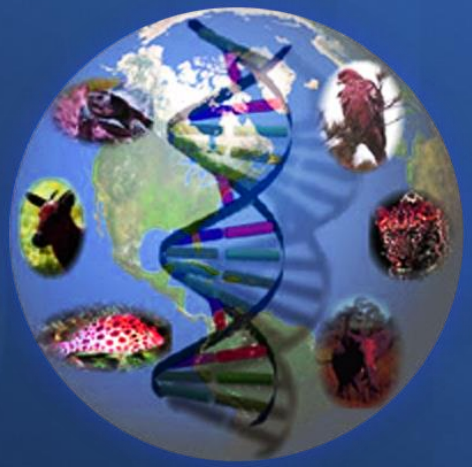
Using genetics to evaluate patterns of invasion for the marine mussel *Mytella charruana*



Eric A. Hoffman
University of Central Florida
Department of Biology

Invasion | Population Genetics | Conservation

Using genetics to evaluate patterns of invasion for the marine mussel *Mytella charruana*

Linda Walters

Savio Calazans

RESEARCH ARTICLE

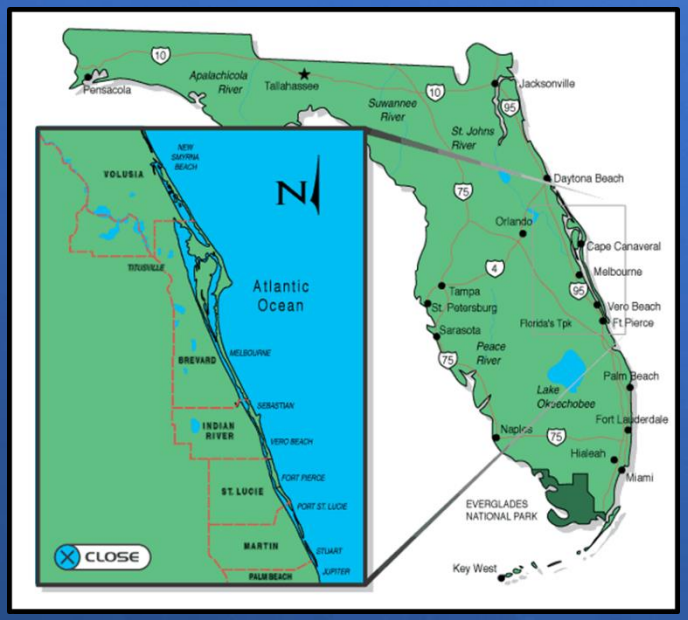
Genetic structure provides insights into the geographic origins and temporal change in the invasive charru mussel (Sururu) in the southeastern United States

Sávio H. Calazans C[1,2], Linda J. Walters[3], Flavio C. Fernandes[2], Carlos E. L. Ferreira[1], Eric A. Hoffman[3]*

1 Department de Biologia Marinha, Universidade Federal Fluminense - UFF, Niterói, Rio de Janeiro, Brazil, **2** Department de Oceanography, Instituto de Estudos do Mar Almirante Paulo Moreira - IEAPM, Arraial do Cabo, Rio de Janeiro, Brazil, **3** Department of Biology, University of Central Florida, Orlando, Florida, United States of America

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

Non-Natives Attached to Live Oysters in the Indian River Lagoon

***Perna viridis* (2002)**

***Mytella charruana* (2004)**

***Megabalanus coccopoma* (2006)**

Mytella charruana

First Documented Introduction (US)

- Jacksonville, Florida in October 1986
- Large numbers of *Mytella* found on water intake filters for power plant
- None seen in March 1987; assumed extirpated due to cold temperatures

Current U.S. distribution of *M. charruana*

Georgia

Savannah, GA

Jacksonville, FL

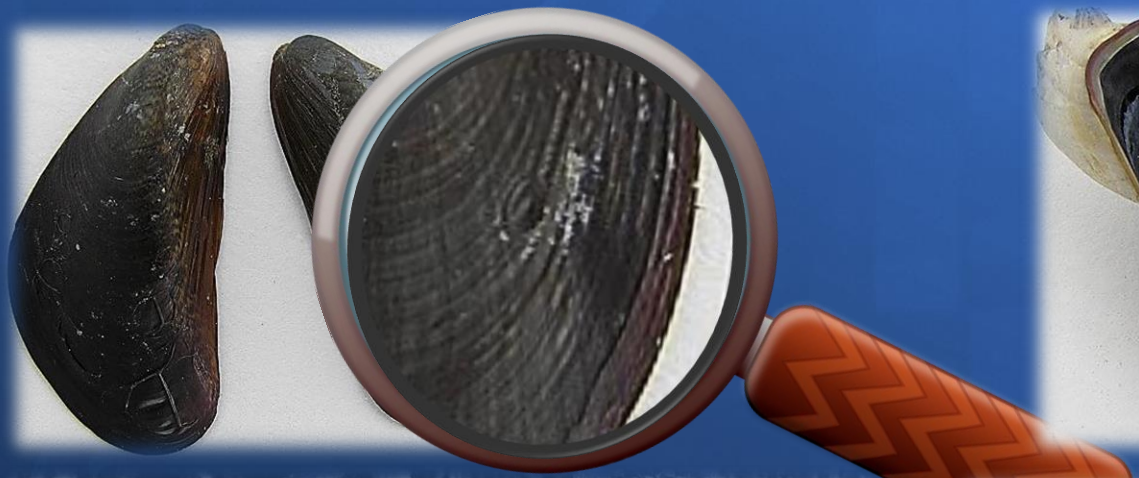
Florida

Cape Canaveral, FL

Current distribution of *Mytella charruana*

M. charruana
native distribution

Mytella charruana



Densities up to 11,000 individuals/m^2 with estimates up to 61 million mussels in a single population (Sibaja, 1985; Pereira *et al*., 2003)

New invasion: *Mytella charruana*

Rev. Bras. Cienc. Farm.
Braz. J. Pharm. Sci.
vol. 40, n. 4, out./dez., 2004

RBCF

Perfil de ácidos graxos, composição centesimal e valor calórico de moluscos crus e cozidos com leite de coco da cidade de Maceió-Al

Giselda Macena Lira[1*,4], Jorge Mancini Filho[2], Lea Sílvia Sant'ana[3], Rosângela Pavan Torres[2], Alane Cabral de Oliveira[4], Cristhiane Maria Bazílio de Omena[4], Maria de Lourdes da Silva Neta[4]

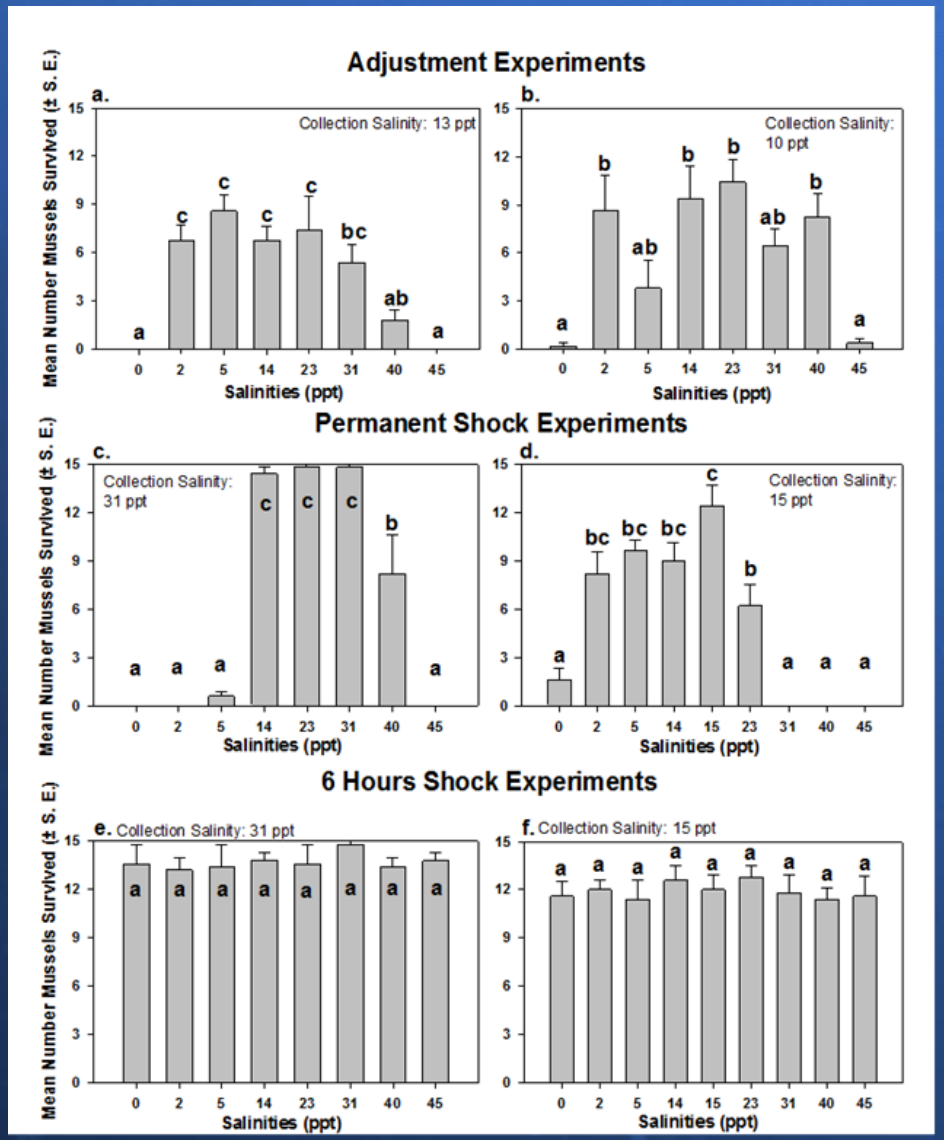
Fatty acids composition, chemical composition and caloric value of raw and boiled mollusks with coconut milk in the city of Maceió, Alagoas, Brazil

New invasion: *Mytella charruana*

Fatty acids composition, chemical composition and caloric value of raw and boiled mollusks with coconut milk in the city of Maceió, Alagoas, Brazil

Ecology of species invasion

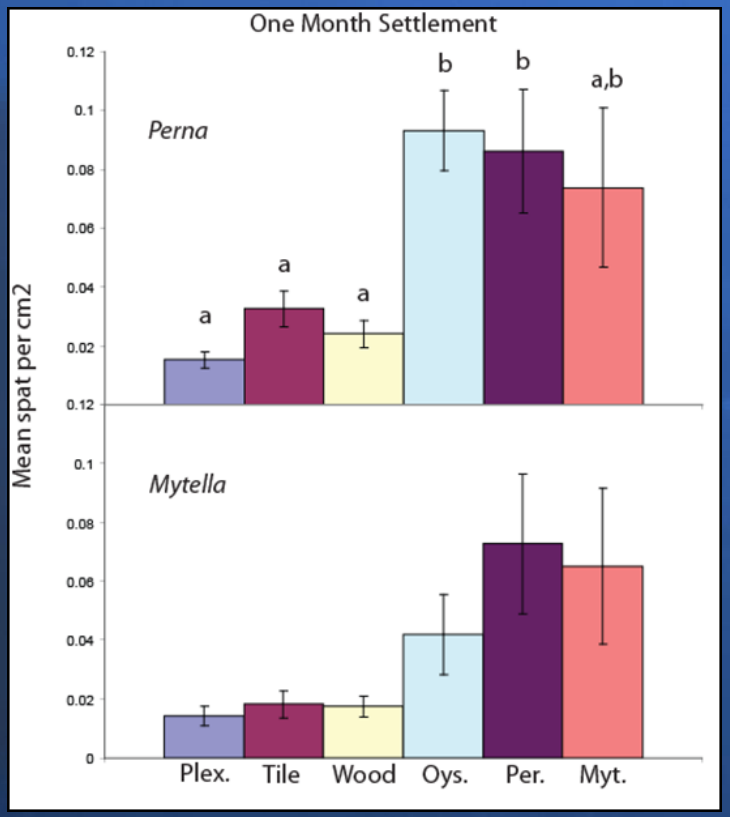
Salinity Tolerance Trials



Yuan, Wei, Linda J. Walters, Kimberly R. Schneider and **Eric A. Hoffman**. 2010. *Journal of Shellfish Research* 29:415-422

Ecology of species invasion

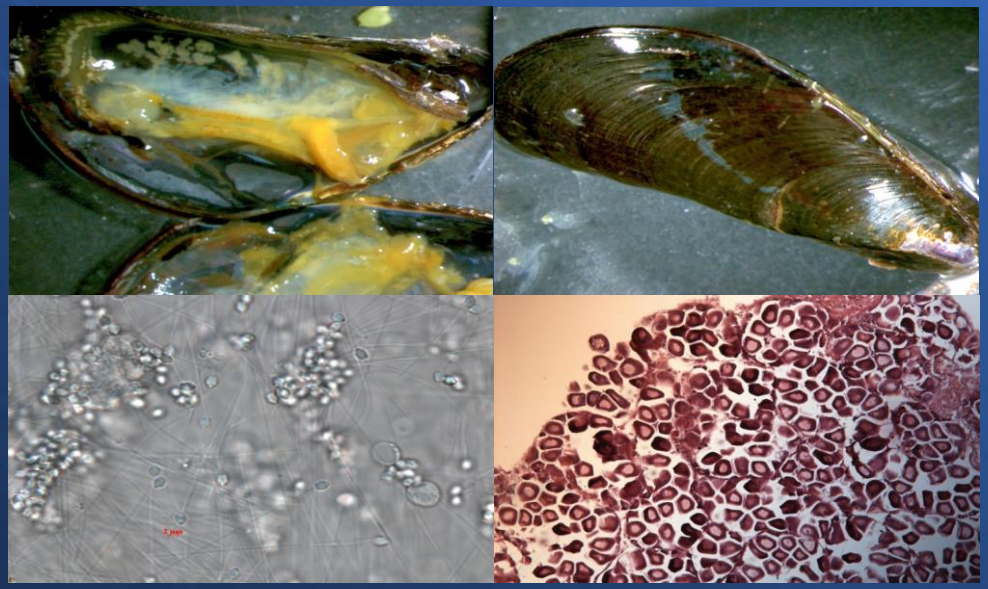
Substrate Preferences



Gilg, Matthew R., **Eric A. Hoffman**, Kimberly R. Schneider, Josiah Ryabinov, Christine El-Khoury, and Linda J. Walters. *Journal of Molluscan Studies* 76:333-339

Ecology of species invasion

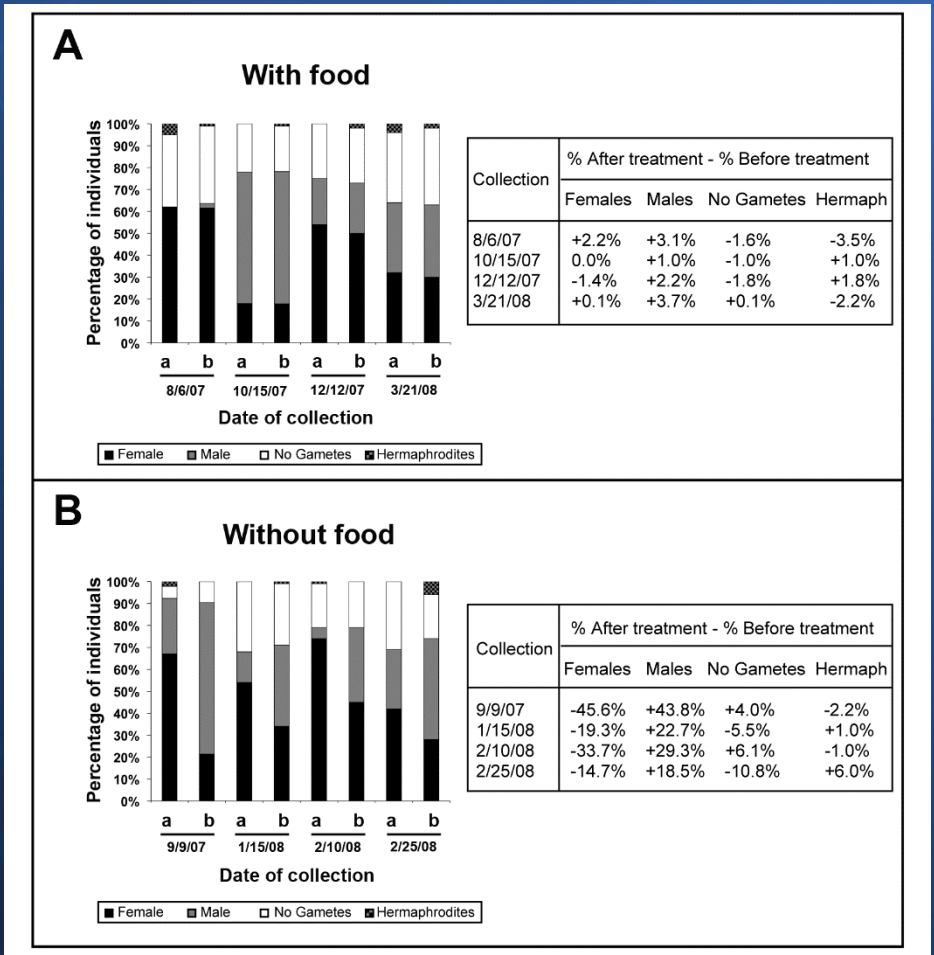
Development of *M. charruana*



Stenyakina, Anastasia*, Linda J. Walters, **Eric A. Hoffman** and Cristina Calestani. 2010. *Molecular Reproduction and Development*, 77:222-230

Ecology of species invasion

Development of *M. charruana*



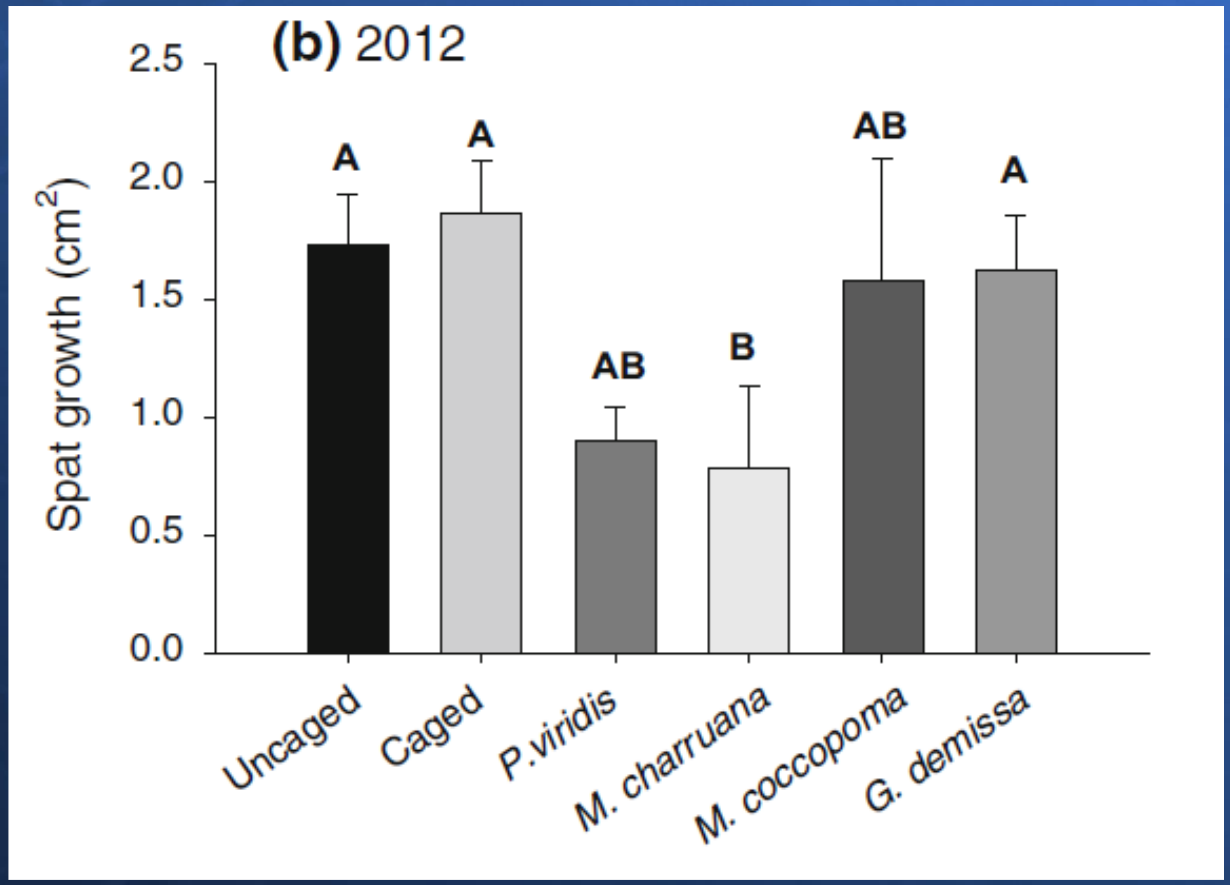
Collection	% After treatment - % Before treatment			
	Females	Males	No Gametes	Hermaph
8/6/07	+2.2%	+3.1%	-1.6%	-3.5%
10/15/07	0.0%	+1.0%	-1.0%	+1.0%
12/12/07	-1.4%	+2.2%	-1.8%	+1.8%
3/21/08	+0.1%	+3.7%	+0.1%	-2.2%

Collection	% After treatment - % Before treatment			
	Females	Males	No Gametes	Hermaph
9/9/07	-45.6%	+43.8%	+4.0%	-2.2%
1/15/08	-19.3%	+22.7%	-5.5%	+1.0%
2/10/08	-33.7%	+29.3%	+6.1%	-1.0%
2/25/08	-14.7%	+18.5%	-10.8%	+6.0%

Stenyakina, Anastasia*, Linda J. Walters, **Eric A. Hoffman** and Cristina Calestani. 2010. *Molecular Reproduction and Development*, 77:222-230

Ecology of species invasion

Impacts on native oysters



Growth of *C. virginica* spat over 6 weeks

Wei Samantha Yuan, **Eric A. Hoffman**, and Linda J. Walters. 2016. Effects of nonnative invertebrates on two life stages of the eastern oyster *Crassostrea virginica*. *Biological Invasions*, 18:689-701.

Ecology of species invasion

Impacts on native oysters

Table 2 Summary of results for all oyster larvae and spat experiments

	Larvae of *Crassostrea virginica*				Spat of *Crassostrea virginica*			
	Settlement		Settlement Pattern		Survival		Growth	
	2011	2012	2011	2012	2011	2012	2011	2012
M. coccopoma	*	**	*	*	X	X	X	X
P. viridis	*	X	*	*	*	*	X	X
M. charruana	–	X	–	*	–	*	–	*
G. demissa	–	X	–	*	–	X	–	X

Settlement refers to whether oyster larvae differentially settled on oyster shell with various other substrates present. Settlement pattern refers to whether oyster spat settled differentially on oyster versus non-native shell within treatments

* Significant difference between nonnative species and control

** Significant difference between nonnative species and native *G. demissa* only

X No statistical difference was found between treatment and control

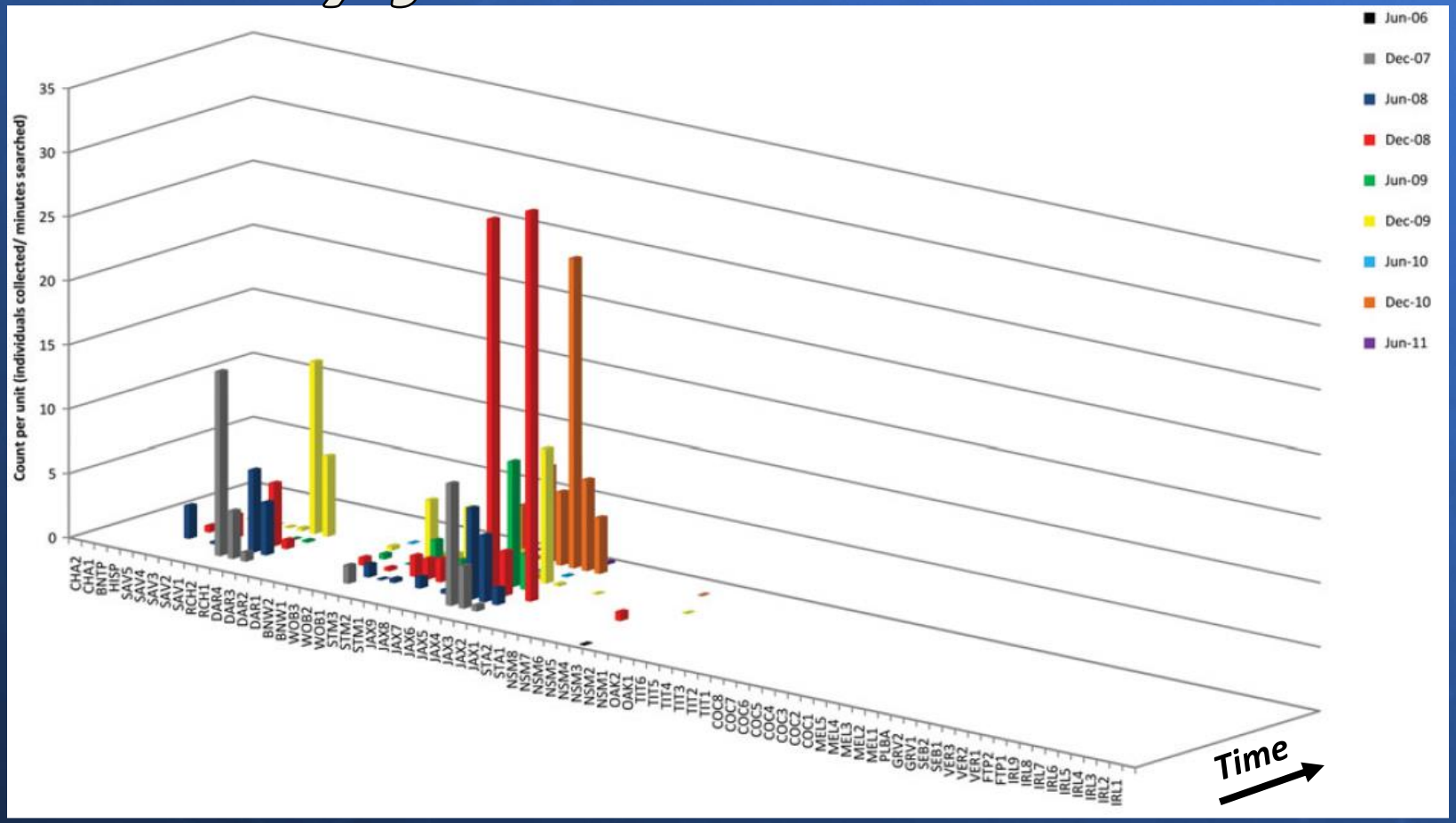
– Not tested in 2011

Wei Samantha Yuan, **Eric A. Hoffman**, and Linda J. Walters. 2016. Effects of nonnative invertebrates on two life stages of the eastern oyster *Crassostrea virginica*. *Biological Invasions*, 18:689-701.

Maximum Range: 82 locations spanning 894 km checked twice/yr from 2006 – 2011

Spinuzzi, Schneider, Walters, Yuan & Hoffman. 2013. *Marine Biodiversity Records* 6:1-13

Density fluctuation



Spinuzzi *et al.* 2013

894 km checked twice/yr from 2006 – 2011

Study Objectives

1) Investigate the genetic structure of the native and invasive distributions.

   A – Identify diversity of populations

   B - Determine which native populations are the source of invasion

Predictions

- Non-native populations are different from native populations
- The possible source being the South Caribbean

Objectives

1) Investigate the genetic structure of the native and invasive distributions.

   A – Identify diversity of populations

   B - Determine which native populations are the source of invasion

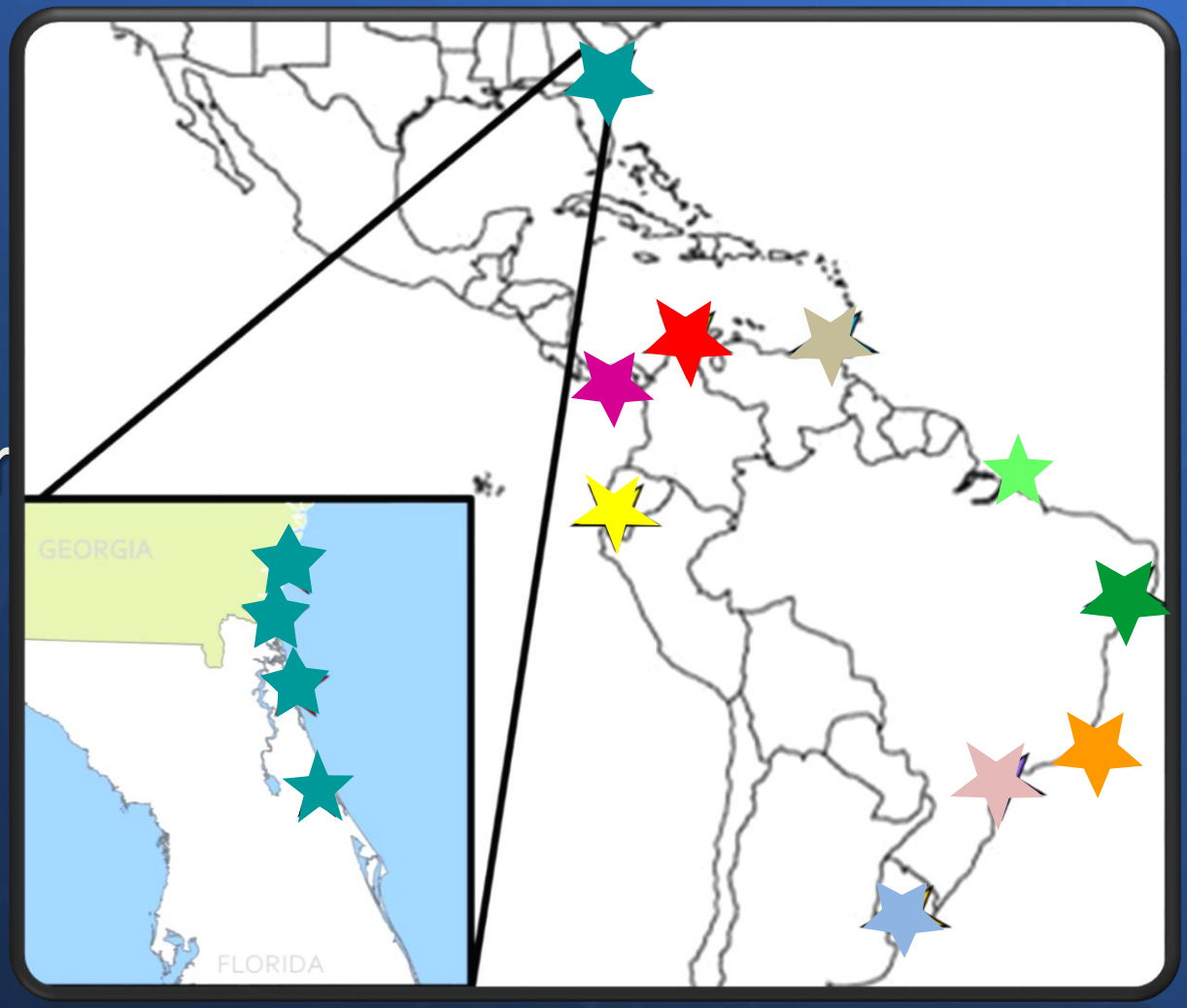
2) To determine if genetic diversity changes over time in invasive populations

Predictions

- Expect change in genetic composition through time based on density fluctuations influenced by reintroduction

Methods

- 9 natives; 4 Non-natives
- ~40 samples per locations
- 722 bp mtDNA gene COI.

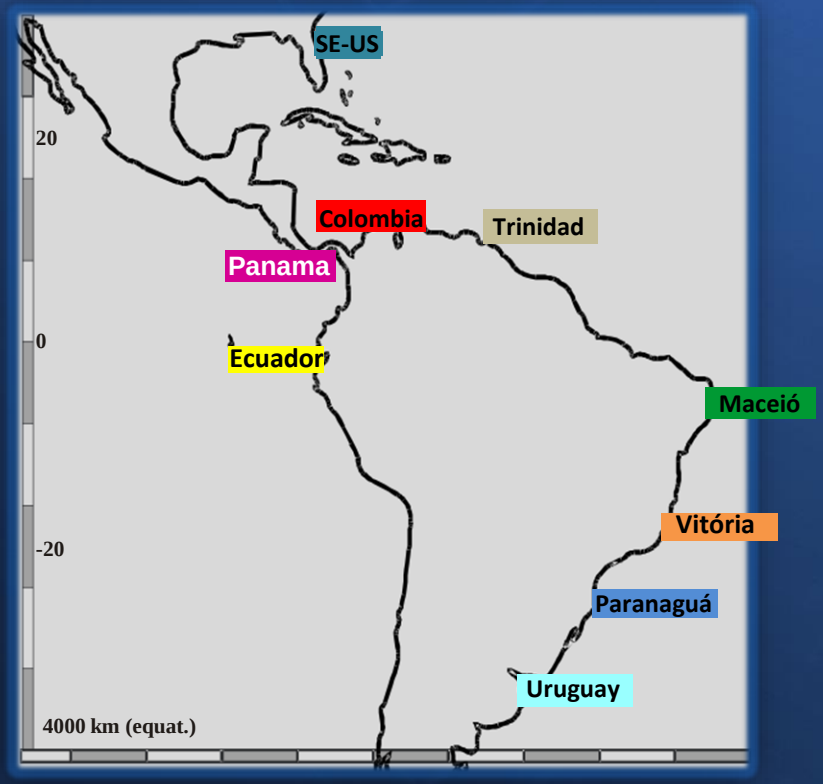


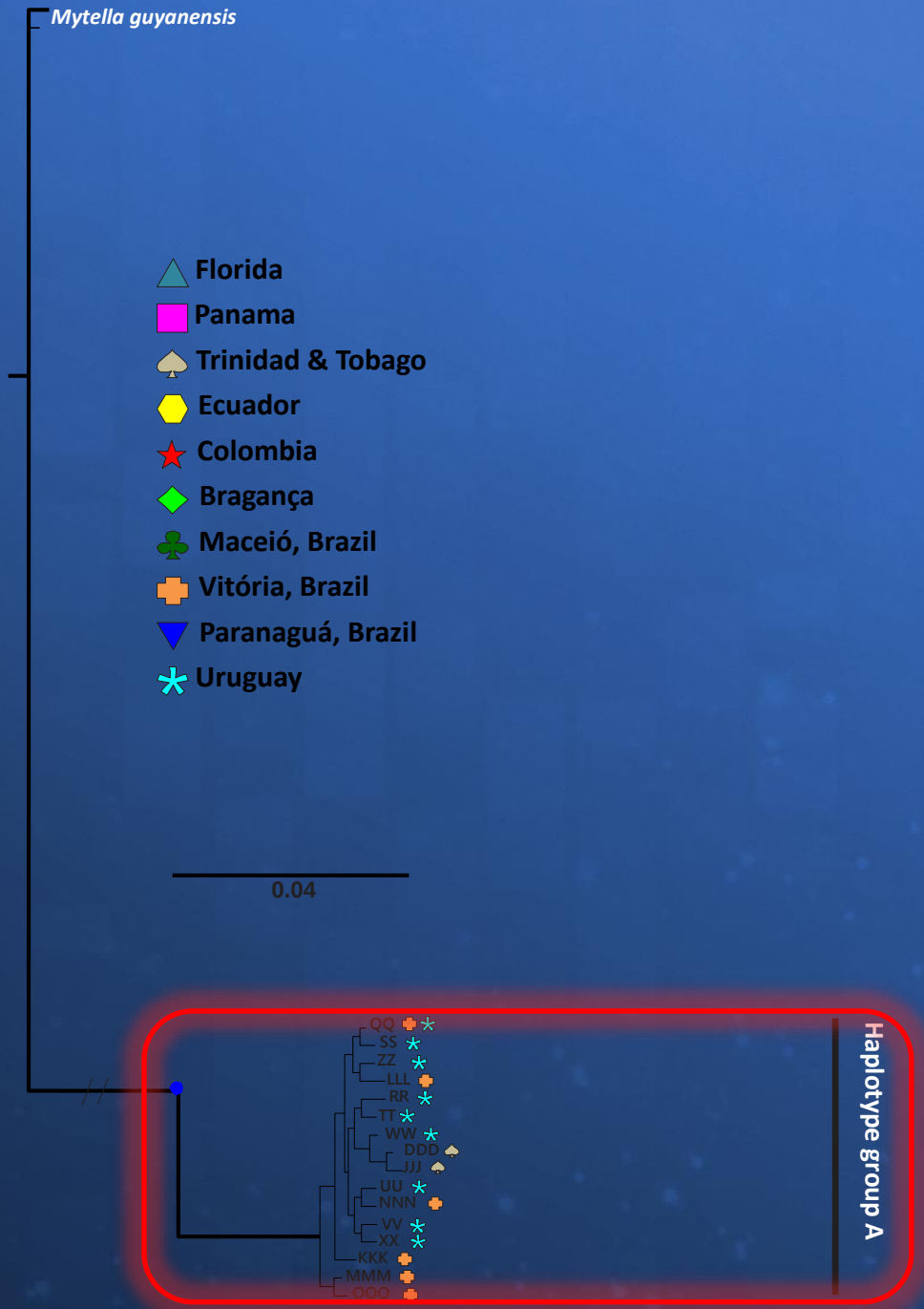
Methods

Objective 1a – identify diversity and genetic structure

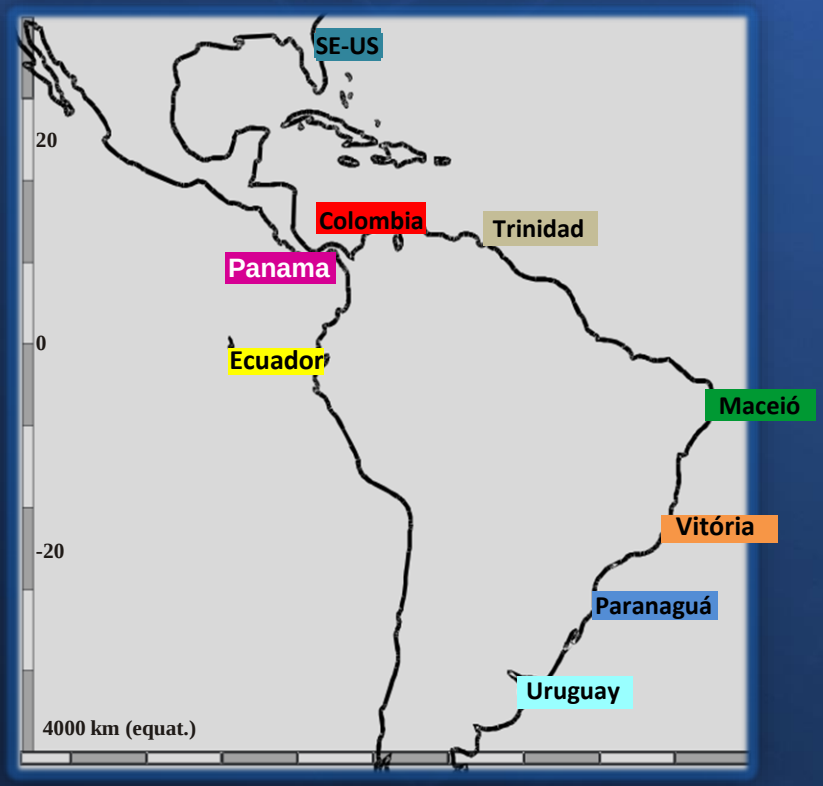
1. **Phylogenetic reconstruction in MrBayes 3.2.2**
2. **Haplotype network in TCS v. 1.21**
3. **Isolation by distance (Mantel test)**
4. **Analysis of molecular variance (AMOVA) in Arlequin**

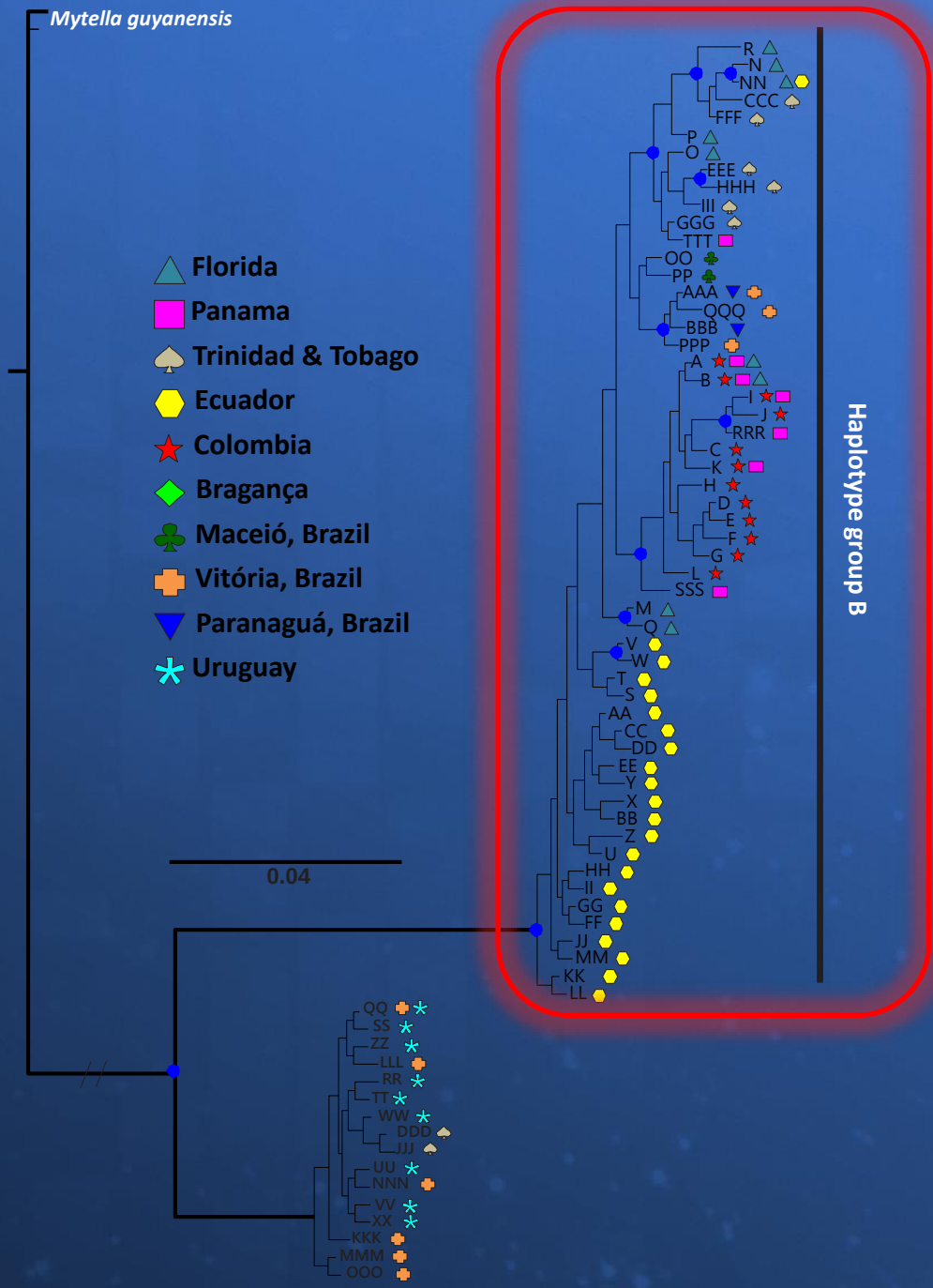
Results: Phylogenetic reconstruction



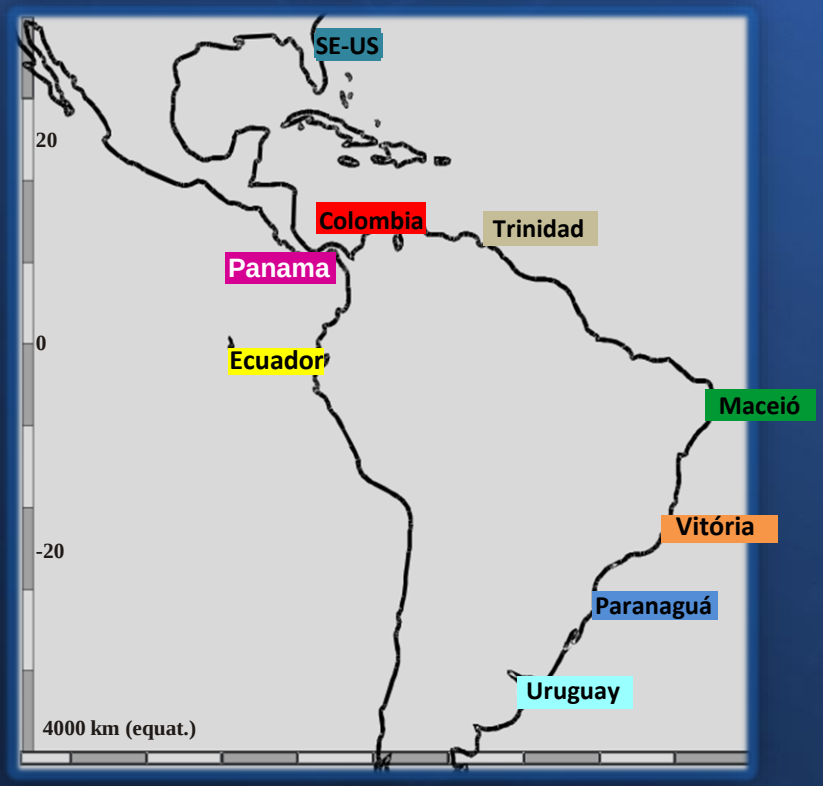


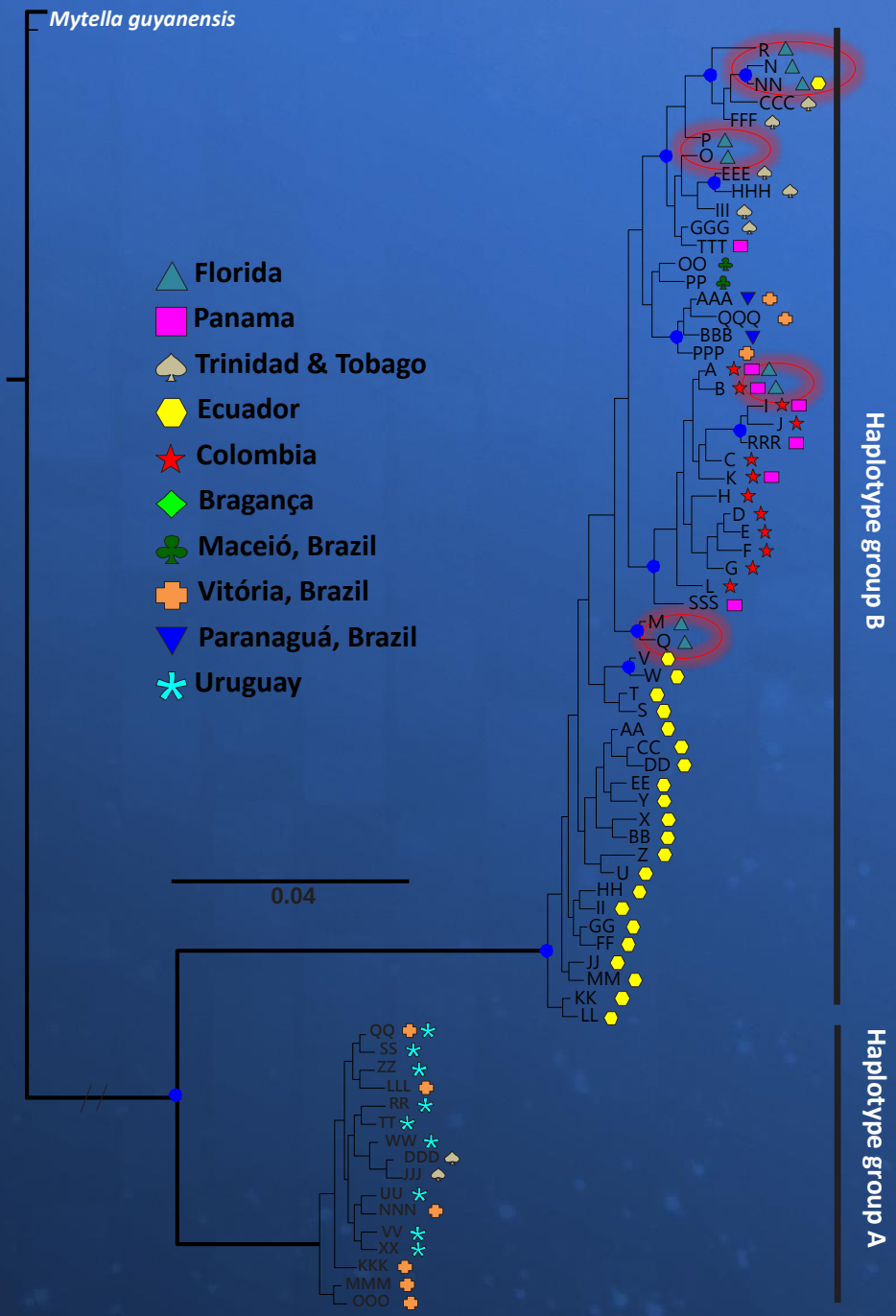
Results: Phylogenetic reconstruction



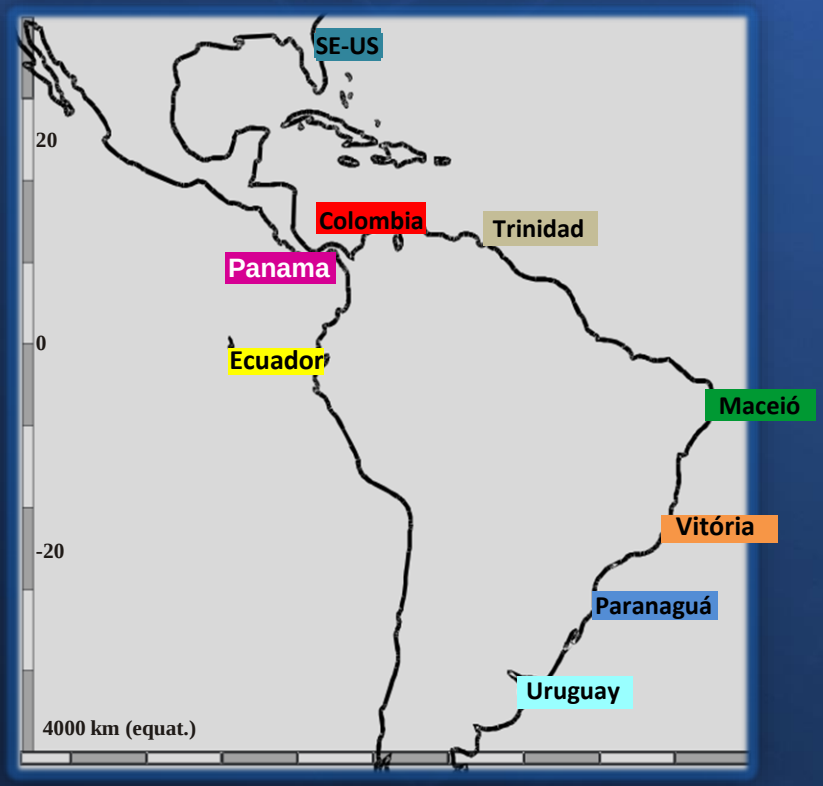


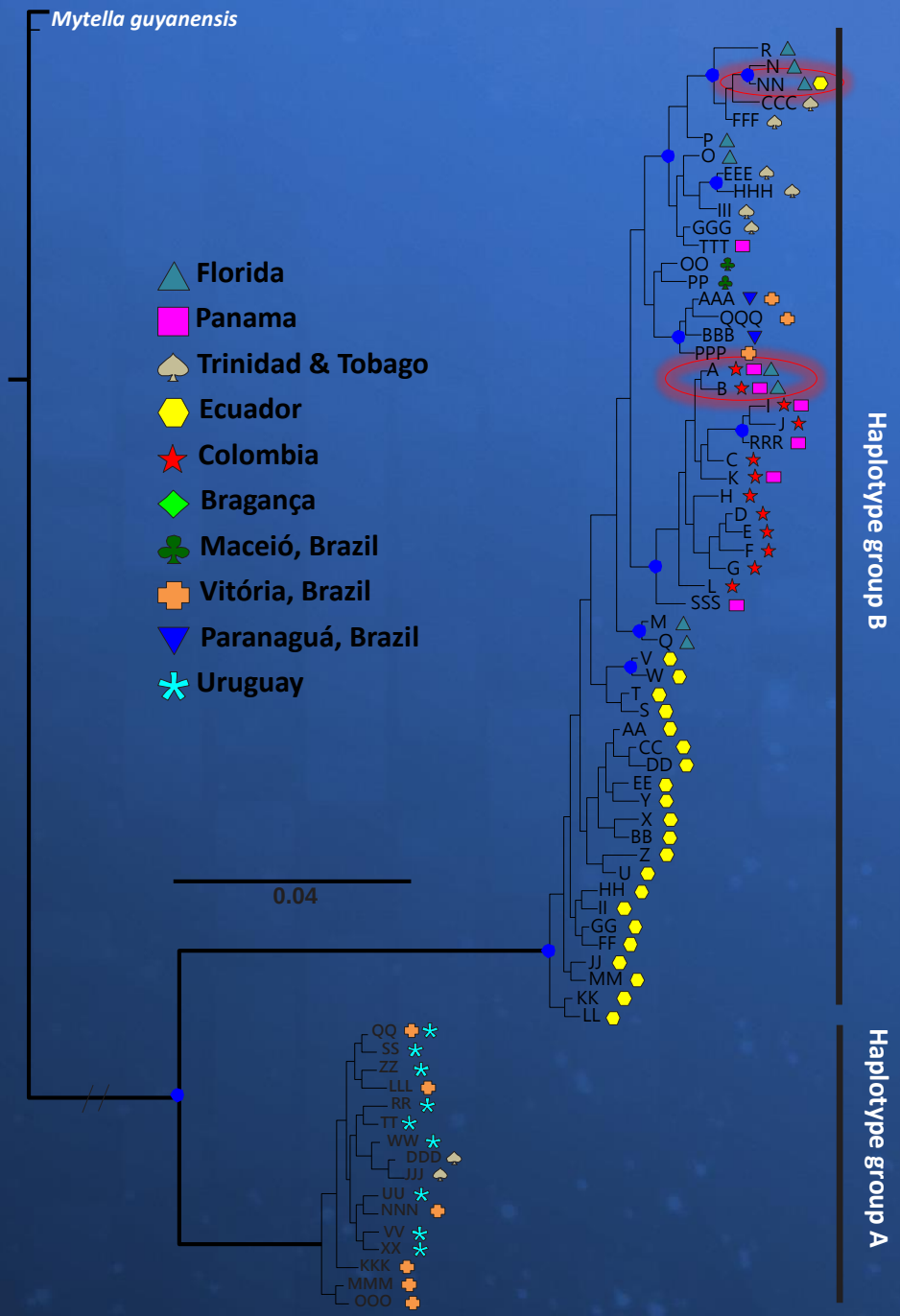
Results: Phylogenetic reconstruction



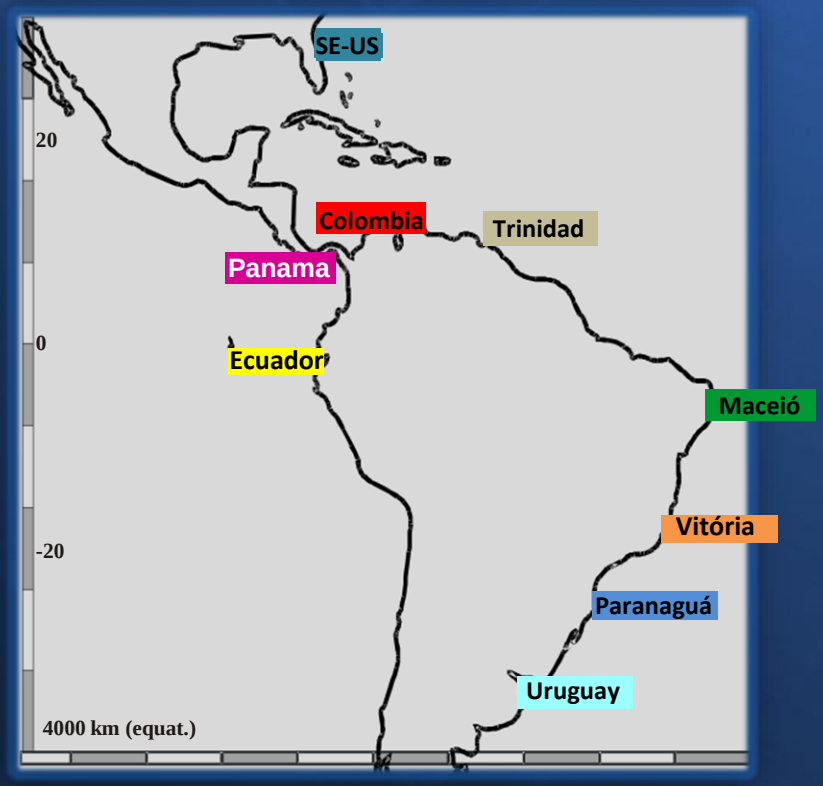


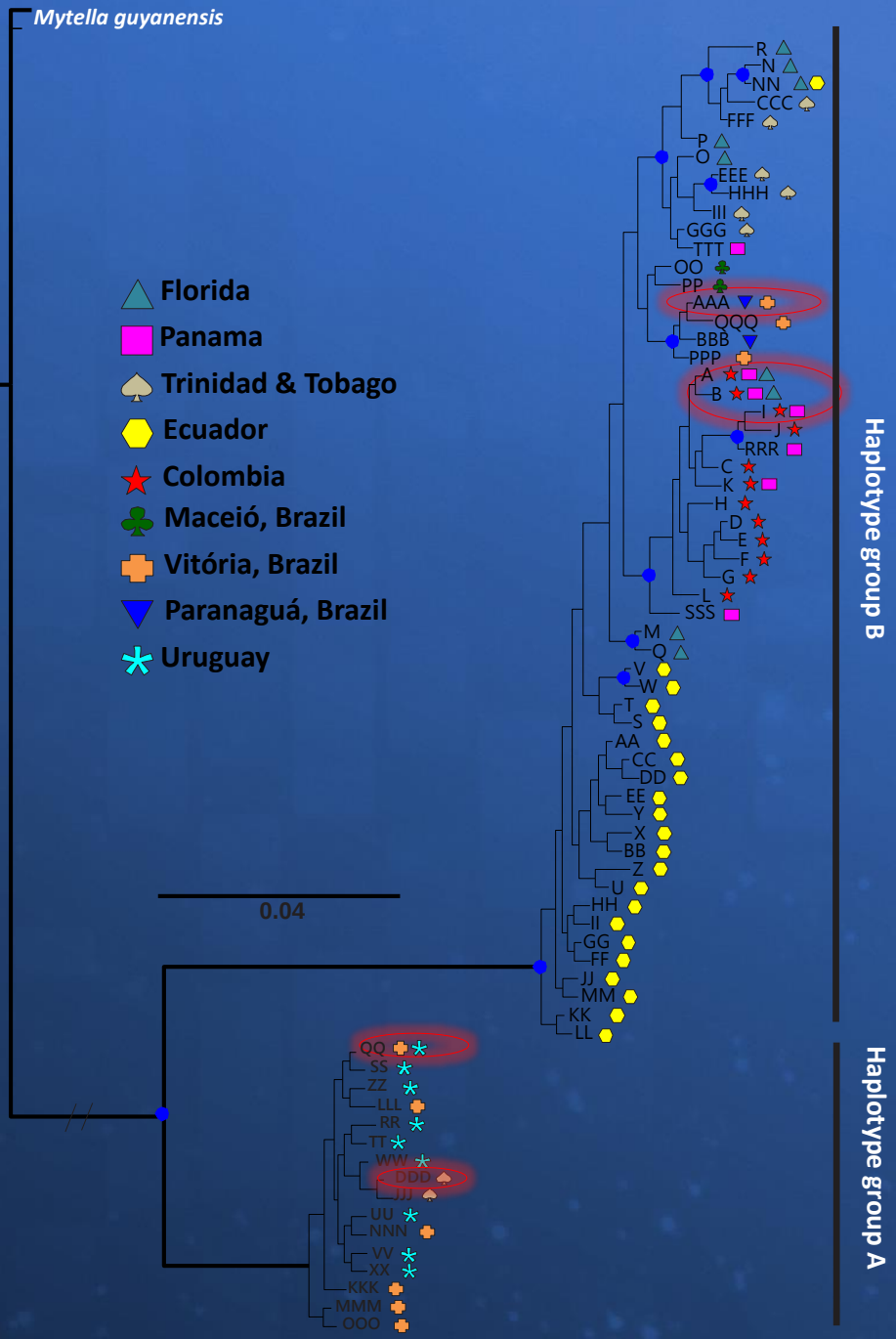
Results: Phylogenetic reconstruction



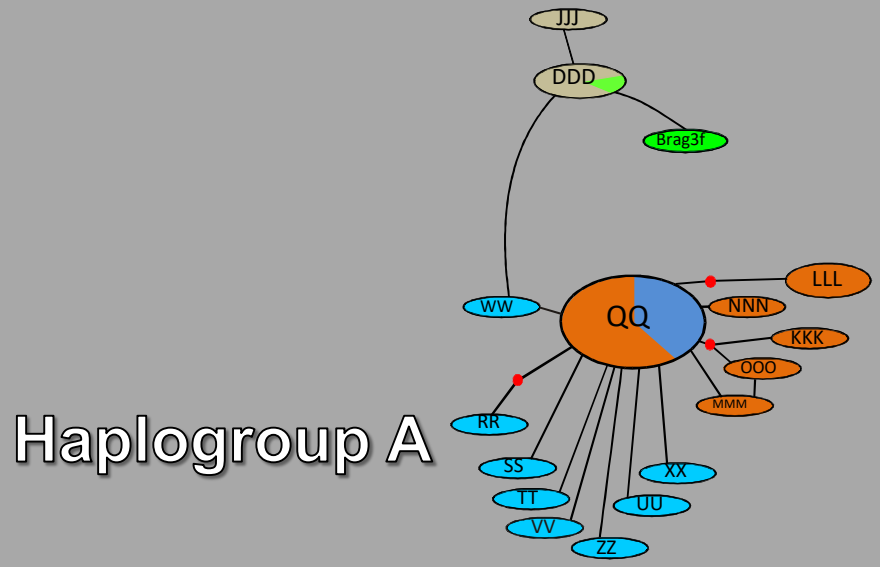


Results: Phylogenetic reconstruction



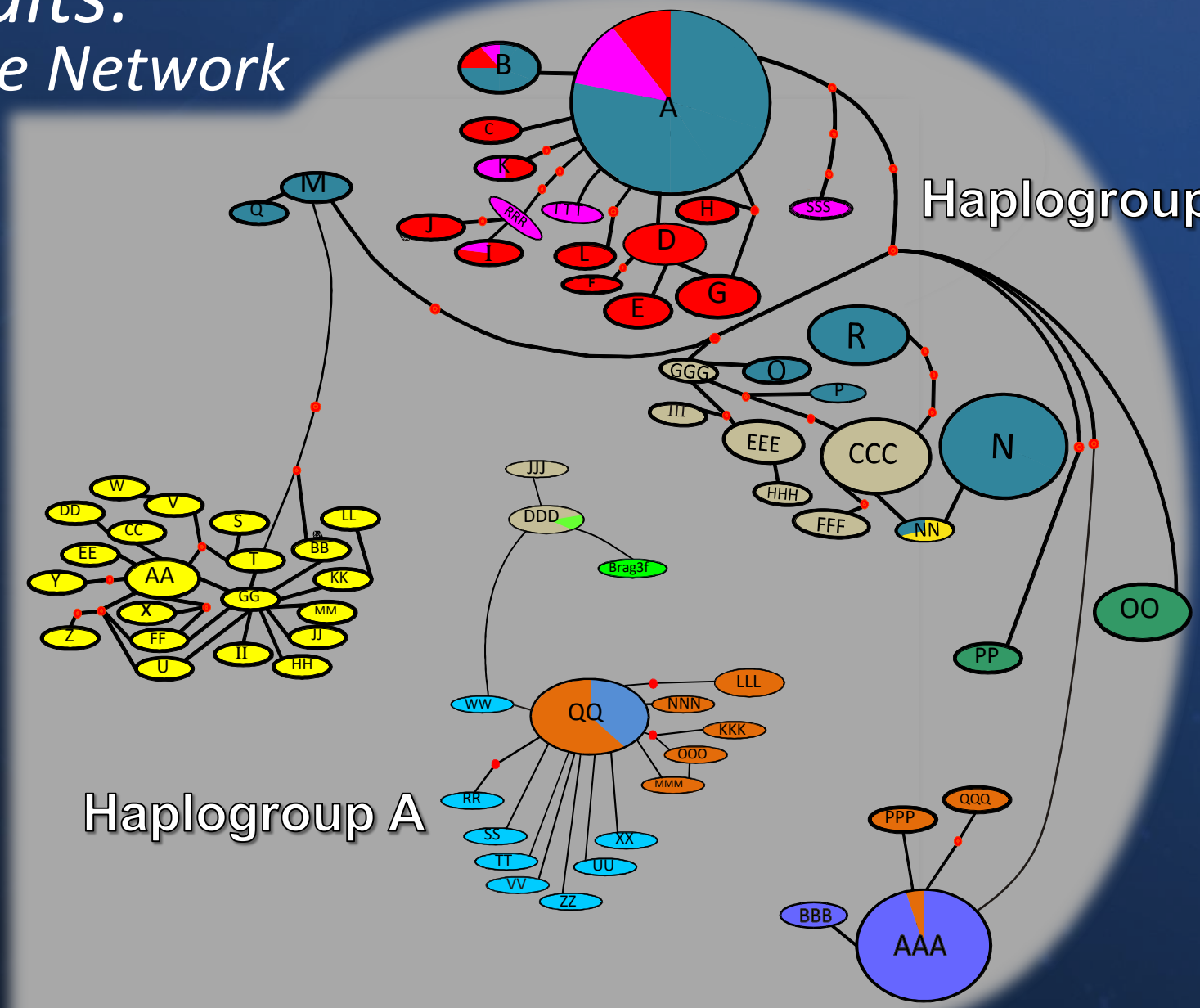


Results:
Haplotype Network

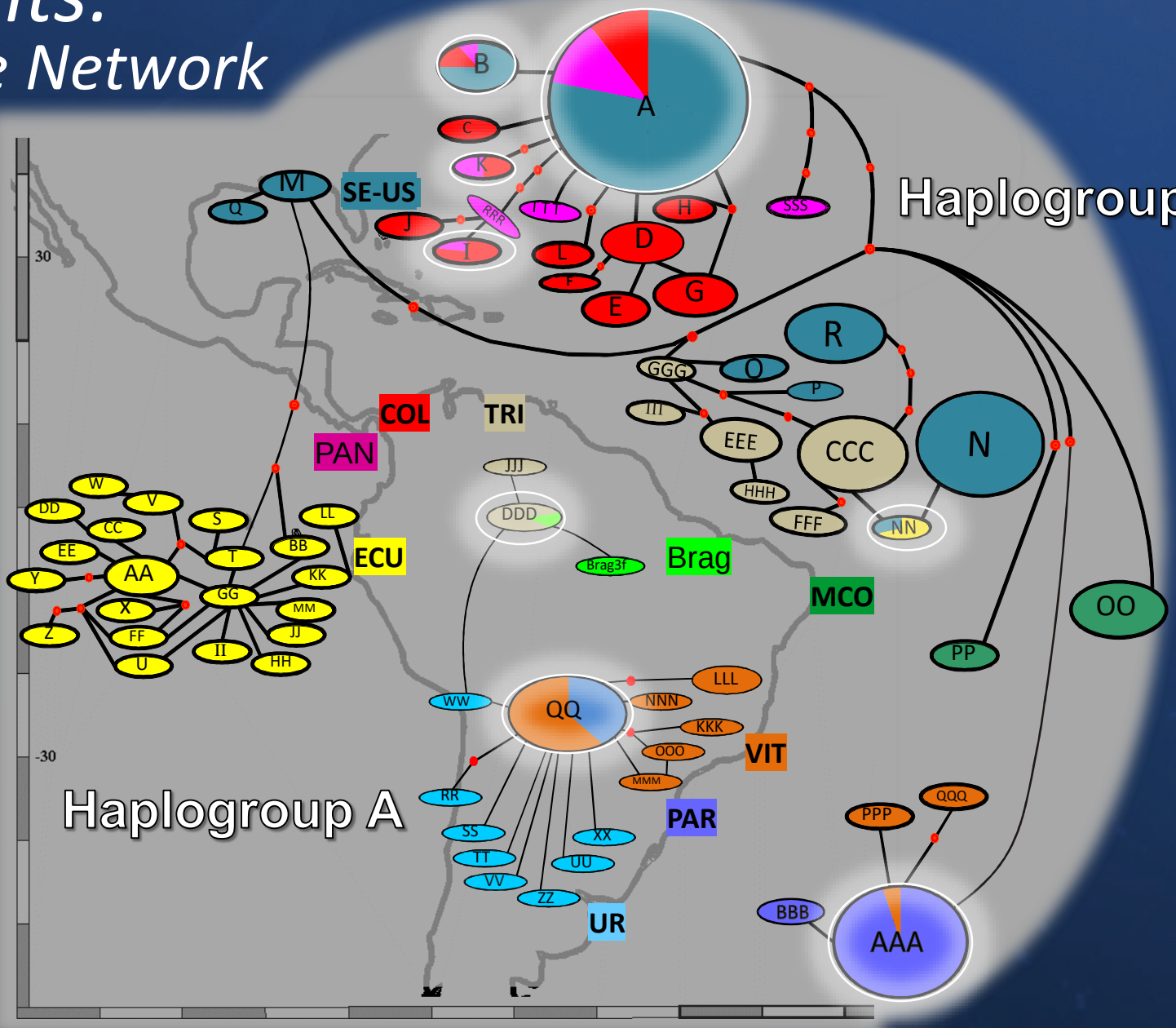


Haplogroup A

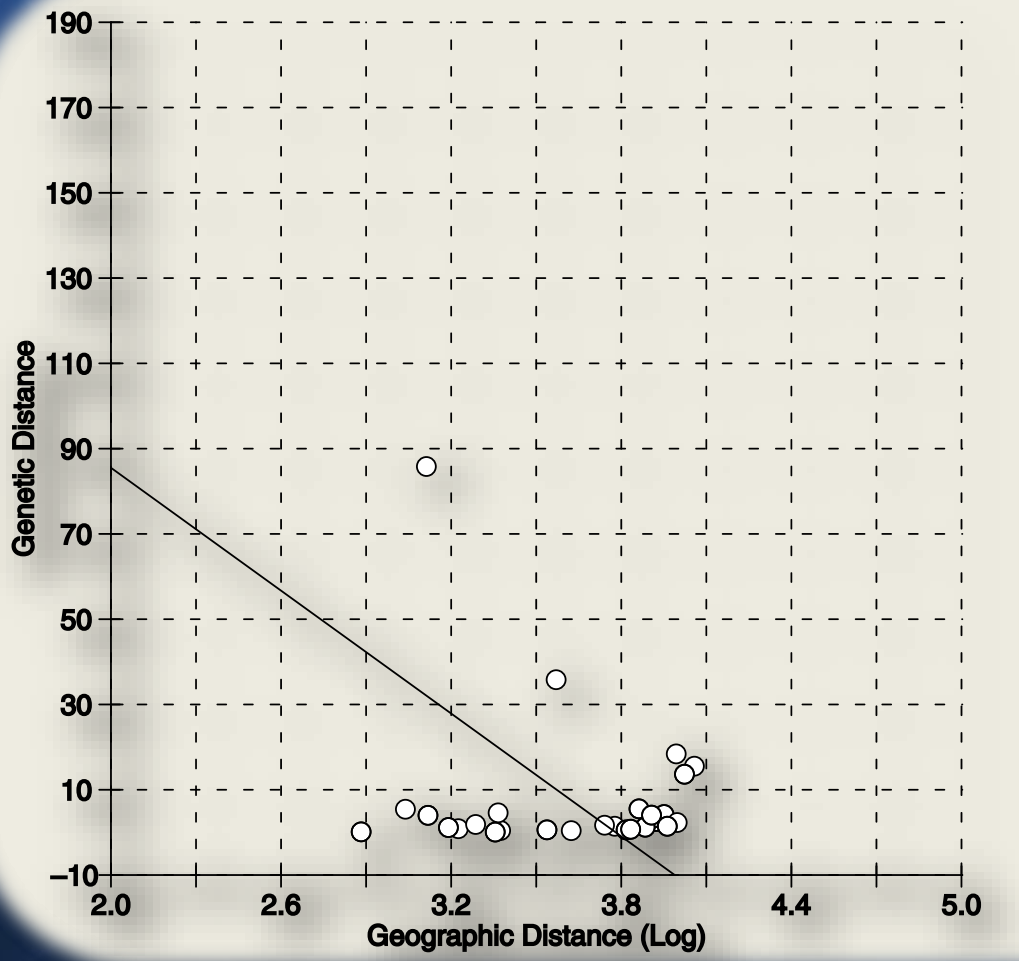
Results:
Haplotype Network



Results:
Haplotype Network



Results: Isolation By Distance



$Z = 761.9835$

$r = 0.1576$

$p = 0.7840$

Results:

Genetic structure: Analysis of Molecular Variance

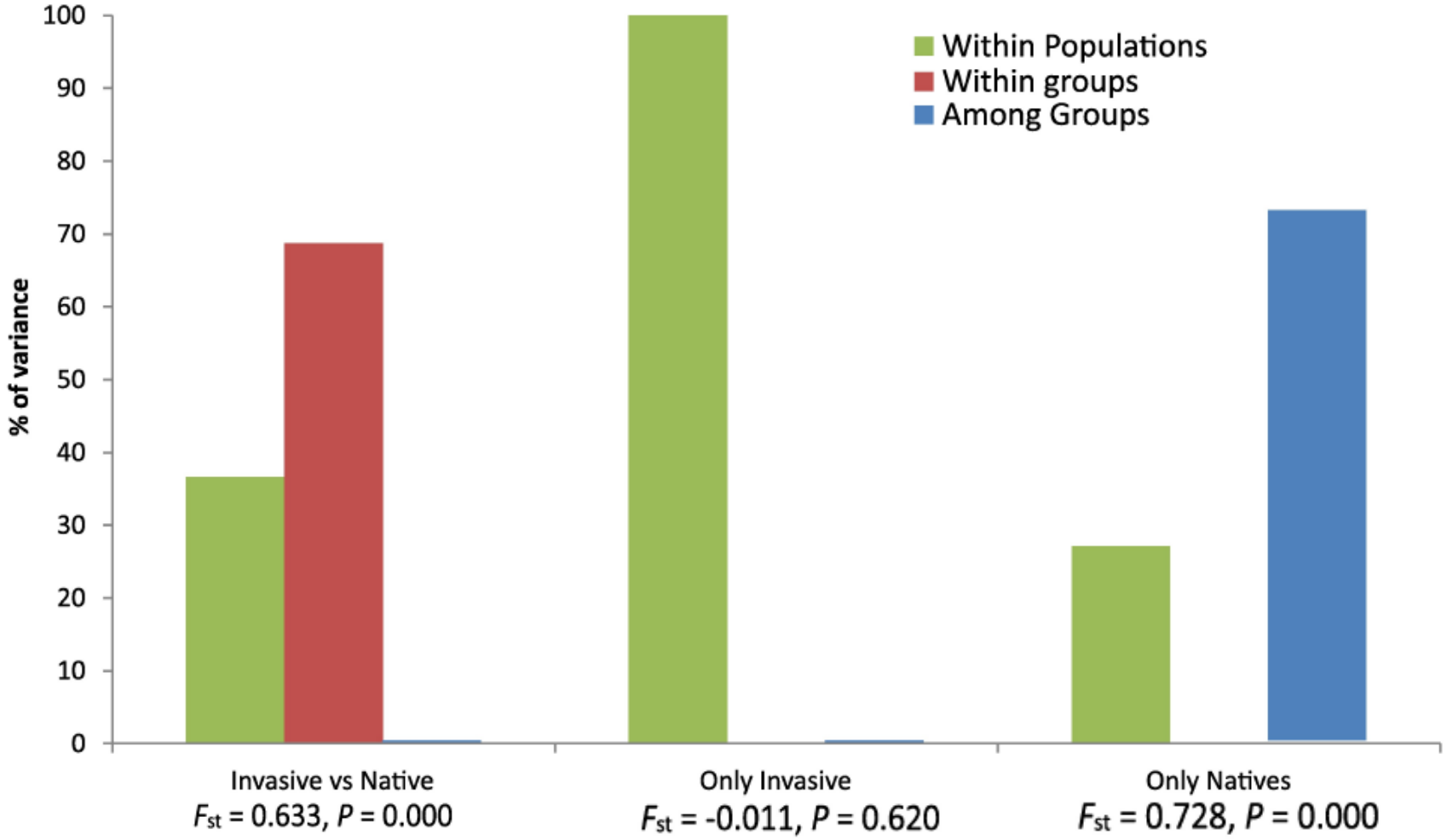


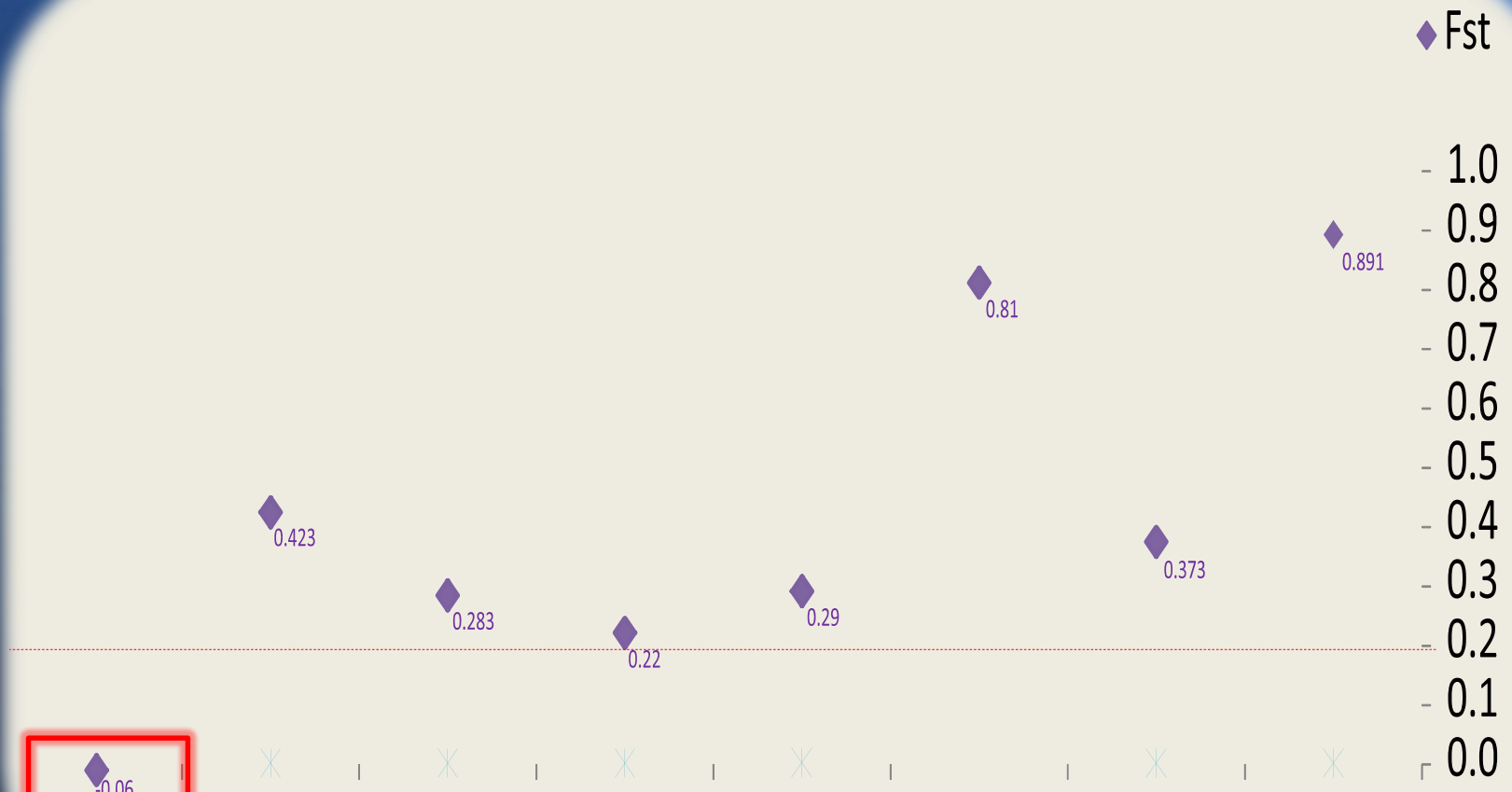
Fig 4. Graphs of the results from three analyses of molecular variance (AMOVA). Each analysis is separated by populations included in the analysis (invasive versus native populations, invasive populations only, and native populations only). For each analysis, columns indicate the percent of variance explained. Below columns are global F_{ST} and *p*-values for a null hypothesis of no genetic structure.

Methods

Objective 1B – Source of invasion

Analysis of molecular variance (AMOVA) in Arlequin

Results:
Molecular Variance



P-value	0.686	0.000	0.000	0.000	0.019	0.000	0.000	0.000

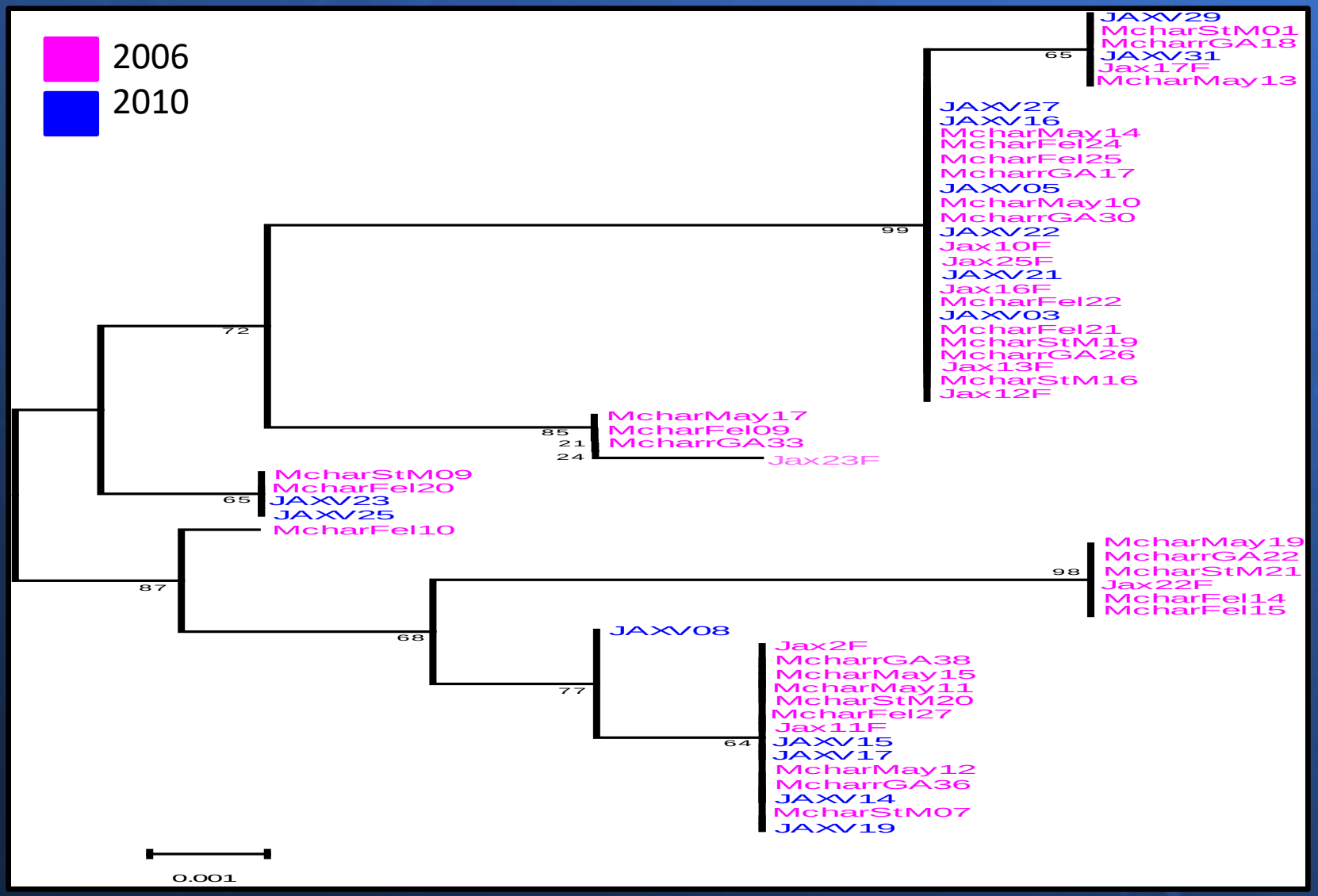
SE-US invasive V.S. Natives

Methods

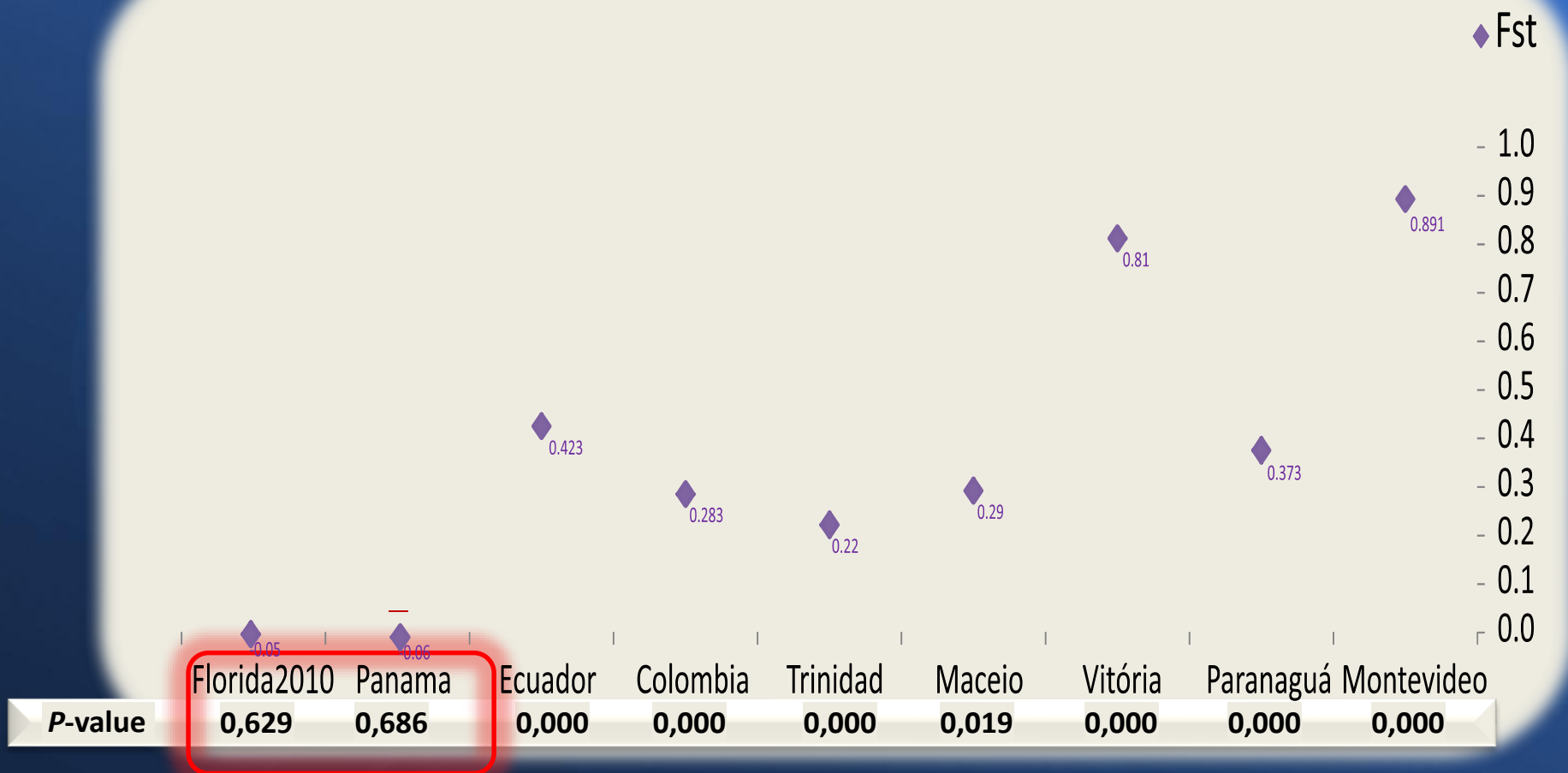
Objective 2 – Change over time

Analysis of molecular variance (AMOVA) in Arlequin: Comparing Invasive range samples from 2006 vs. 2010

How are nonnative populations changing over time?



Results:
Molecular Variance



	Florida2010	Panama	Ecuador	Colombia	Trinidad	Maceio	Vitória	Paranaguá	Montevideo
***P*-value**	**0,629**	**0,686**	**0,000**	**0,000**	**0,000**	**0,019**	**0,000**	**0,000**	**0,000**

2006 SE-US vs. JAX2010

Summary

1 - Native populations exhibit high genetic differentiation from each other

2 - Panama was the only native population indistinguishable from the invasive population

3 – Invasive genetic composition was largely unchanged over time

Acknowledgments:

Linda Walters
Nancy Gillis
Tamara Downs
Wei (Sam) Yuan
Flavio Fernandez
Savio Calazans
Kimberly Schneider
Matt Gilg

University of Central Florida

USDA

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Protecting and Restoring
National Estuary Program
20 Years


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EXPRESSION