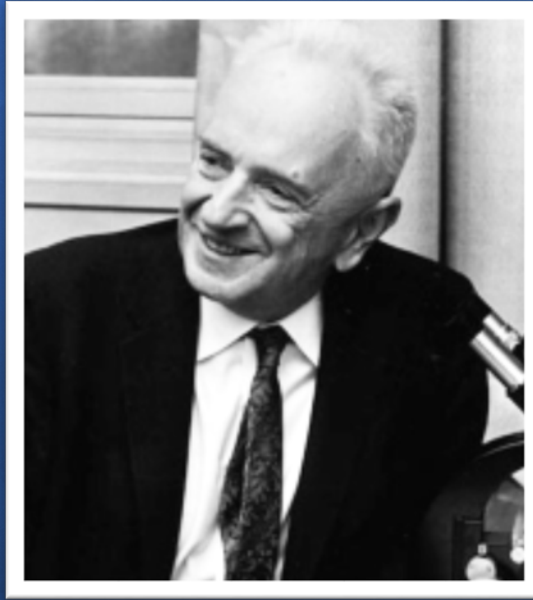


Using Genetics to Understand the Invasion Dynamics of *Megabalanus coccopoma* (Titan Acorn Barnacle)



Eric A. Hoffman
University of Central Florida
Department of Biology

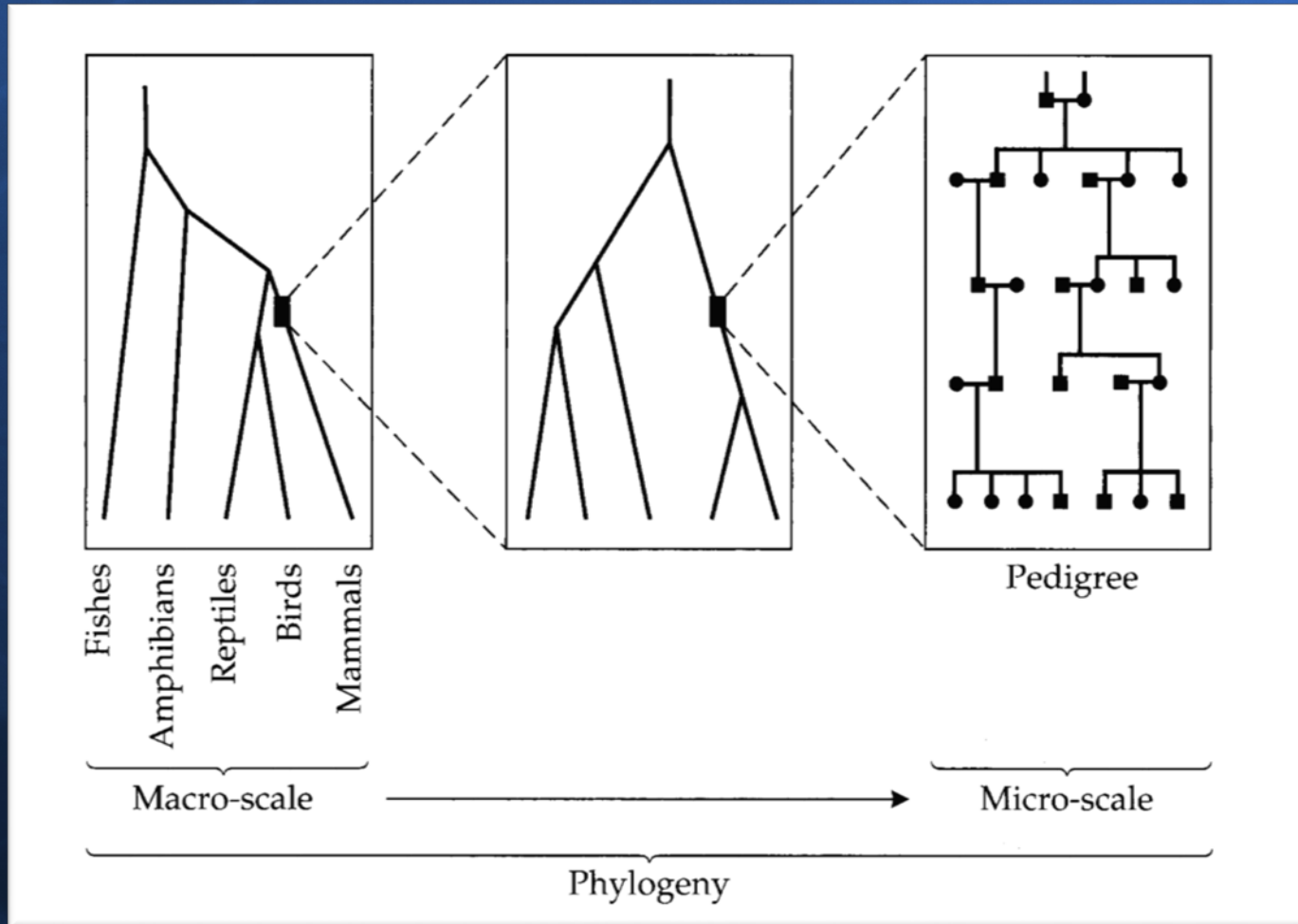


“Nothing in biology makes sense
except in light of evolution”

“much in evolution makes even more sense in the light of historical genealogy”



Molecular markers are used to estimate genetic relationships

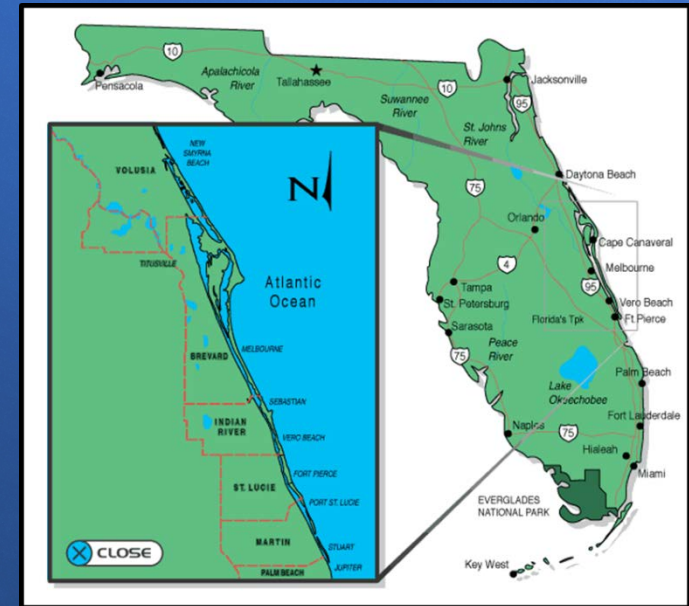


Indian River Lagoon, Florida, USA



Indian River Lagoon, Florida, USA

- Extends over 250 kilometers along the east coast of central Florida
- Home to over 4000 species of plants and animals
- Is classified as an Estuary of National Significance
- In 2005, retail sales associated with recreational fishing within just the *northern* half of the lagoon totaled \$262.9 million



Indian River Lagoon, Florida, USA



Aquatic Invasives

High rate of transfer for many species via shipping:

Hull fouling

Ballast water



Florida Aquatic Invasives



Two recent marine invaders



Megabalanus coccopoma, the Titan Acorn barnacle



M. coccopoma native range



M. coccopoma



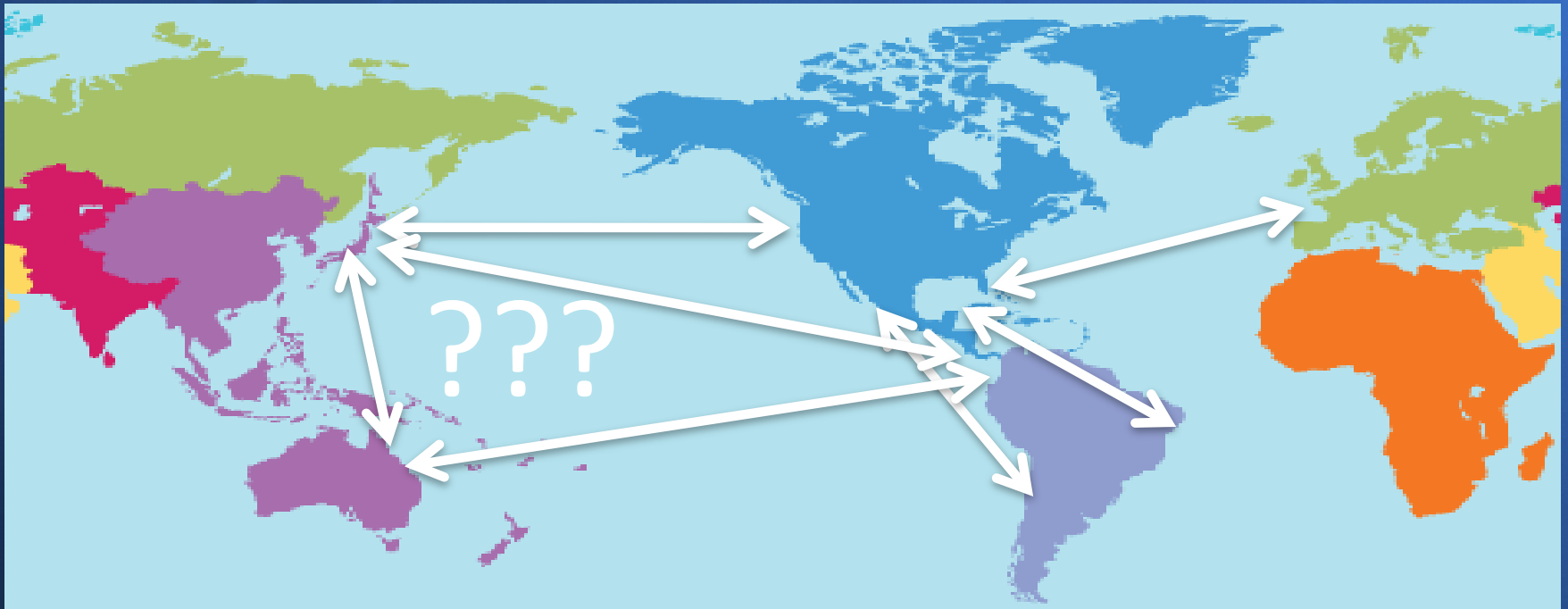
- First invaded report in US (2001, Caribbean); Atlantic in 2006
- Pan-global invader (e.g. Japan, Brazil, Australia, US, Europe)
- Unknown number of species in genus...

Are all samples collected *M. coccopoma*?

- Morphological data vs. Genetic data
- Phenotypic plasticity in barnacles



Megabalanus coccopoma invasion



Megabalanus coccopoma Invasive??

	Larvae of Crassostrea virginica				Spat of Crassostrea virginica			
	Settlement		Settlement Pattern		Survival		Growth	
	2011	2012	2011	2012	2011	2012	2011	2012
<i>M. coccopoma</i>	*	**	*	*	X	X	X	X
<i>P. viridis</i>	*	X	*	*	*	*	X	X
<i>M. charruana</i>	-	X	-	*	-	*	-	*
<i>G. demissa</i>	-	X	-		-	X	-	X

* indicates a significant difference between nonnative species and control.

** indicates a significant difference between nonnative species and native *G. demissa* only.

X indicates no statistical difference was found between treatment and control.

- indicates not tested in 2011.

Data from: Yuan *et al.* Biol Invasions (2016) 18:689–701

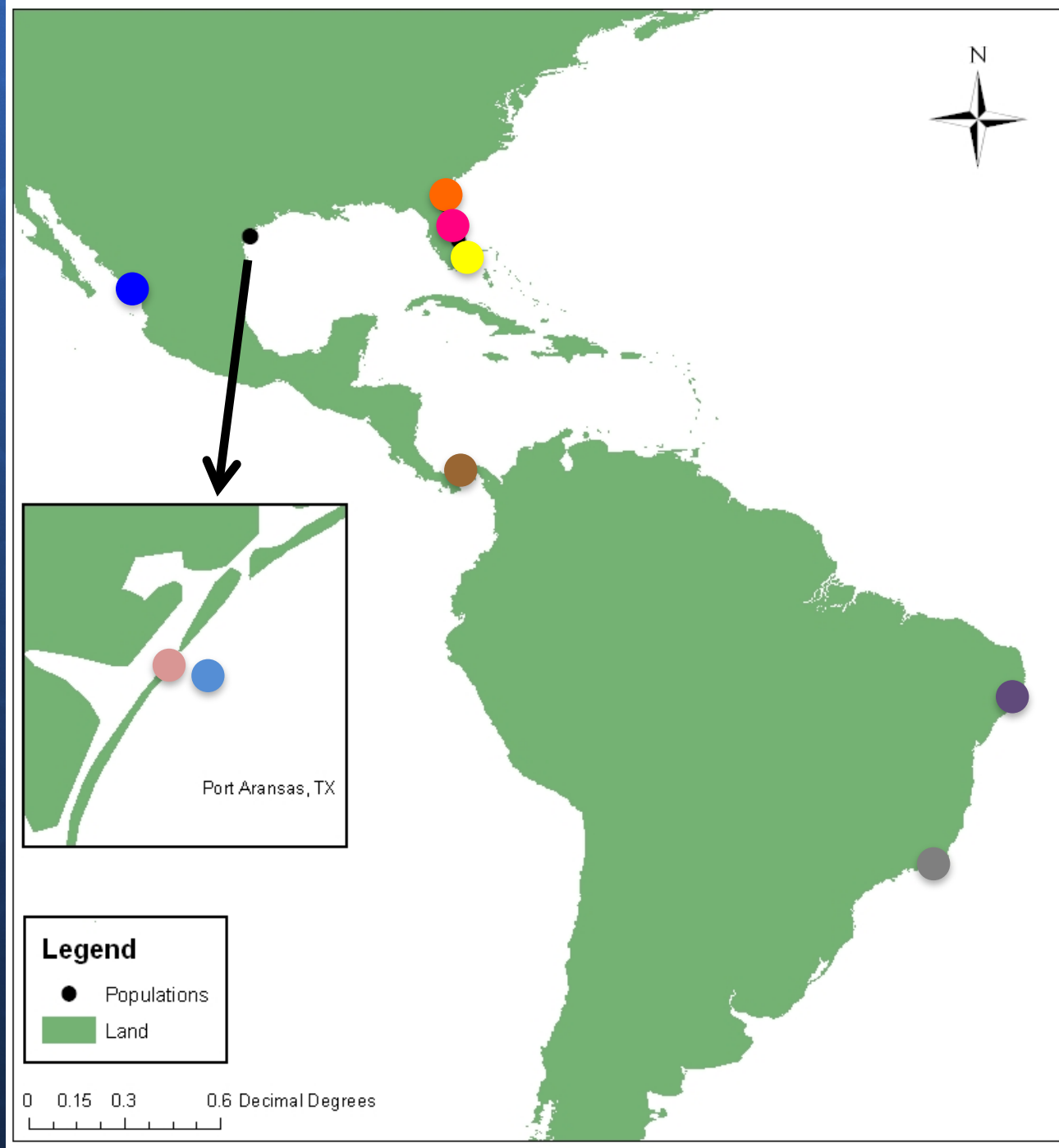
Patterns of genetic diversity for *M. coccopoma*

- 1) What species is invading?
- 2) From where did the invading species originate?
- 3) How do levels of genetic diversity compare between native and non-native populations?



Sample Locations

- N. Florida ●
- C. Florida ●
- S. Florida ●
- Texas Pier ●
- Texas Rig ●
- N. Brazil ●
- S. Brazil ●
- N. Mexico ●
- Panama ●

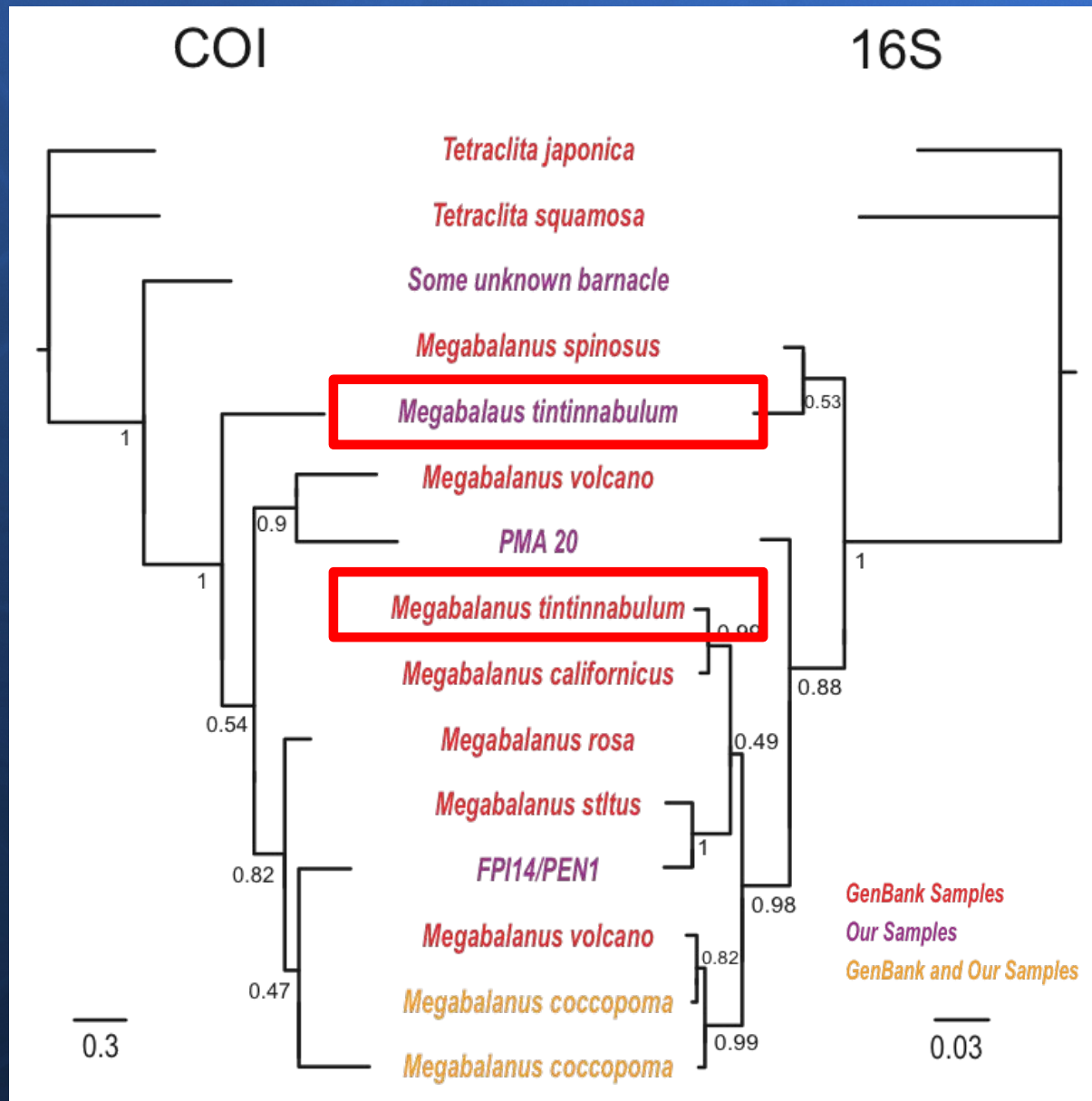


Molecular Analysis

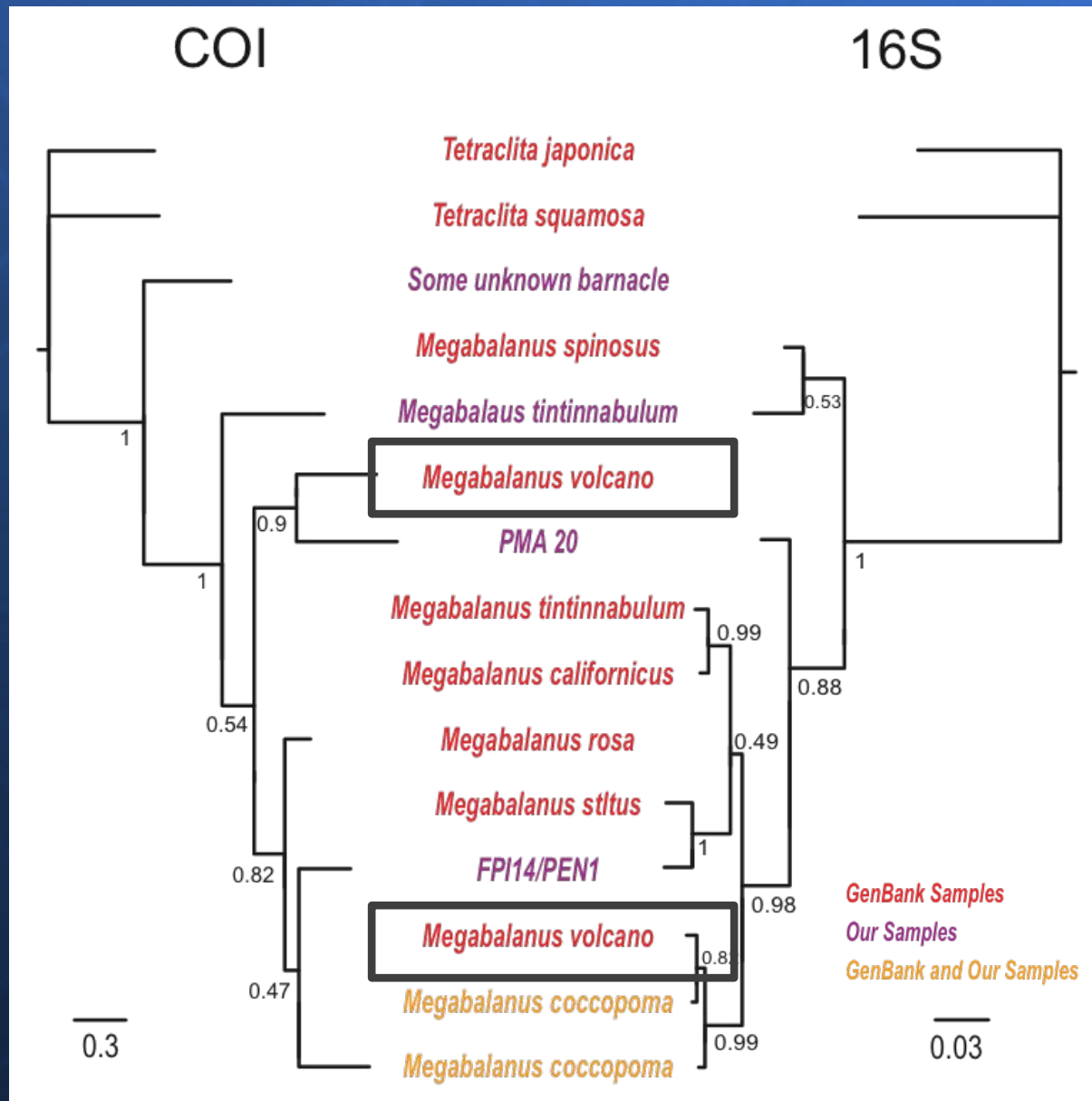
- 608 base pairs of COI
- 521 base pairs of 16S (for some individuals)
- Sequenced approximately 20 individuals each location
- Added 7 other *Megabalanus* species from Genbank
- Compared COI and 16S phylogenies



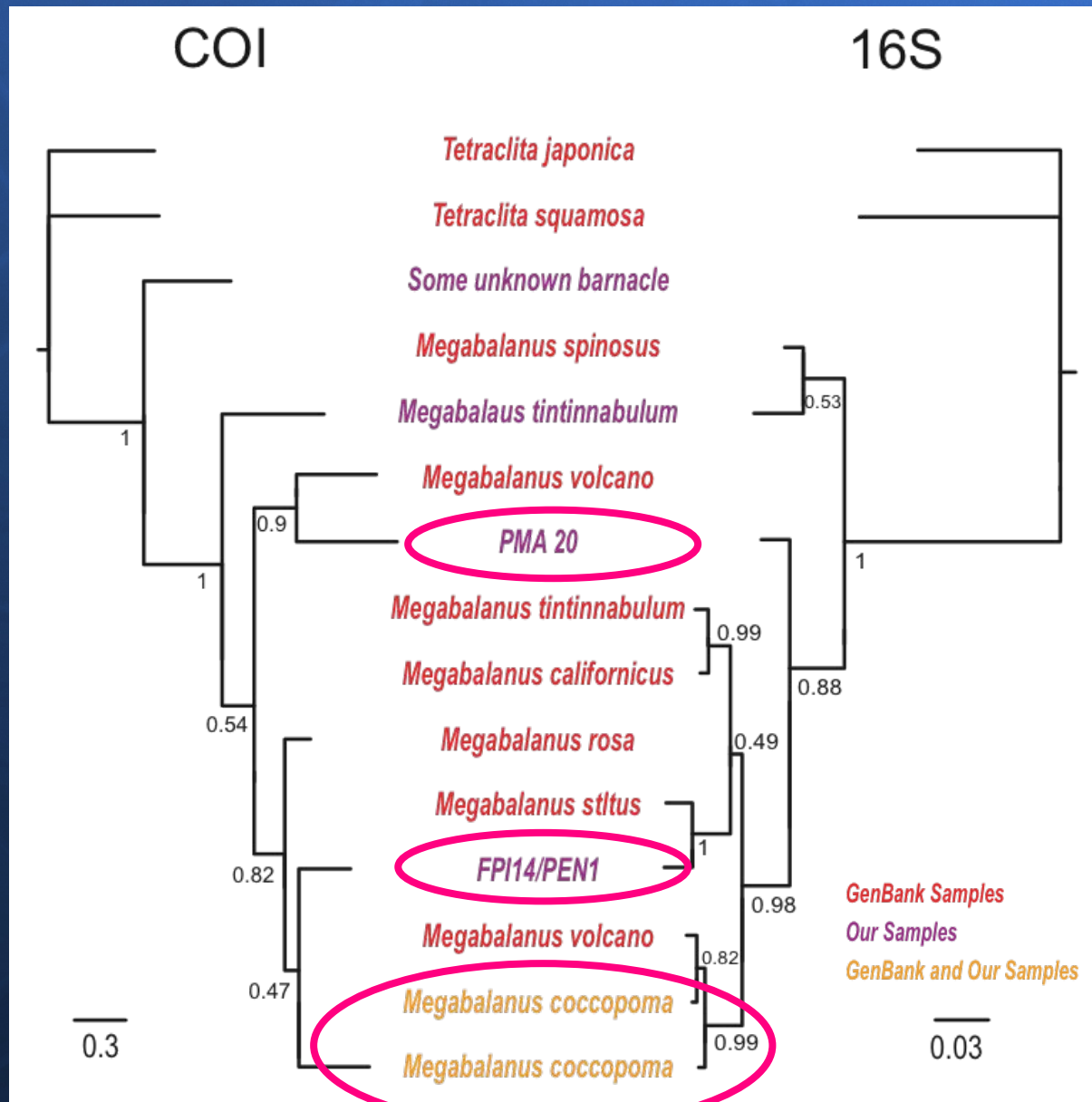
Phylogeny of *Megabalanus* sp.



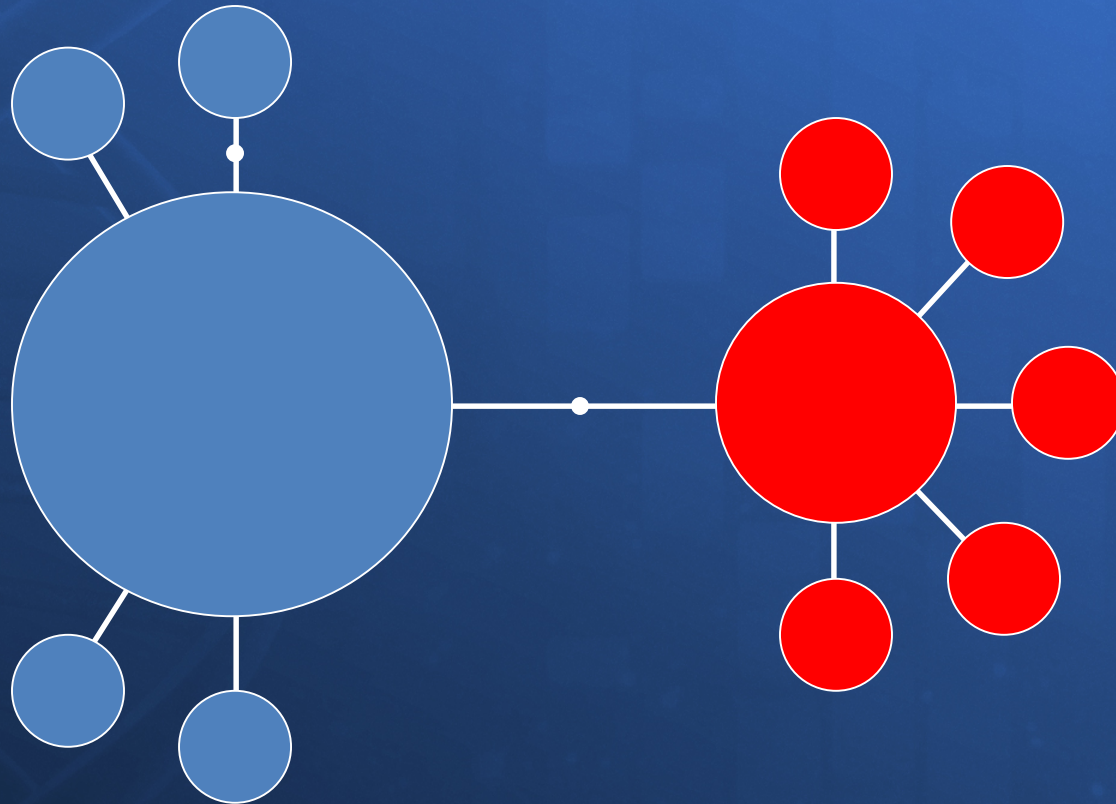
Phylogeny of *Megabalanus* sp.



Phylogeny of *Megabalanus* sp.

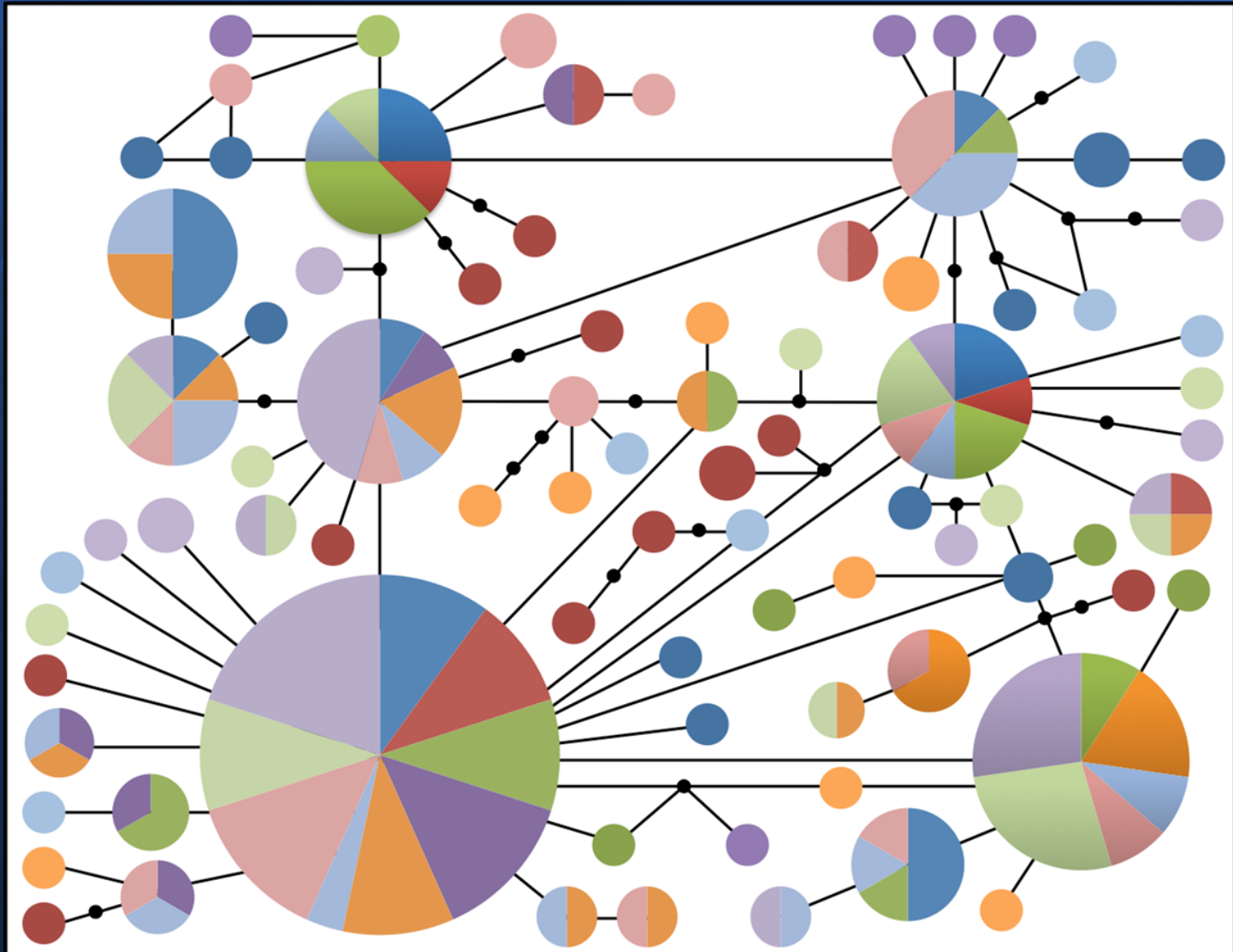


Example haplotype network identifying population of origin



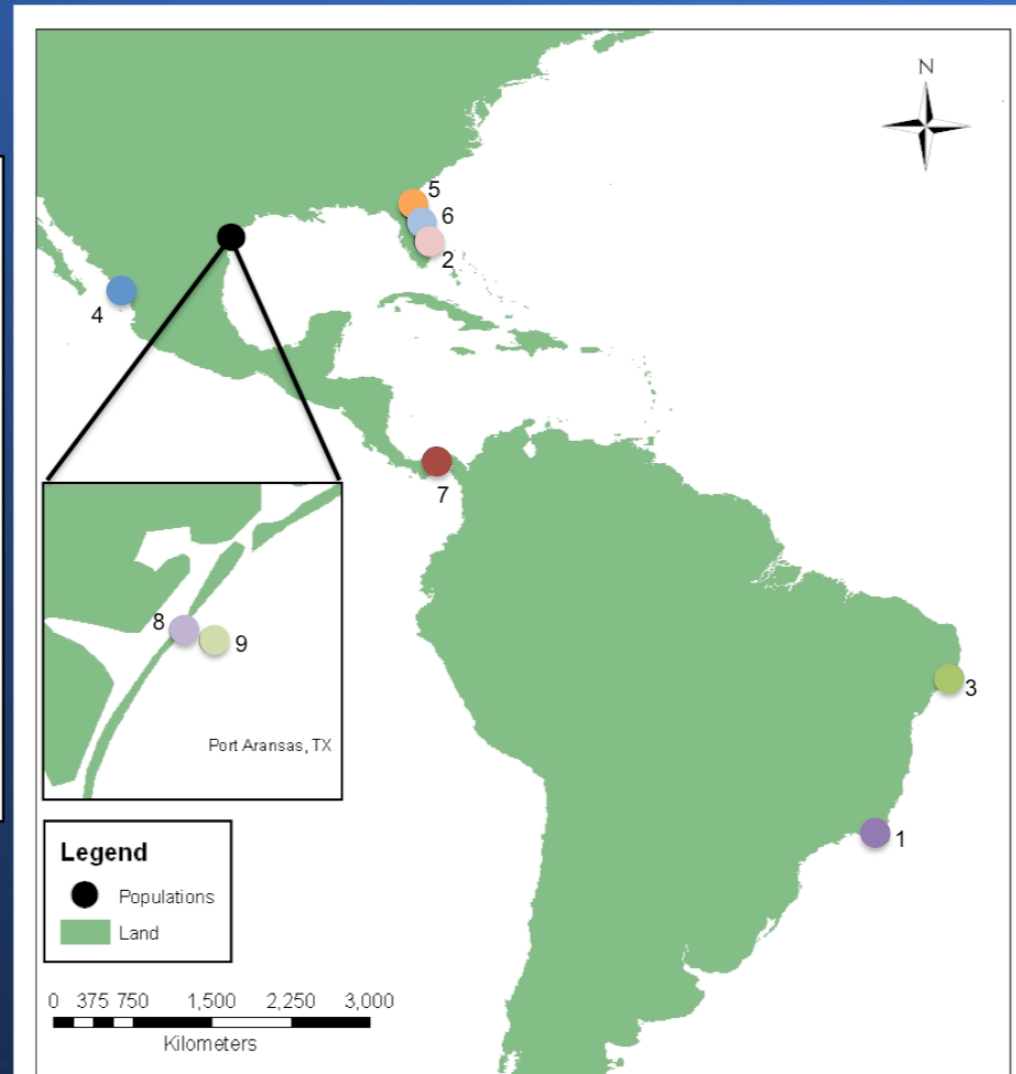
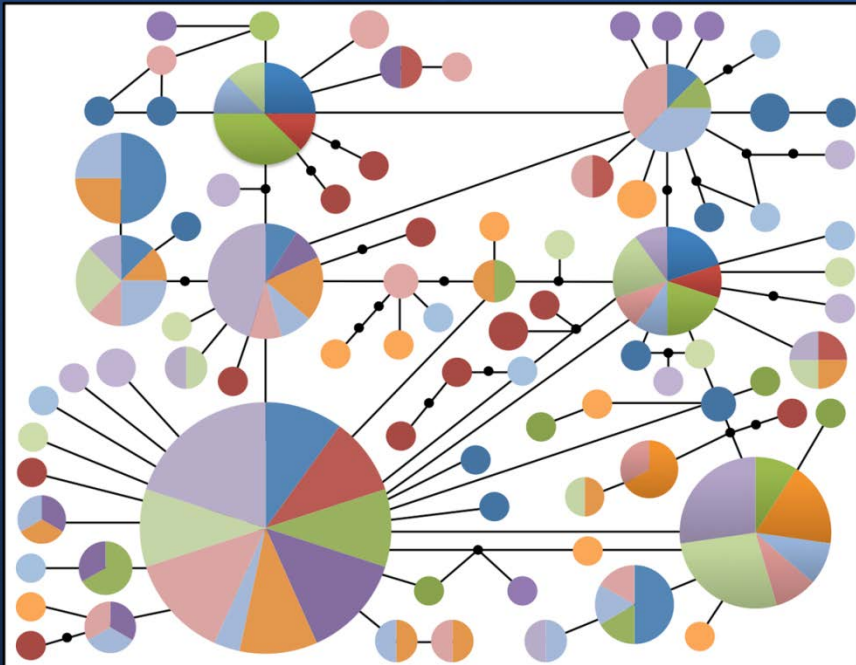
From where did the invading species originate?

M. coccopoma haplotype network (COI)



From where did the invading species originate?

M. coccopoma haplotype network (COI)



Are population genetically differentiated?

Global $F_{ST} = 0.0153$

Table: AMOVA Non-native versus Native Populations

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among groups	1	4.249	0.02249 Va	1.17
Among populations within groups	7	15.976	0.01760 Vb	0.91
Within populations	200	377.196	1.88598 Vc	97.92
Total	208	397.421	1.92607	

Are population genetically differentiated?

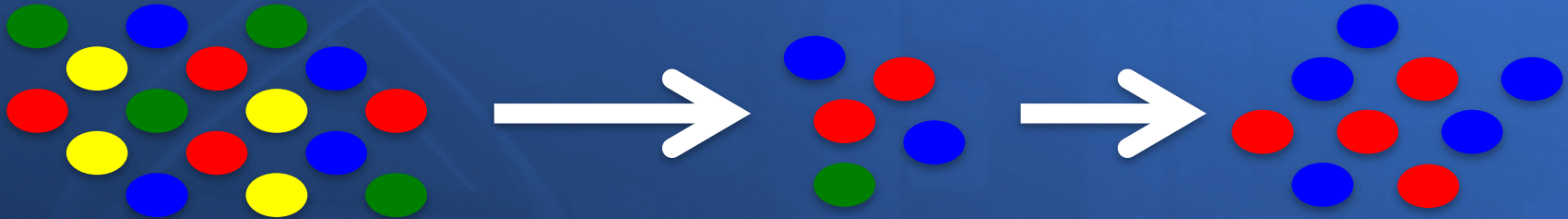
TABLE: Population Pairwise Fst

	POIN	NAV	ADB	FPI	MAC	TXP	TXR	MAZ
PMA	0.01972	0.05943	-0.02429	-0.00830	0.00200	0.02959	0.01485	0.03088
MAZ	-0.01817	0.05200	0.01307	-0.00778	0.05551	0.04335	0.03795	
TXR	0.00676	-0.00723	0.00238	0.01171	-0.02312	-0.01255		
TXP	0.00474	-0.00093	0.00183	0.01680	-0.00084			
MAC	0.02602	0.01613	-0.01294	0.00727				
FPI	-0.01252	0.03042	-0.03289					
ADB	-0.00962	0.03231						
NAV	0.01462							



How do levels of genetic diversity compare between native and non-native populations?

1. Bottleneck

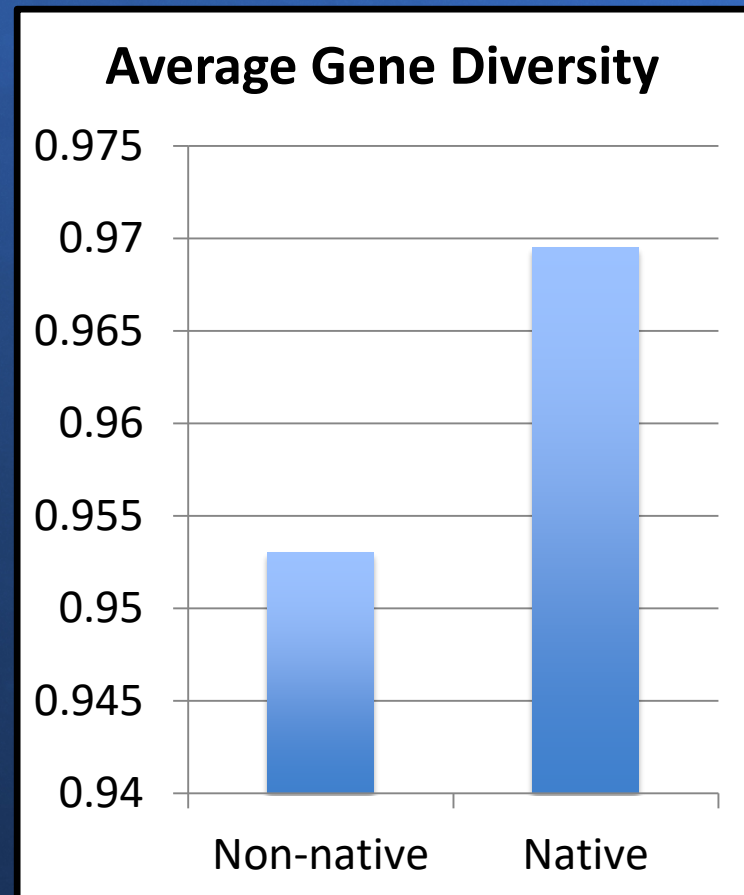
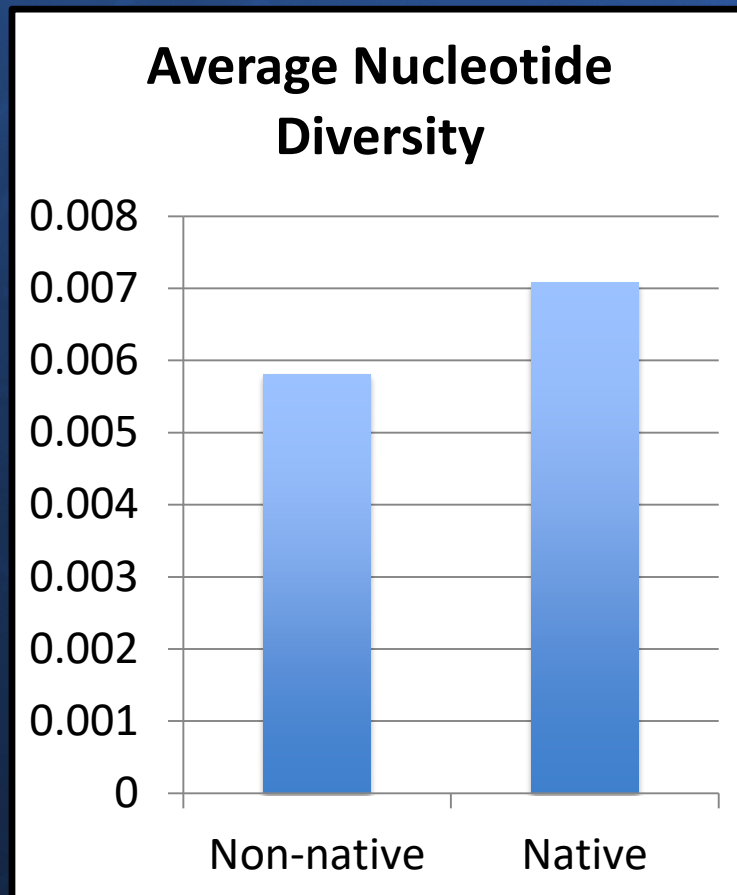


2. Admixture



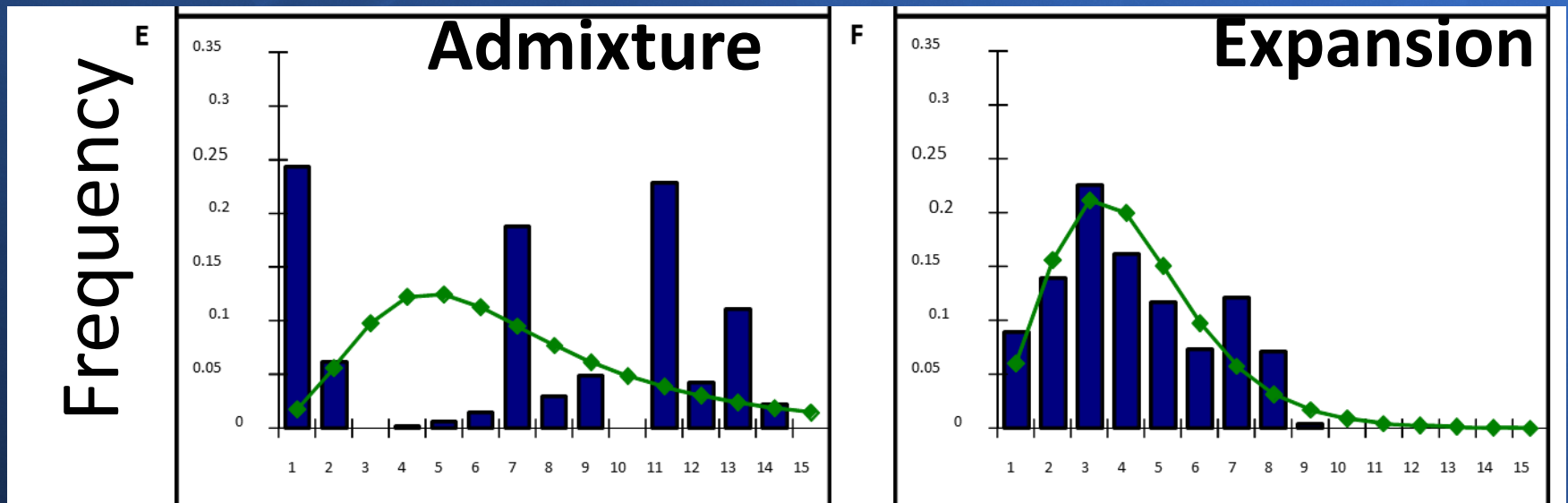
How do levels of genetic diversity compare between native and non-native populations?

Estimates of *M. coccopoma* COI genetic diversity



How do levels of genetic diversity compare between native and non-native populations?

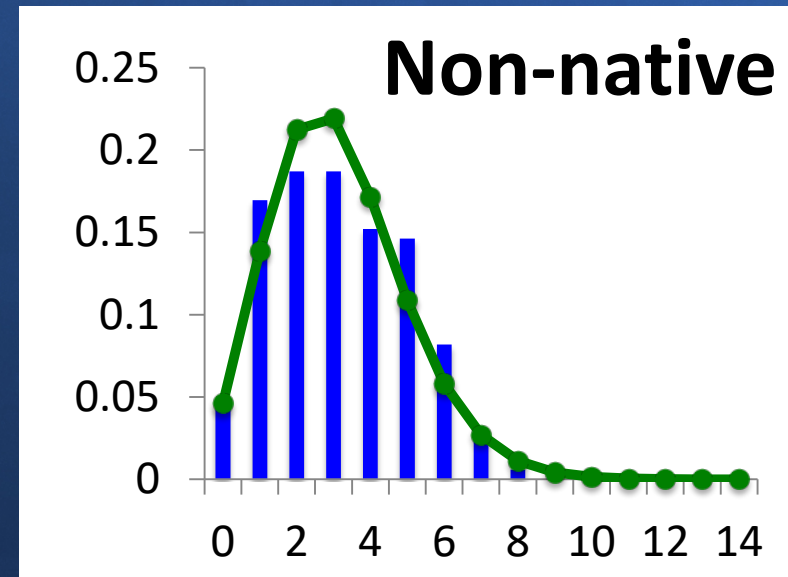
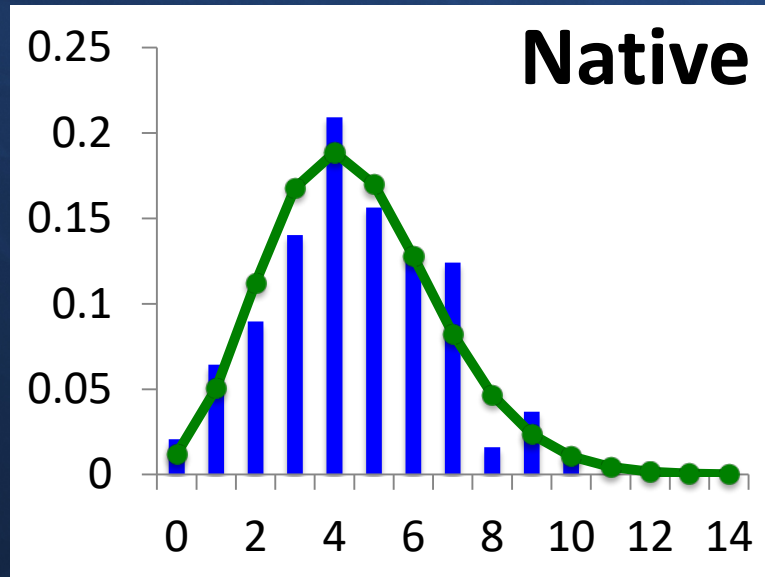
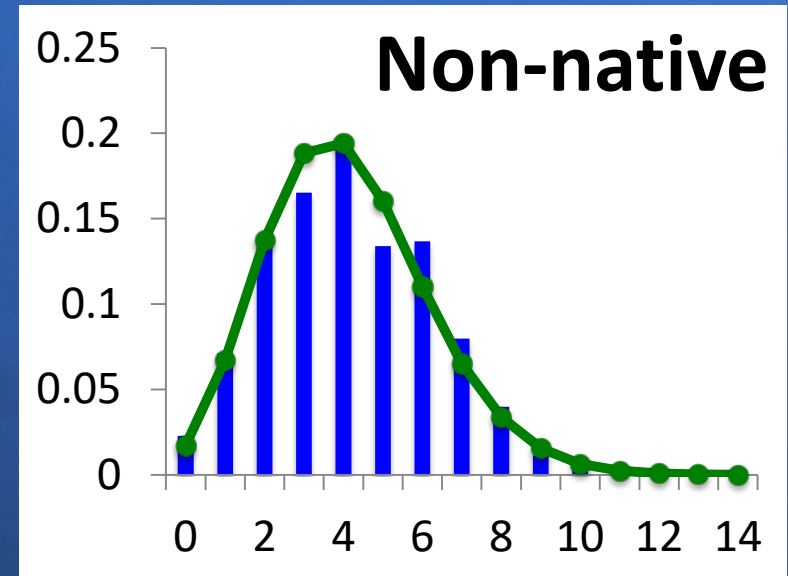
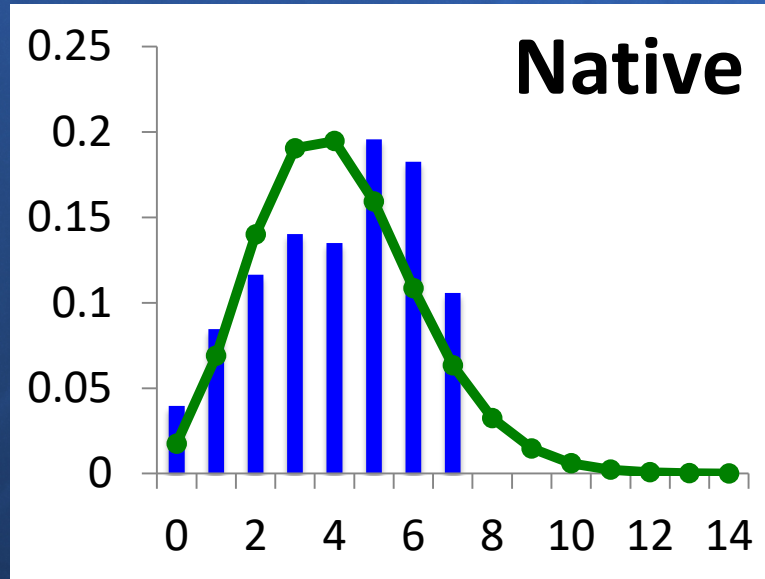
Sample mismatch distribution analysis data



Pairwise Differences

Mismatch distribution analysis for *M. coccopoma*

Frequency



Pairwise Differences

Conclusions for *M. coccopoma*

1) What species is invading?

- **Multiple genetic lineages (species) invading Florida coast**
- **Morphology and genetics are inconsistent**
- **Most samples were *M. coccopoma***

2) From where did the invading species originate?

- **Little genetic differentiation among populations, so unable to determine where invasion originated**

3) How do levels of genetic diversity compare between native and non-native populations?

- **No statistical differences between native and invasive populations for measures of genetic diversity – no evidence of admixture.**

Vector Strength Data

Data collected from National Ballast Water Information Clearinghouse:

21/6505 (0.3%) ballast tanks dumped in JAX originated from the native range of *M. coccopoma*.

47% of all dumped water originated from San Juan, Puerto Rico.



Ongoing and Future Research Directions

- 1) Further study of species complex
- 2) Compare temporal differentiation within non-native populations
- 3) Use microsatellites to investigate genetic structure using faster evolving molecular markers



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