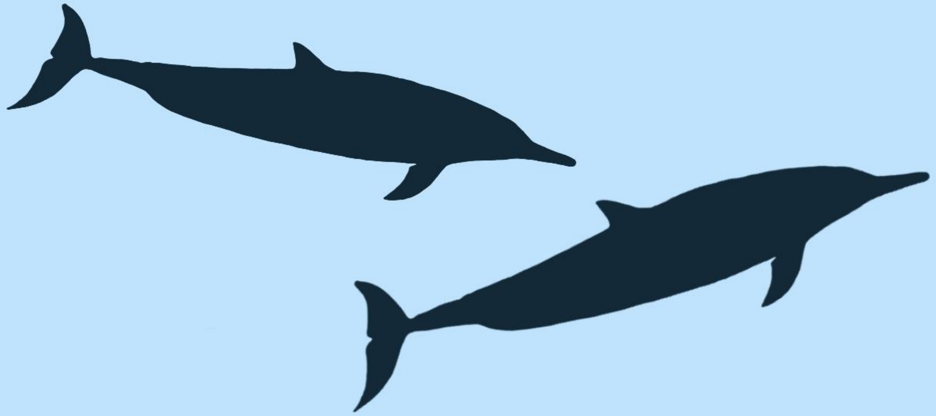
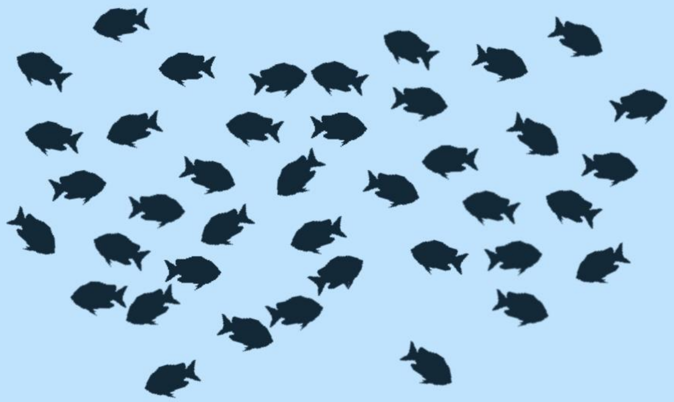
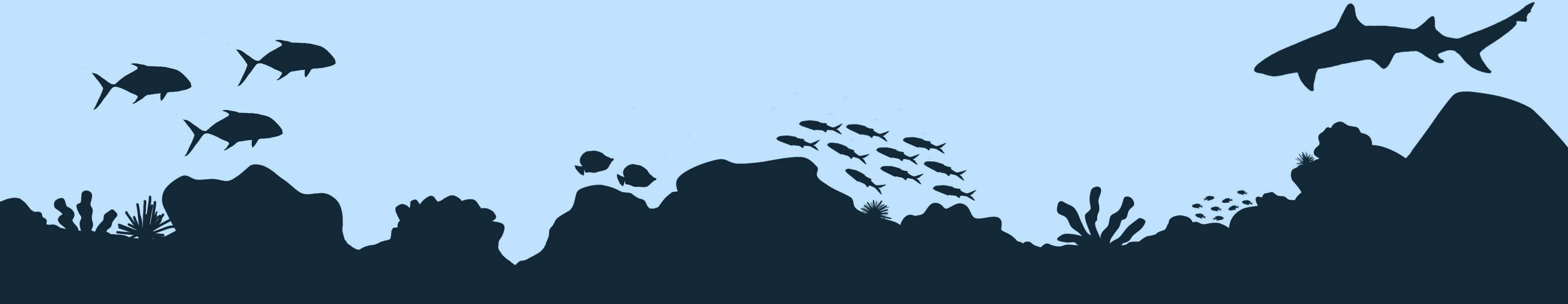
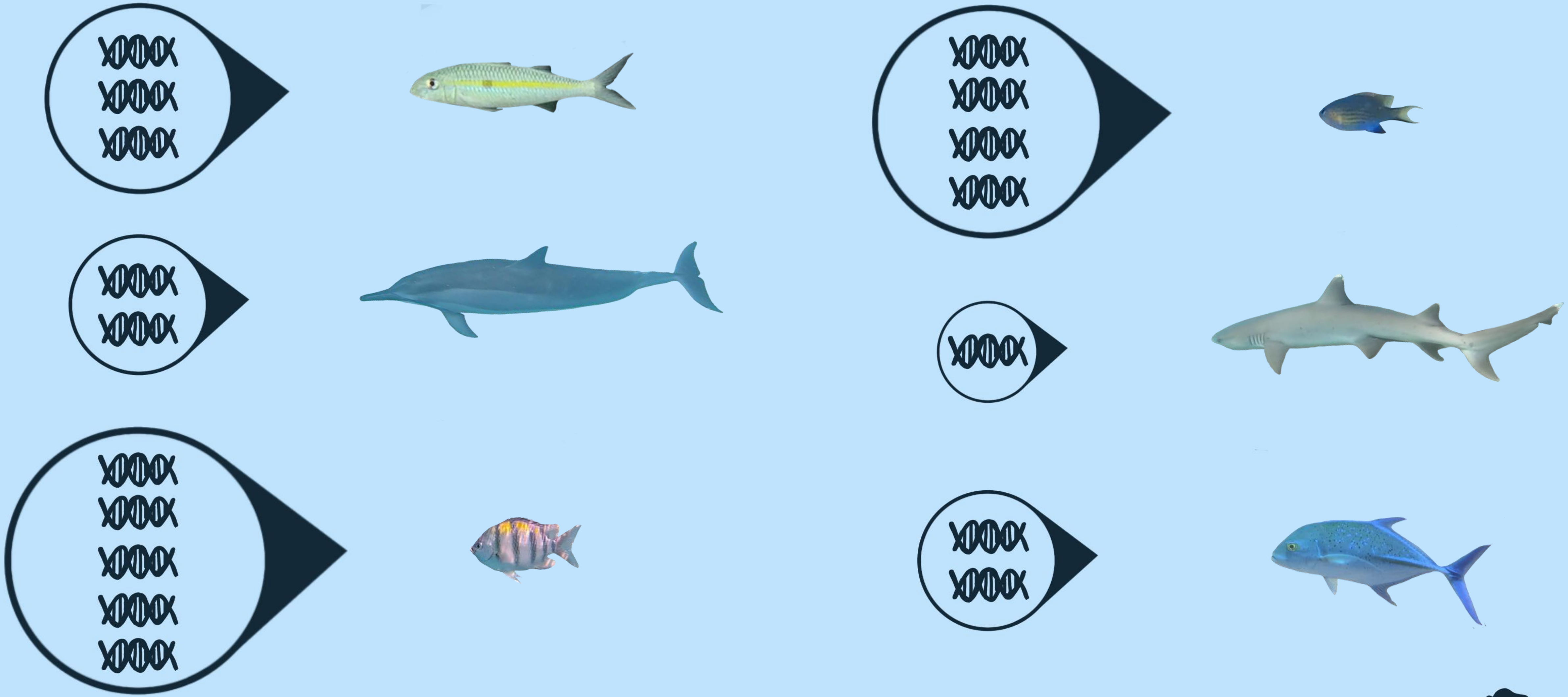




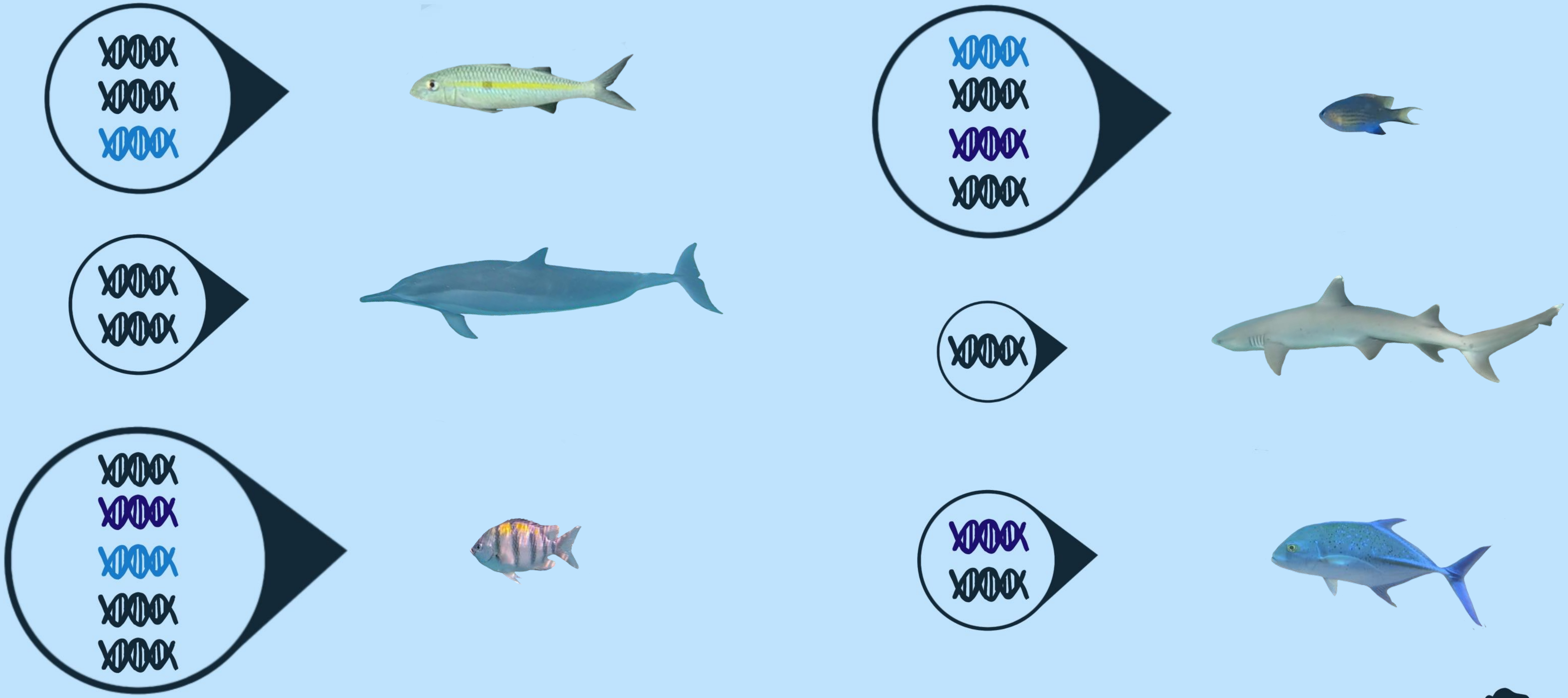
Population Genetics of Marine Species in Hawai‘i using eDNA



Species Detections

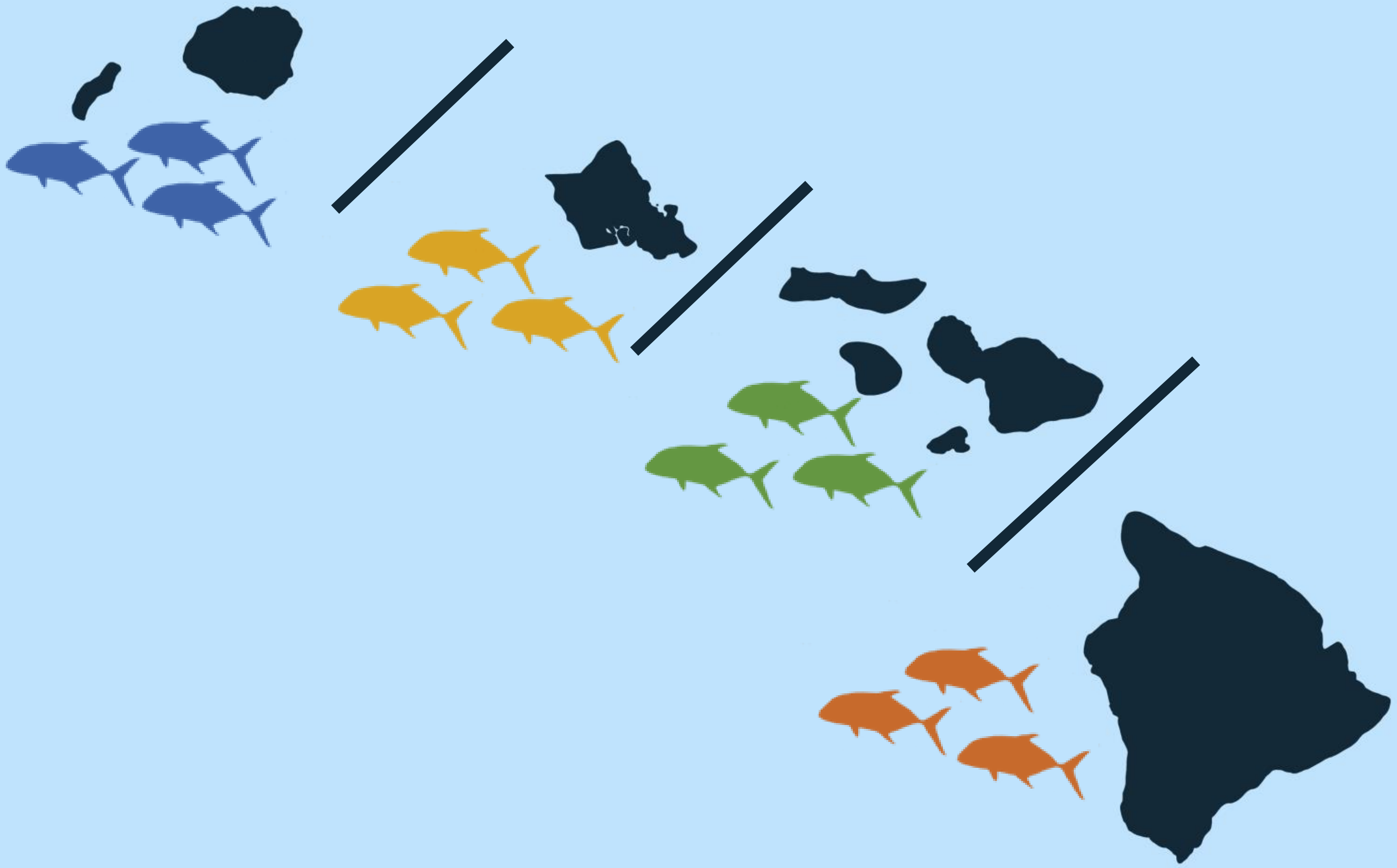


Intraspecific variation often ignored



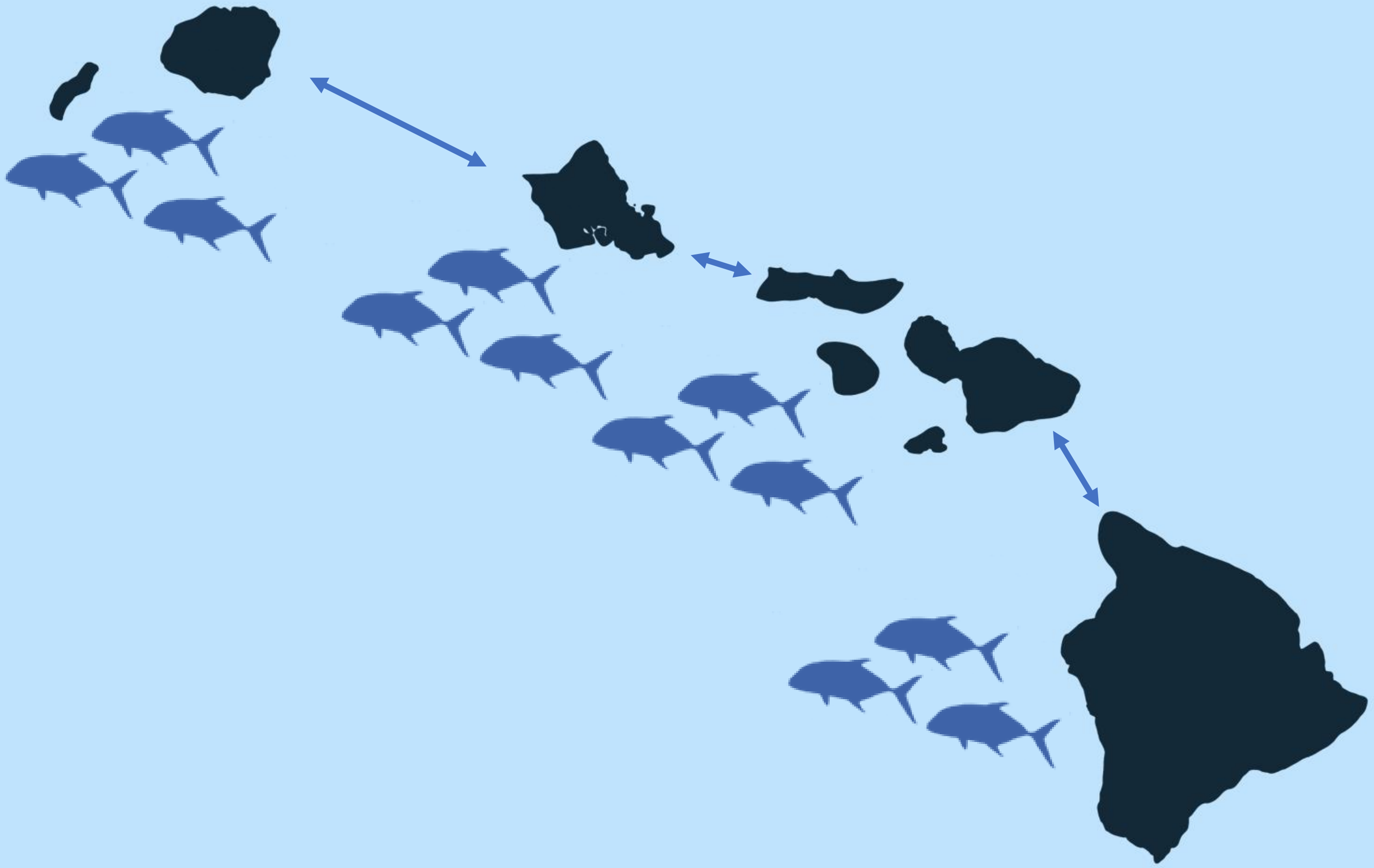
Intraspecific variation can reveal population structure

Separate Populations



or

All 1 population

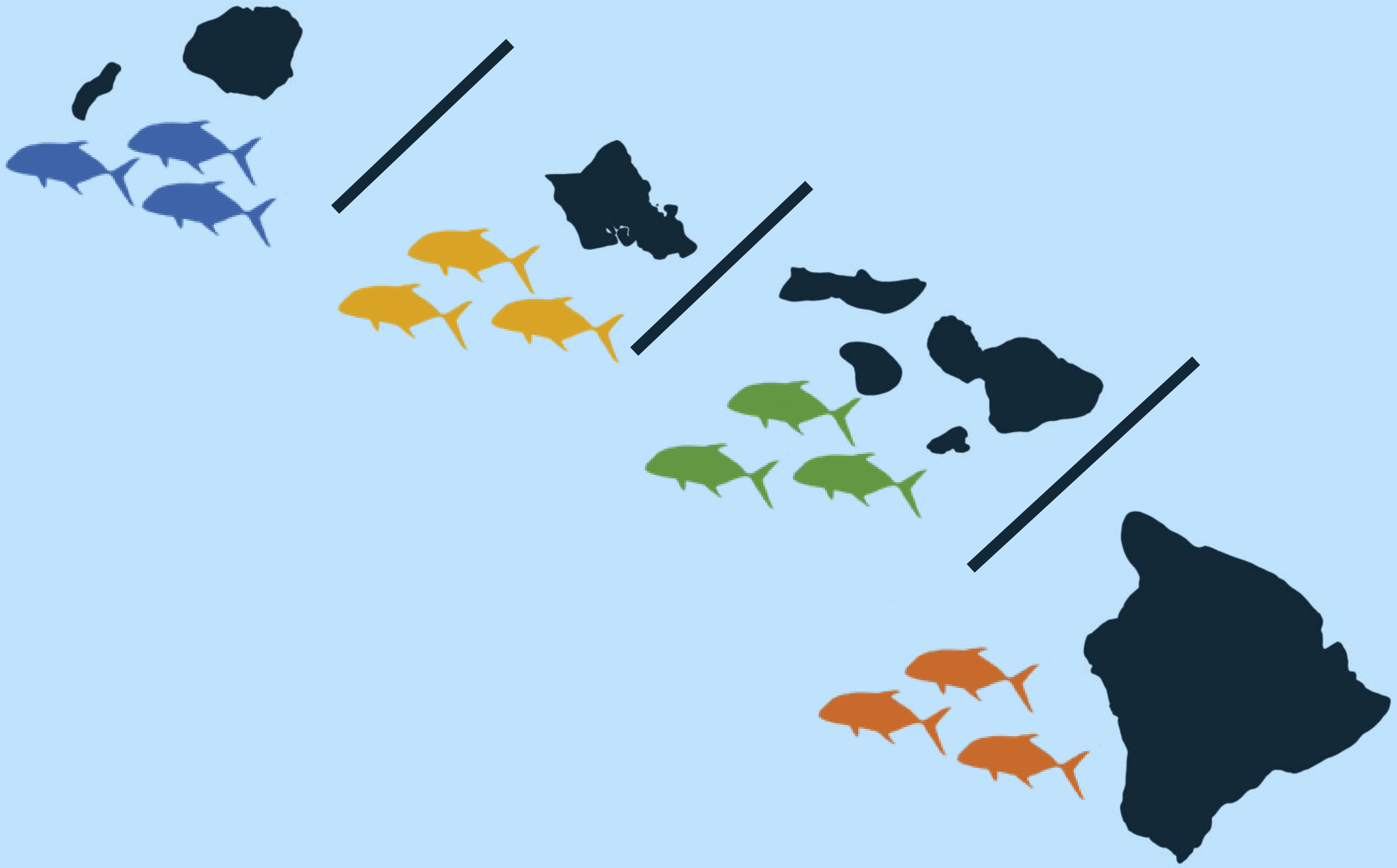


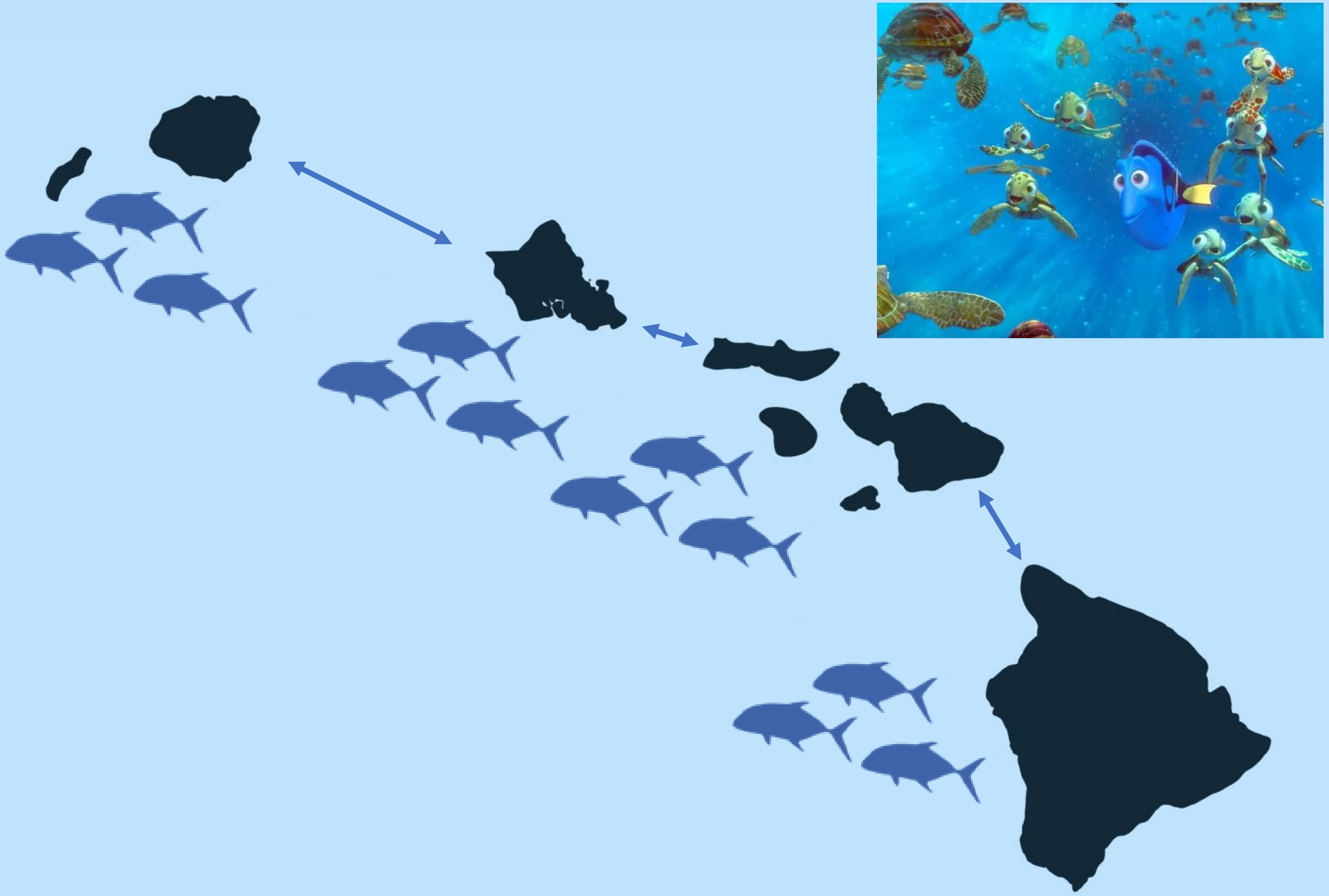
Intraspecific variation can reveal population structure

Separate Populations

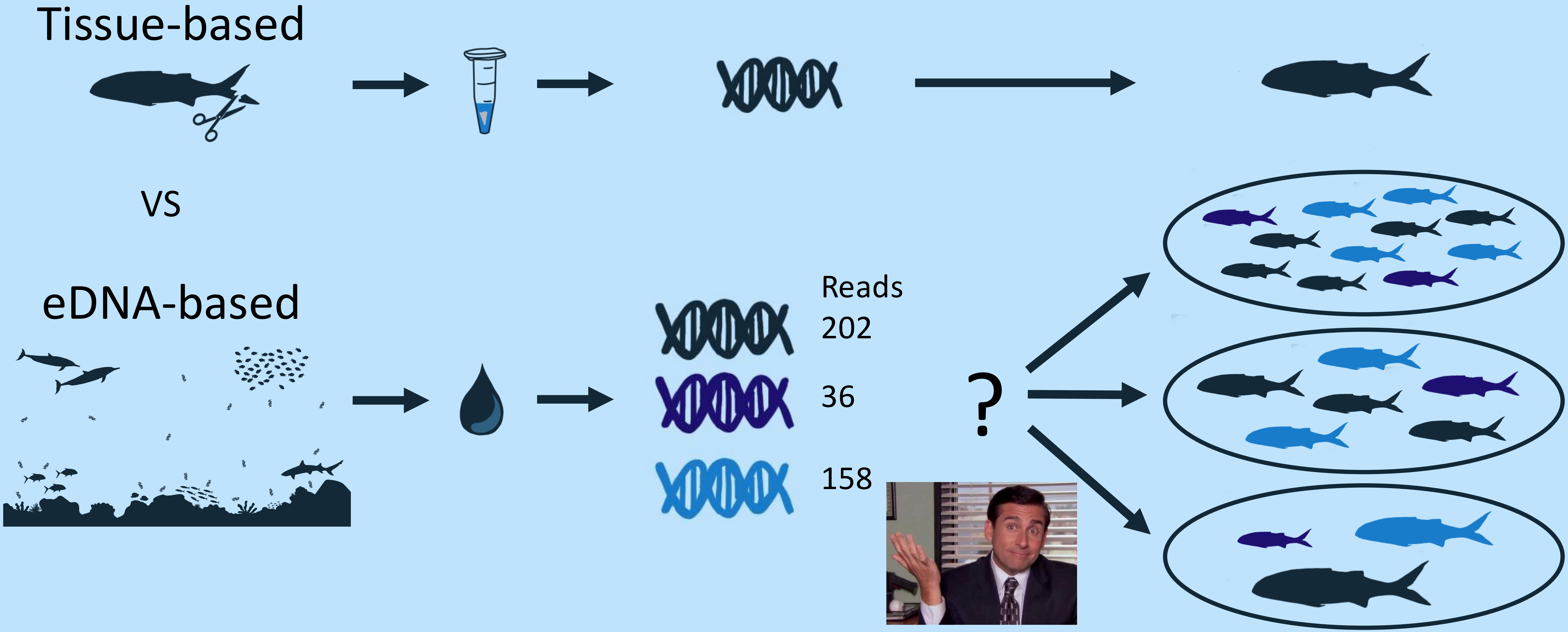
or

All 1 population





Problem with eDNA:
eDNA does not reveal no. of individuals



Tissue-based

vs

eDNA-based

Reads

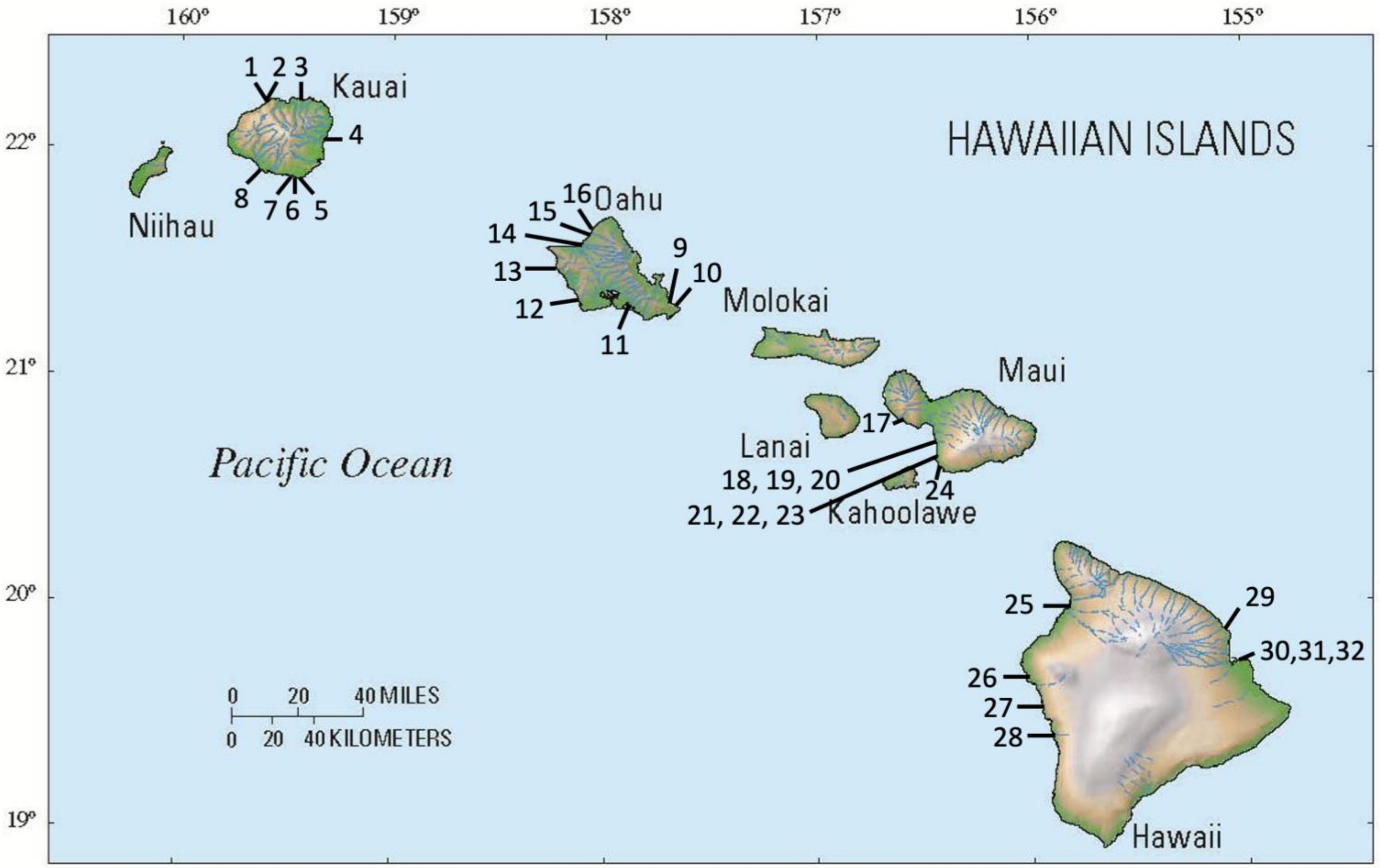
202

36

158

?

Comparing eDNA to Tissue



Per Site

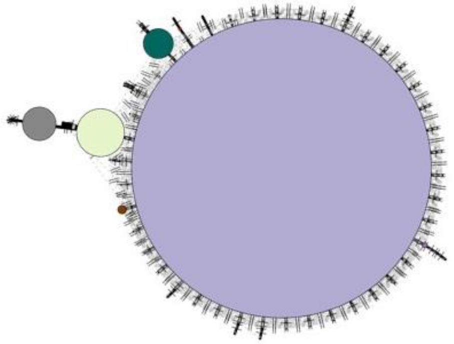
8 Sites Per Island

In Total: **64** Samples per Island

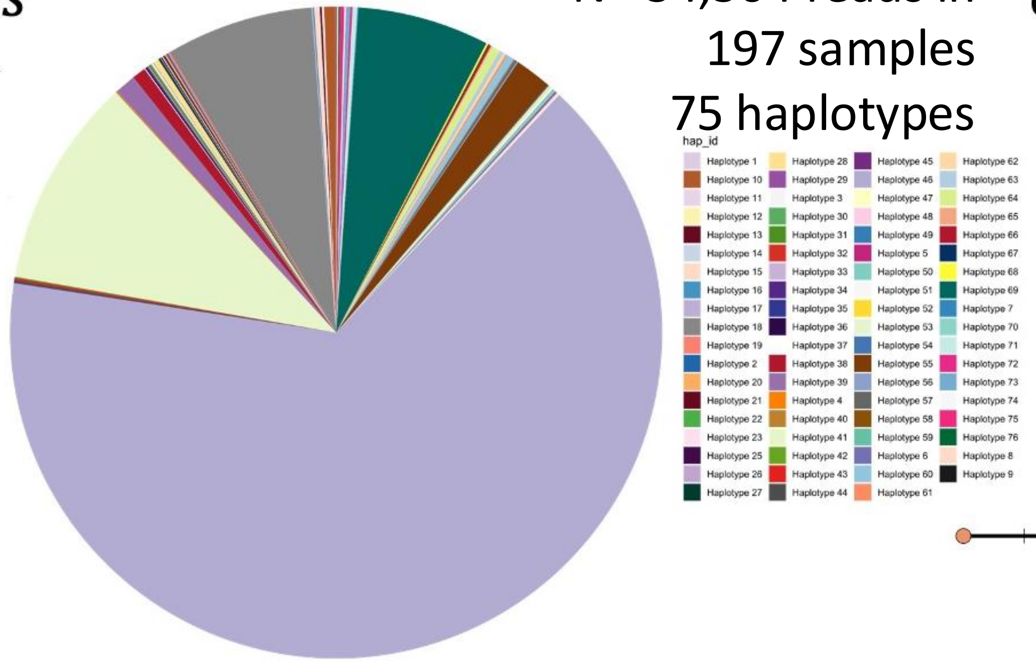
Haplotype Frequencies

Acanthurus nigrofuscus

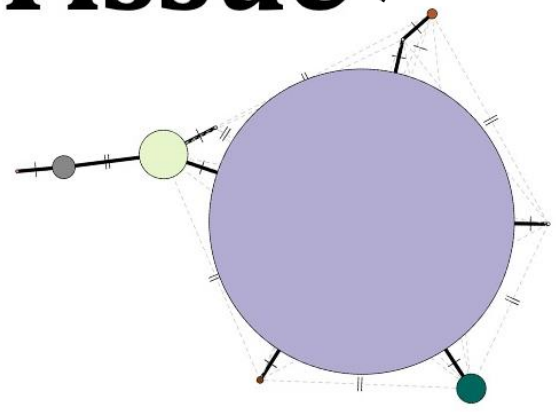
eDNA



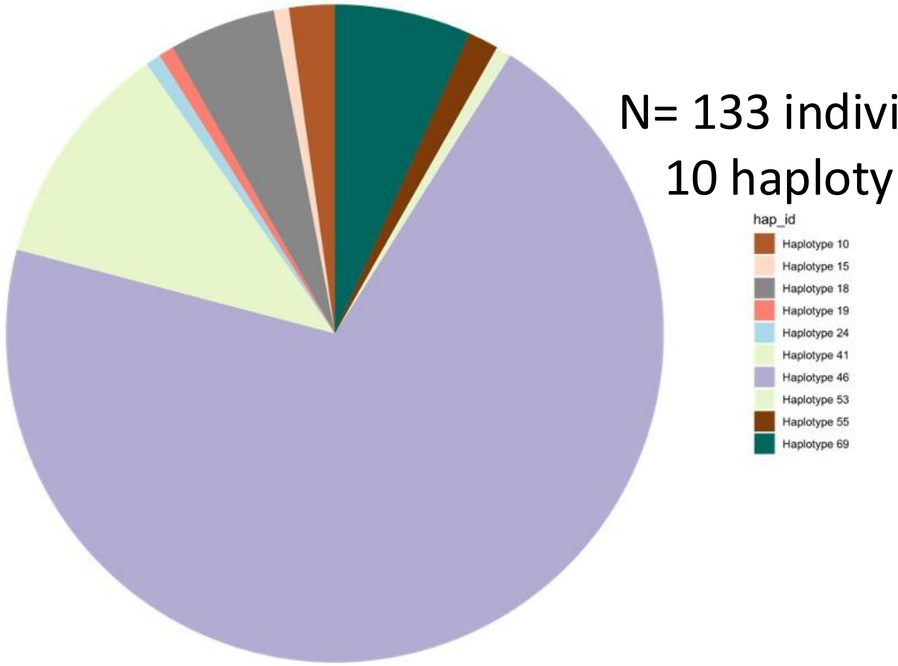
N= 34,504 reads in
197 samples
75 haplotypes



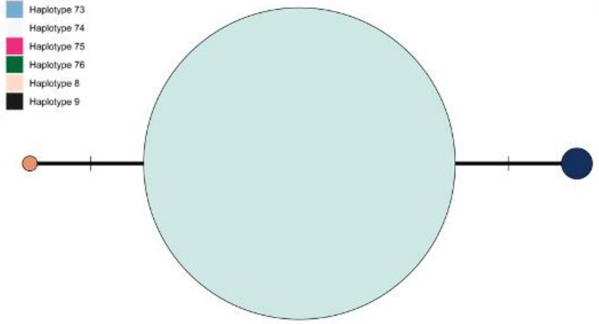
Tissue



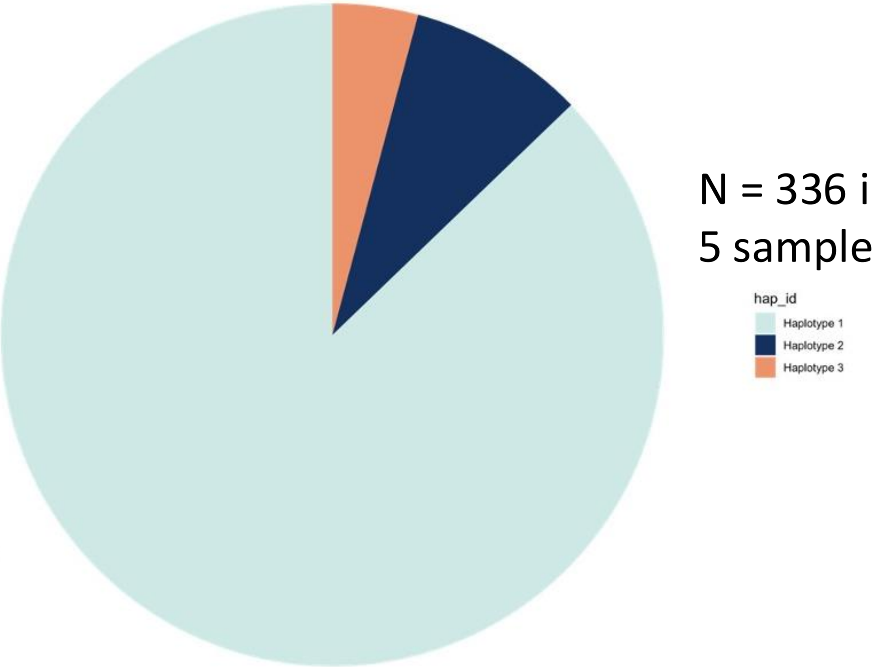
N= 133 individuals
10 haplotypes

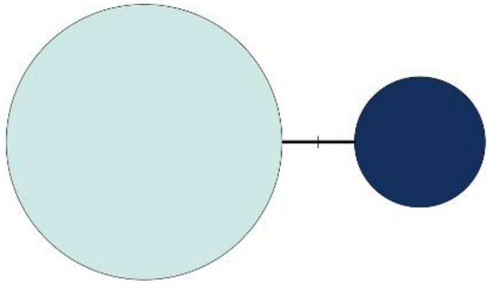


Chaetodon miliaris

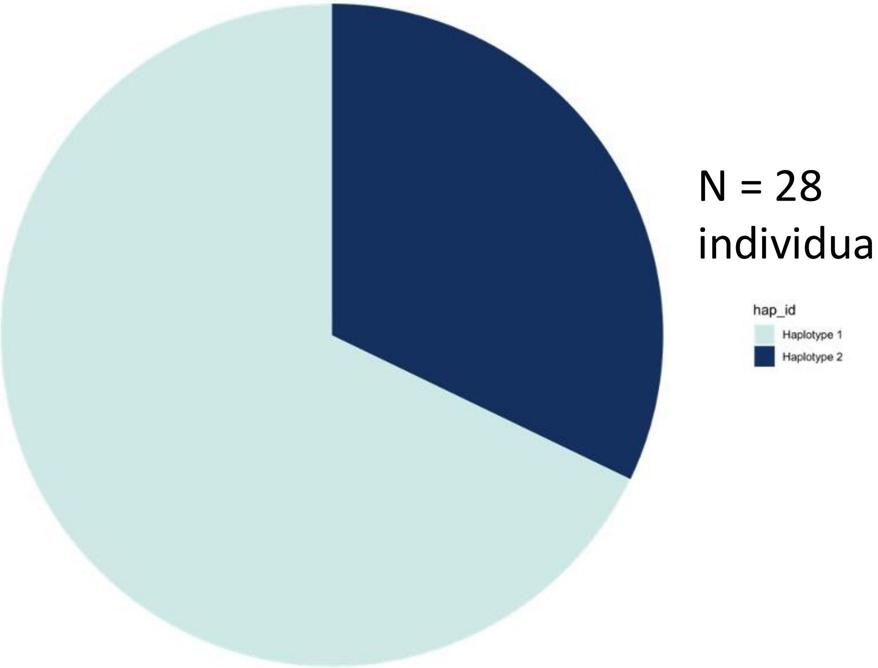


N = 336 in
5 samples

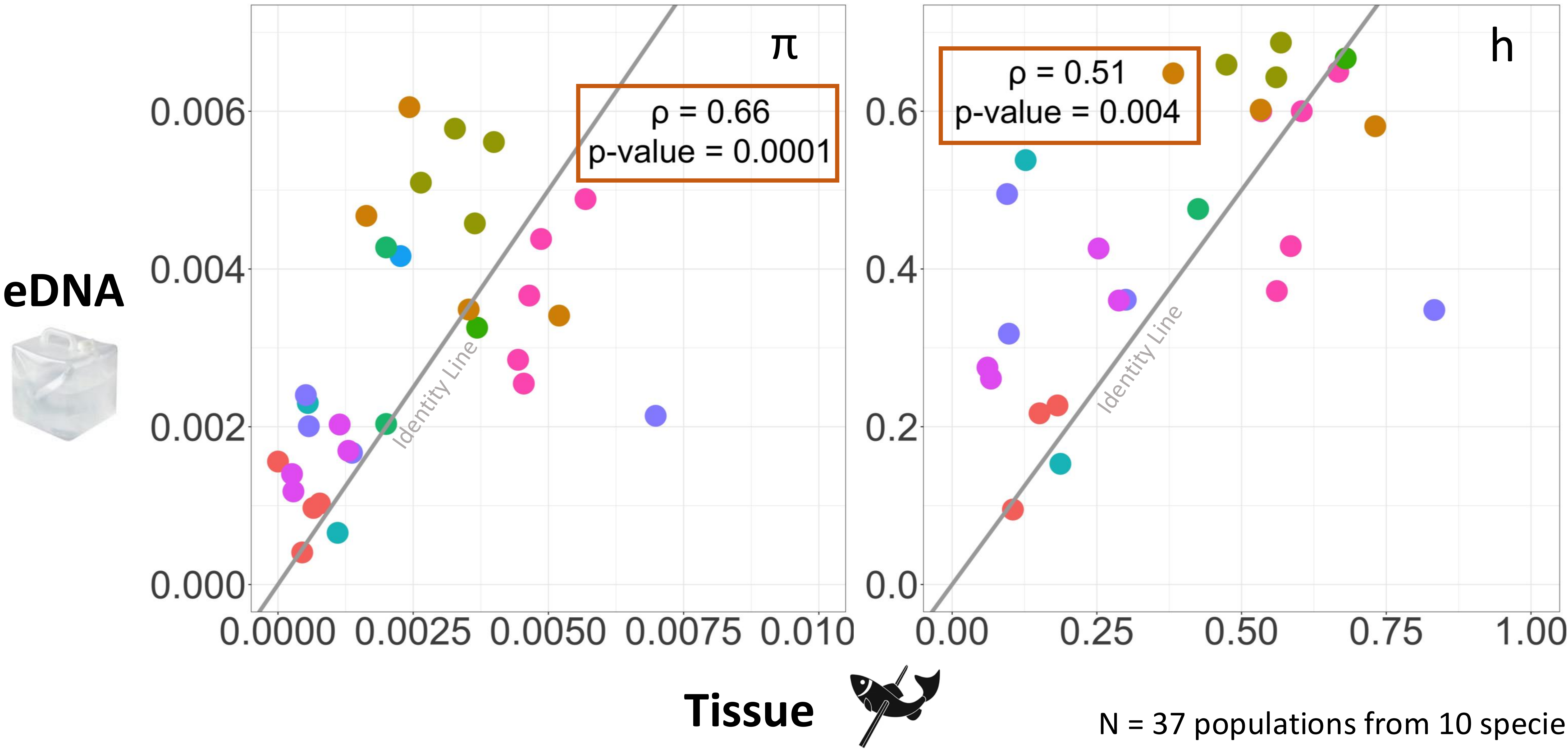




N = 28
individuals

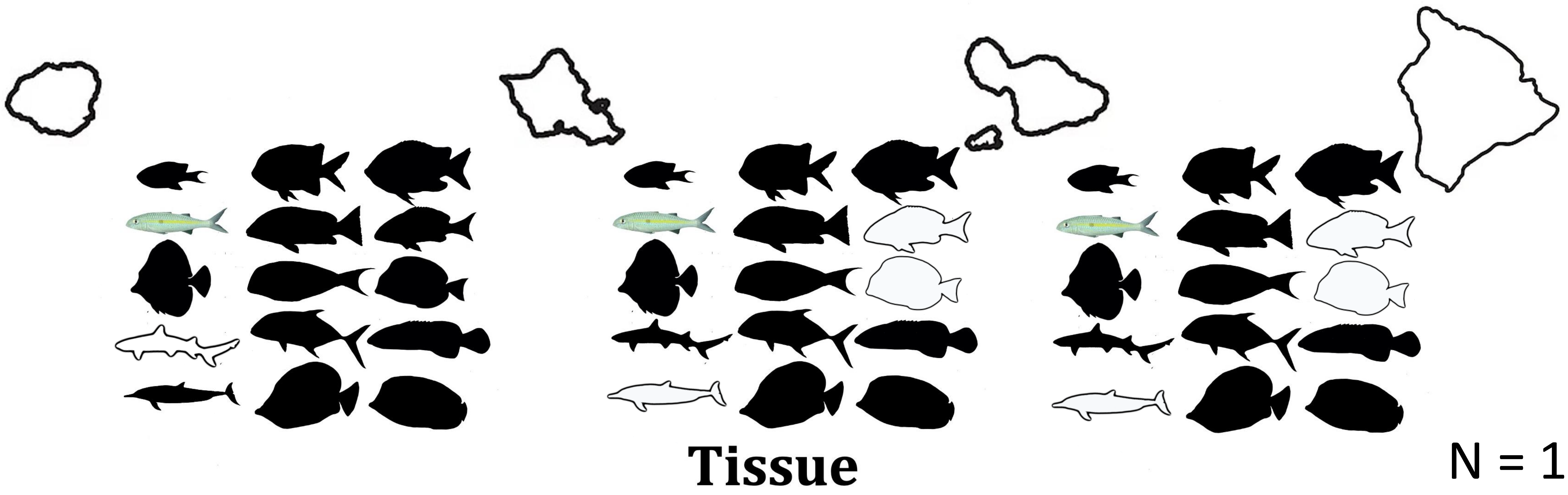


Genetic diversity is correlated



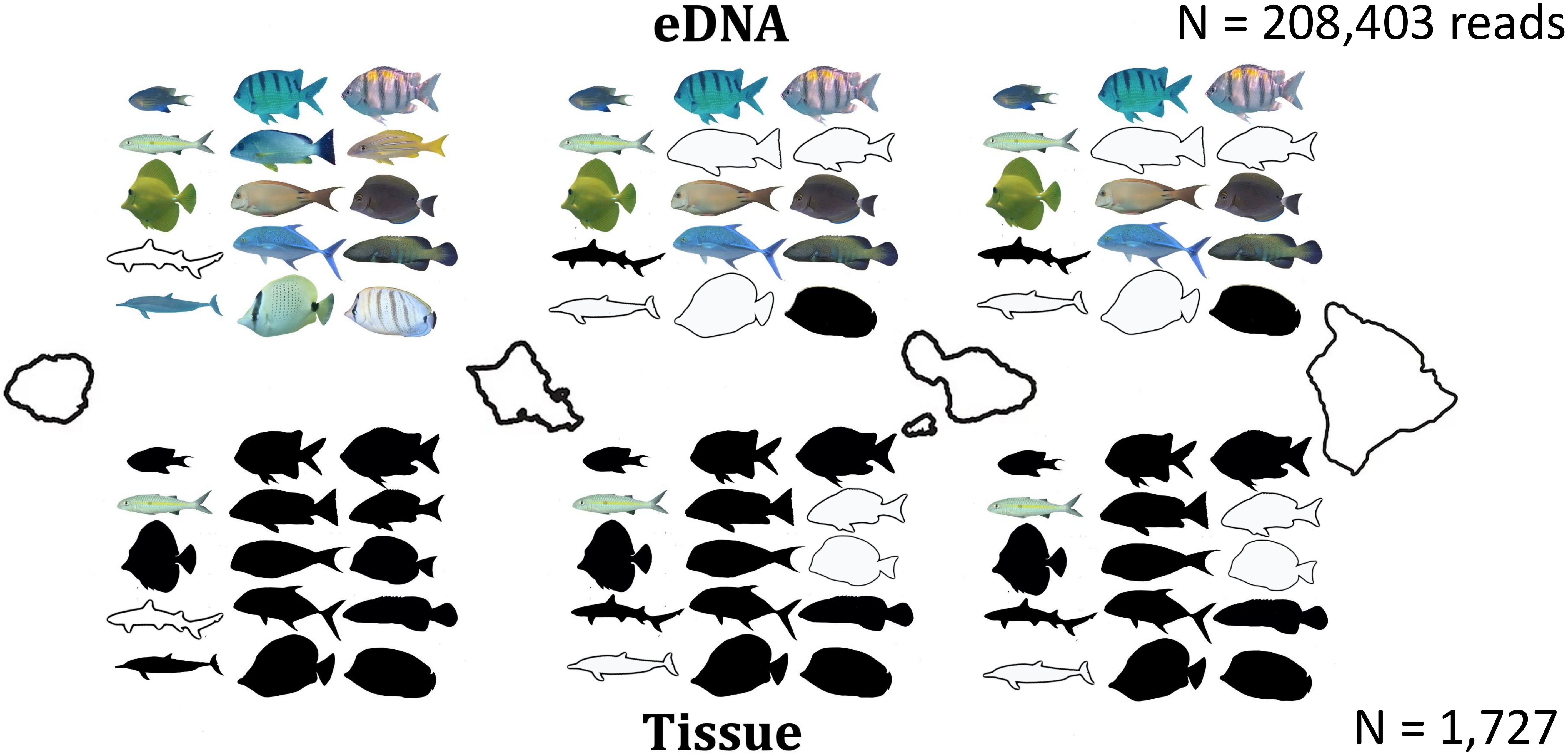
N = 37 populations from 10 species

Only 1 significant genetic break (Φ_{ST}) with tissue



N = 1,727

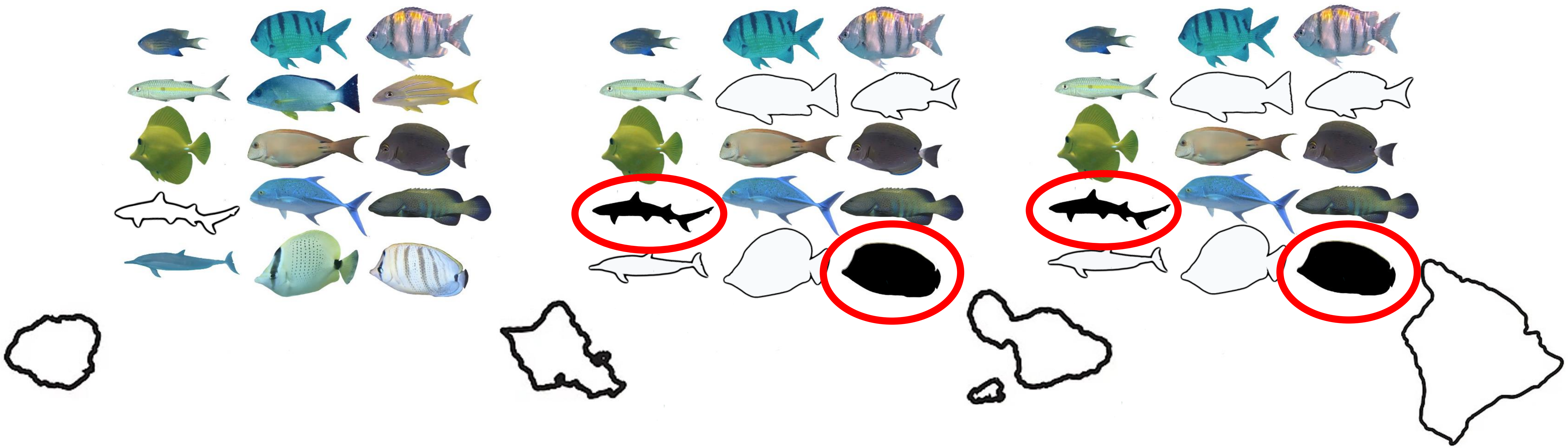
More significant genetic breaks (Φ_{ST}) with eDNA



Patterns of significant genetic breaks (Φ_{ST}) with eDNA

eDNA

N = 208,403 reads



Deepest and Widest Channel
116 km wide
3,400 m deep

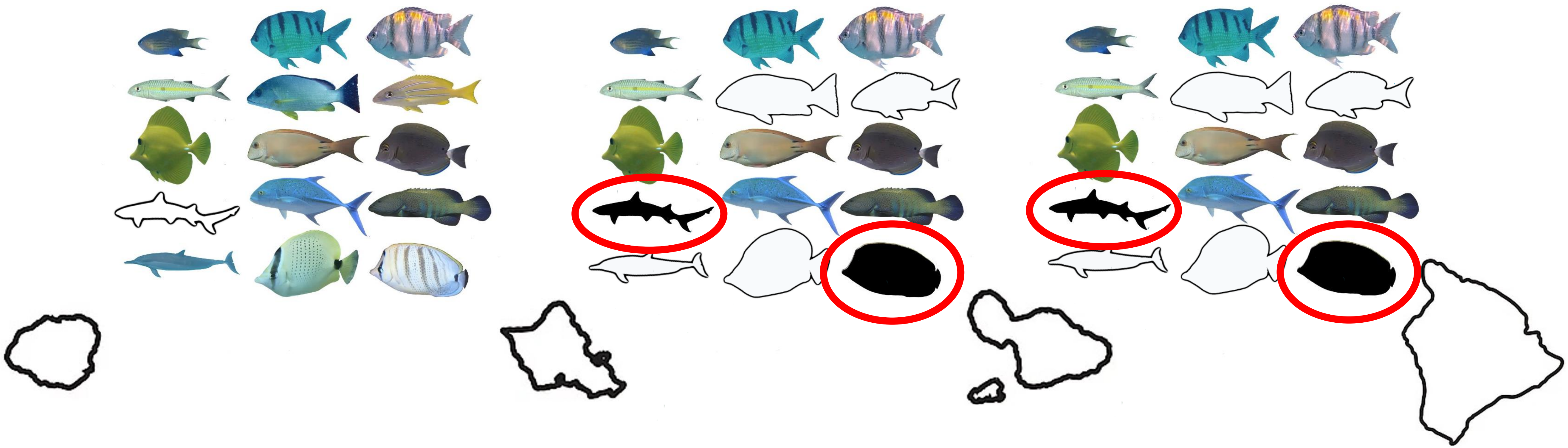
42 km wide
700 m deep

48 km wide
1,900 m deep

Patterns of significant genetic breaks (Φ_{ST}) with eDNA

eDNA

N = 208,403 reads



Is each island really a different population???

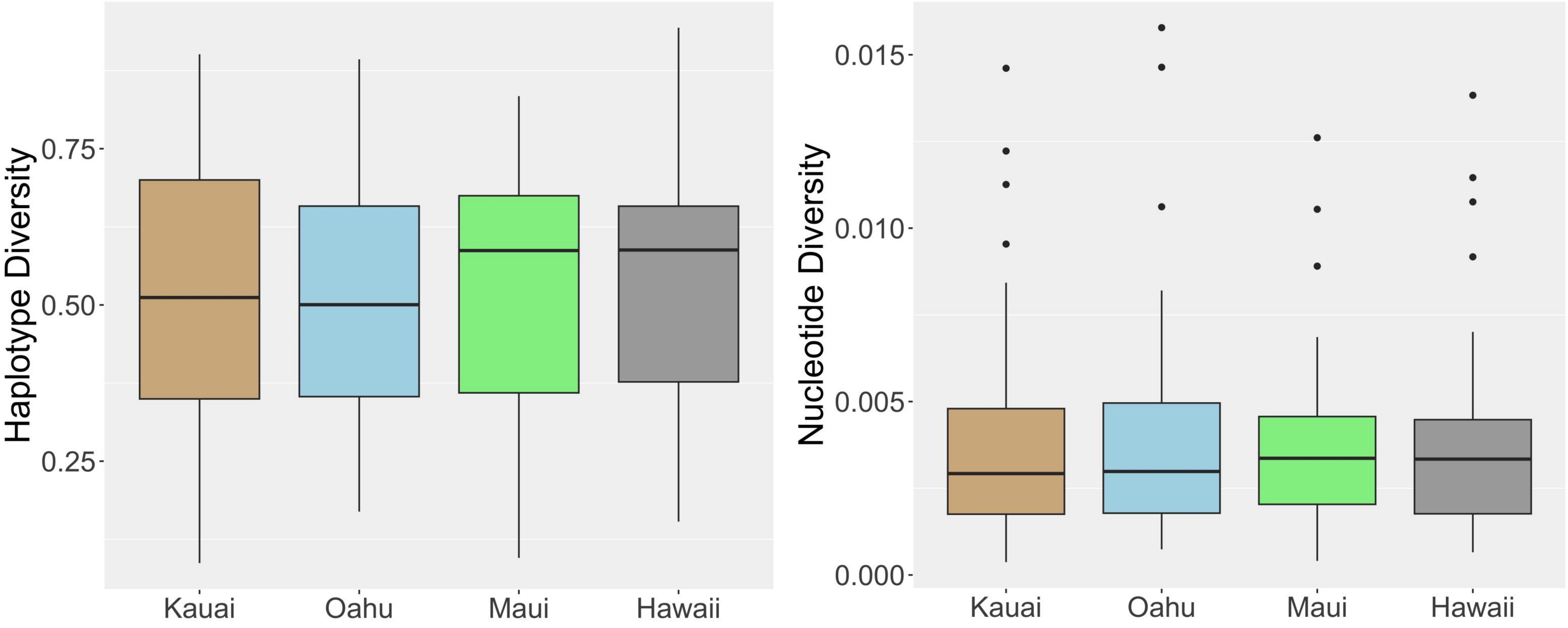
Total genetic diversity detected

155 marine taxa
- 4 classes
- 32 orders
- 46 families
- 80 genera
- 131 species level

No. Haplotypes Per Taxa

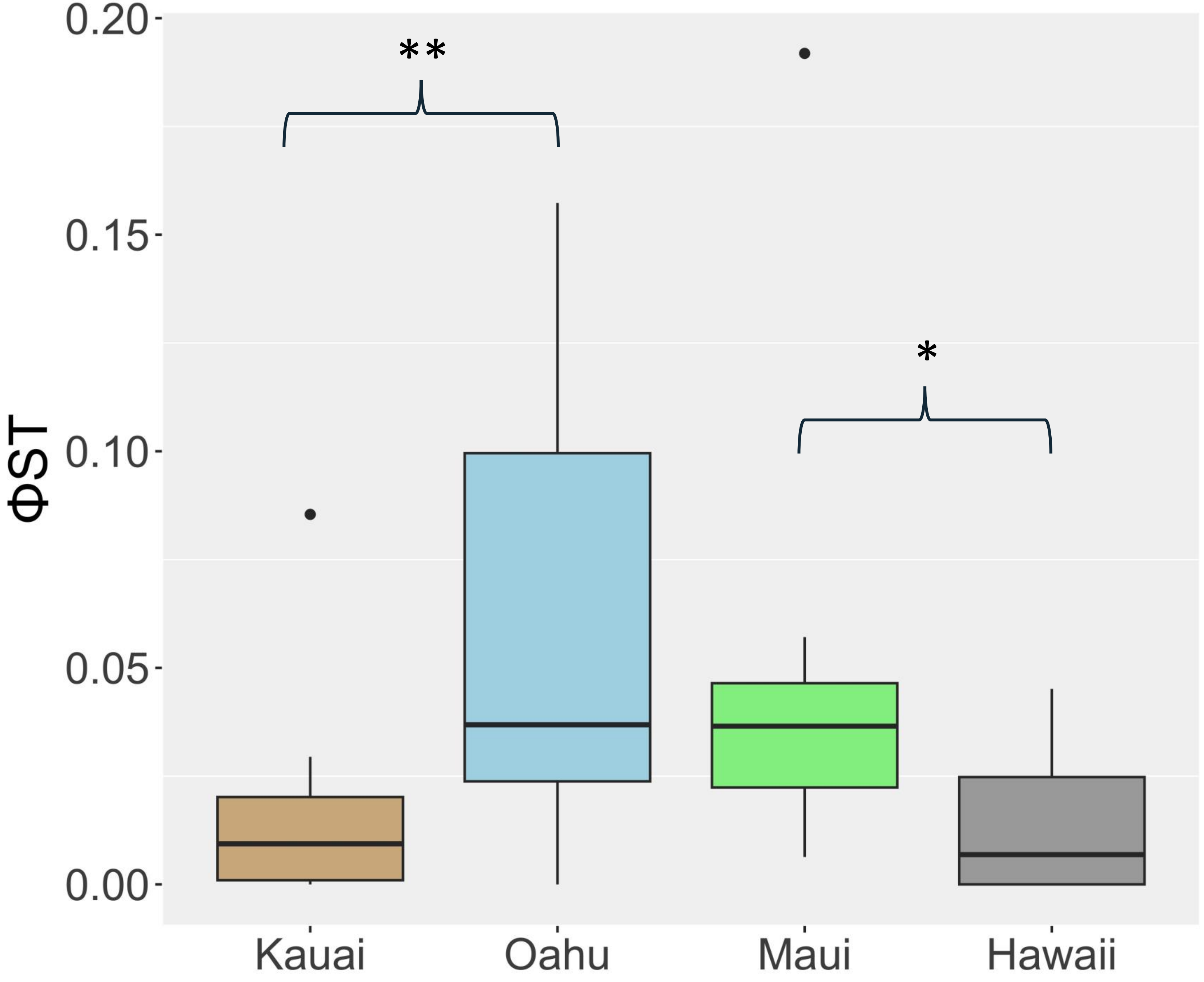
Mean ± SE	12 ± 1
Min	1
Max	150

No variation in genetic diversity across shared species



Paired t-test
79 Species

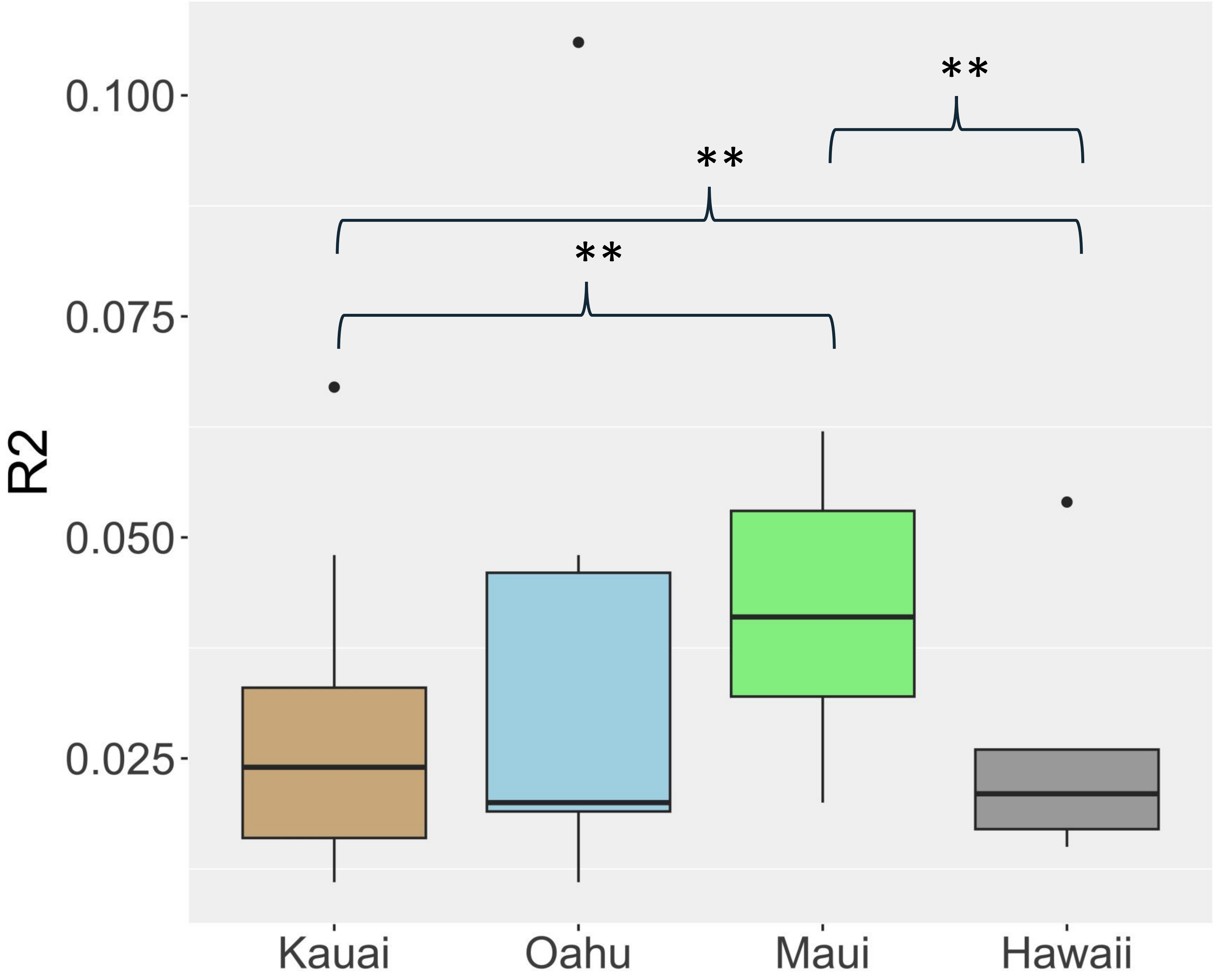
Genetic structure is greater for O‘ahu across shared species



Paired t-test
12-20 Species

* = p-value < 0.05
** = significant after FDR correction

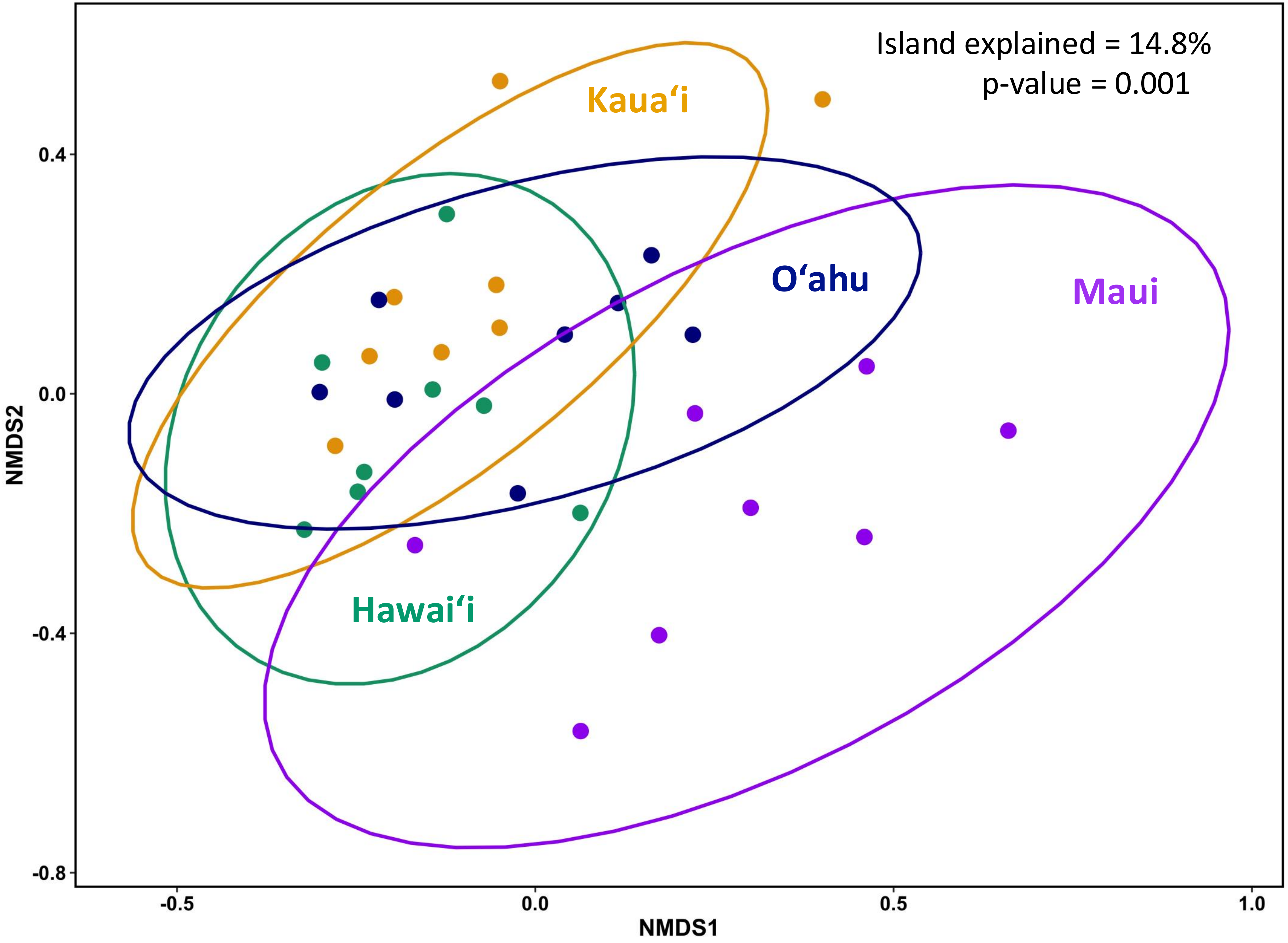
Demographic history at each island varies across species



Paired t-test
12-20 Species

* = p-value < 0.05
** = significant after FDR correction

Relative abundance of haplotypes of all taxa



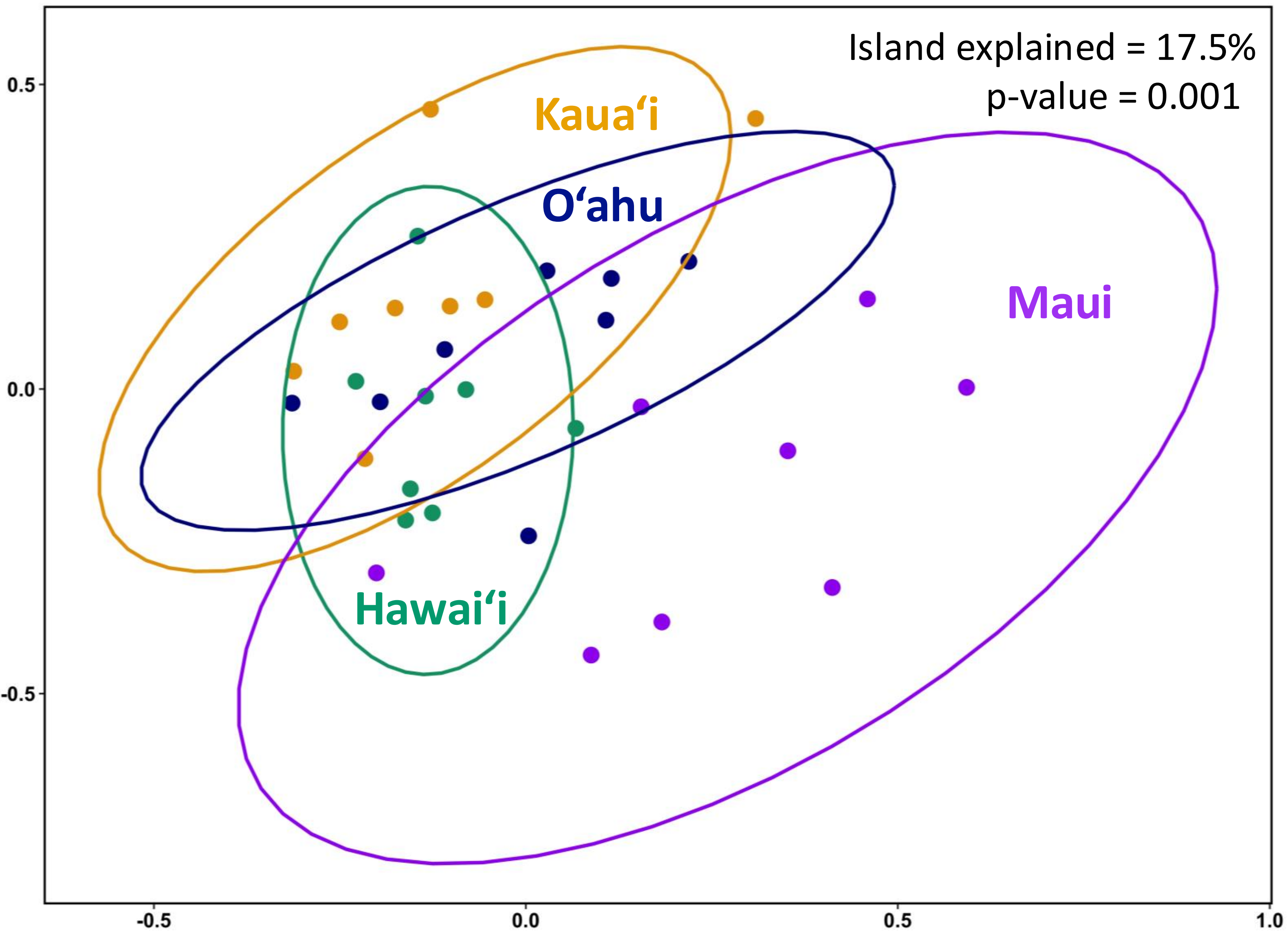
Unique Haplotypes

Hawai‘i	652
Kaua‘i	531
O‘ahu	506
Maui	323

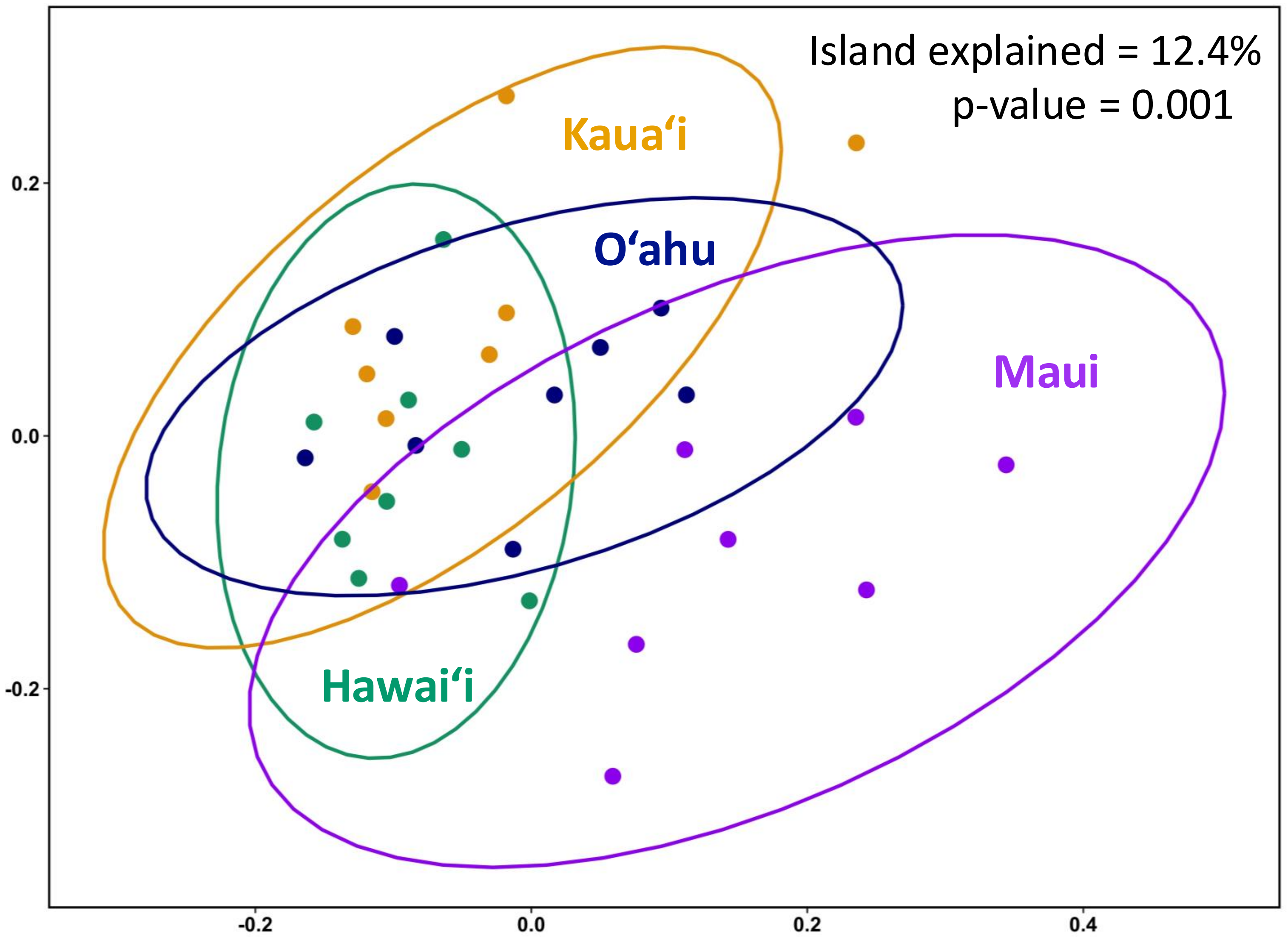
155 Taxa
2,507 Unique Sequences
NMDS
Bray-Curtis Distances
PERMANOVA

Betadisp p-value = 0.03

Haplotypes of shared taxa



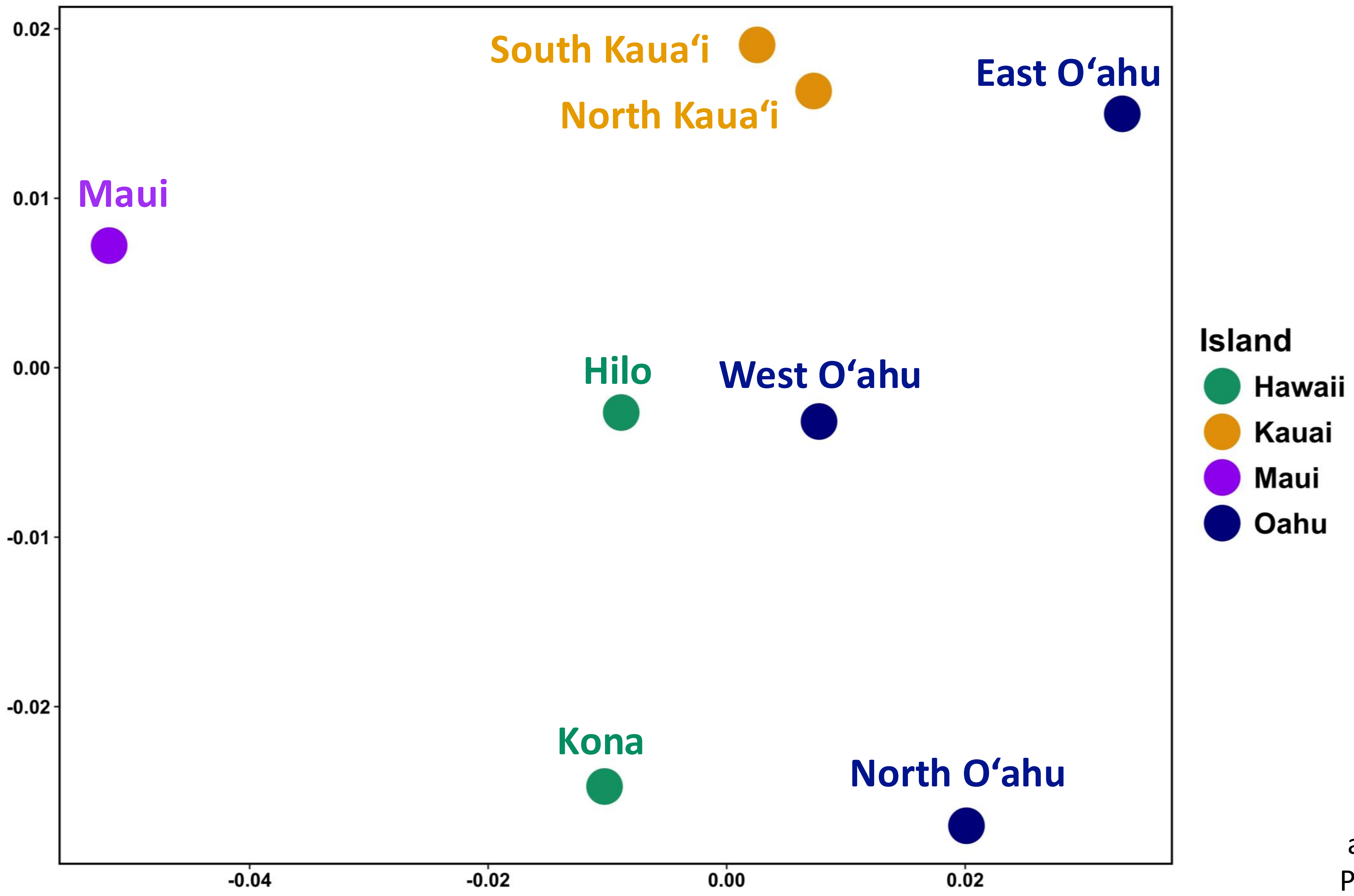
Relative abundance
Bray-Curtis



Presence Absence
Jaccard

79 Species, 2,094 Unique Sequences
NMDS, PERMANOVA

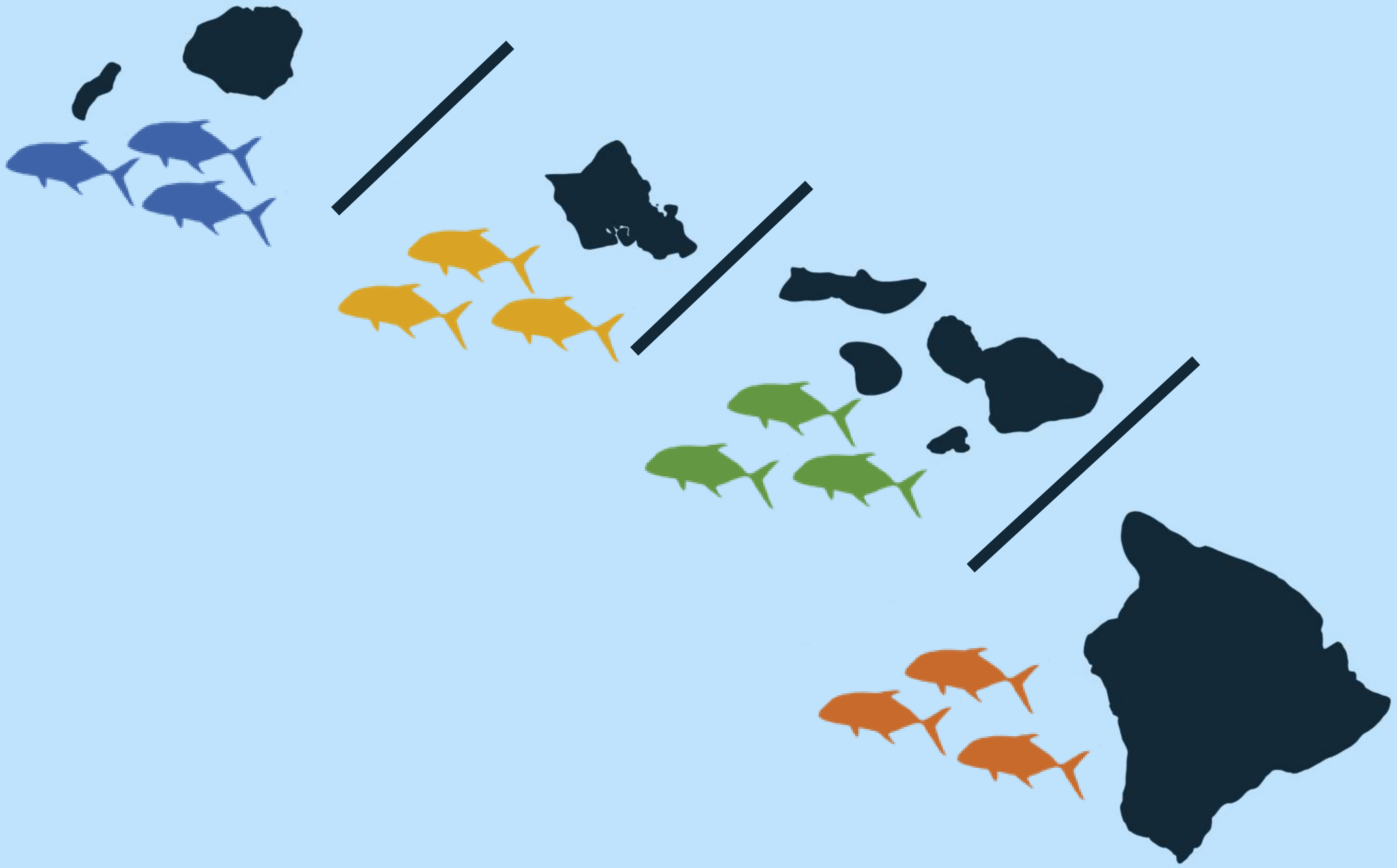
Average pairwise Φ_{ST} different by region and island across shared taxa



8 Species
NMDS
average pairwise Φ_{ST}
PERMANOVA, not sig.

eDNA works for population genetics but statistical power is unknown

Separate Populations

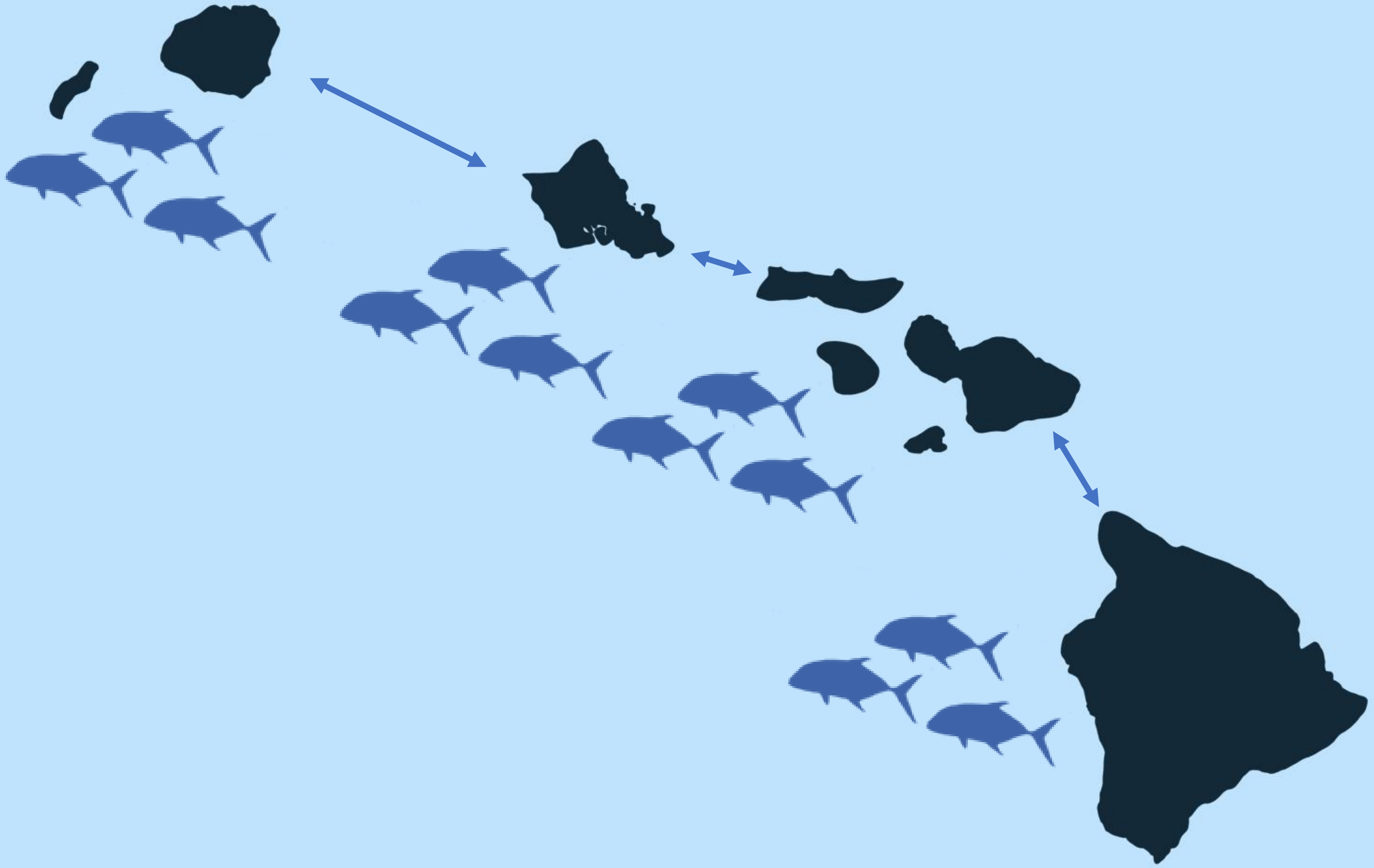


Support:

Φ_{ST}, R2, NMDS

or

All 1 population



Support:

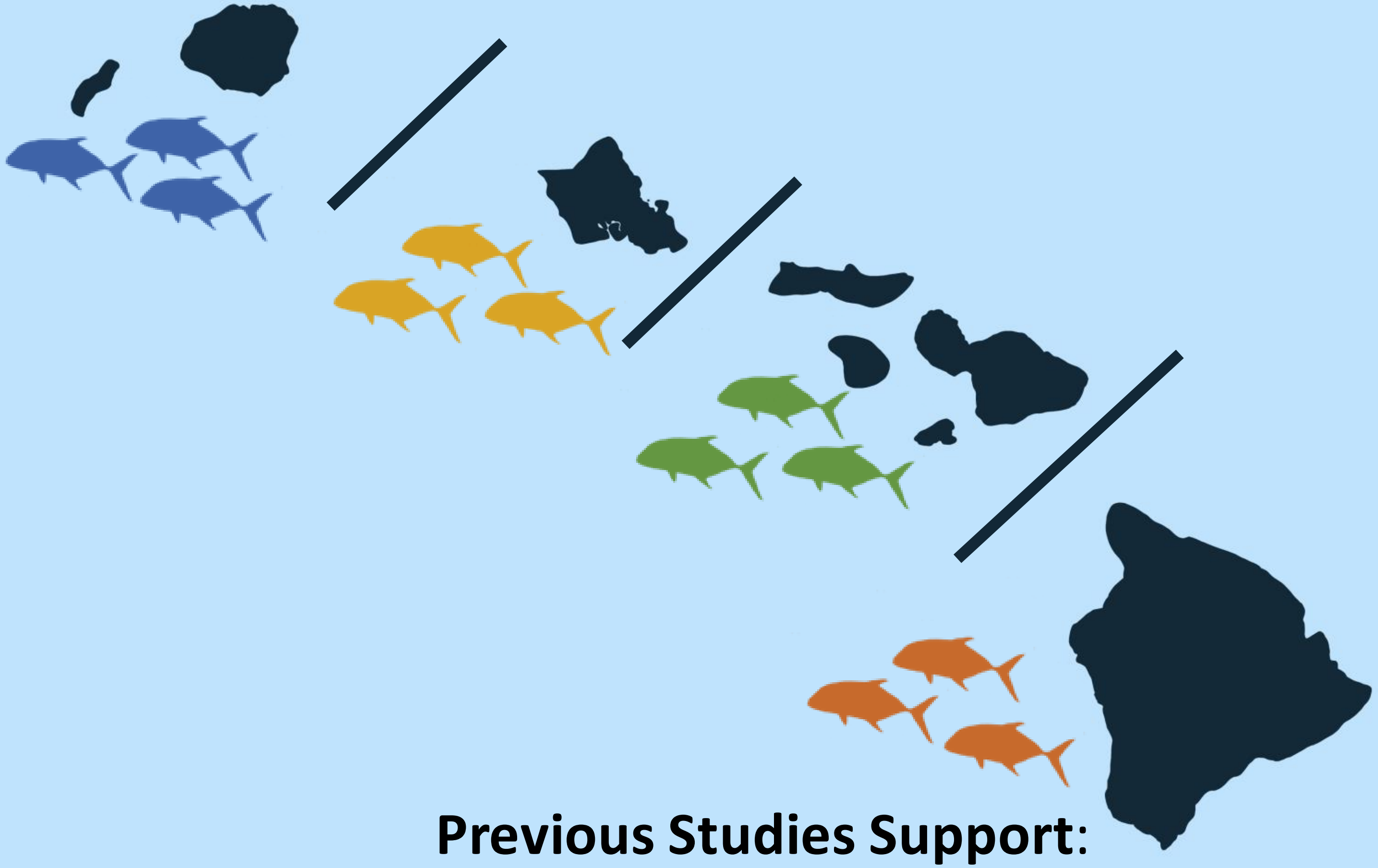
h, π

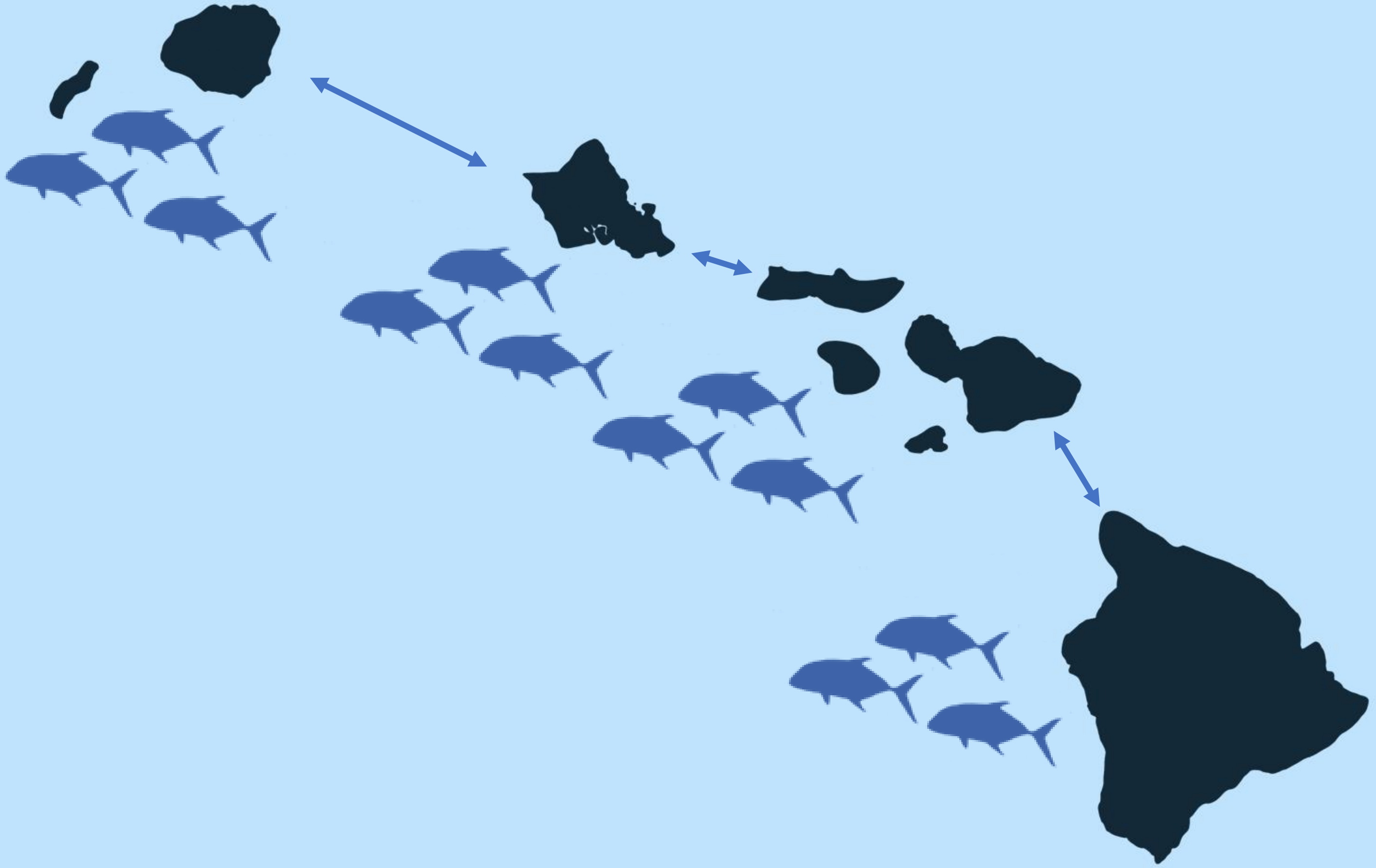
eDNA works for population genetics but statistical power is unknown

Separate Populations

or

All 1 population





Previous Studies Support:

Pairwise Φ_{ST} of invertebrates (Toonen et al. 2011),
Demographics of Cephalopholis argus (Donovan et al. 2013),
Tagging of Caranx ignobilis (Meyer et al. 2007)

Previous Studies Support:

Pairwise Φ_{ST} of fish (Toonen et al. 2011),
Size differences of some fish (Nadon et al. 2015)

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1907

Questions?