Genetic Evaluation of the Remnant White River Lake Sturgeon Population: A Suitable Source for Ohio River Reintroductions?

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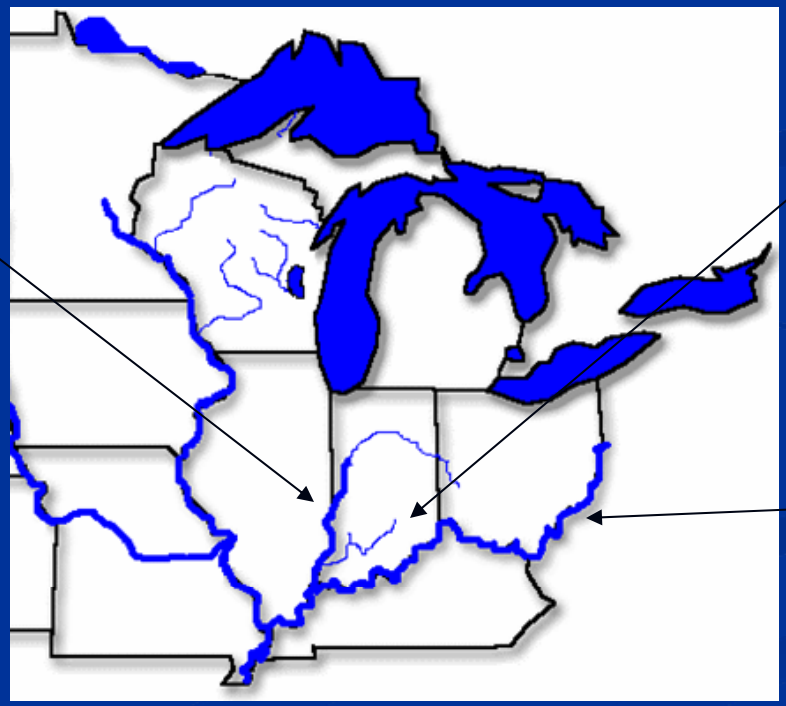
Talk Overview

- White River Lake Sturgeon
- Genetic Criteria for Source Evaluation
  - Genetic Variability
  - Genetic Distinctiveness
  - Genetic Integrity
- Methods Summary
- Is the White River a Suitable Source?
- Management Implications

Background

- Lake sturgeon once abundant in Ohio River system
- Currently, only single population of lake sturgeon exists in Ohio River drainage (White River, E. Fork)



White River Background

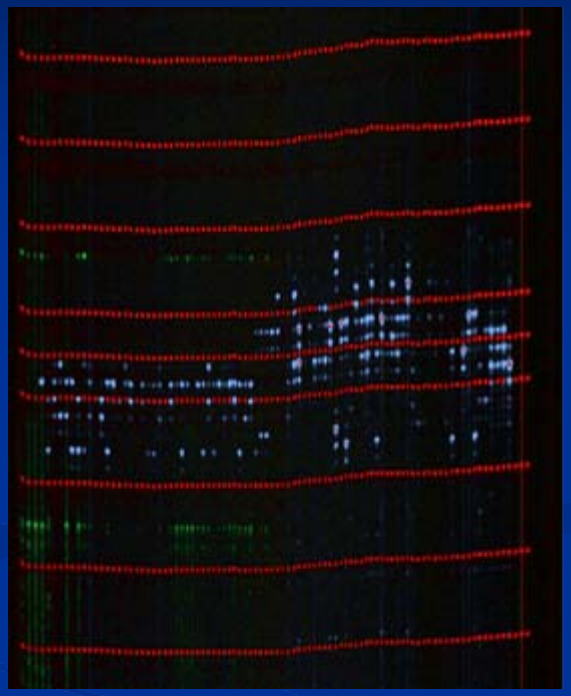
- White River seems like an obvious choice to be used as source for Ohio River reintroductions
- However…
  - Little known about the genetic characteristics of the White River population
    - Small, isolated population → inbreeding, genetic drift
    - Relationship to other lake sturgeon populations unknown
    - Genetic composition?

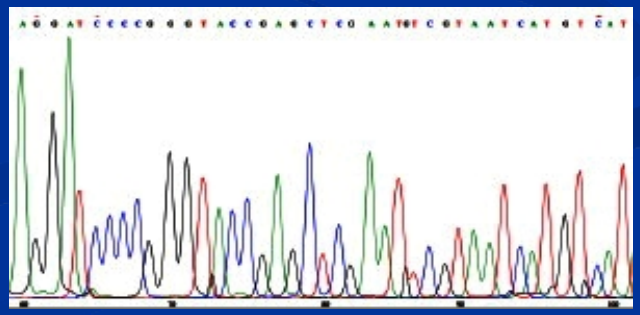
Objectives

- Characterize the White River lake sturgeon population and assess its suitability as a source for Ohio River reintroductions
  - Genetic Variability
    - Maximize genetic variability → adaptability over time
  - Genetic distinctiveness
    - Can be evidence of adaptive divergence
  - Genetic integrity
    - Immigrants (especially non-native or hatchery sources) can "contaminate" genetic lineages

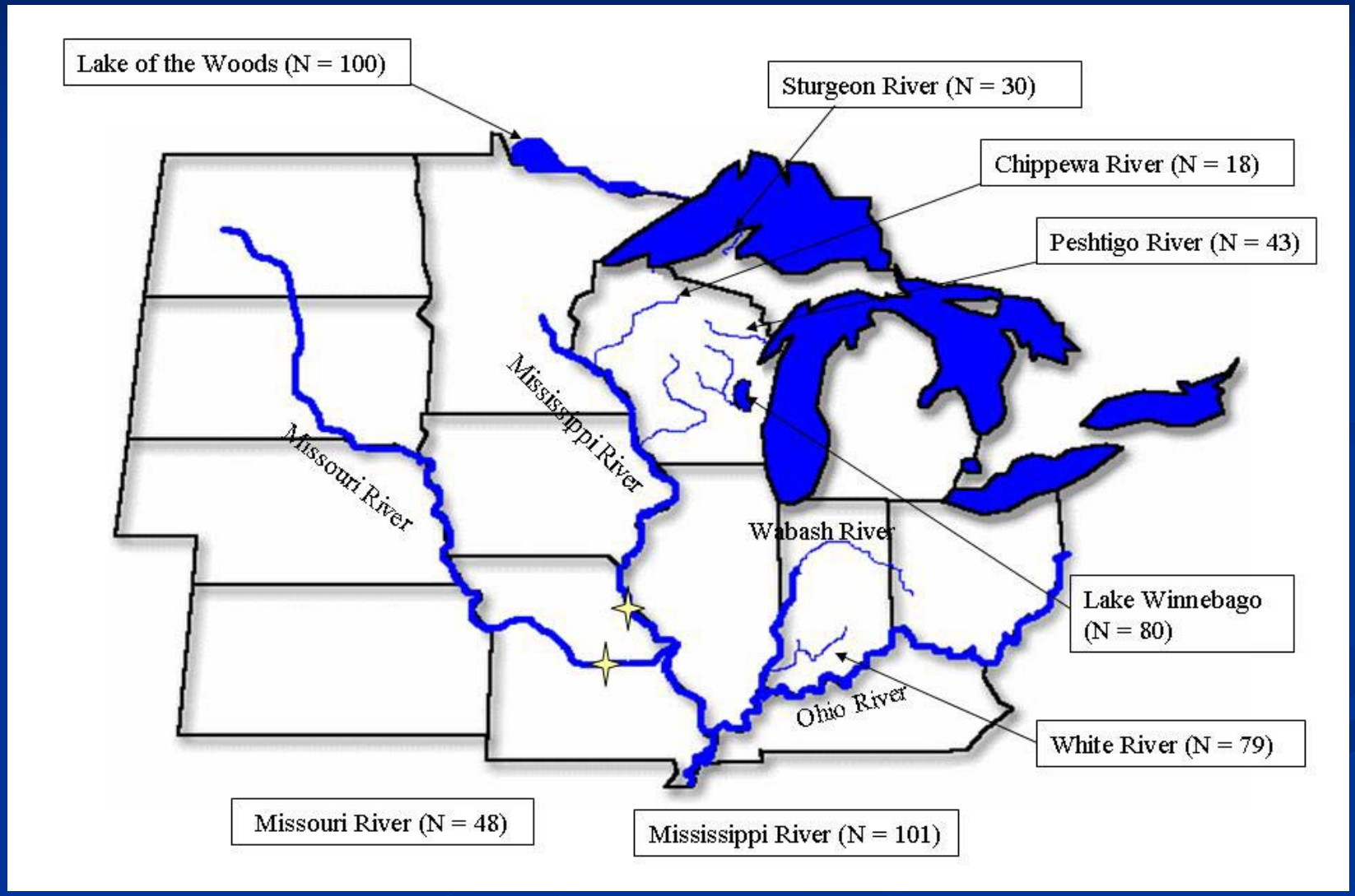
Methods Summary

- Collected microsatellite (10 loci) and sequence data from mitochondrial control region for 8 lake sturgeon populations



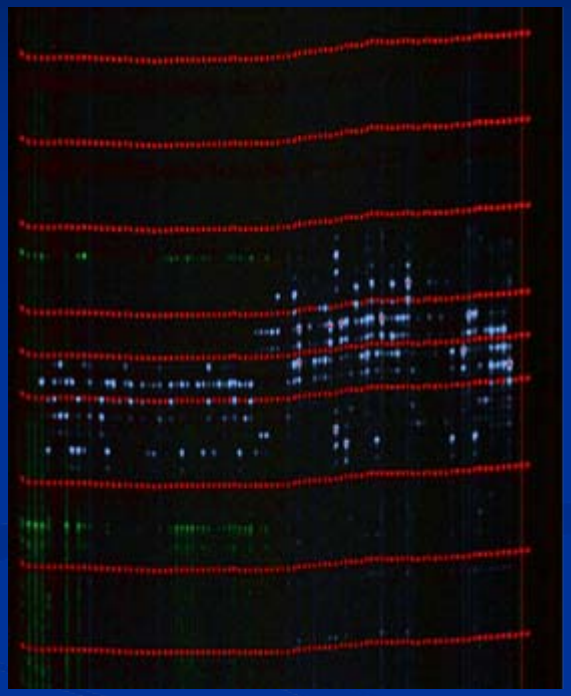


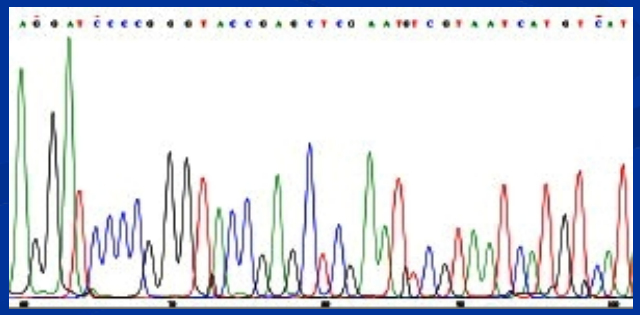
Study Populations



Methods Summary

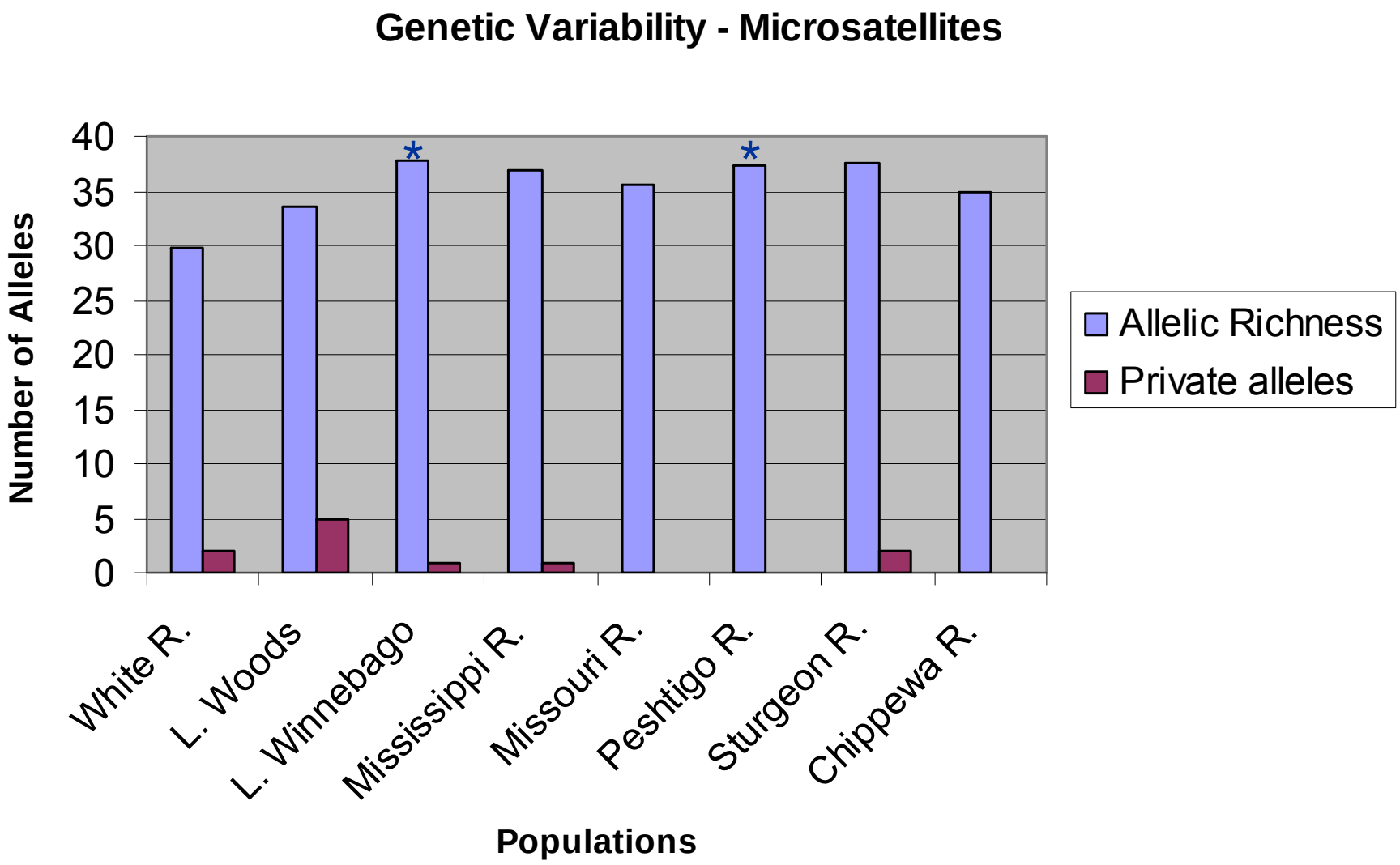
- Collected microsatellite (10 loci) and sequence data from mitochondrial control region for 8 lake sturgeon populations
- Variability: Estimated genetic variability in White River population (N=79)
- Distinctiveness: Examined genetic structure of Midwestern lake sturgeon populations
- Integrity: Conducted population assignment testing with White River and possible migration sources



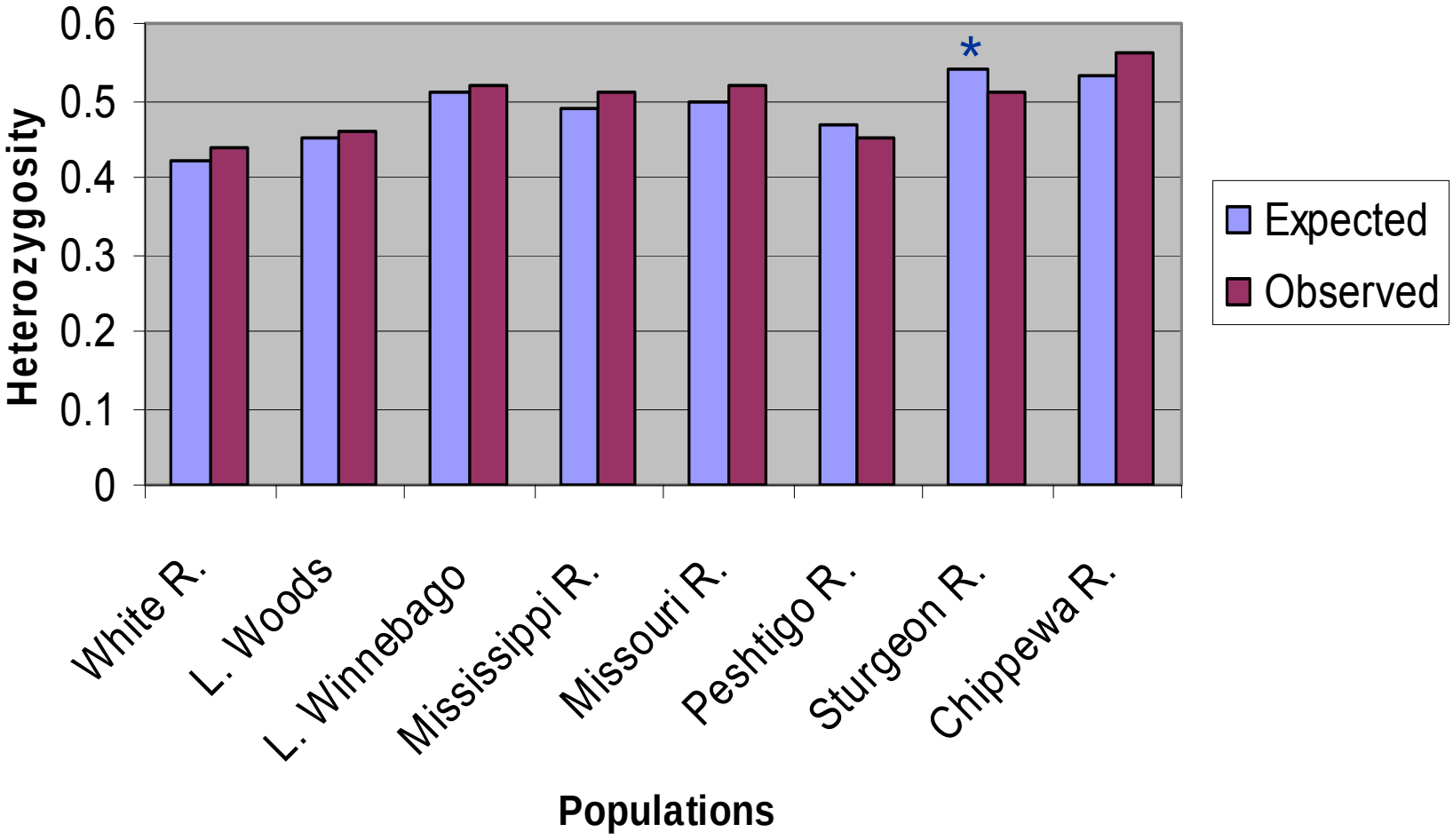


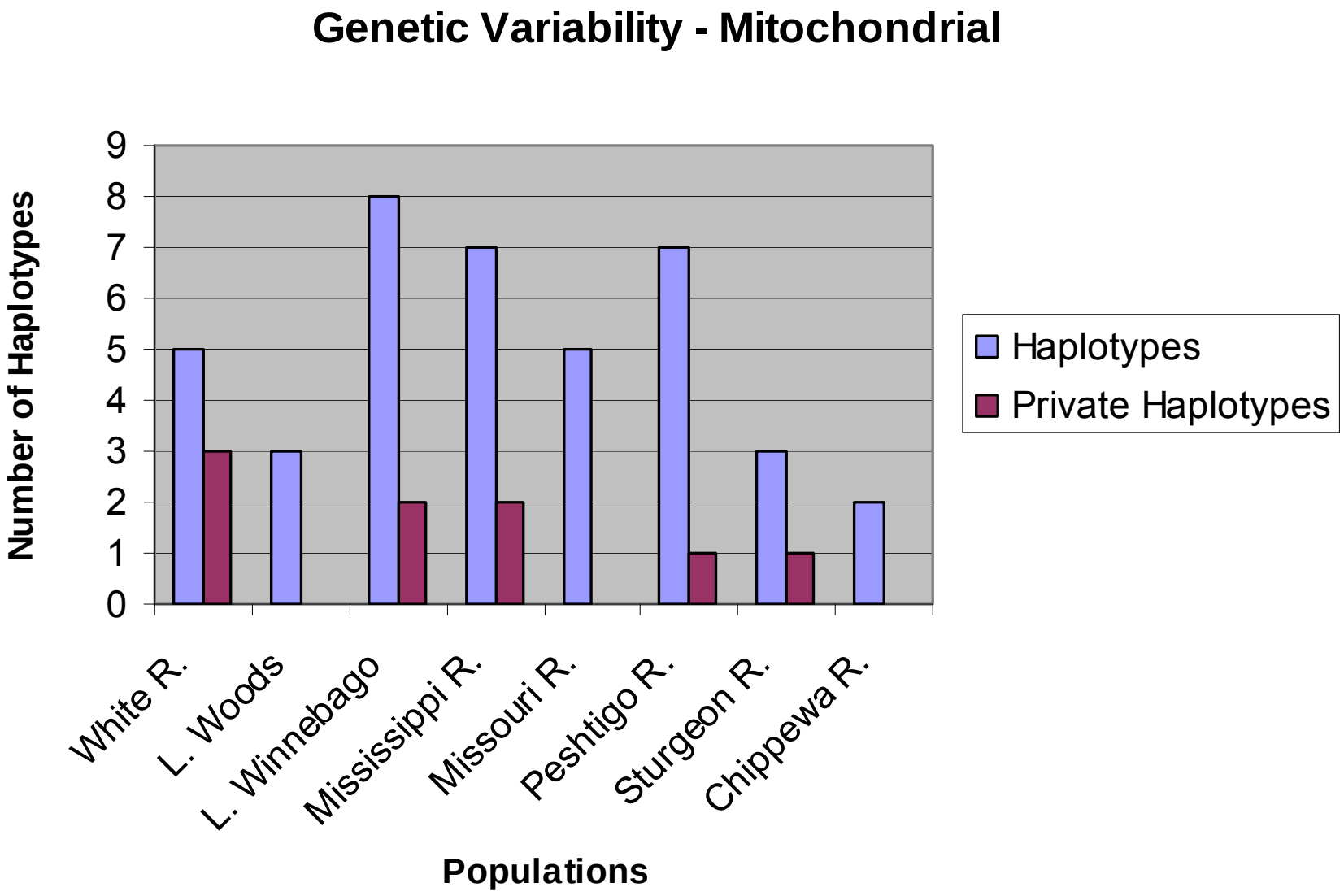
Results

- 499 lake sturgeon genotyped at ten microsatellite loci
- 382 bases of control region sequence for 414 lake sturgeon
  - 20 haplotypes identified


Genetic Variability - Microsatellites
Number of Alleles
40
35
30
25
20
15
10
5
0
*
*
White R.
L. Woods
L. Winnebago
Mississippi R.
Missouri R.
Peshtigo R.
Sturgeon R.
Chippewa R.
Populations
Allelic Richness
Private alleles

Genetic Variability - Microsatellites II




Genetic Variability - Mitochondrial
Number of Haplotypes
0
1
2
3
4
5
6
7
8
9
White R.
L. Woods
L. Winnebago
Mississippi R.
Missouri R.
Peshtigo R.
Sturgeon R.
Chippewa R.
Populations
Haplotypes
Private Haplotypes

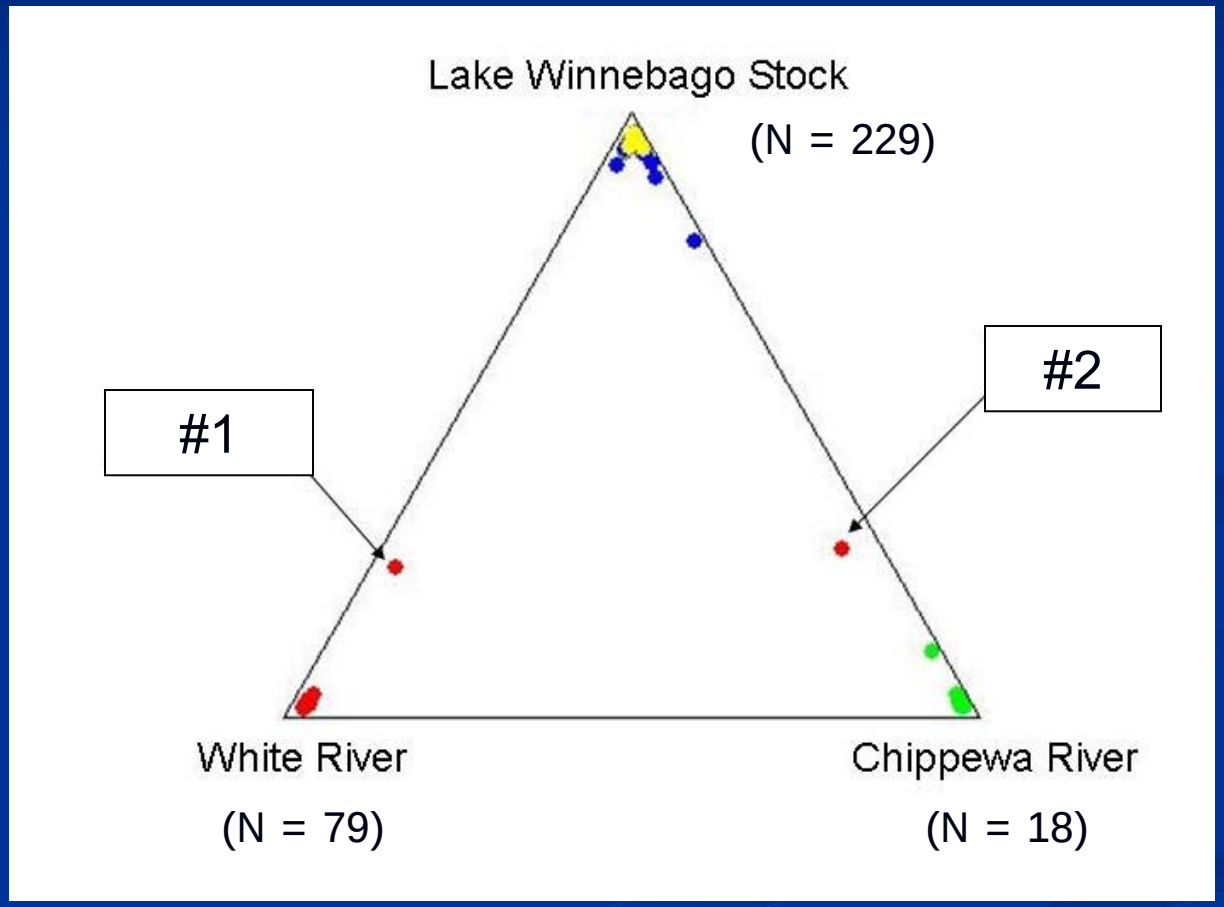
Genetic Distinctiveness : Population Structure

- Significant $F_{ST(microsat)} = 0.12$
- $F_{ST(mtDNA)} = 0.34$
- Pairwise $F_{ST\ (microsat)} = 0.09 – 0.16$
- Pairwise $F_{ST(mtDNA)} = 0.37 – 0.72$

White River population appears to be ….

- As genetically variable as other potential sources
- Genetically distinct from other lake sturgeon populations

Genetic Integrity: Population Assignment



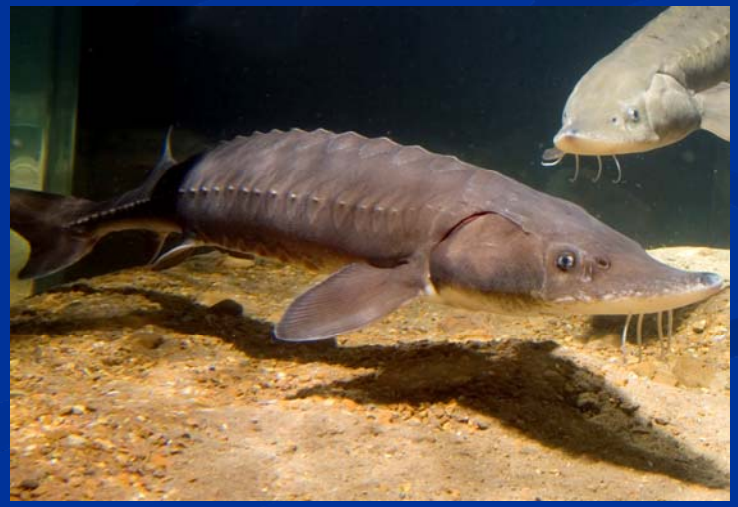
White River population does not appear to be contaminated by non-native stocks.

These data suggest that the White River lake sturgeon population represents the best source for reintroductions in the Ohio River

Management Implications

- Benefits of using White River as source
  - Possible adaptive differences between White River and other lake sturgeon populations
  - Persistence insurance → decrease likelihood that a single event could devastate the Ohio River genetic stock

- However….



Lake sturgeon spawning behavior in the White River is not well characterized. Couldn't we use another source in the meantime?

- Possible alternative sources
  - Lake Winnebago
  - Chippewa River
- Lake Winnebago used for many lake sturgeon reintroductions… maybe too many?
  - Concerns about genetic homogenization
- Chippewa River = Not enough data!
  - Need to examine a larger sample to genetically characterize

Using a single non-native source could permanently compromise the genetic integrity of the Ohio River lake sturgeon genetic stock!

We recommend that management efforts focus on preserving and reintroducing the White River lake sturgeon stock to conserve this unique genetic lineage.

Acknowledgements

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AFS 2007 Annual Meeting Symposium

Bridging the Gap: Addressing Critical Uncertainties in North American Sturgeon Conservation and Recovery

Pairwise F_{ST}

Mt / Msat

	WH	LoW	LW	MS	MO	PS	SR	CR
WH	------	0.720*	0.377*	0.374*	0.401*	0.411*	0.474*	0.492*
LoW	0.159*	--------	0.536*	0.409*	0.517*	0.342*	0.568*	0.562*
LW	0.086*	0.207*	--------	0.035	0.040	0.130*	0.234*	0.042
MS	0.094*	0.216*	0.006	--------	-0.015	0.117*	0.221*	0.072
MO	0.104*	0.230*	0.006	0.005	--------	0.133*	0.243*	0.095
PS	0.138*	0.231*	0.050*	0.050*	0.045*	-------	0.033	0.127
SR	0.112*	0.160*	0.083*	0.092*	0.094*	0.066*	--------	0.278
CR	0.099*	0.172*	0.054*	0.056*	0.063*	0.073*	0.052*	--------

*Statistically significant comparisons (table-wide $\alpha = 0.002$)

Genetic Variability - Microsatellites

	A_R	A_P	H_e	H_o	F_{IS}[a]
White R. (79)	29.8	2	0.419	0.439	-0.047
L. Woods (100)	33.5	5	0.454	0.457	-0.007
L. Winnebago (80)	37.8[b]	1	0.512	0.521	-0.017
Mississippi R. (101)	37.0	1	0.486	0.507	-0.044
Missouri R. (48)	35.6	0	0.498	0.521	-0.046
Peshtigo R. (43)	37.4[b]	0	0.473	0.449	0.053
Sturgeon R. (30)	37.5	2	0.537[b]	0.512	0.047
Chippewa R. (18)	35.0	0	0.526	0.561	0.070

[a]F_{IS} values not significant different from zero ($P > 0.05$)
[b]Significantly different from White River population ($P < 0.05$)

Genetic Variability – Control Region

	H_T	H_P	H_d	k
White R. (58)	5	3	0.493	1.10
L. Woods (88)	3	0	0.109	0.40
L. Winnebago (66)	8	2	0.778	3.07
Mississippi R. (81)	7	2	0.735	4.24
Missouri R. (37)	5	0	0.716	4.27
Peshtigo R. (41)	7	1	0.714	2.44
Sturgeon R. (26)	3	1	0.582	2.23
Chippewa R. (17)	2	0	0.538	1.08