

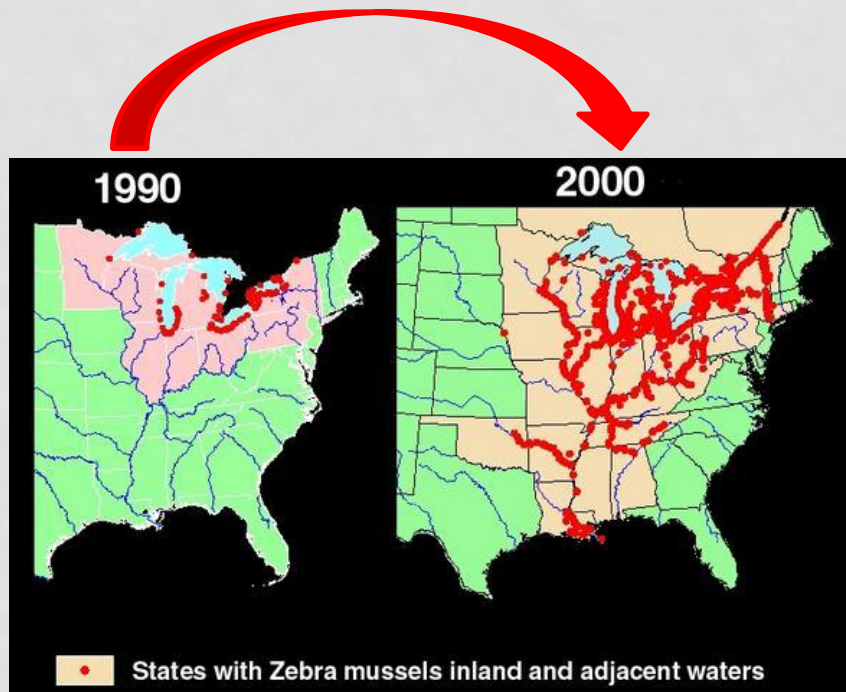
INVASIONAL GENETIC PATTERNS ACROSS TIME AND SPACE IN NORTH AMERICAN DREISSENA MUSSELS

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GENETICS AND GENOMICS GROUP

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SOLVING INVASION MYSTERIES WITH BIOGEOGRAPHY, GENETICS & GENOMICS

1. Rapid detection & accurate identification of taxa
2. Determine invasion population source(s), sinks, & number(s)
3. Analyze variation within & among population sites, testing for founder effects & mixing from sources
4. Test whether the genetic structure & genomic adaptations of exotic populations change over space & time



NORTH AMERICA *DREISSENA* MUSSEL INVASION

- Native to Ponto-Caspian region
- **Zebra mussel invade GL ~1986**
- Quagga mussel invade GL ~1989



Zebra



Quagga



- Negative economic and ecological impacts

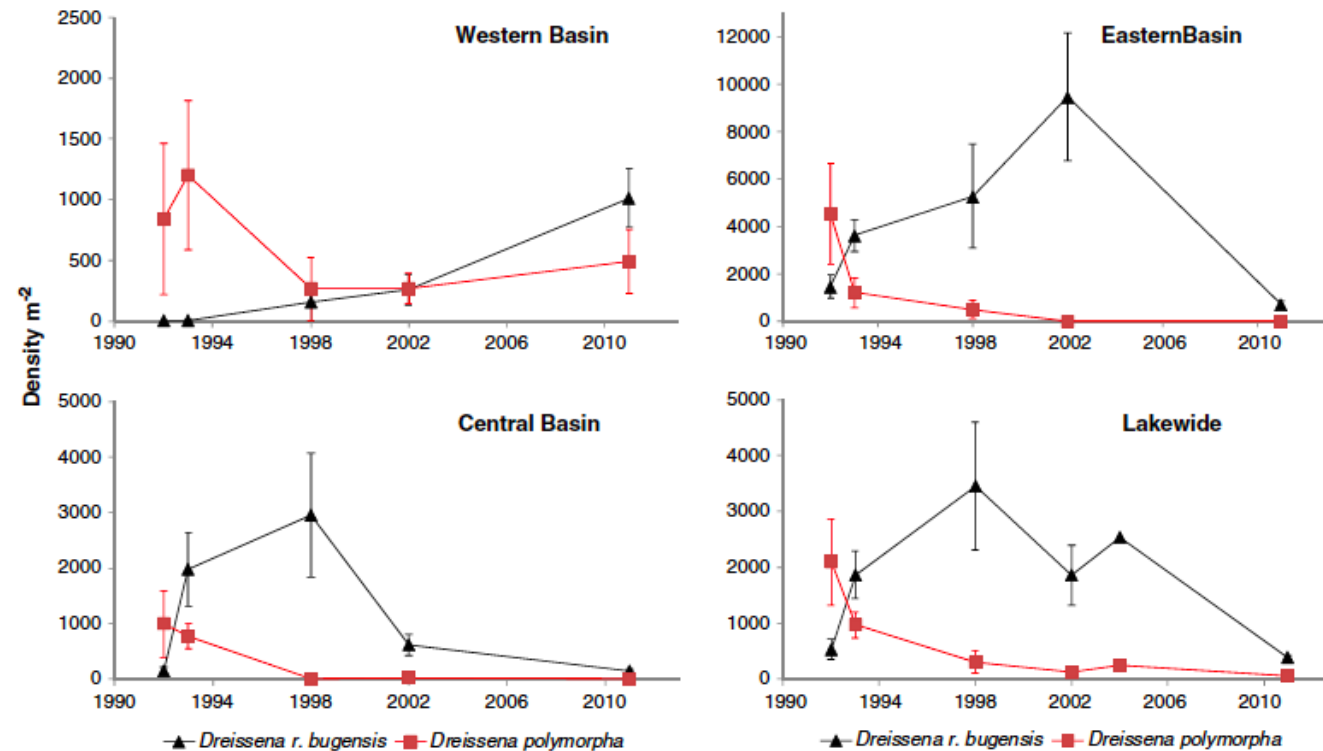
TEMPORAL POPULATION DYNAMICS

Invasive species tend to go through population crashes following explosive population growth

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Lake Erie



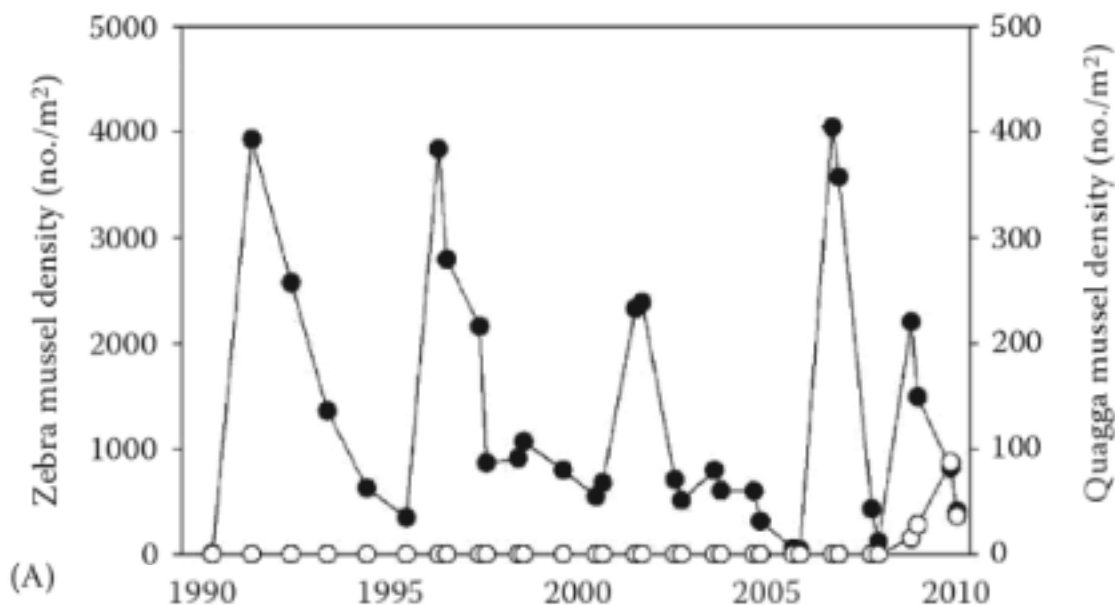
- ZM populations reached capacity within 3-5 years, then crashed
- QM take longer to reach capacity, but follow a similar trend

Karatayev et al. 2014

TEMPORAL POPULATION DYNAMICS

Invasive species tend to go through population crashes following explosive population growth

Hudson River

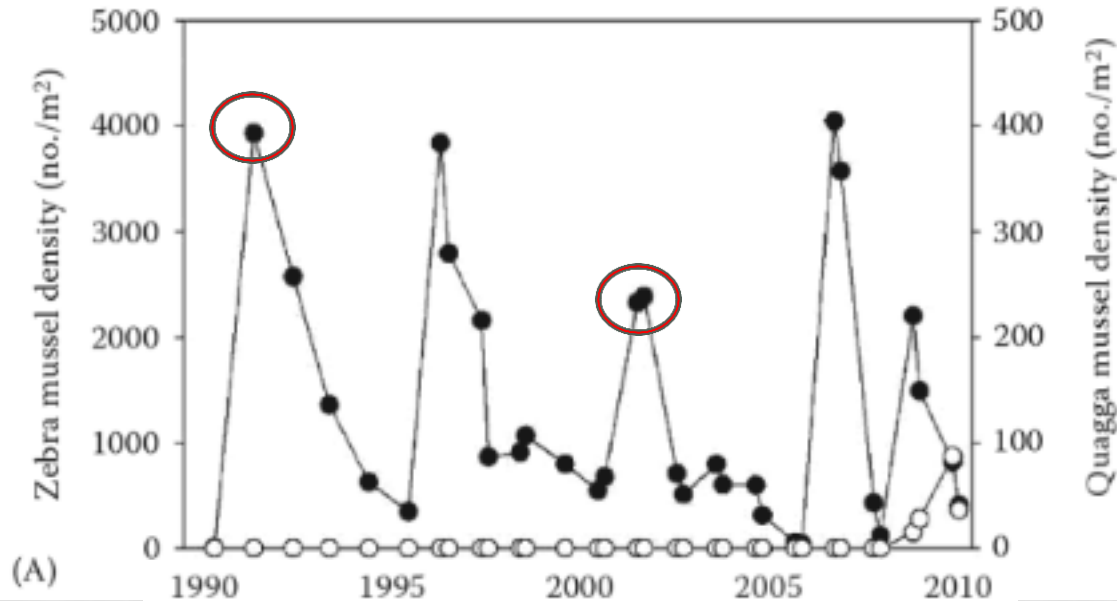


- ZM populations reached capacity within 3-5 years, then crashed
- However, ZM display cyclical pattern of growth and decline
- QM is a recent invader (2010)

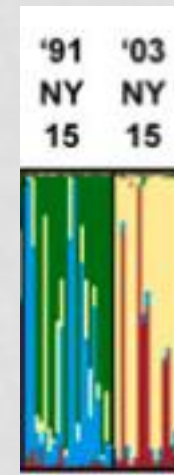
TEMPORAL POPULATION DYNAMICS

Invasive species tend to go through population crashes following explosive population growth

Hudson River



Strayer & Malcom 2013



Brown & Stepien 2010

- Appears to be genetic turnover between growth cycles

POPULATION GENETIC HYPOTHESES & QUESTIONS

Research Questions

- 1) Single or multiple introductions?
- 2) Founder effect?
- 3) How are invasive populations structured?
- 4) What changes have occurred over time?
- 5) Do the genetic types that establish first persist?

Hypotheses

A. Genetic Stasis

- Founder takes all/most
- Genotypes stay relatively consistent over time

B. Genetic Supplement

- Genetic diversity may increase after founding
- New genotypes arrive & become established

C. Genetic Replacement

- Later arriving genotypes replace originals
- Significant differences in composition

Data Sets

- a) mitochondrial & nuclear DNA sequences
- b) 15 nuclear DNA microsatellite loci
- c) Genomic SNPs (single nucleotide polymorphisms)

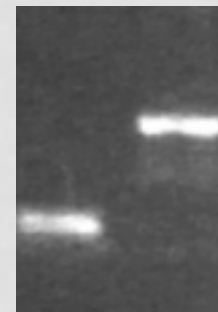
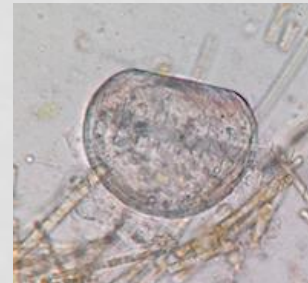
METHODS

Use 15 μ sats for 50 individuals per sample group to examine:

1) Temporal population genetics within the Hudson River and Lake Erie (early, middle, present)

- Are the trends similar for two distinct invasive locations
- Are the trends similar for two invaders (Zebra and Quagga)

2) Genotypes of veligers and adults



ZM QM

- Individuals identified to species with genetic assay

Ram et al. 2011

QUAGGA MUSSEL RESULTS

5 μ sats analyzed for 5 QM samples

Fst divergence value calculated in Arlequin

	HR10	HR16	LE98	LE11
HR16	0.016*			
LE98	0.004	0.010		
LE11	0.003	0.011	0.002	
LE16	0.012*	0.029**	0.001	0.009

** significant after Sequential Bonferroni Correction

* significant before Sequential Bonferroni Correction

- No difference temporally within **LE**
- Slight difference in **HR**
- Sites become more divergent over time

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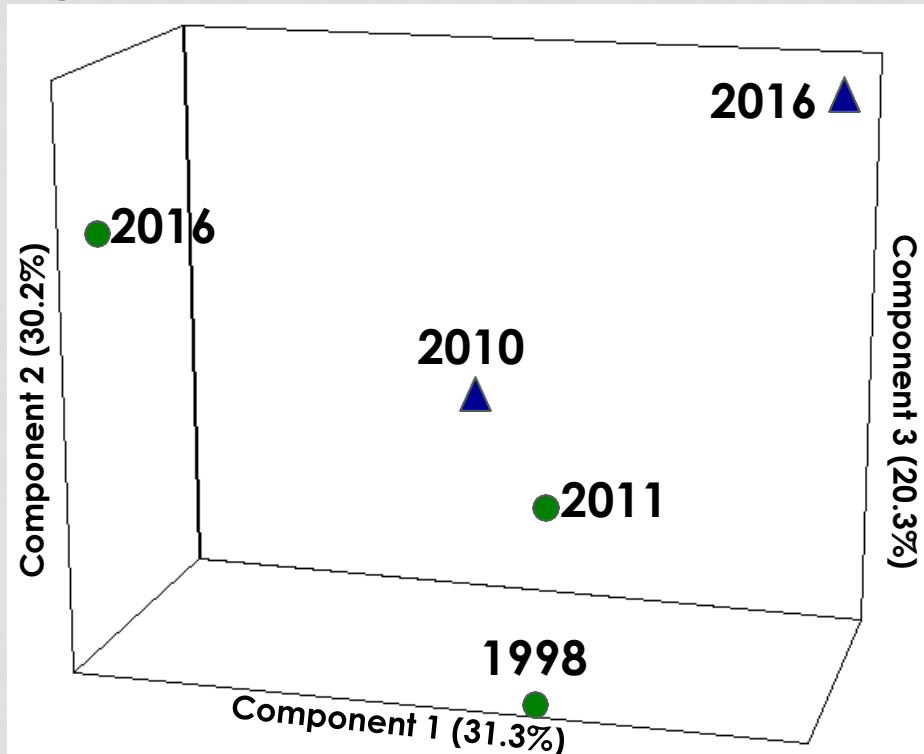
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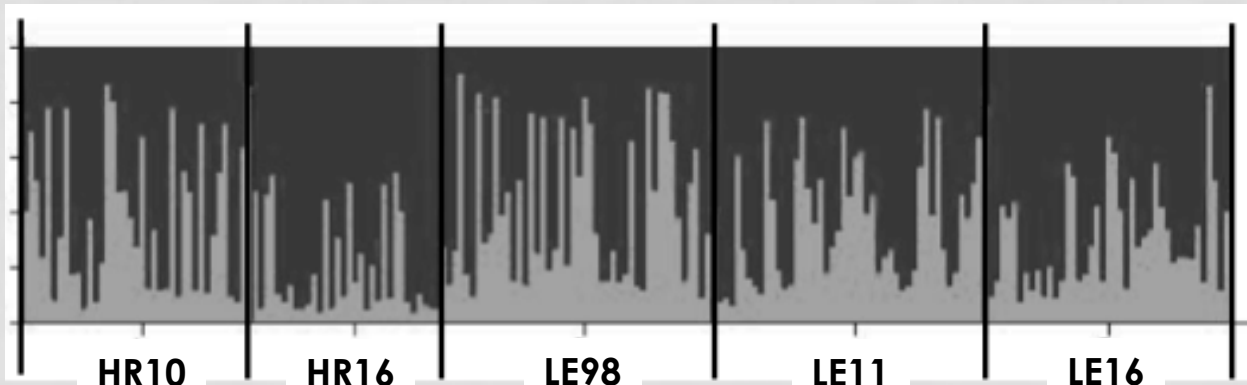
QUAGGA MUSSEL RESULTS



Genetix v4.05 (Belkhir et al. 2004)

● Lake Erie
▲ Hudson River

- 3dFCA shows divergence over time between **HR** and **LE**
- Explains 81.8% of the data



- No population structure seen with individual assignment tests

Structure v 2.3.3 (Pritchard & Wen 2004), Structure Harvester (Evanno et al. 2005, Earl & vanHoldt 2012)

ZEBRA MUSSEL RESULTS

15 μ sats analyzed for 6 ZM adult samples

Fst divergence value calculated in Arlequin

Fst **HR** vs **LE** 0.004

	HR94	HR03	HR16	LE94	LE03
HR03	0.039**				
HR16	0.008**	0.037**			
LE94	0.011**	0.020**	0.007*		
LE03	0.008**	0.038**	0.006*	0.007*	
LE16	0.009**	0.030**	0.009**	0.007*	0.009**

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- No difference spatially between **LE** & **HR**
- Low Fst temporally within **LE**
- Two genetic turnovers in **HR**
- Sites become more similar over time

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15 μ sats analyzed for 6 ZM adult samples

Fst divergence value calculated in Arlequin

Fst **HR** vs **LE** 0.004

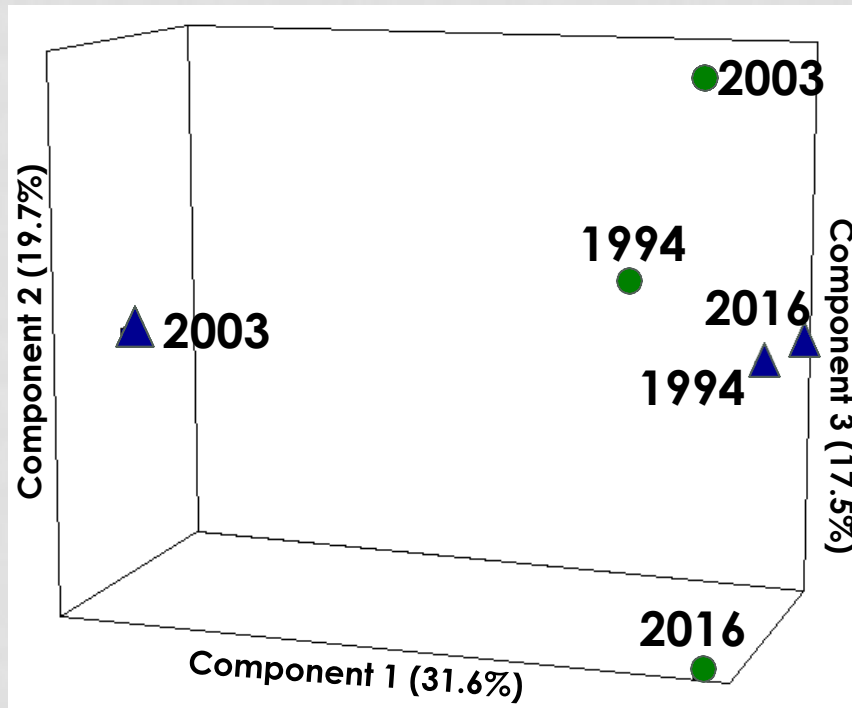
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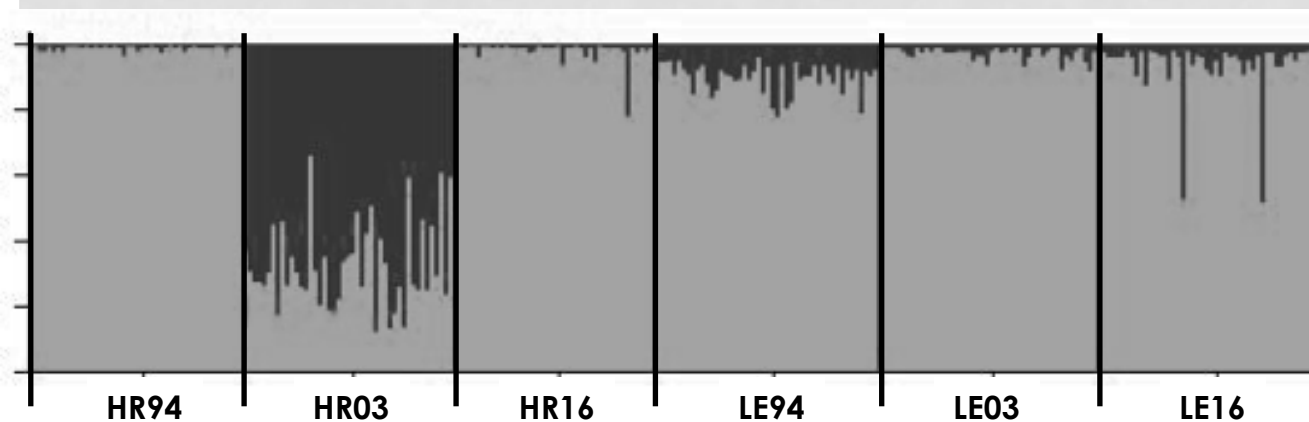


- Lake Erie
- ▲ Hudson River

- 3dFCA shows temporal genetic changes in **HR**
- Explains 68.8% of the data

Genetix v4.05 (Belkhir *et al.* 2004)

- Population structure seen in the middle **HR** sample with individual assignment



Structure v 2.3.3 (Pritchard & Wen 2004), Structure Harvester (Evanno *et al.* 2005, Earl & vanHoldt 2012)

ZEBRA MUSSEL VELIGER LARVAE RESULTS

15 μ sats analyzed for 1 ZM veliger sample from Lake Erie

Fst divergence value calculated in Arlequin

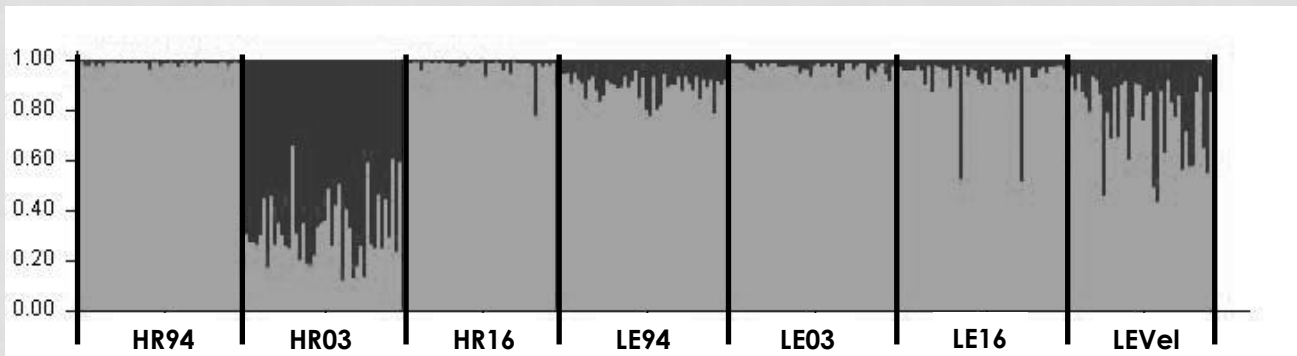
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LE03	0.008**	0.038**	0.006*	0.007*		
LE16	0.009**	0.030**	0.009**	0.007*	0.009**	
LE16-Vel	0.022**	0.032**	0.012**	0.003	0.008**	0.012**

- Fst highest compared with **HR** adults

** significant after Sequential Bonferroni Correction

* significant before Sequential Bonferroni Correction

Arlequin v3.5.1.3 (Excoffier & Lischer 2010)



- Veliger individuals assigned slightly different from **LE** adults

CONCLUSIONS: DREISSENID GENETIC PATTERNS OVER TIME AND SPACE

1. Some divergence between **HR** & **LE** in QM, much greater in ZM
 - Possibly founding from **LE** in QM **HR**
 - Likely different founding sources for ZM
 - QM set is currently limited in # loci (being increased to 15)
2. **HR** and **LE** QM populations appear to be diverging more over time
3. ZM in **HR** shows two major population genetic changes, possibly related to cyclical population dynamics
 - **Genetic Replacement** and/or **Genetic Stasis** of original genotypes?
4. ZM Veliger larvae show some sig. divergence from adult community
 - Differences in timing of adult spawning?
 - Drift from other ZM communities?



Support: Past and Present members of the Stepien Lab

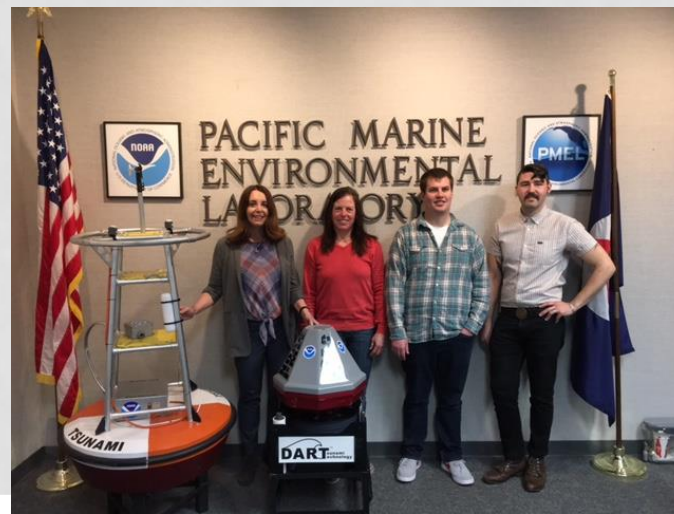
Sampling: Cary Institute (Dr. Dave Strayer, Heather Malcom, David Fischer), Dr. John Hageman



Funding: USEPA Great Lakes Restoration Initiative

Hudson River Foundation Mark B. Bain Graduate Fellowship

University of Toledo Robert N. Whiteford Scholarship



Questions?



FUTURE WORK

1. Add 10 more loci for QM
2. Add veliger samples for QM and ZM
3. Test for hybrids
 - Hybridization could lead to higher invasion success or swamp out one species
 - Laboratory trials show evidence for viable hybrid veligers
 - Only one study has found a hybrid in the wild (*Voroshilova et al. 2010*)
 - 1 out of 37 individuals tested from the Volga River
 - No evidence thus far in our dataset



The Great Lakes: *Freshwater Seas*

A Venue for Invasions

L. Superior



Facts

- 90% US & 22% world's surface freshwater
- 186+ aquatic invasive spp. (AIS)
- Most AIS from ballast water
- **World's largest freshwater fisheries: \$4-7 U.S. billion/year**

L. Michigan

L. Huron

L. Ontario

L. Erie

Lake Erie Center



500 km