INVASION GENETICS OF THE EURASIAN ROUND GOBY: CHANGES VERSUS STASIS OVER TIME AND SPACE

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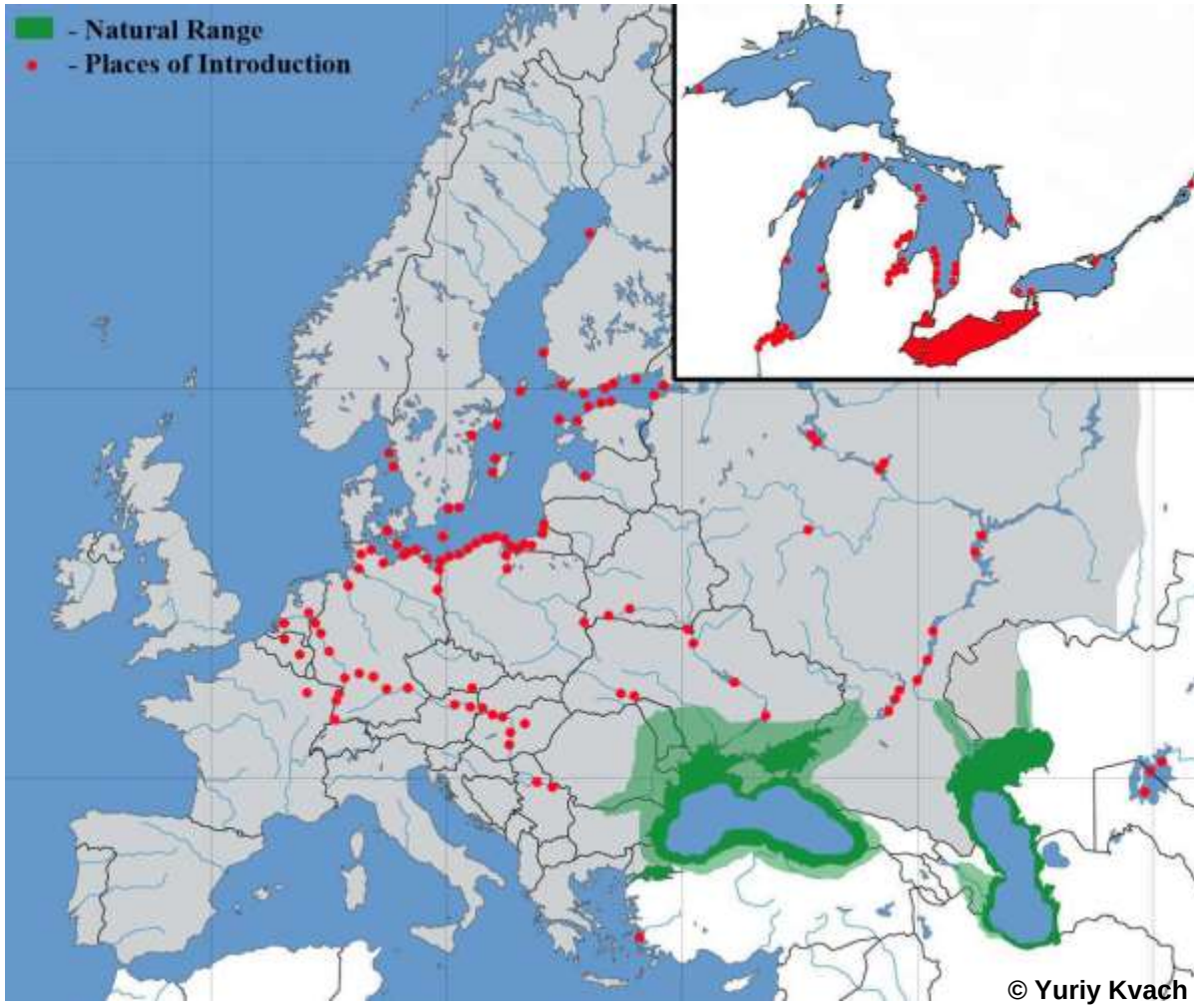
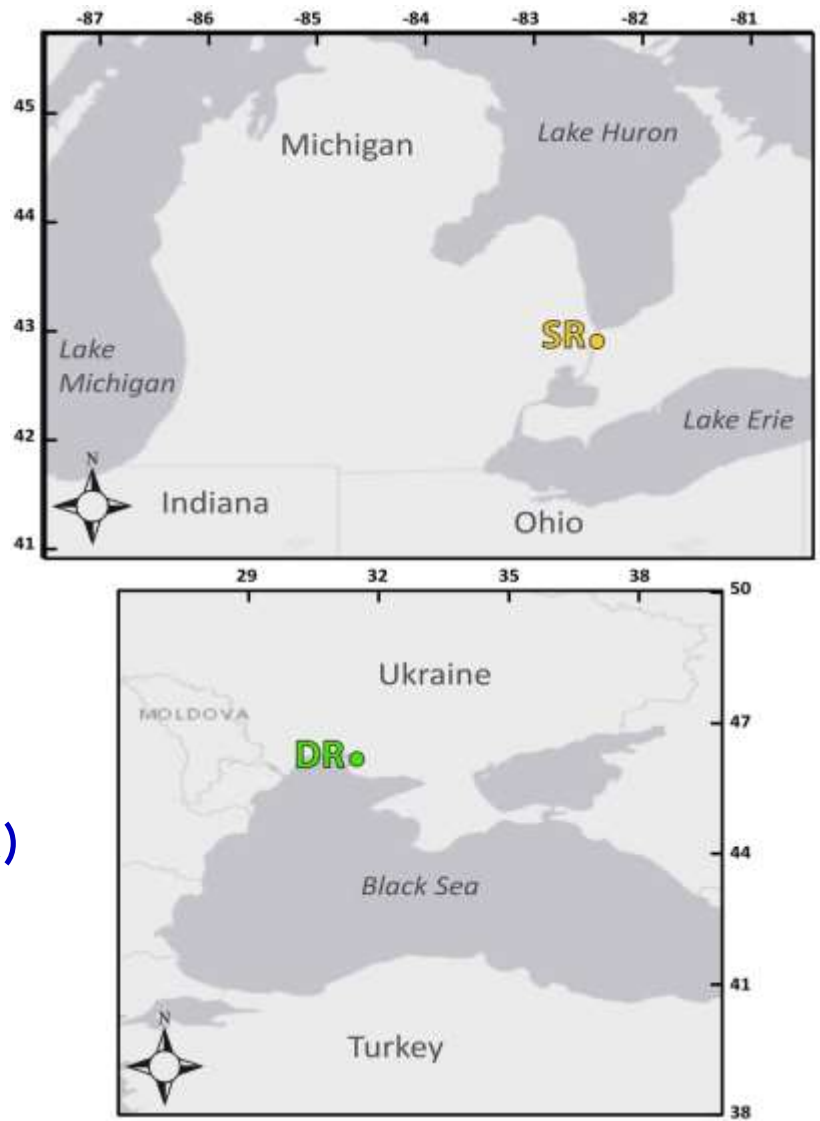
The round goby

- *Neogobius melanostomus* (Fam. Gobiidae, Subfam. Benthophilinae)
- Native to Ponto-Caspian region of Eurasia
- Benthic invertivore, ovivore, and piscivore
- Invasive in Baltic Sea, Great Lakes, the middle East, and much of Europe
- Tolerates a wide range of temperature and salinity



The round goby in the Great Lakes

- **GL invasion established via ballast water transport initially in St. Clair River (SR)**
- **Arrived in 1990, spread throughout region by 1995**
- **Extensive economic & ecological effects**
  - **Predator on benthic fish eggs**
  - **Habitat and diet overlap with several native fishes**
  - **Prey for several native fishes**
- **Primary GL source: Dnieper River Delta (DR) in the Black Sea (Brown & Stepien. *Molecular Ecology*. 2009)**



Objective

Test for genetic changes over multiple geographic and temporal scales

Hypotheses

Hypothesis	Description
1. Genetic Stasis	**Genotypes of the initial established colonists have persisted over time**
2. Genetic Replacement	**Genotypes of the initial established colonists were replaced by later-arriving genotypes from single or multiple sources**
3. Genetic Supplement	**Genotypes of the initial established colonists have persisted, along with later-arriving genotypes from single or multiple sources.**

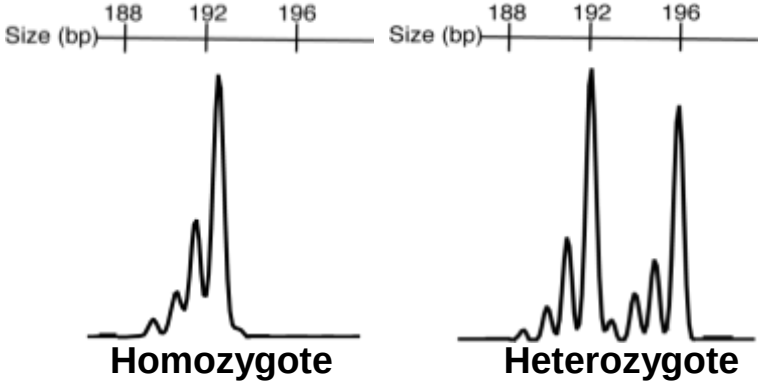
Assumptions about invasion genetics

- **Invasive species will display a founder effect**
- **Little to no differentiation across the invasive range**
- **Early arriving individuals & genotypes will be supplemented by later arrivals across all temporal scales**

Methods: 2 genetic data sets

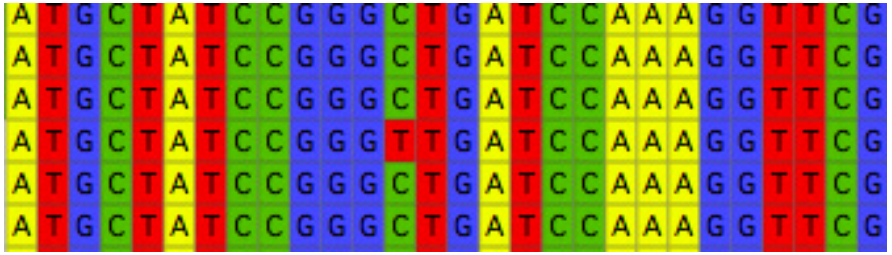
Nuclear DNA microsatellite (μsat) loci

- Short tandem repeating sequences (GACGACGAC….)
- Using 13 loci
- Replication errors during meiosis create alleles of different lengths
- Mutate rapidly: selectively neutral
- Useful for determining fine scale population differences



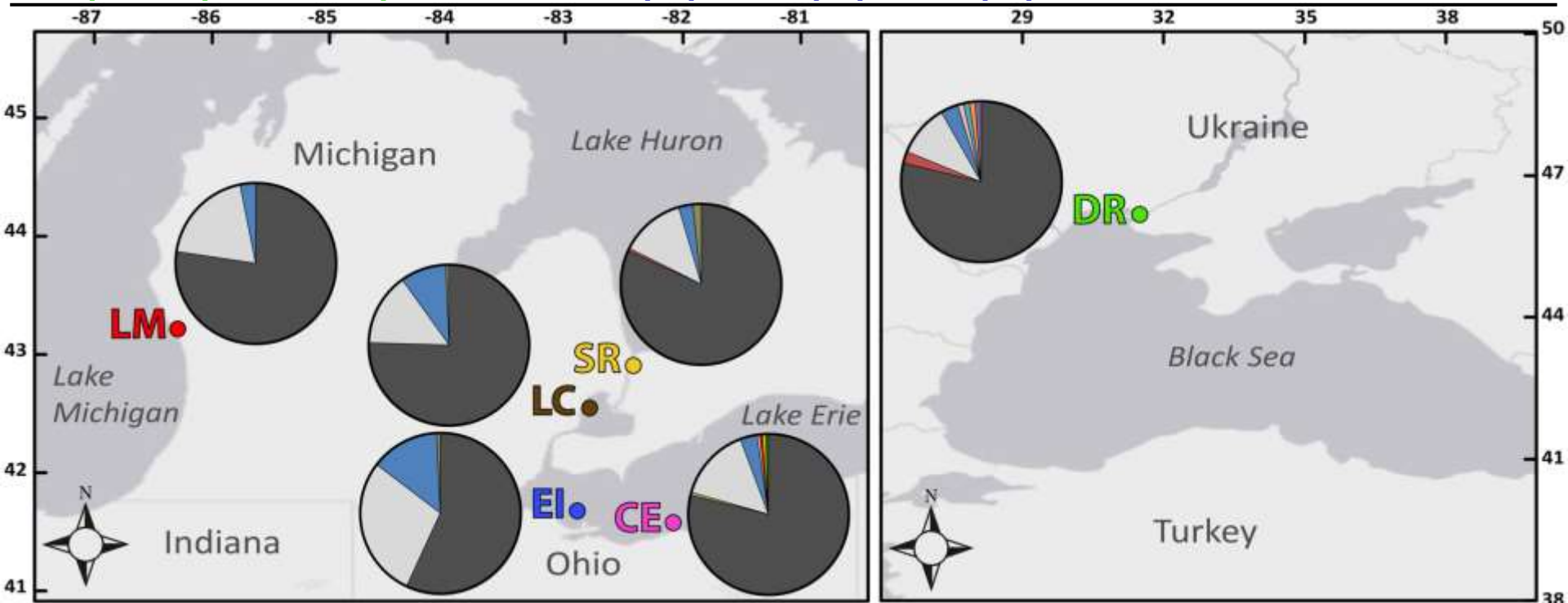
Cytochrome *b* gene sequences

- Mitochondrial (mtDNA) gene: maternally inherited
- Gene sequences: Haplotype (one allele/individual)
- Most mutation is at 3rd codon "wobble"
- Useful for determining biogeographic & phylogenetic histories & some population differences



Methods: sampling design

Site (Map Label, First Sighting)	Sample Years (*N*)
L. Michigan (LM, 1997)	1998 (19), 2007 (50), 2011 (44), 2013 (50)
St. Clair R (SR, 1990)	1993 (45), 2007 (50), 2011 (34), 2013 (50)
L. St. Clair (LC, 1993)	1998 (39), 2007 (50), 2011 (32), 2013 (50)
L. Erie Islands (EI, 1996)	1998 (51), 2002 (50), 2005 (49), 2007 (40), 2011 (45), 2013 (50)
Central L. Erie (CE, 1996)	1998 (24), 2002 (29), 2007 (50), 2011 (48), 2013 (50)
Dnieper R. (DR, Native)	2002 (25), 2007 (24), 2013 (53)



Spatial diversity & composition

A_r = Allelic richness (common measure of genetic diversity)
H_o = observed heterozygosity
h = gene diversity

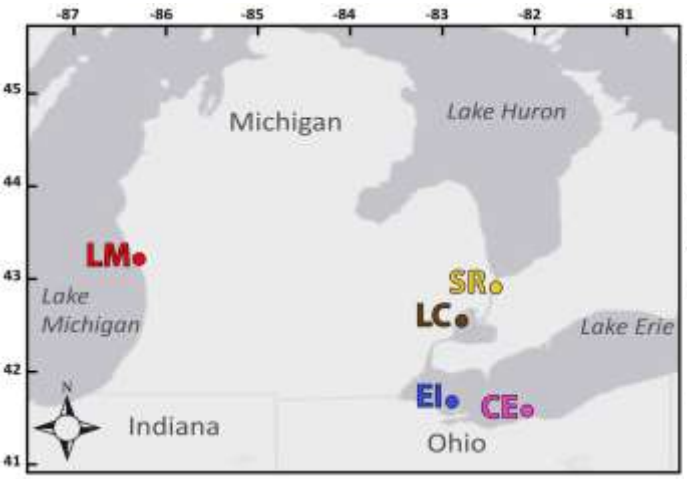
N_H = N haplotypes
N_{PH} = N private haplotypes
* = significant differences

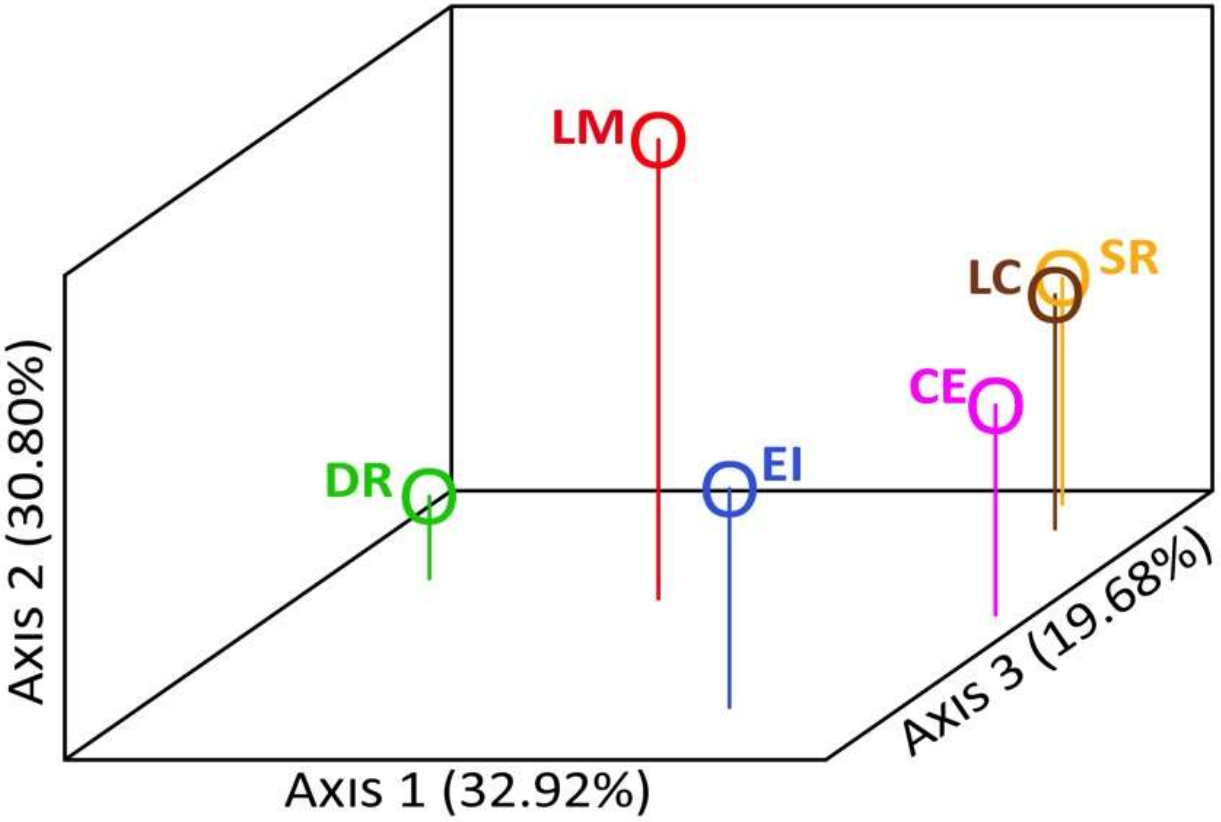
		cytochrome *b*				µsat		
Site	*N*	Haplotypes		*h*	N_H	N_{PH}	*Ar*	*Ho*
L. Michigan	163	1,8,57		0.32	3	0	8.3 *	0.59
St. Clair R.	179	1,7,8,57,88		0.36	5	0	10.0	0.60
L. St. Clair	171	1,8,57,88		0.41	4	0	9.7	0.60
L. Erie Islands	285	1,8,57,88	* All other sites	0.58	5	0	9.1 *	0.59
L. Erie Avon Pt.	201	1,5,8,57,89,94-96		0.33	8	3	8.5 *	0.59
Dnieper R. Delta	102	1,7,8,57,89,91-93		0.37	8	3	14.5	0.62

Arlequin, F-Stat

Spatial 3DFCA

L. Michigan (LM)
St. Clair R. (SR)
L. St. Clair (LC)
L. Erie Islands (EI)
Central L. Erie (CE)
Dnieper R. Black Sea (DR)





Genetix

Spatial Divergence

Pairwise θ_{ST} for nuclear DNA microsatellite loci.
***=statistically significant after Bonferroni correction**

	LM	SR	LC	EI	CE	DR
L. Michigan (LM)	~					
St. Clair R. (SR)	0.042*	~				
L. St. Clair (LC)	0.047*	0.004*	~			
L. Erie Islands (EI)	0.055*	0.014*	0.007*	~		
Central L. Erie (CE)	0.065*	0.020*	0.016*	0.009*	~	
Dnieper R., Black Sea (DR)	0.067*	0.025*	0.026*	0.037*	0.047*	~
mean θ_{ST}:	0.055	0.021	0.020	0.024	0.031	0.040

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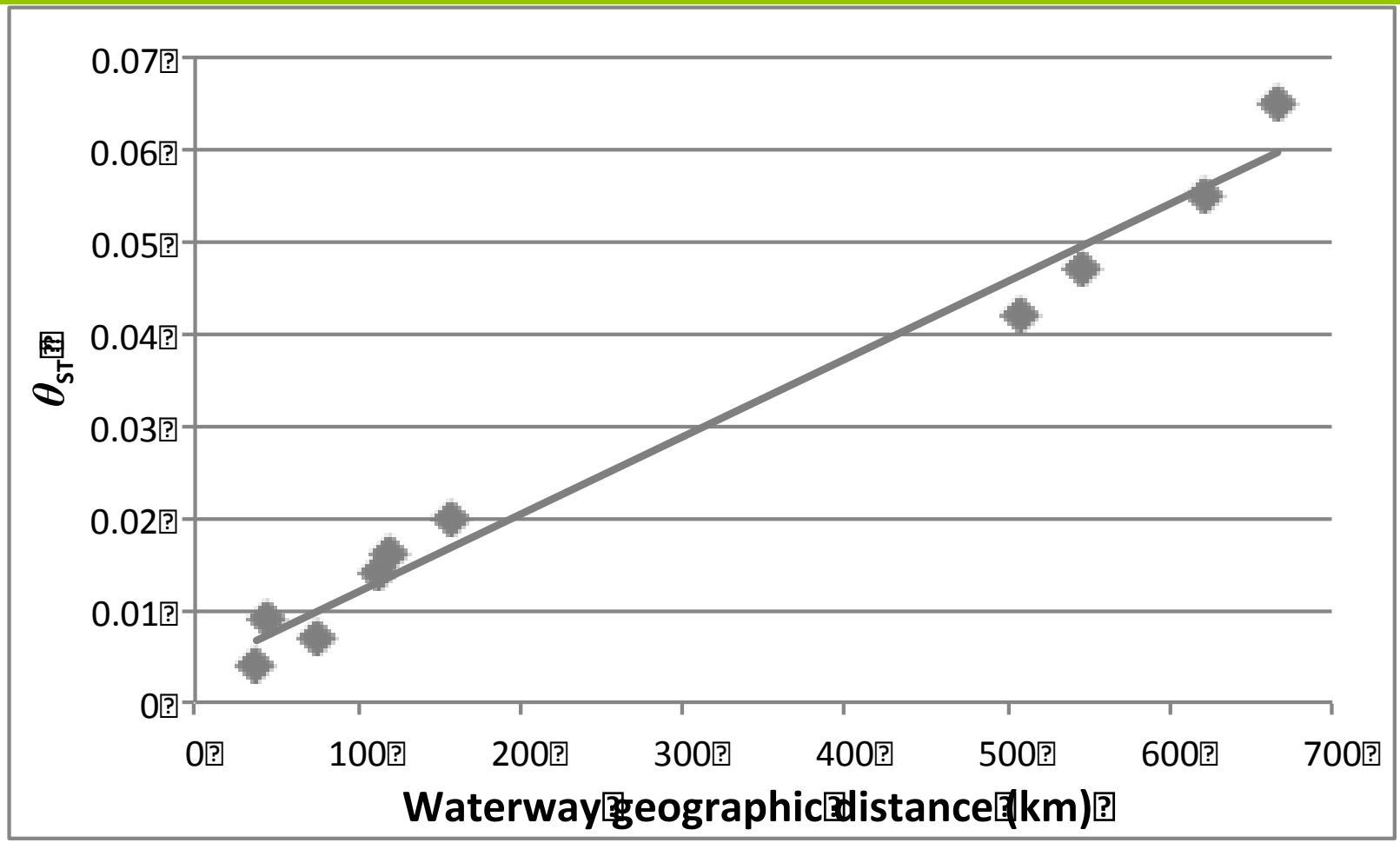

98% of variation in divergence is explained by geographic distance**

F-Stat, R, Excel

Spatial individual assignments

- SR and LC have high assignment to DR (>0.25)
- All other high mis-assignments were back to the invasion core
- LM and DR are very different from all other sites

	Assigned to					
Site	LM	SR	LC	EI	CE	DR
L. Michigan (LM)	0.72	0.06	0.06	–	0.01	0.15
St. Clair R. (SR)	–	0.36	0.31	0.02	0.02	0.29
L. St. Clair (LC)	–	0.08	0.60	0.03	0.01	0.27
L. Erie Islands (EI)	0.01	0.09	0.34	0.32	0.06	0.19
Central L. Erie (CE)	–	0.06	0.28	0.07	0.42	0.15
Dnieper R. (DR)	–	–	–	–	–	1.00

Geneclass2

Temporal results

■ = first sample
◆ = last sample
O = intermediate sample
L. Michigan (LM)
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L. St. Clair (LC)
L. Erie Islands (EI)
Central L. Erie (CE)
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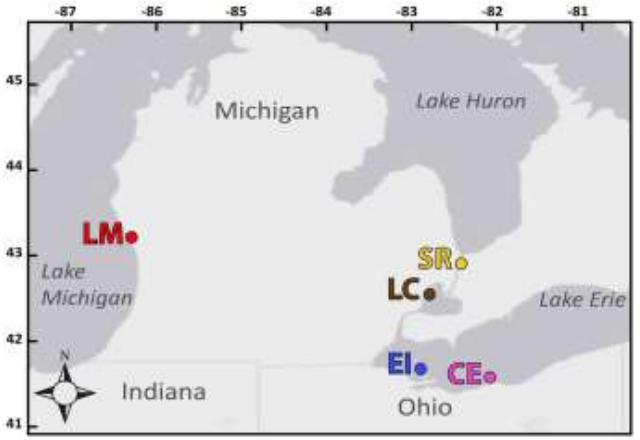
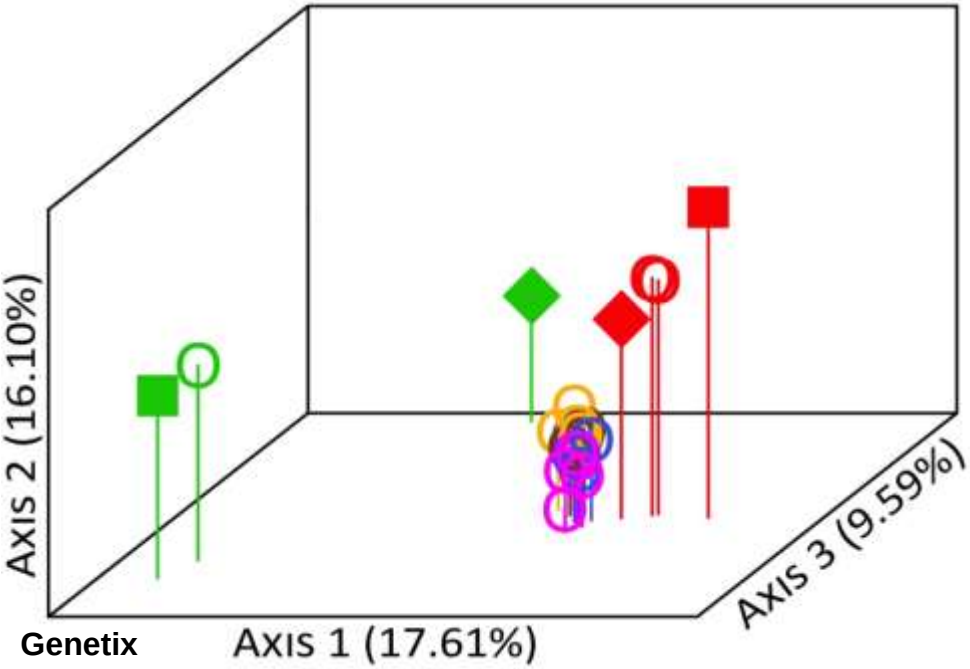
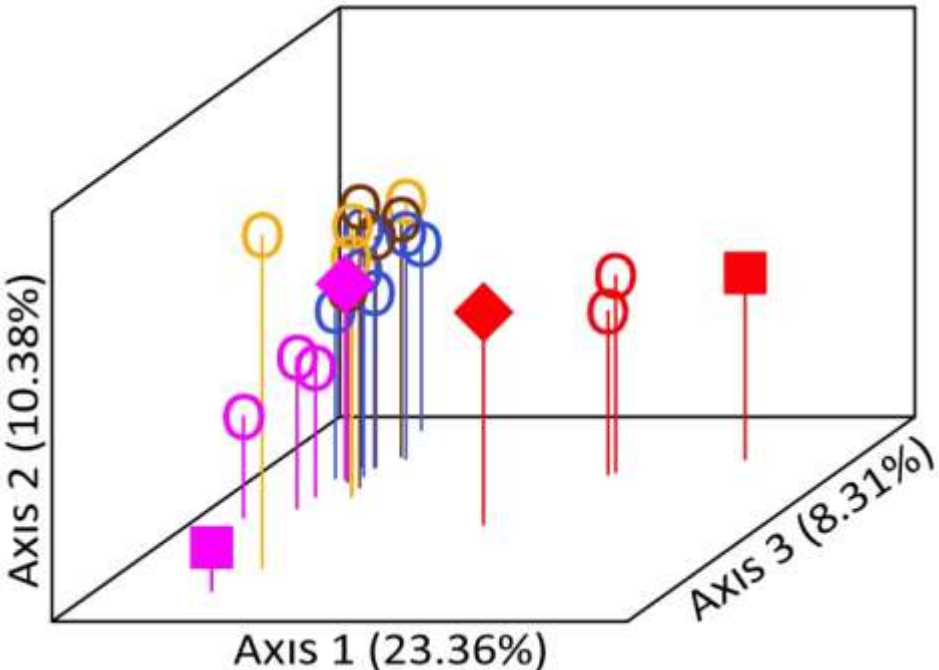
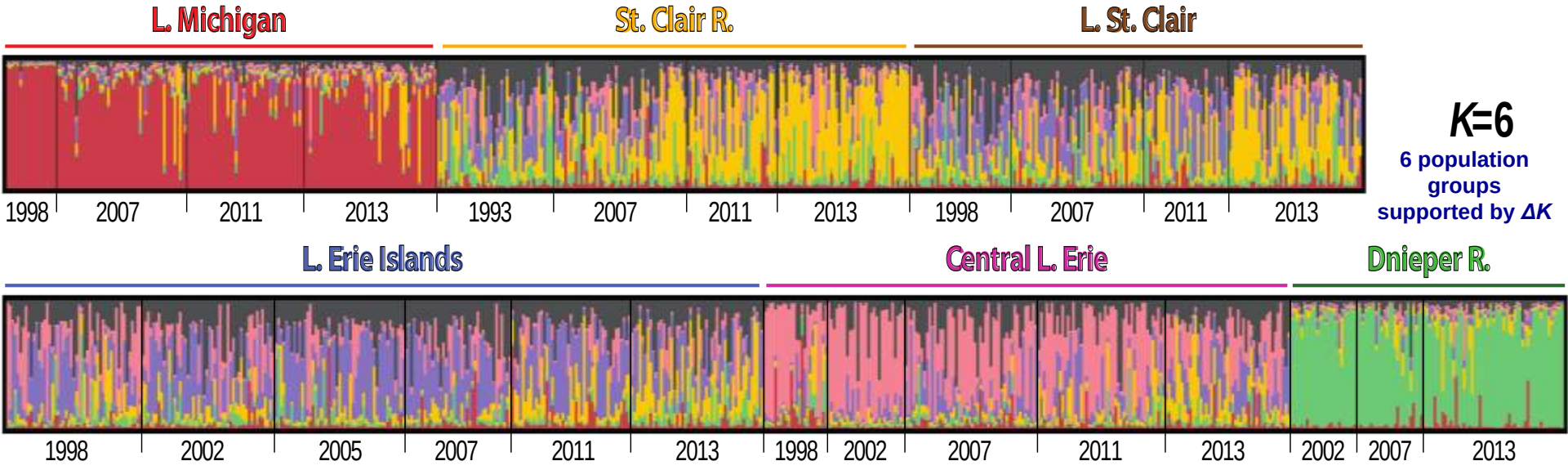






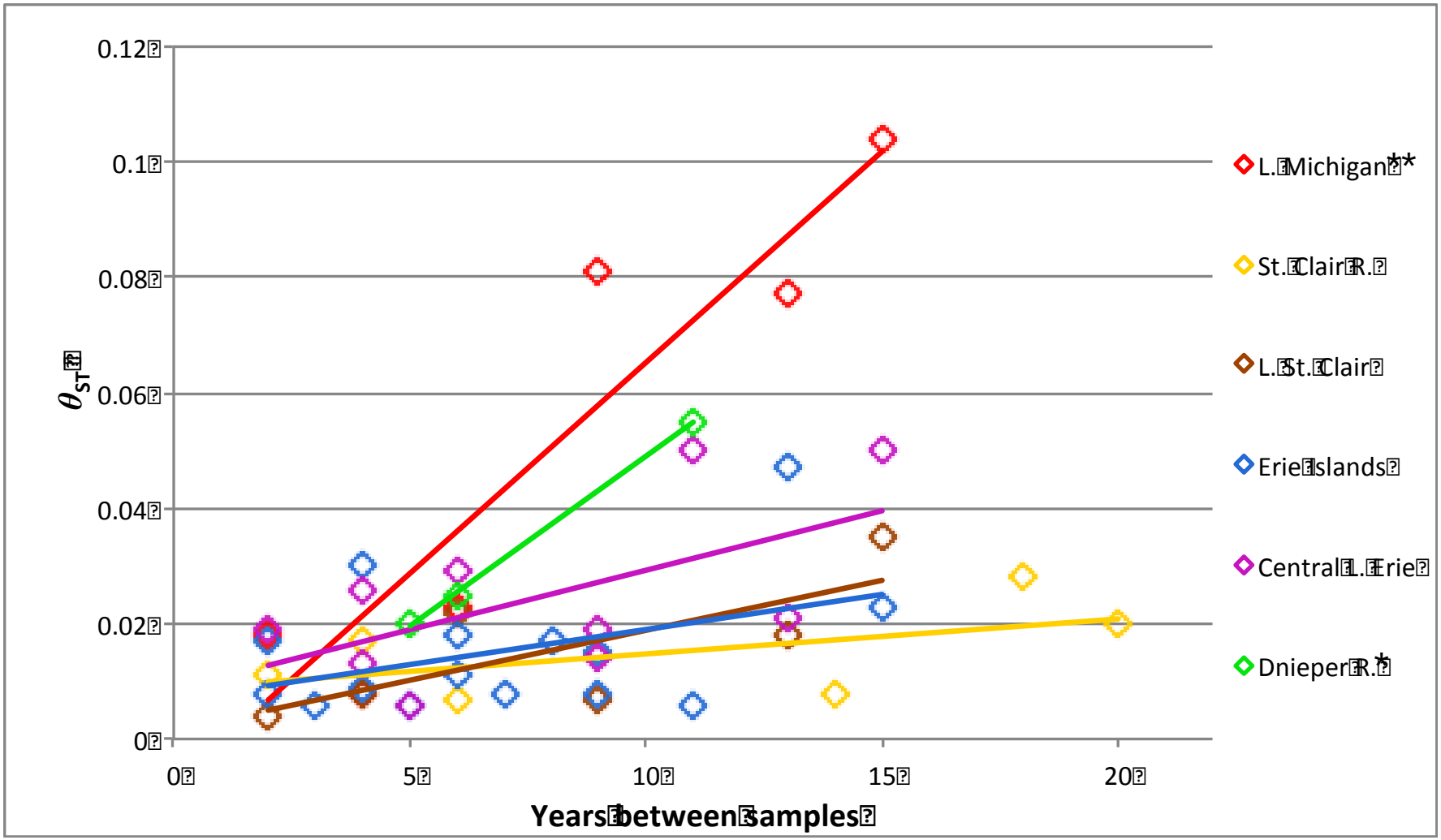
Genetix

Temporal results



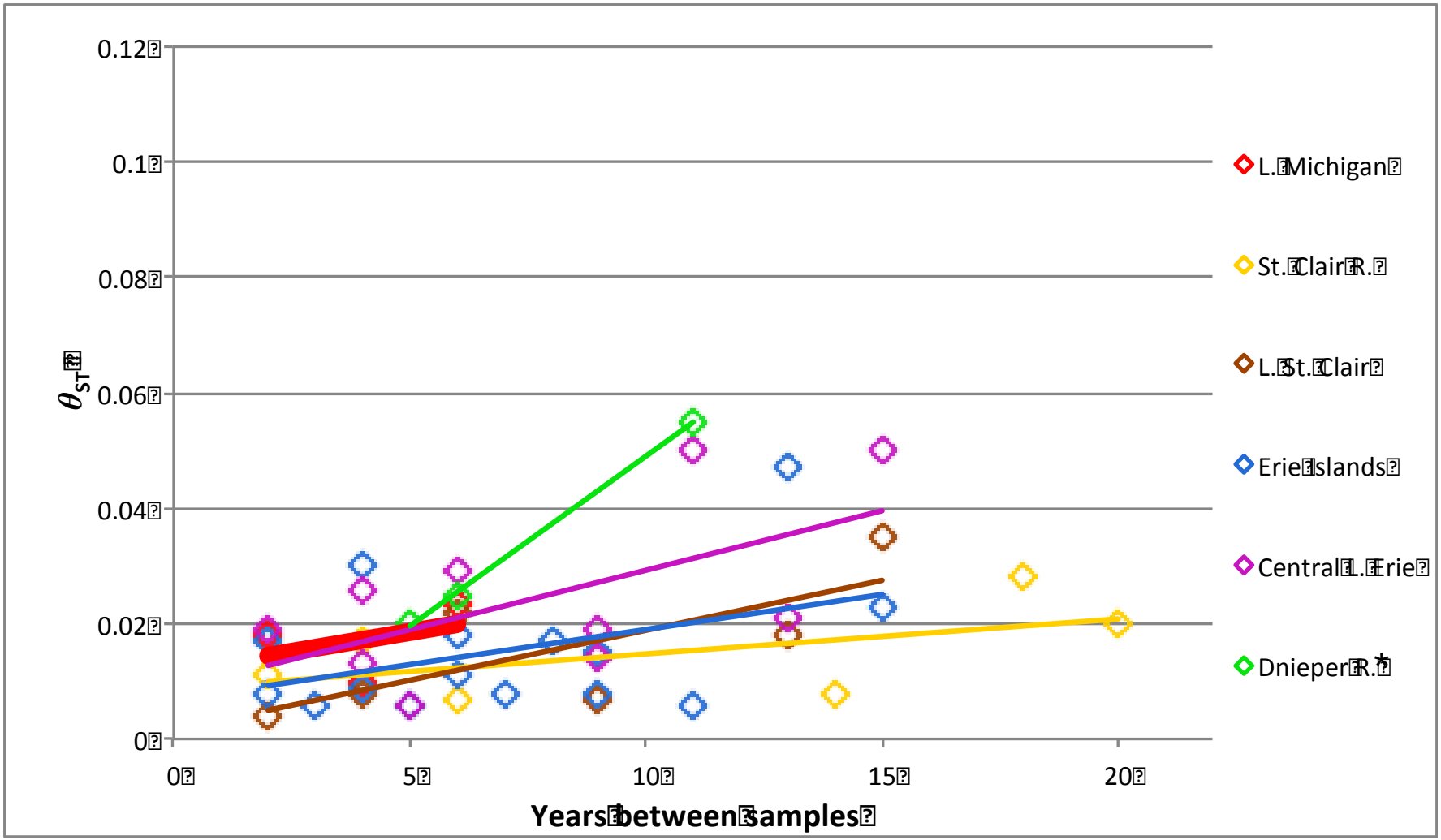
Genetix, Structure, Structure Harvester

Temporal results



F-Stat, R, Excel

Temporal results



F-Stat, R, Excel

Conclusions

1. **Only evidence for founder effect at the early expansion edge**

2. **All sites are significantly divergent from each other; determined by geographic distance**

3. **Spatial & temporal variation in composition between all sites, but no significant changes in diversity over time within sites**

4. **Significant divergence over time within all sites though each remained distinct with small convergence of sites due to slight supplementation at the early invasion periphery**

Conclusions

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Evidence for the “founder takes most” hypothesis

Future directions

- **Developing eDNA assay using HTS specific for currently and potentially invasive gobies**

- **We need water samples!**
  - **Great Lakes & Europe native and invasive**
  - **Especially if multiple goby spp. are sympatric**

- **See me for protocol or email: Matthew.Snyder6@rockets.utoledo.edu**

Thank you!

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Funding sources:

- USEPA CR-83281401-0
- NSF DEB-0456972
- UT University Fellows Program

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OHIO DEPARTMENT OF NATURAL RESOURCES

GRAND VALLEY STATE UNIVERSITY

Questions?

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Spatial Divergence

Pairwise θ_{ST} for cyt *b* (above diagonal) and μsat (below).
***=statistically significant after Bonferroni correction**

	LM	SR	LC	EI	CE	DR	Mean cyt *b* θ_{ST}
L. Michigan (LM)	~	0.003	0.015	0.040*	-0.002	0.009	0.013
St. Clair R. (SR)	0.042*	~	0.015	0.061*	-0.003	-0.005	0.014
L. St. Clair (LC)	0.047*	0.004*	~	0.020*	0.006	0.007	0.013
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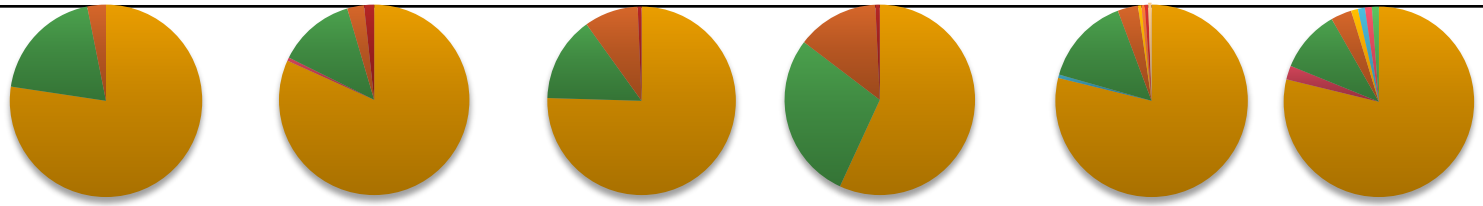
Dnieper R., Black Sea(DR)	0.067*	0.025*	0.026*	0.037*	0.047*	~	0.012
mean μsat θ_{ST}:	0.055	0.021	0.020	0.024	0.031	0.040	



Arlequin v3.5.1.3 (Excoffier & Lischer 2010), *F*stat v2.9.3.2 (Goudet 1995, 2002)