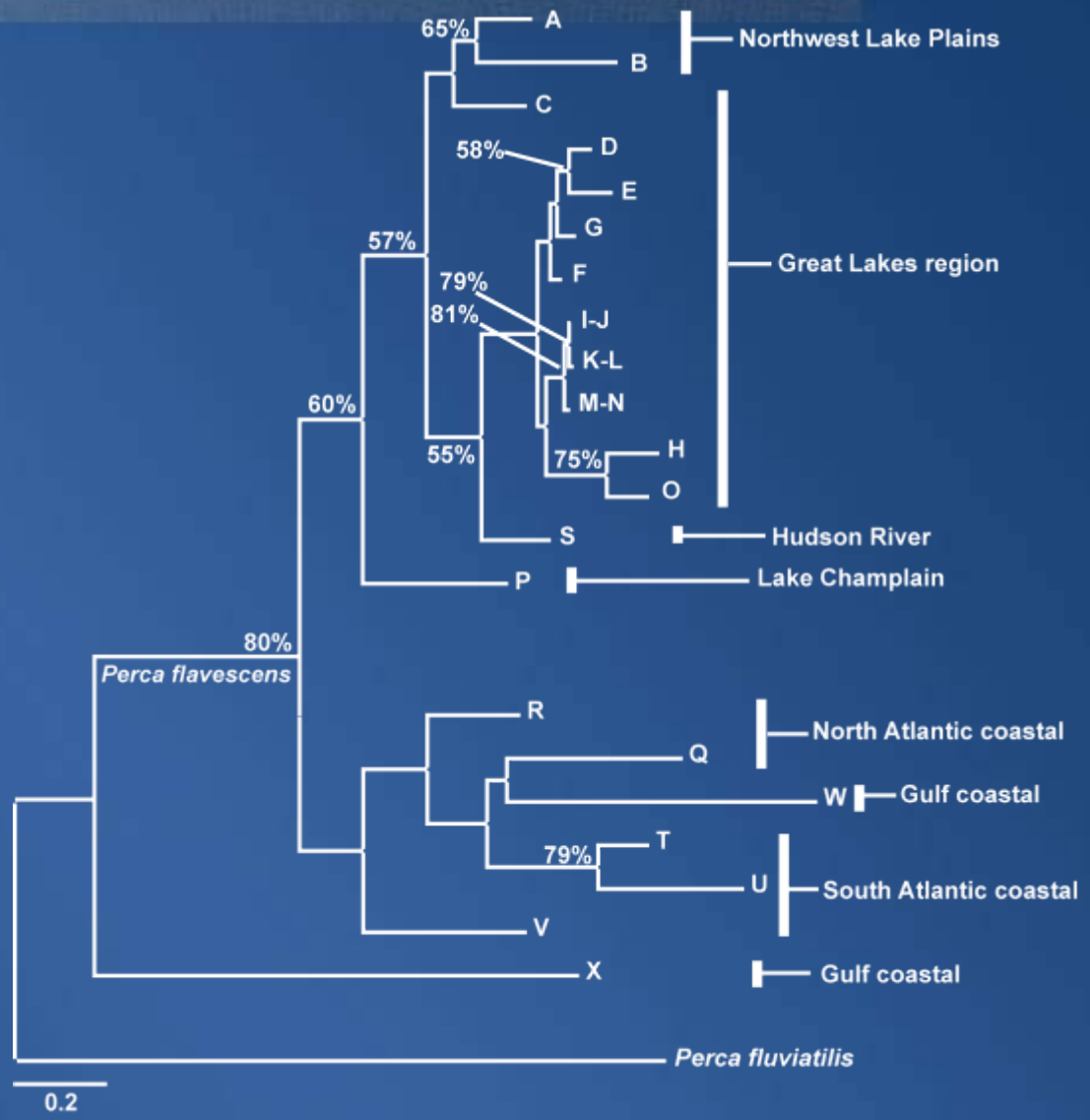
- **Interpretation: Most Great Lakes haplotypes closely related, North Atlantic coastal haplotypes most distant from all others.**



Relationships among sampling sites

Neighbor-joining tree using msats

- **Primary split into midwest / coastal groups**
- **Southernmost site is basal to other NA sites**
- **North Atlantic coastal site in midwest group**



AMOVA: Influence of connectivity in North vs. South

- **Interpretation: Connected systems in North vs. South explain the largest % of variation among all scenarios of genetic structure.**

		% variation	Significance (*P*-value)
(a) *μ*sat	5. Between connected groups in north vs. south	24.82	*0.013*
	Among populations within connected groups	7.97	*0.001*
	Within populations	67.22	*0.001*
(b) mtDNA	5. Between connected groups in north vs. south	79.69	*0.018*
	Among populations within connected groups	7.31	*0.001*
	Within populations	13	*0.001*

Testing distribution scenarios

Analysis of molecular variance (AMOVA)

- **Interpretation: The influence of the six geographic regions is the second highest scenario tested.**

Marker	Scenario and hierarchies tested	% variation	Significance (*P*-value)
(a) *μ*sat loci	1. Among the 6 regions	18.04	*0.001*
	Among sampling sites within regions	7.56	*0.001*
	Within the sampling sites	74.4	*0.001*
(b) mtDNA	1. Among the 6 regions	49.75	*0.002*
	Among sampling sites within regions	24.99	*0.001*
	Within the sampling sites	25.27	*0.001*

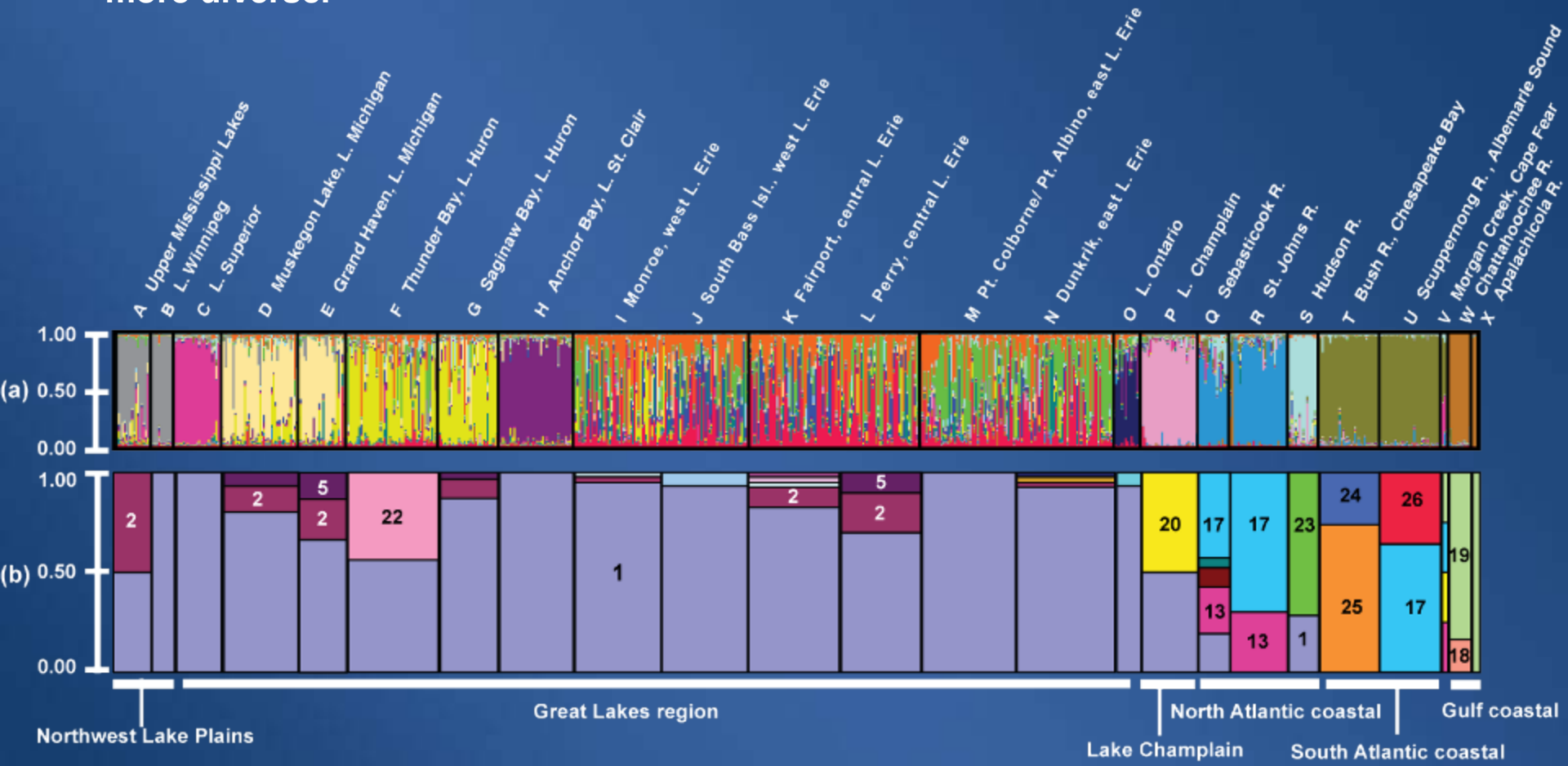
AMOVA: Testing influence of glacial refugia

- **Interpretation: The influence of glacial refugia is third highest scenario tested.**

		% variation	Significance (*P*-value)
(a) *μ*sat	2. Among 4 glacial refugia/ relict groups	14.93	*0.001*
	Among the sampling sites within groups	9.84	*0.001*
	Within the sampling sites	75.59	*0.001*
(b) mtDNA	2. Among 4 glacial refugia/ relicts	36.51	*0.018*
	Among the sampling sites within refugia	36.87	*0.001*
	Within the sampling sites	26.62	*0.001*

Genetic structure across the range

- **Interpretation: Most sampled sites in GL region have unique assignments, Atlantic and Gulf coastal sites have more regional identities.**
- **Midwest sites dominated by single haplotype, Atlantic and Gulf coastal sites are more diverse.**

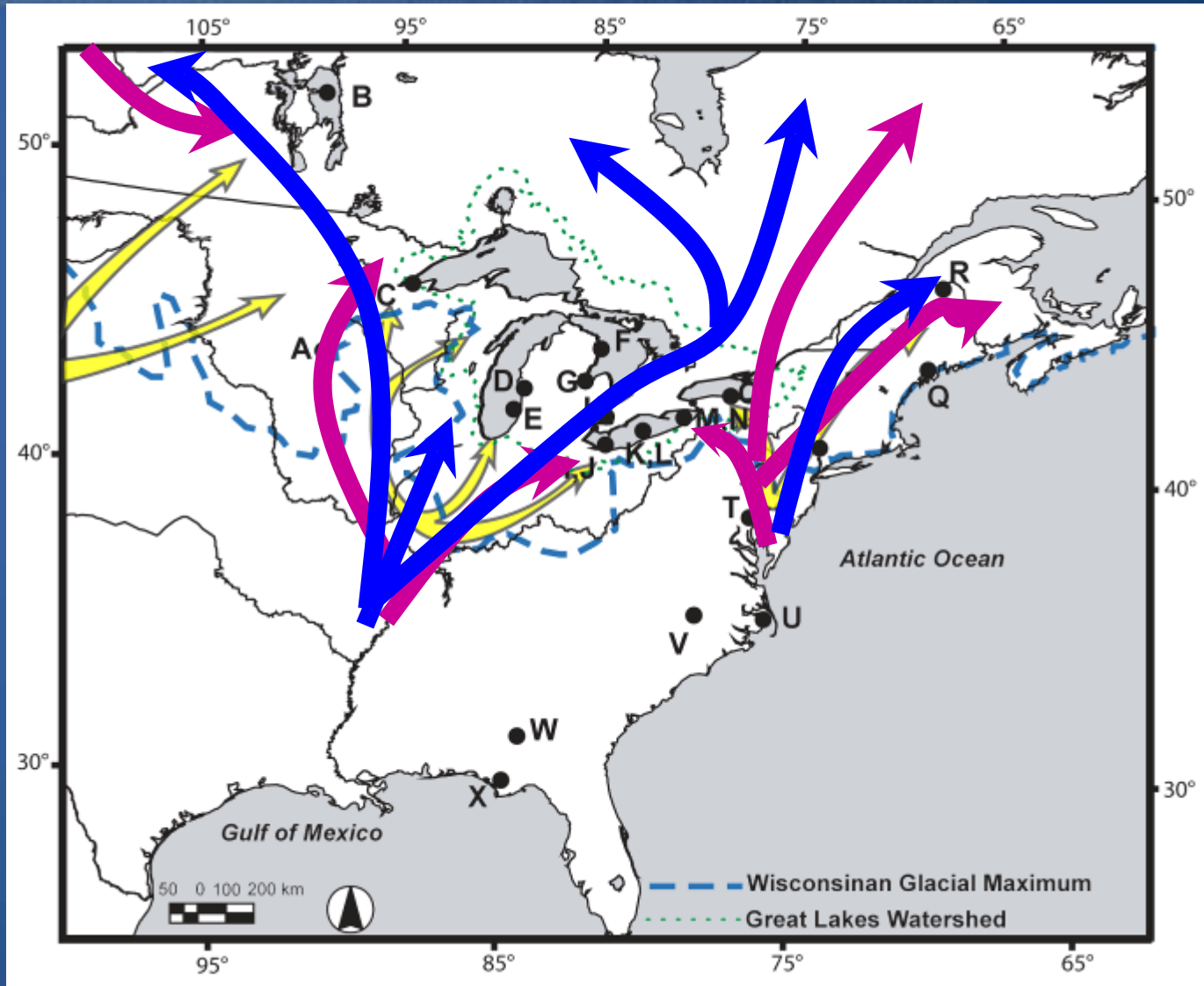


Assignment of samples to glacial refugia

	Missourian refugium	Mississippian refugium	Atlantic coastal refugium and relicts	Gulf coastal relicts
Upper Mississippi R. sites	6	94	---	---
L. Winnipeg, MB	37	---	3	---
St. Louis Bay, MN, L. Superior	96	4	---	---
Muskegon L., MI, L. Michigan	---	95	---	---
Grand Haven, MI, L. Michigan	---	83	---	---
Thunder Bay, MI, L. Huron	---	100	---	---
Saginaw Bay, MI, L. Huron	---	103	---	---
Anchor Bay, MI, L. St. Clair	---	97	---	---
Monroe, MI, L. Erie	---	100	---	---
South Bass Isl., OH, L. Erie	---	100	---	---
Fairport, OH, L. Erie	---	100	---	---
Perry, OH, L. Erie	---	100	---	---
Pt. Colborne/Pt. Albino, ON, L. Erie	---	100	---	---
Dunkirk, NY, L. Erie	---	100	---	---
Rochester, NY, L. Ontario	---	93	---	---
Burlington, VT, L. Champlain	---	---	100	---
Sebasticook R., ME	---	---	88	---
St. Johns R., ME	---	---	82	---
Hudson R., NY	---	6	94	---
Bush R., Chesapeake Bay, MD	---	---	94	---
Scuppernong R., Albemarle S., NC	---	---	100	---
Morgan Ck., Cape Fear, NC	---	---	100	---
Chattahoochee R., Gulf coast, GA	---	---	---	100

Likely post-glacial dispersal routes

- Contributions from three refugia
- Missourian refugium founded Northwest/ Lake Superior
- Mississippian founded GL
- Atlantic expanded northwards and west
- Gulf did not significantly contribute to other sites



Conclusions for broad-scale investigation

- **1- Genetic diversity is higher in connected population systems, in comparison to isolated sites. Genetic divergence is greater among isolated populations, both in formerly glaciated and unglaciated regions.**
- **2- There is a significant positive relationship between geographic distance and genetic divergence, consistent with isolation by distance, across the native North American range of yellow perch.**
- **3- contribution from at least three primary glacial refugia to the analyzed samples: Missourian to Northwest Lake Plains, Mississippian to GL region, and Atlantic to L. Champlain and Maine.**
- **4- Genetic diversity overall is higher in unglaciated populations versus previously glaciated ones. Isolation provided the strongest driver.**

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