POPULATION GENETIC STRUCTURE OF WALLEYE IN THE EASTERN HIGHLANDS AND ADJACENT REGIONS



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A FAVORITE GAMEFISH



Widely stocked, including outside its native range

Just what *is* its native range is debated:

- Jenkins and Burkhead wrote that it is native to the Tennessee and Big Sandy drainages of Virginia; work done by George Palmer et al. says that it *is* native also to the New River drainage.

- Controversy as to whether it is native to Montana and Alberta; some want to declare it introduced and manage to *extirpate* it.





 MtDNA data from 1990s suggest its expansion from three glacial refugia
 Eastern Highlands, Lower Mississippi, Northwest

The Eastern Highlands component had not been well studied

NATURAL HISTORY





 Evaluate genetic differentiation among walleye populations in the Eastern Highlands and adjacent regions, and

GOALS

 Provide the basis for genetically appropriate conservation and management plans for the region

METHODS

- Samples from 38 populations
 within six major drainages:
 - Great Lakes in pink
 - Ohio River in red
 - Mississippi River in yellow
 - Tennessee River in purple
 - New River in blue
 - Alabama river system in green
 - N = 1279 individuals



METHODS

A study of *recent* genetic differentiation – we screened microsatellite DNA markers.

- Began with 19 candidate marker loci not all amplified consistently in our regional populations
- \odot More detailed evaluation of 12 loci
- Screened 8 polymorphic loci for characterizing population genetic structuring

Locus	Size Range (bp)
Svi5	130-192
Svi6	126-164
Svi16	175-299
Svi17	99-113
Svi18	110-142
Svi33	73-95
SviL1	151-209
SviL7	135-269

DATA ANALYSES

GeneMarker

Scoring of microsatellite genotypes

\circ MicroChecker

- $\,\circ\,$ Assessment of null alleles and artifacts
- Arlequin and GENEPOP
 - \odot Assessment of population structuring

○ STRUCTURE

- $\,\circ\,$ Bayesian identification of multilocus genotypic clusters,
- Assignment of individuals to cluster(s)

\circ NeEstimator v2

 \odot Estimation of effective population sizes

\circ MLRelate

 \odot Estimation of likelihood of relatedness



RESULTS

I'll present results mostly at the drainage level...

Much more nuance at the population-by-population level...

 Mean numbers of alleles per locus (A) were high, though not all loci were polymorphic across sampling locations

GENETIC DIVERSITY

Observed heterozygosities < expected heterozygosities
 (e.g., 0.50 < 0.77 in New R.; 0.36 < 0.79 in Tennessee R.)

M-ratios were all below 0.68 (e.g., 0.12 in New R., 0.09 in upper Tennessee R.), suggesting recent bottlenecks

Population	Number of Polymorp hic Loci	Number of Gene Copies	Number of Alleles	H _o	H _e	Allelic Range	M-Ratio
Alabama	6	110	4.00	0.23	0.54	71.17	0.22
Samples	0	110	(1.67)	(0.40)	(0.07)	(65.83)	(0.23)
Mississippi	0	210	14.75	0.36	0.80	164.88	0.09
River	Ο	310	(5.70)	(0.14)	(0.08)	(52.20)	(0.03)
Tennessee	Q	500	17.63	0.36	0.79	276.00	0.09
River	8 392	372	(7.25)	(0.18)	(0.16)	(253.14)	(0.03)
Now Divor	No	720	23.25	0.50	0.77	179.75	0.12
New River o	/ 30	(16.04)	(0.24)	(0.22)	(70.18)	(0.04)	
Ohio Divor	0	354	16.88	0.44	0.81	159.75	0.13
Onio River 8	0		(8.54)	(0.22)	(0.11)	(77.02)	(0.12)
Croat Lakos	7	120	13.29	0.48	0.81	134.43	0.21
Great Lakes		438	(0.77)	(0.29)	(0.08)	(102.40)	(0.22)

ESTIMATED EFFECTIVE NUMBERS OF BREEDING INDIVIDUALS

- \circ Aggregate $N_{\rm e}$ s shown here...
- All N_e estimates for individual populations were low, many ~10s, for example:
 - \circ Clinch/Powell 8.9
 - New N_e undefined it's a mix!
- Low N_es could be attributable both to natural processes (unequal reproductive success, bottlenecks) and to stocking (Ryman and Laikre effect)

Population	N	Estimated N _e	95% C.I.	JackKnife Estimate
Alabama Samples	59	19.4	7.4 – 58.1	2.7 - 68016.5
Mississippi River	159	17.4	14.9 - 20.4	13.8 – 22.0
Tennessee River	296	21.7	18.9 – 24.7	17.4 – 26.7
New River	369	22.2	19.5 – 25.3	18.5 – 26.5
Ohio River	177	15.9	13.8 – 18.4	11.9 – 21.1
Great Lakes	219	6.9	5.4 - 8.3	4.8 - 8.7

MAXIMUM LIKELIHOOD ESTIMATION OF RELATEDNESS

- High frequency of relatedness in these (aggregated) populations
 - Perhaps attributable to small N_es due to natural processes and stocking
- Similar profiles of relatedness estimations for all watersheds, including the New River
- Stocking in New has not elevated relatedness within the population



INBREEDING COEFFICIENTS

Population	F _{IS}	P(Random F _{IS} ≥ Observed F _{IS})	
Alabama Samples	0.58	0.0	
Mississippi River	0.55	0.0	
Tennessee River	0.54	0.0	
New River	0.34	0.0	
Ohio River	0.46	0.0	
Great Lakes	0.41	0.0	

 \circ $F_{
m IS}$ for all assemblages of populations were significantly greater than zero

- At watershed level, however, not necessarily caused by inbreeding
- May be because of Wahlund Effect (mixing of populations) or high frequencies of null alleles
- \circ Some populations did have $F_{IS} > 0$, suggesting ongoing inbreeding.

STRUCTURE — CLUSTERING AND INDIVIDUAL ASSIGNMENT



Results for K = 4:

- Alabama populations quite distinctive separate glacial refugium, isolated \sim 1.7 MY, drift and local adaptation
- Missouri (Mississippi drainage) distinctive, evidence of admixture
- Tennessee River to some degree distinctive, some mixing with other clusters, \leftarrow extensive stocking
- New River mixed background, but sharing ancestry with Ohio and Great Lakes
- Ohio River and Great Lakes similar background

Other K values \rightarrow additional inferences...breaking up of these four clusters

ANALYSIS OF MOLECULAR VARIANCE

Source of Variation	d.f.	Sum of Squares	Variance Components	Percentage of Variation
Among populations	5	668.38	0.32	9.50
Within individuals	1273	2114.50	1.65	49.55
Total	2557	8366.23	3.34	

Highest percentage of variation (49.6%) was within individuals and populations (41.0%)
 Typical for vertebrate species, though much between individuals within populations

Lower percentage of variation among watersheds (9.5%)

• Not so very low for vertebrates

May have been reduced by stocking across drainages

DIFFERENTIATION AMONG POPULATIONS - $F_{\rm ST}$

Populations across all watersheds were significantly differentiated

- Alabama populations were most differentiated from other populations
 All values above 0.2 (moderate F_{ST})
- Virginia populations:
- New River differentiated from:
 Ohio 0.030
 Missouri (Mississippi River) 0.102
 Great Lakes 0.115

• Tennessee differentiated from:

- \circ New 0.274
- Ohio 0.244
- \circ Missouri 0.043

	Alabama	Mississippi	Tennessee	New	Ohio	Great Lakes
Alabama	0.0					
Mississippi	0.233	0.0				
Tennessee	0.233	0.043	0.0			
New	0.274	0.102	0.094	0.0		
Ohio	0.244	0.072	0.050	0.030	0.0	
Great Lakes	0.305	0.074	0.027	0.115	0.067	0.0

SO, THEN, WHAT *OF* POPULATION GENETIC STRUCTURE OF WALLEYE IN THE EASTERN HIGHLANDS AND ADJACENT REGIONS??



→ HIGH AFFINITY OF NEW RIVER AND GREAT LAKES WALLEYE... *HOW TO EXPLAIN THAT?*

Recent stocking-mediated effects, but...

Also could be due to post-Pleistocene dispersal from Teays River refugium to proto-Lake Erie

East at time of glacial maximum ~ 18,000 YA



Possible glacial refugia

Possible recolonization routes: Proto-Allegheny or proto-Maumee rivers;

HOW DOES ALL OF THIS INFORM CONSERVATION AND MANAGEMENT?



MANAGEMENT UNITS

Two critical concepts:

Management Units (MUs) – populations that are demographically independent of one another; "stocks" as commonly discussed among managers

- Population dynamics are based on local births and deaths
- \circ Units \rightarrow Short-term management for population viability
- Evolutionarily Significant Units (ESUs)
 - Defined by genetic and adaptive differentiation
 - \circ Units \rightarrow Long-term management for evolutionary potential

MANAGEMENT UNITS

<u>MUs</u>: Populations in the respective rivers.

ESUs:

Population genetic variation at eight microsatellite loci supported recognition of differentiated population assemblages in the Alabama, Mississippi River, Eastern Highlands (Tennessee, New, and Ohio rivers), and Great Lakes drainages.

The geographic pattern of population genetic differentiation was consistent with a history of recolonization from glacial refugia in the lower Mississippi, Alabama and upper Teays/ eastern Highlands drainages, with natural secondary contact and recent anthropogenic impacts from stocking.

These are the presumptive ESUs, but we need further analyses of adaptive variation in order to truly differentiate them (e.g., use of riverine spawning habitat and large eggs helped define the New River presumptive ESU).

MANAGEMENT IMPLICATIONS FOR VIRGINIA

Within Virginia, the New River population appears as a mixture of native and several stocked gene pools, and the upper Tennessee drainage populations as mixtures of native, Kentucky and Lake Erie stocks.

We recommend:

Development and implementation of separate management plans for New River and upper Tennessee system populations.

Stocking aimed at restoring native gene pools, as we've done for New River walleye.

More generally across the entire range, management aimed to conserve ESUs and maintain and increase N_e s within the MUs.







VDGIF: John Copeland Bill Kittrell

• VT: Caitlin Miller and Haley Jenkins

• Additional samples:

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