Introduction Histories and Population Genetics of the Nile Monitor (*Varanus niloticus*) and Argentine Black-and-White Tegu (*Salvator merianae*) in Florida

JARED WOOD, STEPHANIE DOWELL, TODD CAMPBELL, ROBERT PAGE

Invasive Species

Invasive species are the second largest threat to global biodiversity

- No natural enemies or competitors → unregulated growth
- Issues → Competitive exclusion, predation, etc.

Florida is especially susceptible to invasion of herpetofauna due to:

1. Robust exotic pet industry
2. Subtropical climate
3. Altered natural environments

Consequently, nonnative lizard species currently **outnumber** native lizard species in Florida.

Nile Monitor

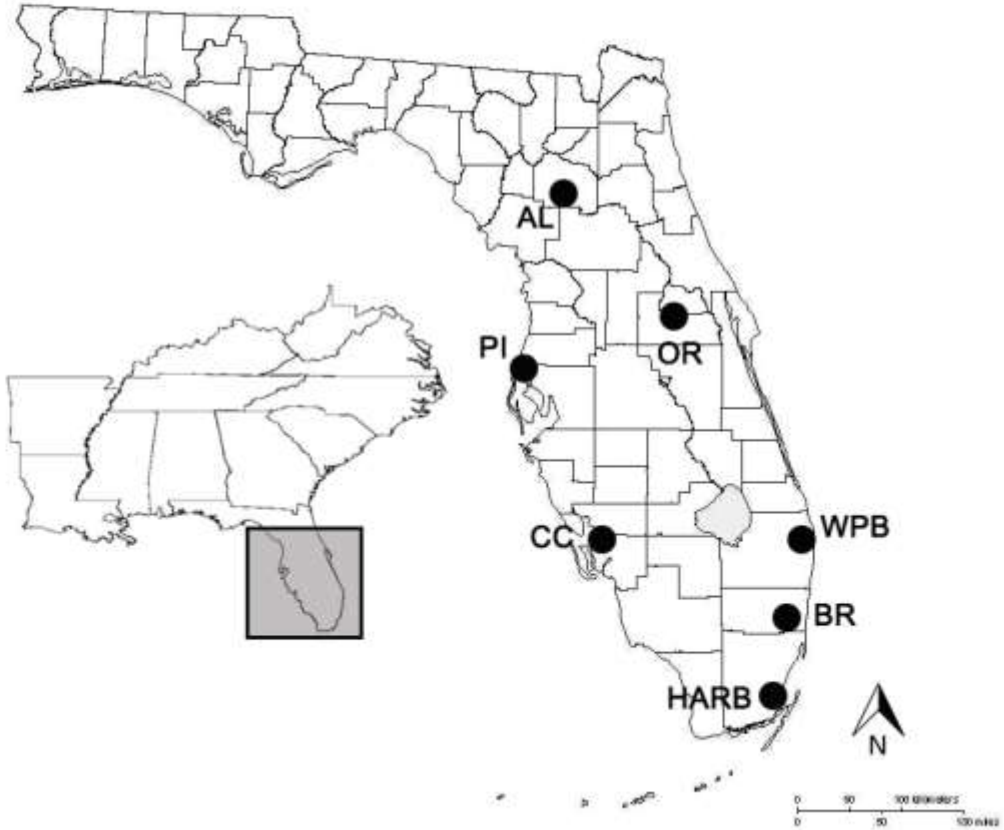
Native to sub-Saharan Africa

First reported in 1990 in Cape Coral, Florida

Most likely introduced through the pet trade

Is of management concern because:
- High reproductive output
- Large generalist predator
- Highly aquatic and mobile
- Adept at burrowing

Study Sites: Nile Monitor



Argentine Black-and-White Tegu

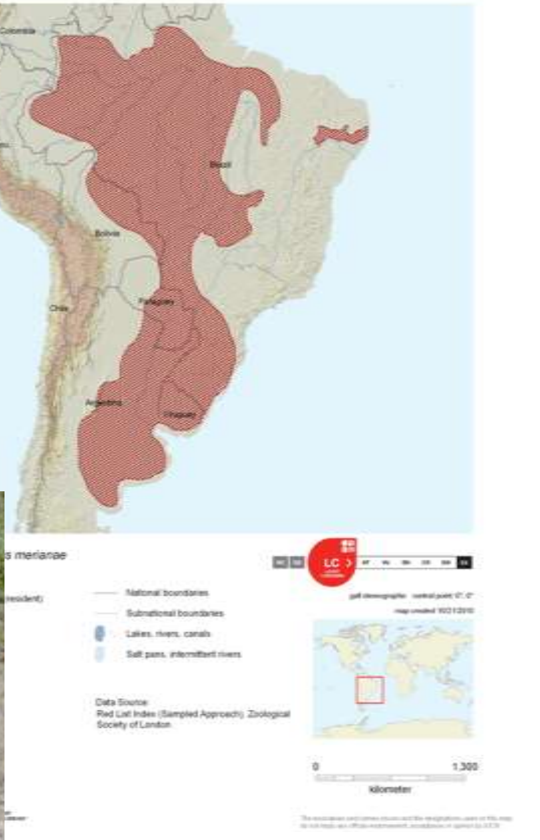
Native to southeastern Brazil, Uruguay, Paraguay, and Argentina

First observed at the Balm-Boyette Scrub Preserve located near Riverview, FL in 2006

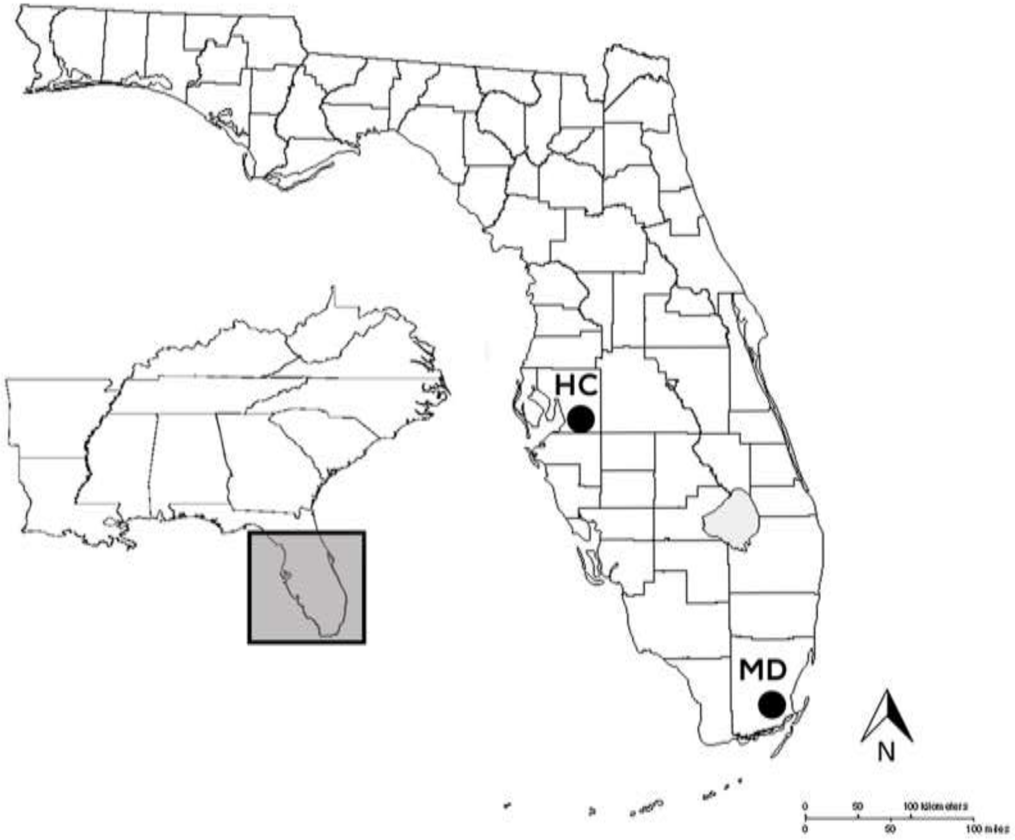
Most likely introduced through the pet trade

Management concerns similar to monitors:

- High reproductive output
- Large generalist omnivore
- Highly aquatic and mobile
- Adept at burrowing



Study Sites: Argentine Black-and-White Tegus



Objectives

1. Gain insight into the amount of genetic variation in Florida's populations
2. Assess whether gene flow and admixture occur among populations
3. Infer the number of introduction events and most likely introduction history
4. Make management recommendations

Catching Lizards

Havahart traps

Shooting

Donations

Nile Monitors

RESULTS

Marker Development

Microsatellite sequences were generated using 454 sequencing

- Generated 43,306,932 bp across 101,489 reads

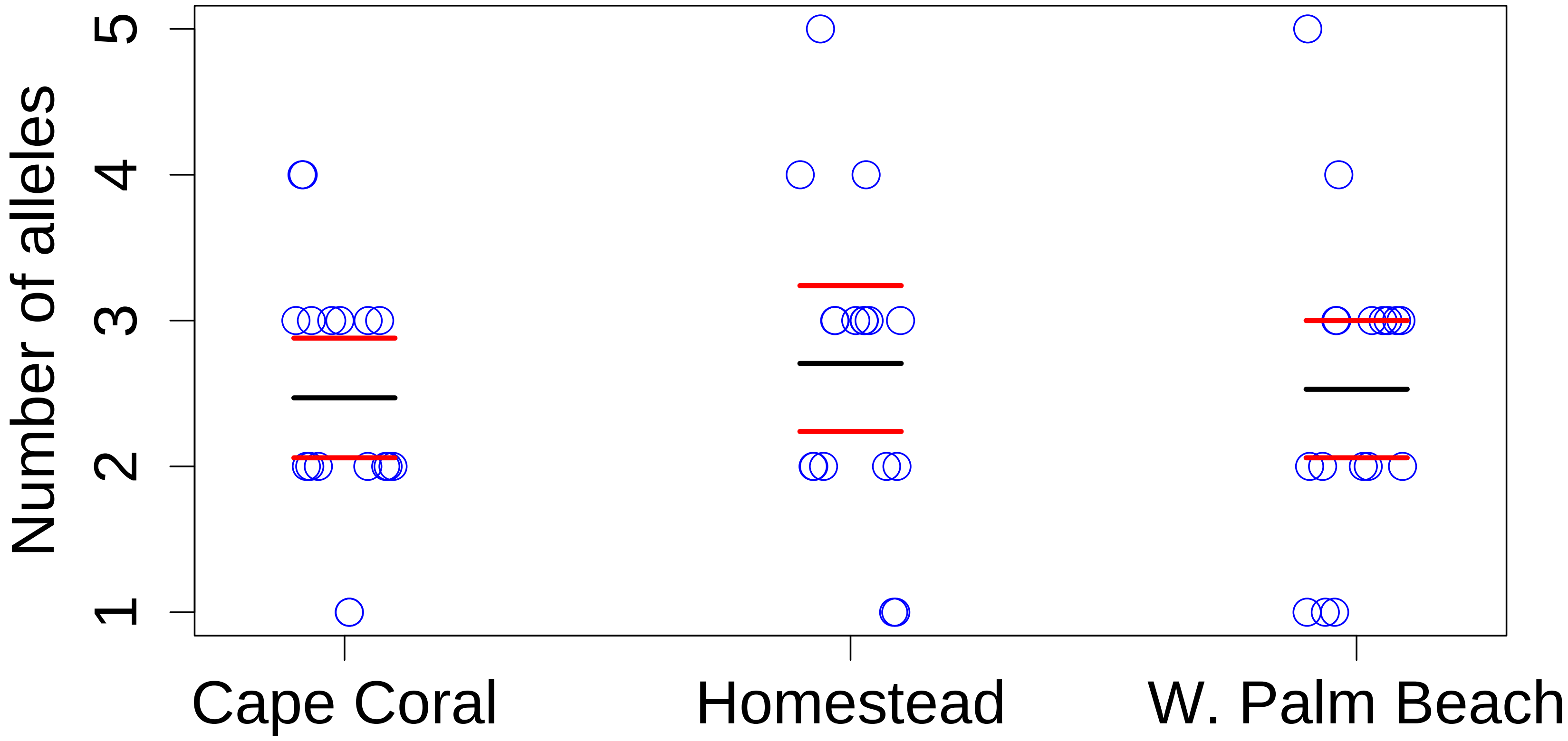
MSATCOMMANDER identified 1,040 potentially amplifiable loci

  - Screened 20 loci using PCR
    - 17 were polymorphic and could be scored reliably
      - 2 additional loci were dropped before performing population-level analyses

Genotyped and analyzed:

- 40 individuals from Cape Coral
- 17 individuals from West Palm Beach
- 10 individuals from Homestead

Genetic richness across 17 microsatellite loci



Assessment of Population Differentiation

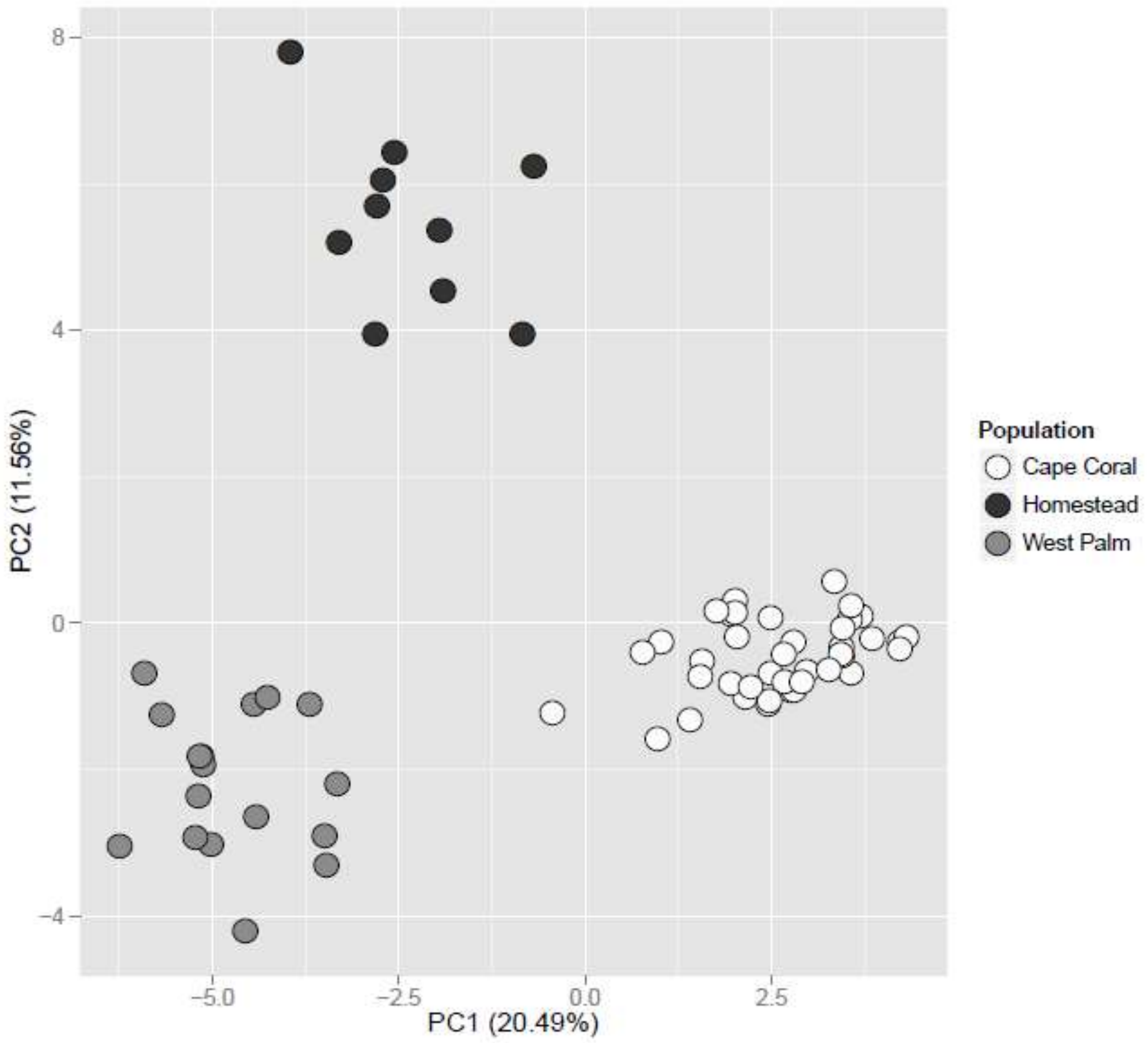
G-Statistics

- Global G_{ST}''= 0.642, *P* = 0.0001
  - Cape Coral vs. Homestead: G_{ST}'' = 0.627, P = 0.0001
  - Cape Coral vs. West Palm Beach: G_{ST}'' = 0.683, P = 0.0001
  - Homestead vs. West Palm Beach: G_{ST}'' = 0.612, P = 0.0001

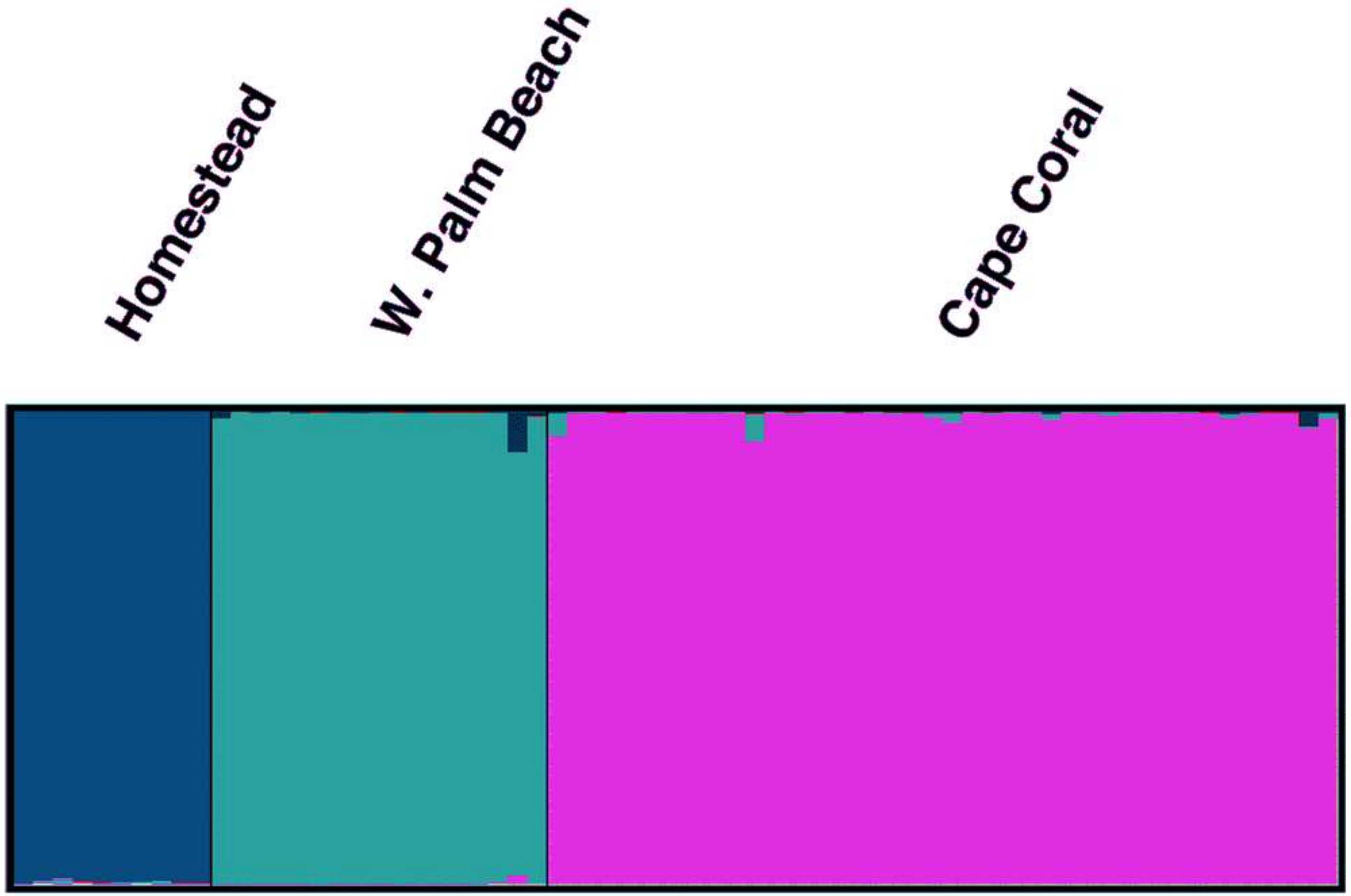
AMOVA

- Fixation indices
  - F_{ST}= 0.38
  - F_{IS} = -0.25

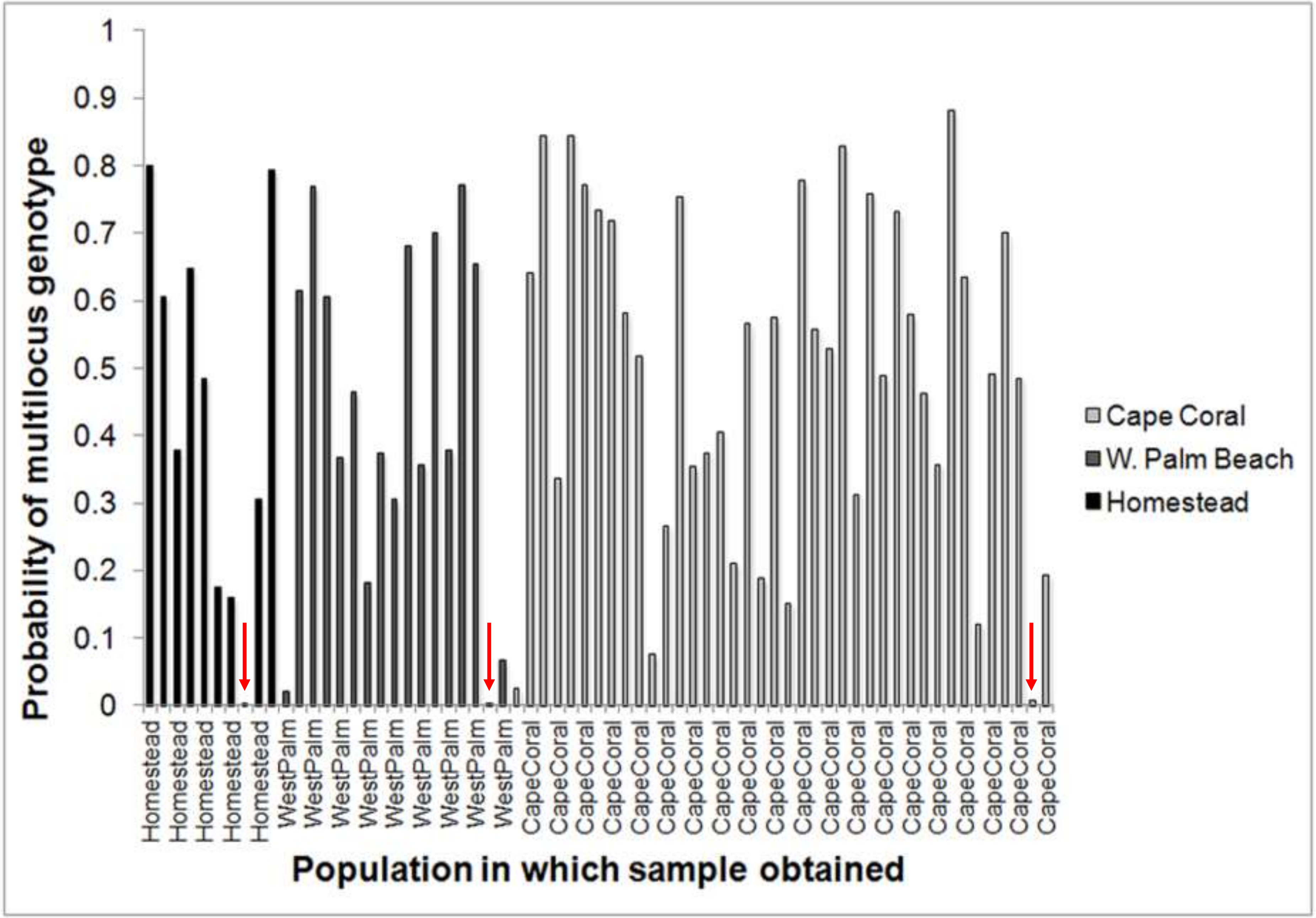
Assessing Population Structure



Assessing Admixture

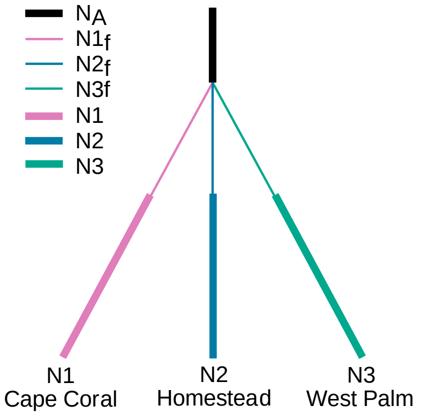


Assessing Gene Flow and Migration

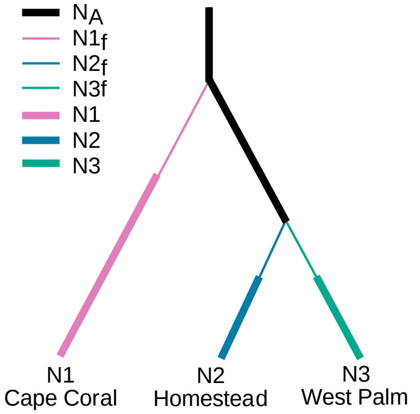


Comparing Possible Introduction Scenarios

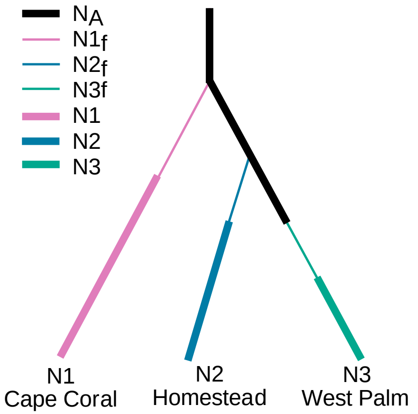
Independent Introductions:



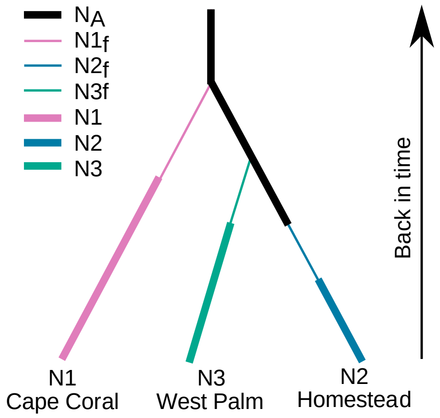
Scenario 1



Scenario 2

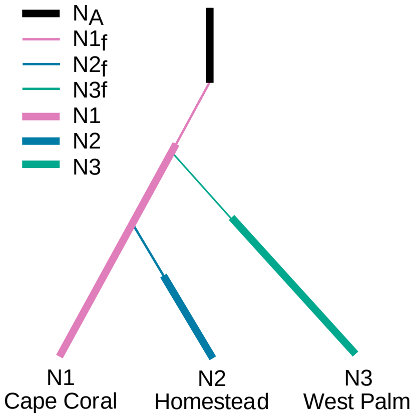


Scenario 3

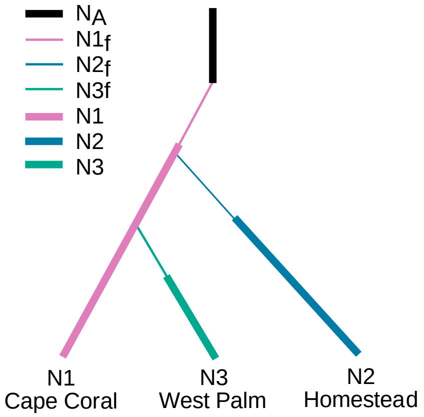


Scenario 4

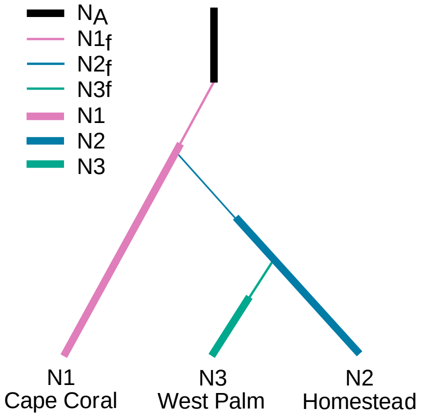
Serial Introductions:



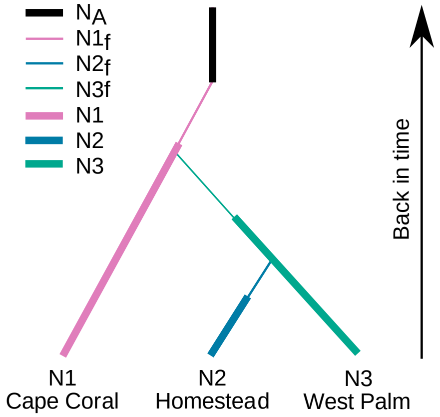
Scenario 5



Scenario 6



Scenario 7



Scenario 8

Conclusions

Still recovering from recent founder effects

- Limited allelic richness and other bottleneck signatures
- Small effective population size estimates

There is marked regional genetic structure

- High self-recruitment, very low/no gene flow
- No admixture among South Florida populations

Three separate introductions from African source

Seem to be in the early phase of invasion

Argentine Black-and-White Tegus

RESULTS

Marker Development

Microsatellite sequences were generated using 454 sequencing

- Generated 127,343,751 bp across 300,675 reads

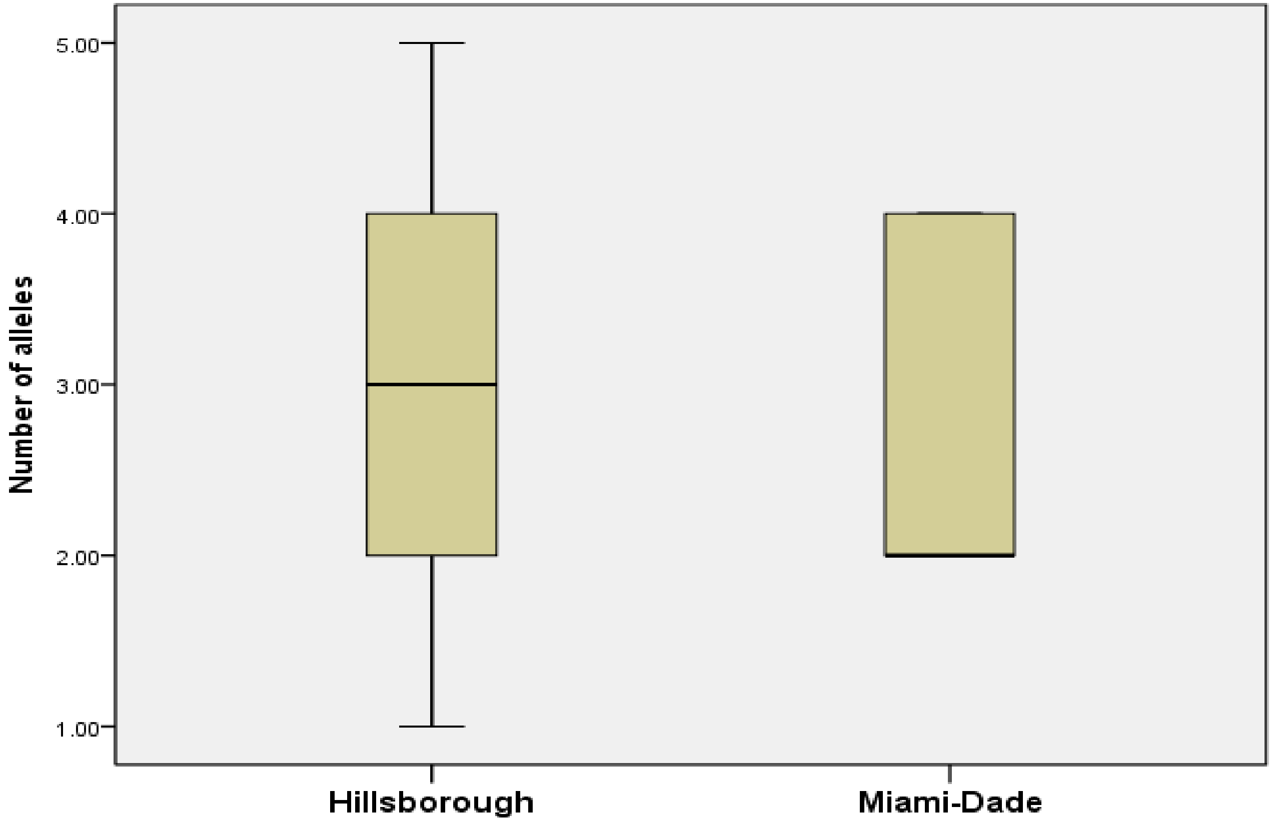
MSATCOMMANDER identified 3,154 potentially amplifiable loci

- Screened 20 loci using PCR
  - 14 were polymorphic and could be scored reliably
    - 4 loci had to be dropped due to quality control issues

Genotyped:

- Tegus:
  - 42 individuals from Riverview
  - 40 individuals from Florida City

Genetic richness across 14 microsatellite loci



Assessment of Population Differentiation

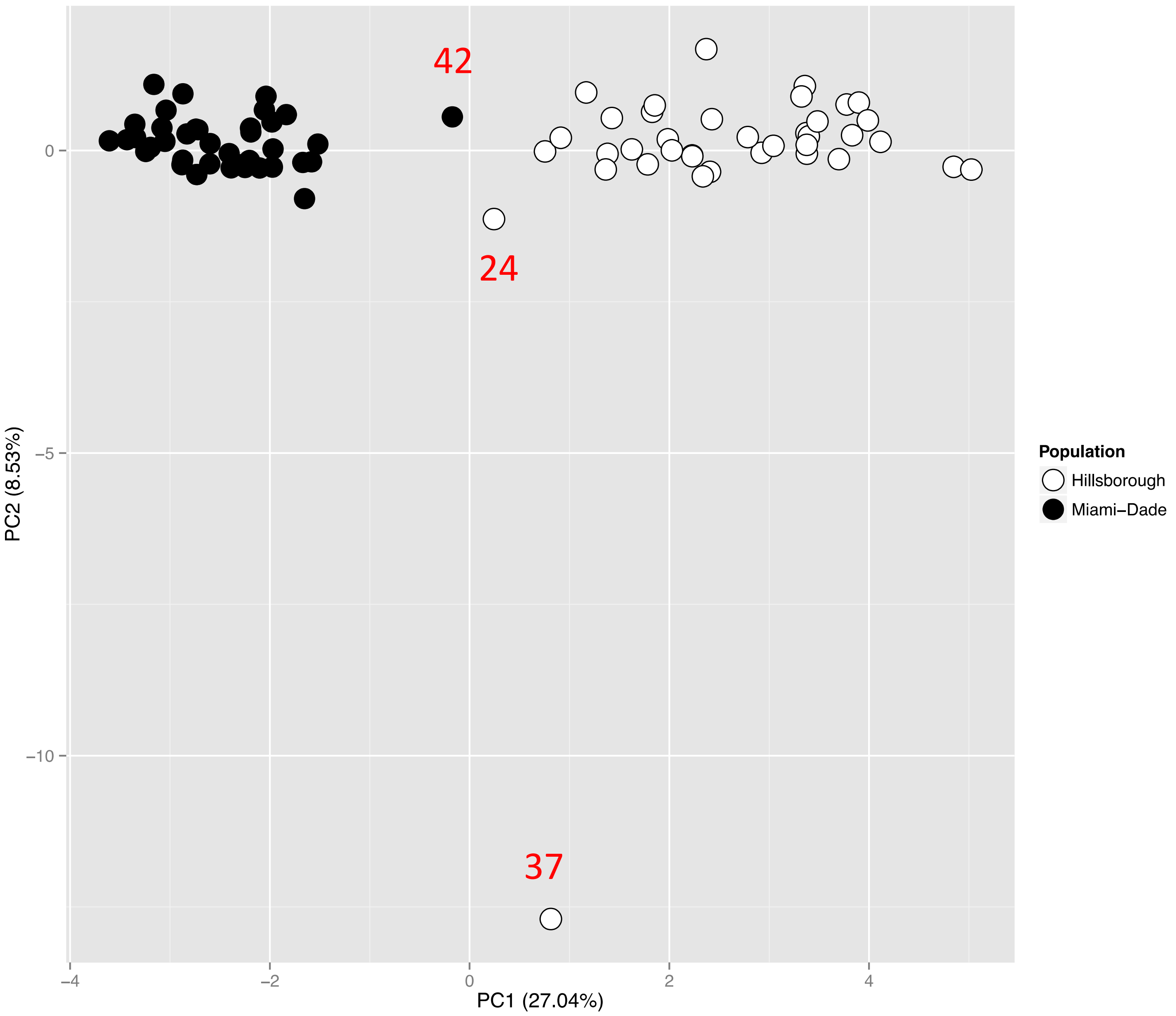
G-Statistics

- Global $G_{ST}''= 0.545$, $P = 0.0001$

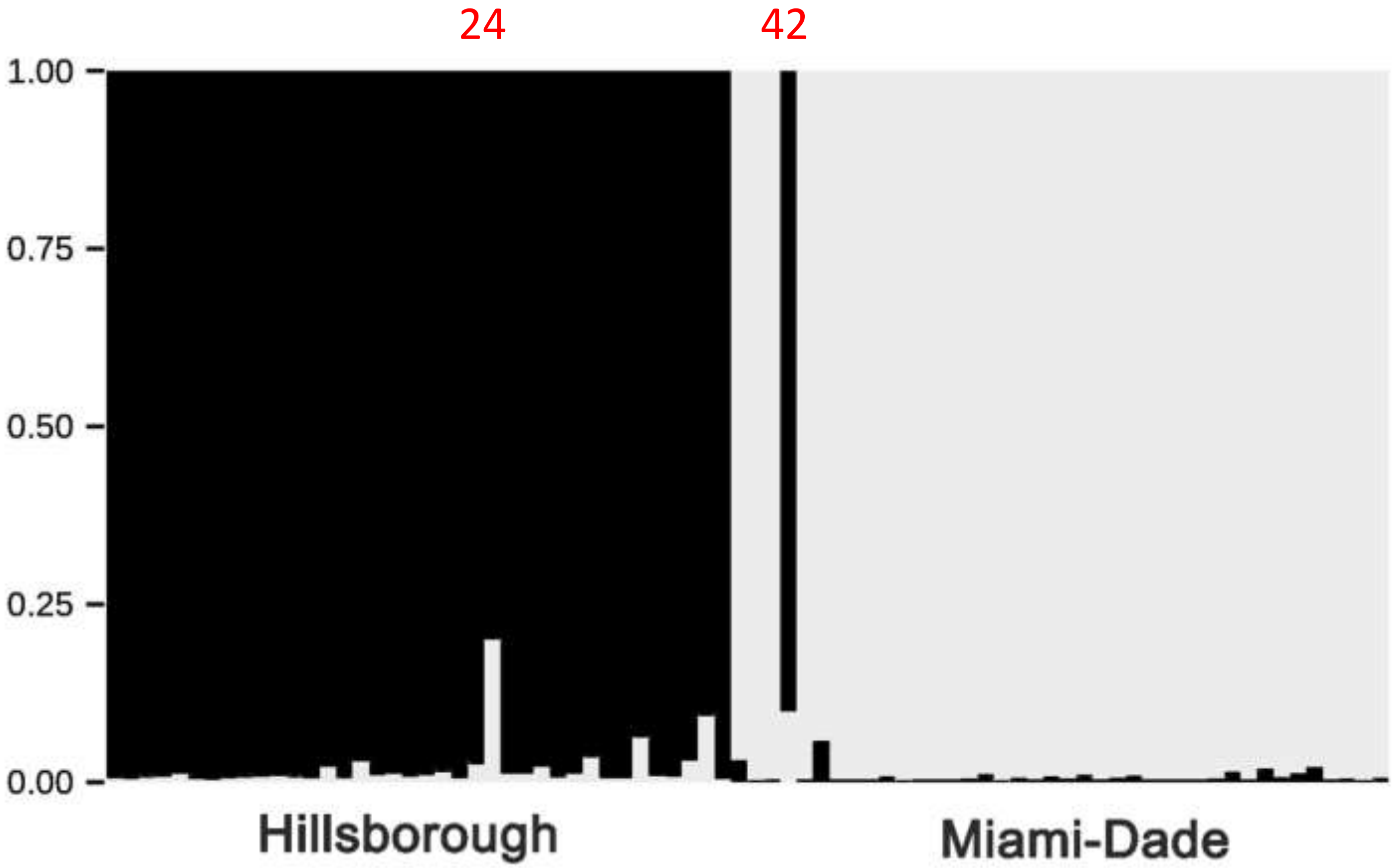
AMOVA

- Fixation indices
  - $F_{ST} = 0.32$
  - $F_{IS} = -0.20$

Assessing Population Structure

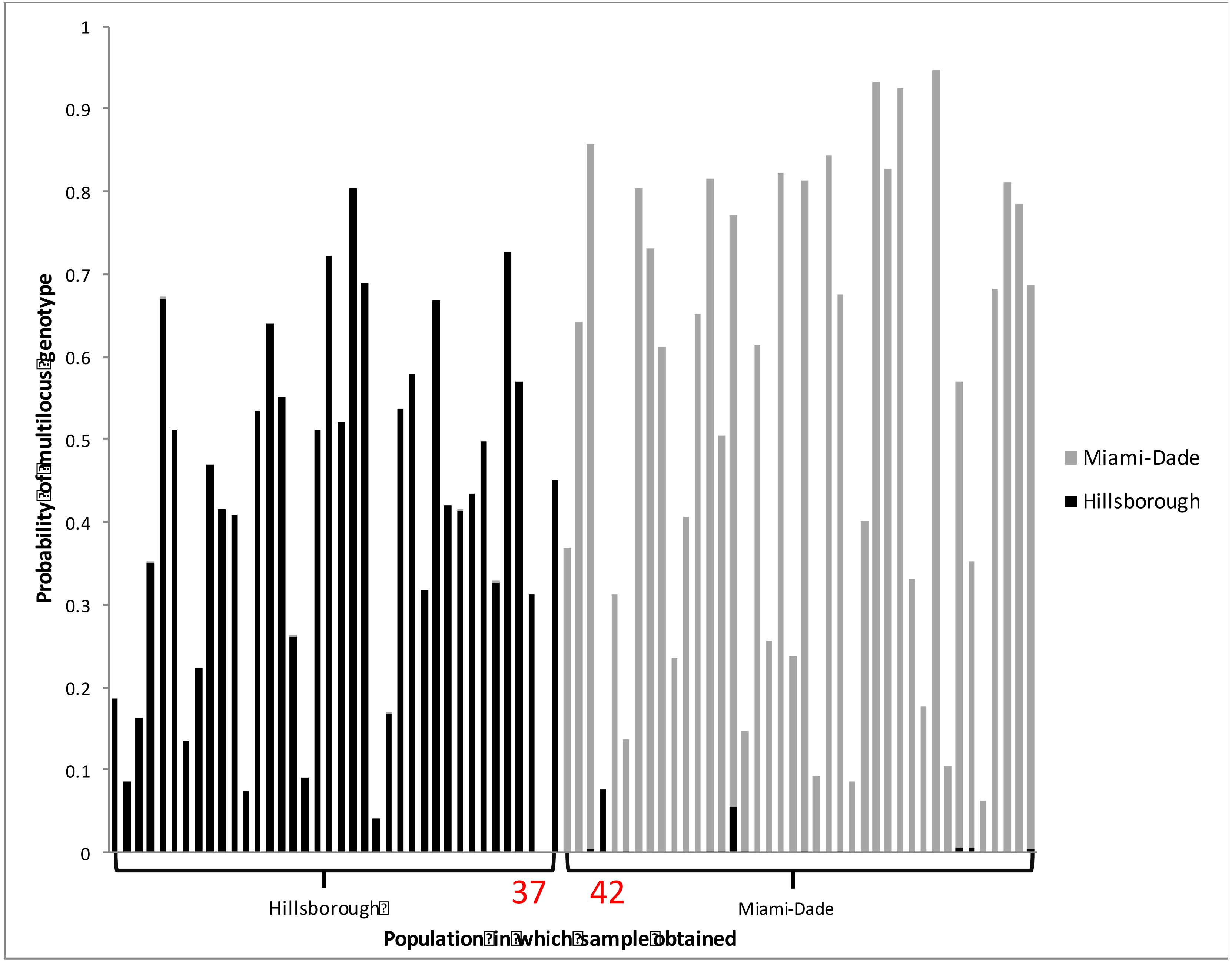


Assessing Admixture

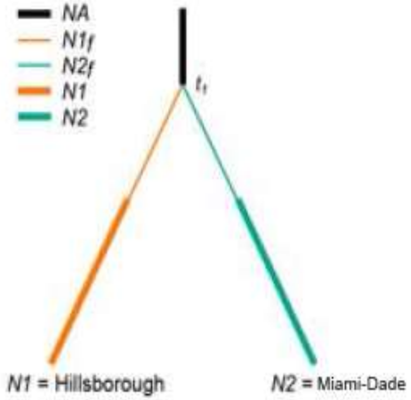


Assessing Gene Flow and Migration

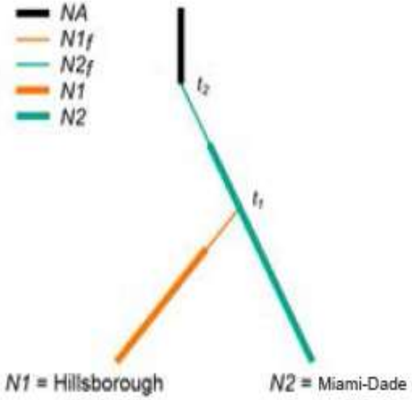
- Migrant Detection Analysis
    - 42
    - 37 (unknown source)



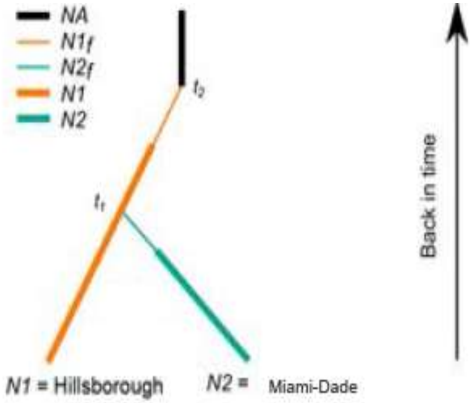
Comparing Possible Introduction Scenarios



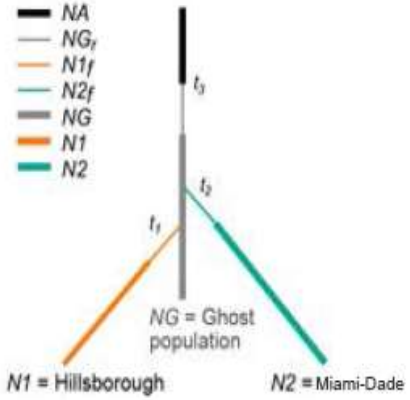
Scenario 1
Independent introduction events



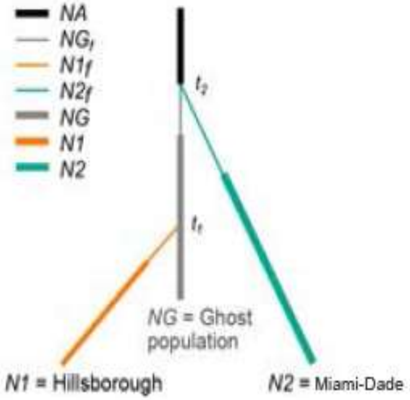
Scenario 2
Serial introduction events



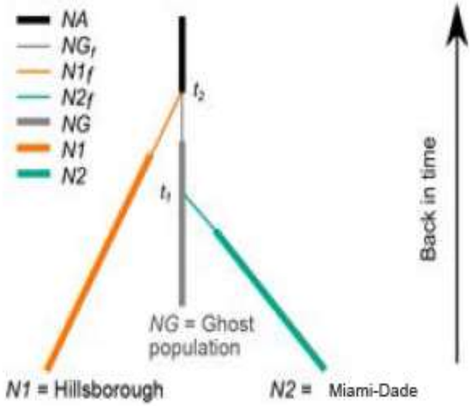
Scenario 3
Serial introduction events



Scenario 4
Unsampled ghost population



Scenario 5
Independent ghost population and introduced population



Scenario 6
Independent ghost population and introduced population

Conclusions

Still recovering from recent founder effects

- Limited allelic richness
- Small effective population size estimates

There is marked regional genetic structure

- However, gene flow is occurring
  - Admixture: tegus 24 and 42
  - Migrants: tegus 42 and 37 (unknown source)

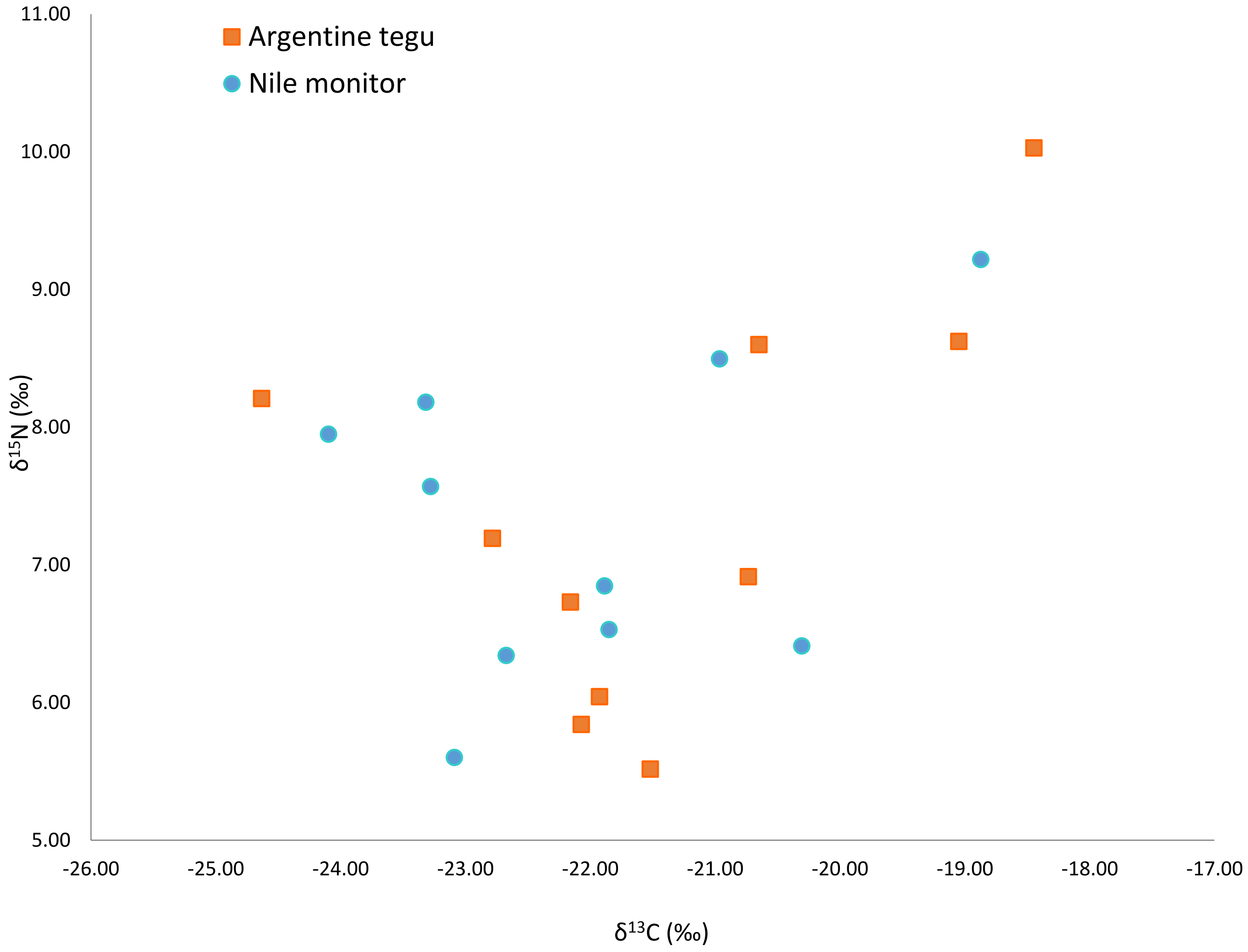
Both populations originated from an undetected "ghost" population

In the early second stage of the invasion process

Answering Our Objectives

1. Gain insight into the amount of genetic variation in Florida's populations
    1. Both species have limited genetic diversity
2. Assess whether gene flow and admixture occur between populations
    1. Negligible admixture among monitor populations
    2. Some gene flow is occurring between tegu populations
3. Infer the number of introduction events and most likely introduction history
    1. Monitors: three separate introduction events from African source
    2. Tegus: both populations originated from a "ghost" population
4. Make management recommendations
    1. Treat each population as separate management units
    2. Focus on containment
    3. Continue to monitor credible sightings and potential migration corridors

Future Directions



Acknowledgements

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It's Happening Here.

FAU

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South Florida Water Management District
sfwmd.gov

Questions?