Genetic Patterns of the Invasive Eurasian Ruffe over Time & Space



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Eurasian Ruffe Gymnocephalus cernua

Native range = Siberia, northern, central, & eastern Europe

Invasive range = southern & western Europe & the Laurentian Great Lakes



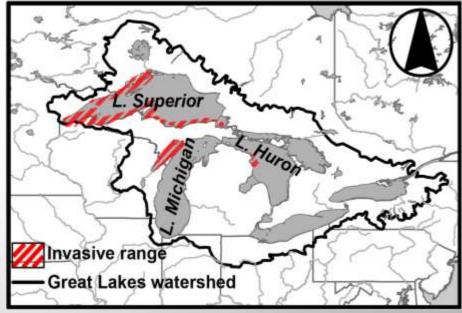
Adapted from: Taxonomy, distribution, and evolution of Percidae (Stepien and Haponski 2015)

Ruffe Invasion History

- 1986 Introduced in St. Louis Harbor via ballast water
 - Spread along L. Superior's southern shore
- 1995 Established in northern Lake Huron
 - Ballast water discharge from intralake shipping
 - Not captured in abundance since ~2003
- 2002 Established in northern Lake Michigan
 - Increasing population densities



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Adapted from: Stepien and Haponski 2015

Ruffe Ecology

Adaptive and tolerant of a wide habitat range

- Salinity (0–12ppt)
- Temperature (4–30°C)
- Depth & flow
- Eutrophic or oligotrophic

High fecundity

- Matures at 1yr (M), 2yrs (F)
- At small size (<10 cm TL)</p>
- Wide spawning range

Consume benthic organisms

Fish eggs & small fishes





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Risk Analysis

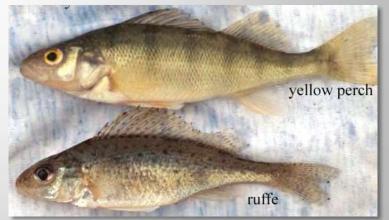
- Rapidly becomes one of the most abundant species at some sites
- Potential predator on coregonids
- Potential competitive threat to yellow perch
 - Habitat & prey overlap
 - Ruffe have feeding advantage

Ruffe proliferate with anthropogenic disturbances



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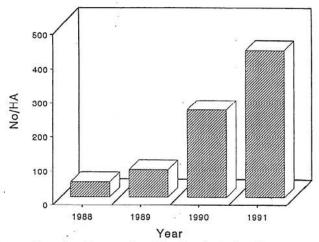


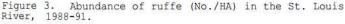


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Past Studies

- Studies in the early 90s at St. Louis Harbor revealed:
 - Ruffe quickly became most abundant species
 - As number of ruffe increased, yellow perch decreased
 - Earlier studies by Stepien et al. have determined:
 - Elbe River, Germany likely source
 - Invasions monotypic for mtDNA control region





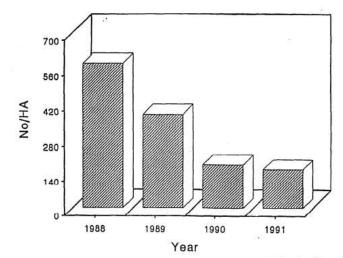


Figure 7. Abundance of yellow perch (No./HA) in the St. Louis River, 1988-91.

Project Objectives

- 1. Determine spatial differentiation patterns
- Analyze whether population genetic composition changed throughout the invasion histories (~30 yrs)



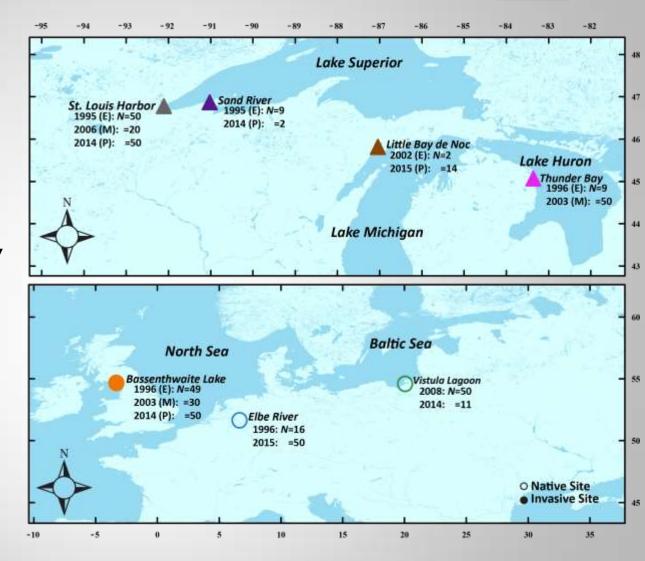


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Study Plan

- Samples representing invasive stages:
 - Early (E)

- Middle (M)
- Present (P)
- Compare to temporally congruent invasion in Bassenthwaite Lake
 - Native samples will be used as a control
- Analyze using 10 nuclear µsat loci



Diversity

- Greater genetic diversity in the native Baltic Sea Region than in either invasive region
- Decreases in N_A and A_R indicate slight initial founder effect

 A_R = allelic richness

Population samples	N	Ho	N _A	A _R
I _a St. Louis Harbor	120	0.41	58	2.81
I _b Sand River	11	0.30	28	2.61
I _c Little Bay de Noc	16	0.42	33	2.62
l _d Thunder Bay	59	0.39	40	2.53
Total GL	206	0.38	70	2.68
II Bassenthwaite Lake	129	0.35	57	2.42
III _a Elbe River	66	0.51	98	4.02
III _b Vistula Lagoon	61	0.55	92	4.10
Total BSR	127	0.53	126	4.05
	I _a St. Louis Harbor I _b Sand River I _c Little Bay de Noc I _d Thunder Bay Total GL II Bassenthwaite Lake III _a Elbe River III _b Vistula Lagoon	IaSt. Louis Harbor120IbSand River11IcLittle Bay de Noc16IdThunder Bay59Total GL206II Bassenthwaite Lake129IIIaElbe River66IIIbVistula Lagoon61	I _a St. Louis Harbor 120 0.41 I _b Sand River 11 0.30 I _c Little Bay de Noc 16 0.42 I _d Thunder Bay 59 0.39 Total GL 206 0.38 II Bassenthwaite Lake 129 0.35 III _a Elbe River 66 0.51 III _b Vistula Lagoon 61 0.55	I I <thi< th=""> <thi< th=""> <thi< th=""> <thi< th=""></thi<></thi<></thi<></thi<>

Arlequin, FSTAT, & Genepop

N = number of individuals H_o = observed heterozygosity

 N_A = number of alleles

Divergence

Strong spatial differentiation among the 3 regions:

- Bassenthwaite Lake is the most divergent
- Baltic Sea Region sites differ slightly
- Single pairwise difference in the Great Lakes

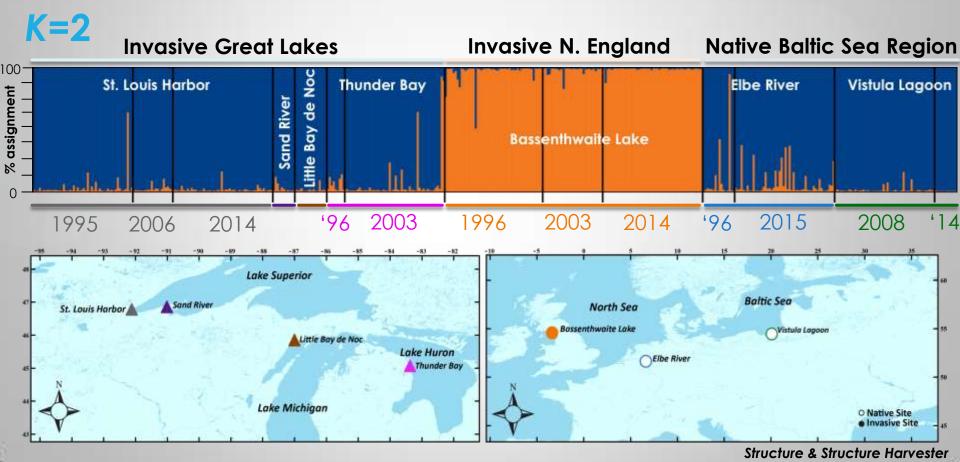
St. Louis Harbor vs Thunder Bay

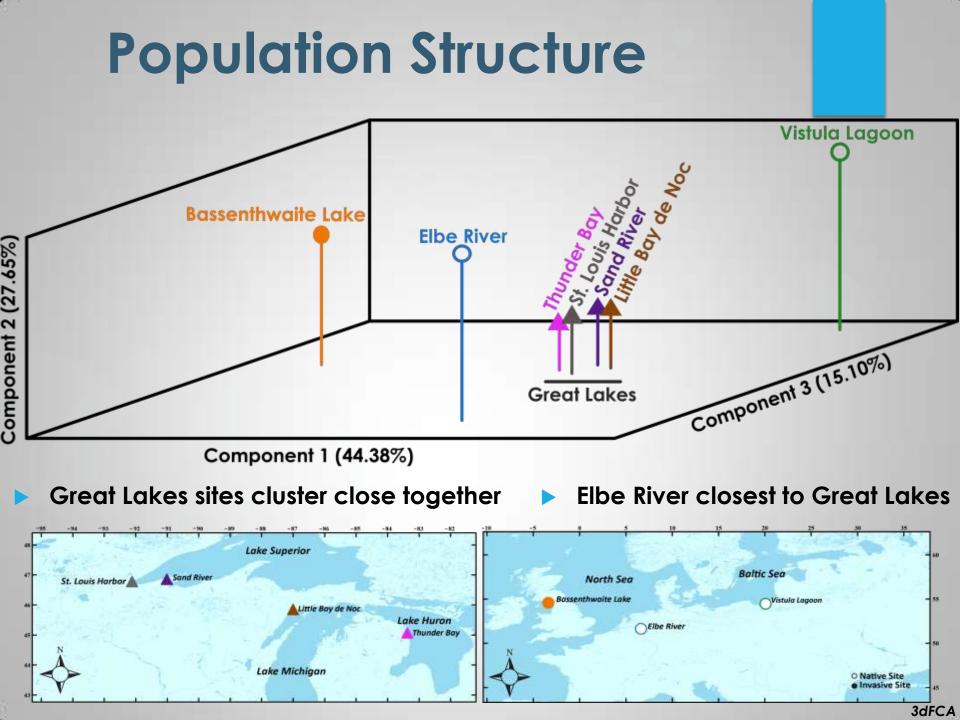
Pairwise genetic divergences (note the difference between I_a and I_d) * = significant after sequential Bonferroni correction

Site	l _a	l _b	I _c	l _d	П	III _a
I _a St. Louis Harbor	-					
I _b Sand River	0.034	-				
I _c Little Bay de Noc	0.017	0.015	-			
l _d Thunder Bay	0.012*	0.043	0.030	-		
II Bassenthwaite Lake	0.177*	0.214*	0.218*	0.178*	-	
III _a Elbe River	0.080*	0.114*	0.068*	0.105*	0.170*	-
III _b Vistula Lagoon	0.110*	0.103*	0.070*	0.125*	0.247*	0.049*

Population Structure

- Each invasion has a separate source
 - Single source of invasion with no additional introductions
- Genetic composition of invasions remained consistent over time







- 1. Strong spatial differentiation among both invasive regions and native Baltic Sea Region
- 2. Elbe River is genetically closest to the Great Lakes
- 3. Slight initial founder effect in both invasions
- 4. Range expansion of original colonists from St. Louis Harbor
- 5. Genetic compositions of both invasions have remained stable with no additional introductions or secondary founder effects

Thank you! Questions?

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ENVIRONME

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Great Lakes RESTORATION

