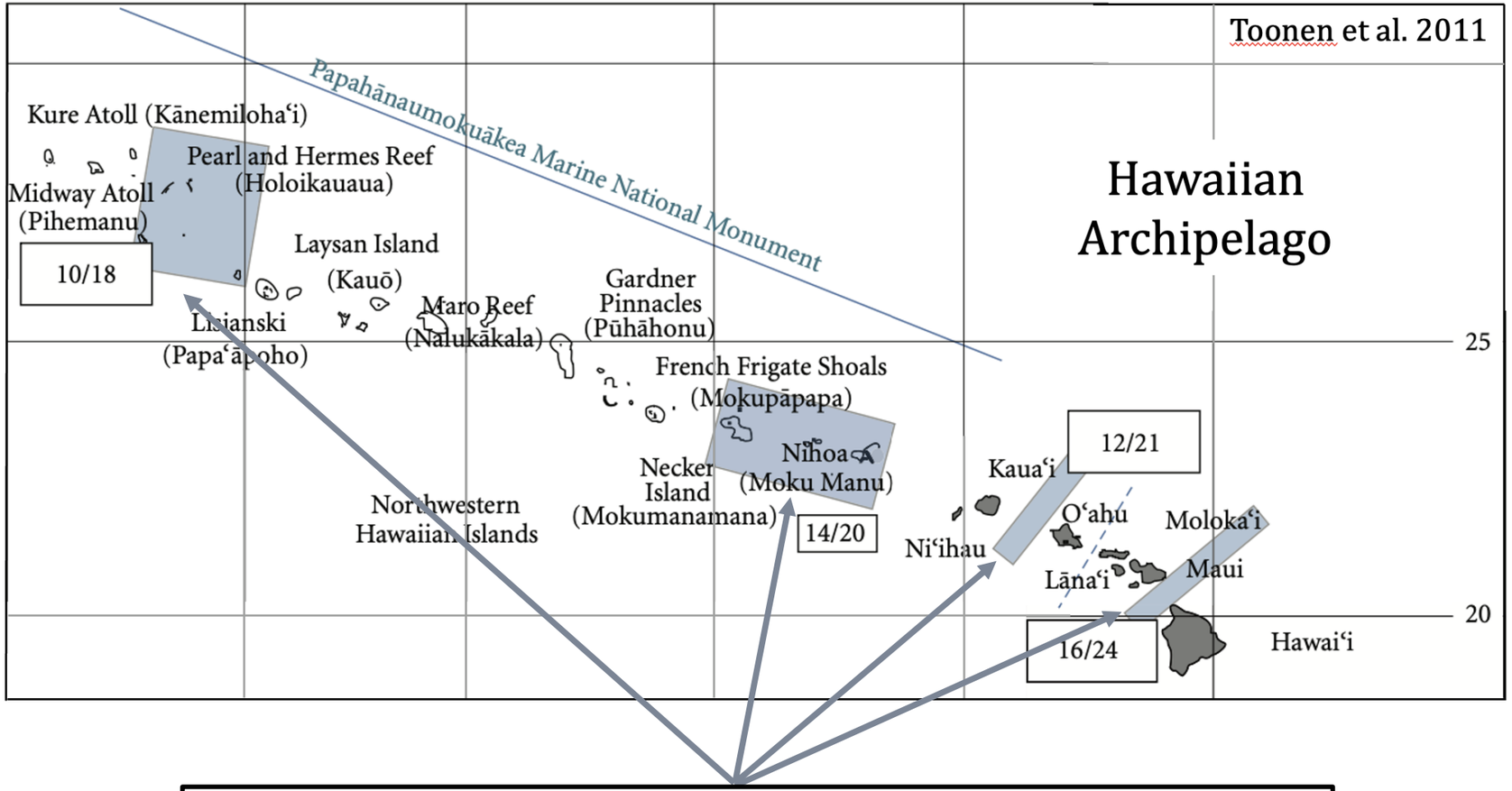
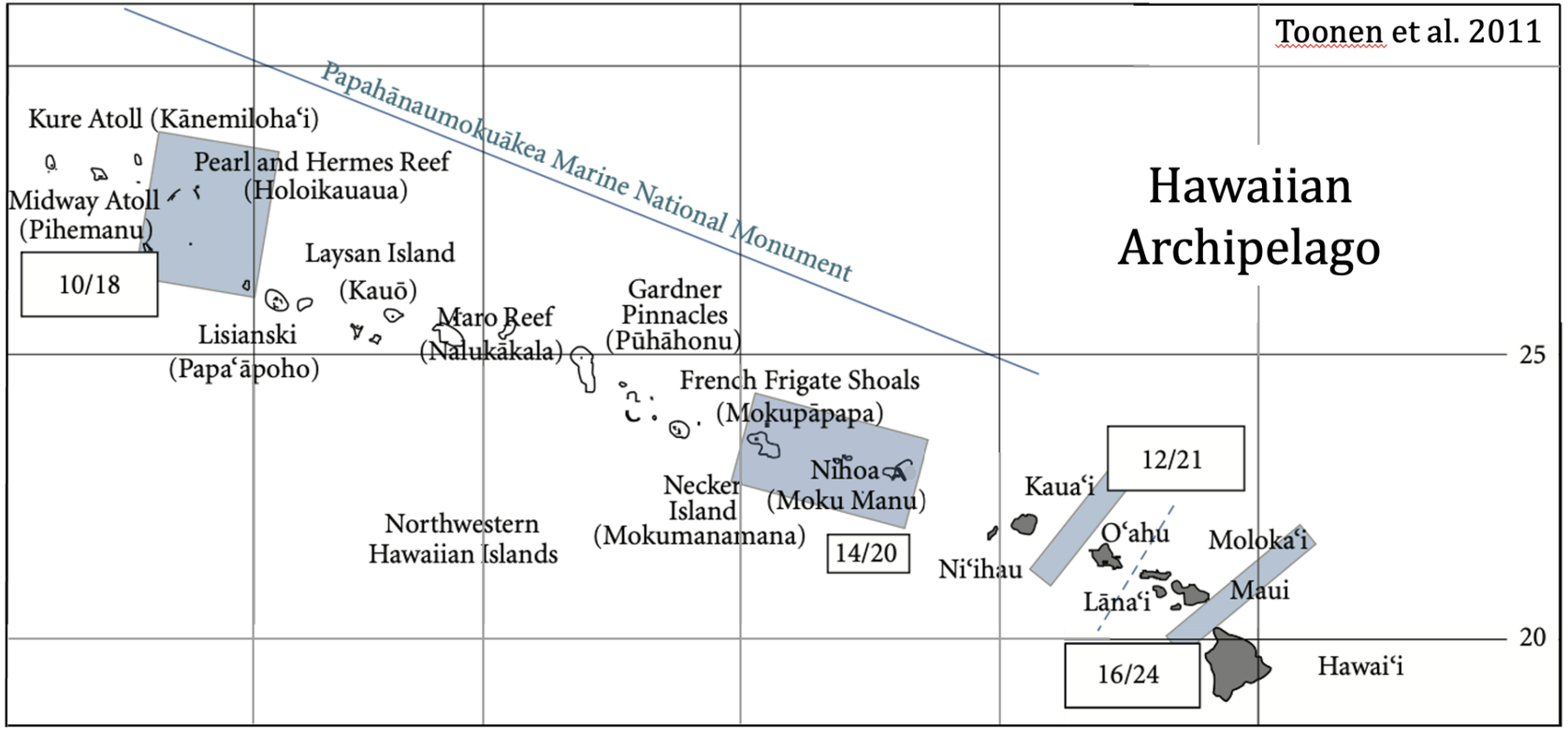
Analysis of eDNA as a community genetics tool

Comparative Population Genetics



4 significant population genetics breaks

Comparative Population Genetics



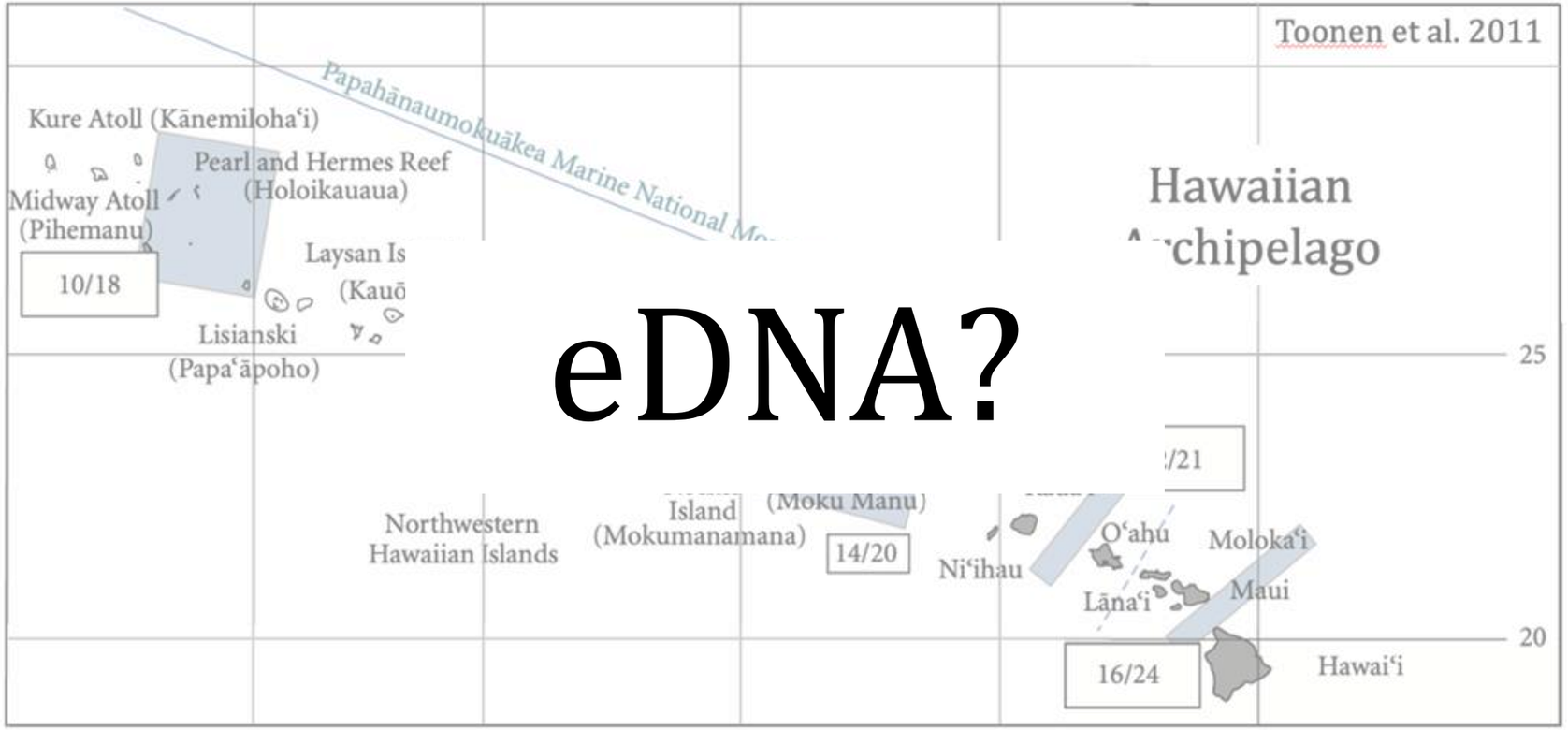
27 Species:

Find and take tissue sample of 9,416 ind.

Permits

15 graduate students' theses

Comparative Population Genetics



eDNA?

27 Species:

Find and take tissue sample of 9,416 ind.

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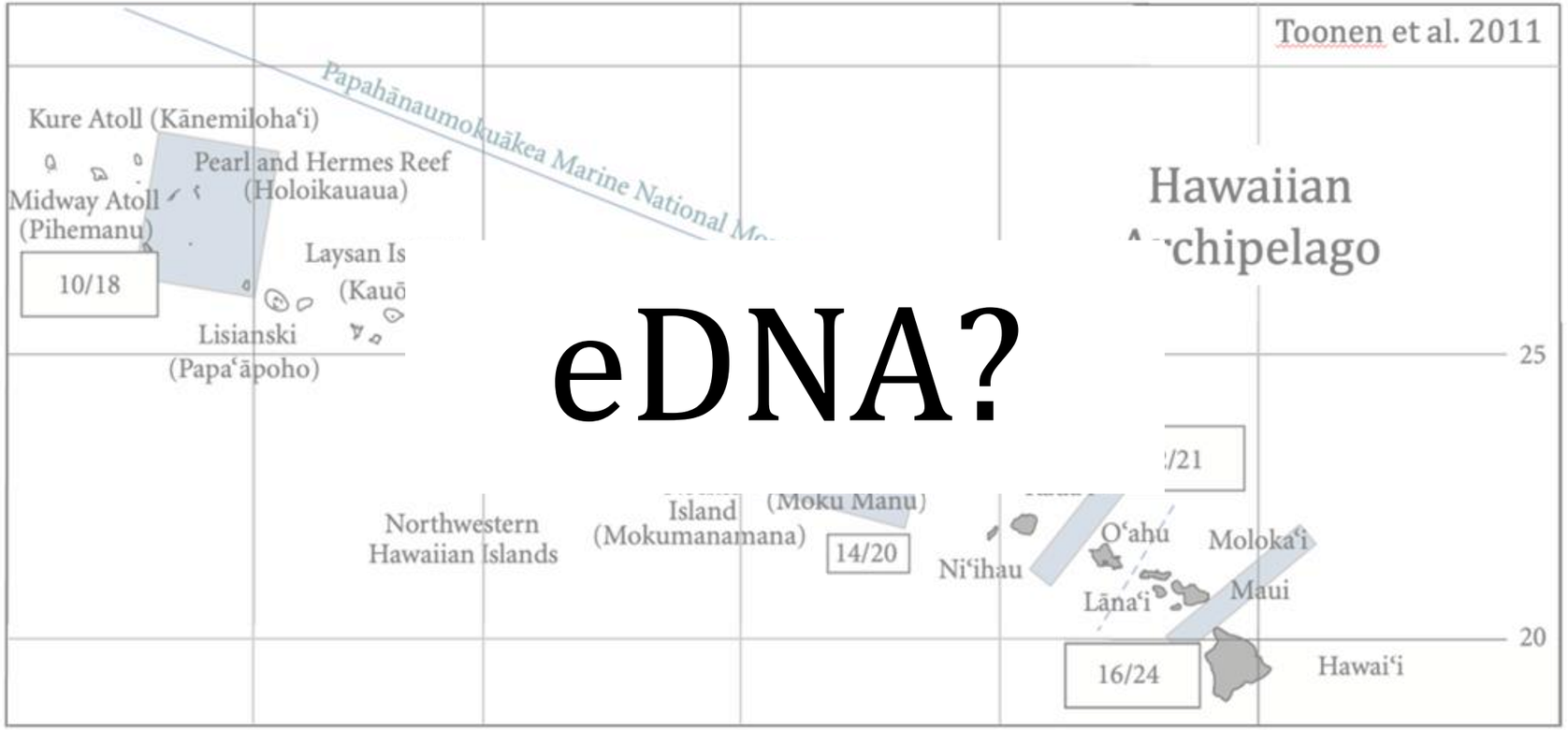
Comparative Population Genetics



eDNA?

100s Species:

Find and take tissue sample of 9,416 ind.

Permits

1 graduate student's thesis

Problem with eDNA:
Unknown Haplotype Frequencies

Individual Sample

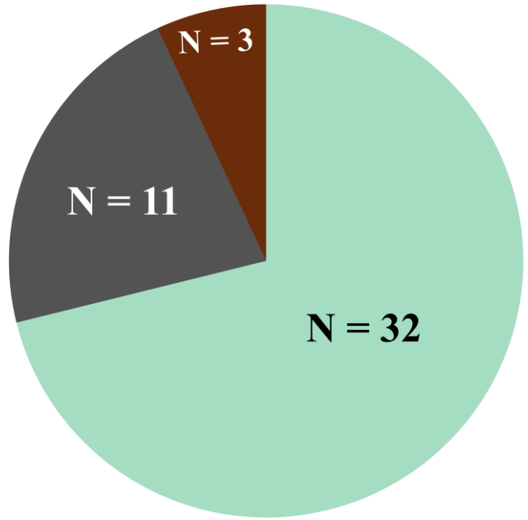
Tissue Sampled

→ Individual 1: TCA GAC ATT GCC ACG GCC …

→ Individual 2: TCA GAC ATT GCC ACG GCC …

→

Number of Individuals



Environmental Sample

Water Sample

→

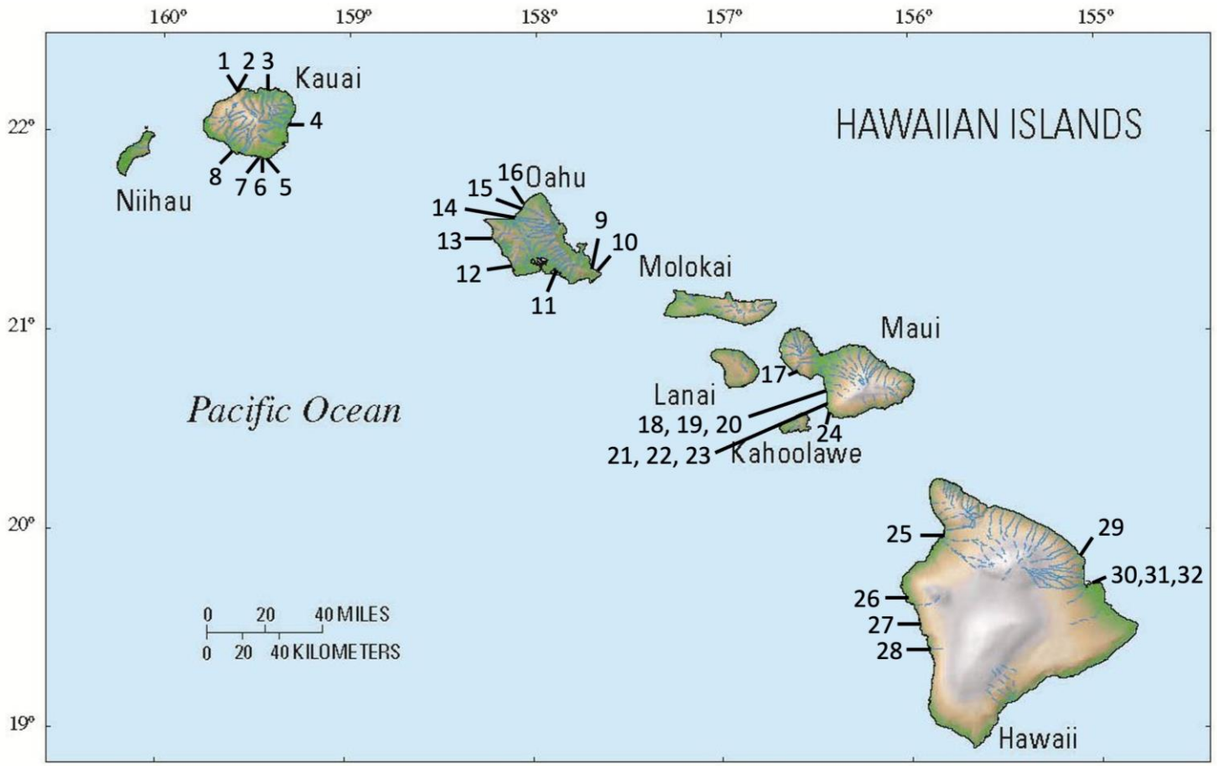
Sequence	Reads
TCA GAC ATT GCC ACG GCC …	201
TCA GAC ATT GCC ACG GCC …	30
TCA GAC ATT GCC ACG GCC …	105
TCA GAC ATT GCC ACG GCC …	74

? →

Number of Individuals

Or

eDNA vs Tissue



Per Site

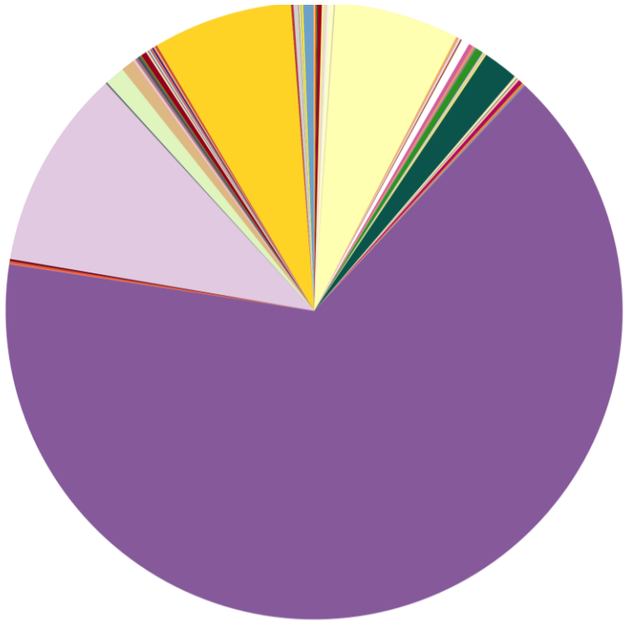
8 Sites Per Island

In Total: **64** Samples per Island

Haplotype Frequencies

Acanthurus nigrofuscus

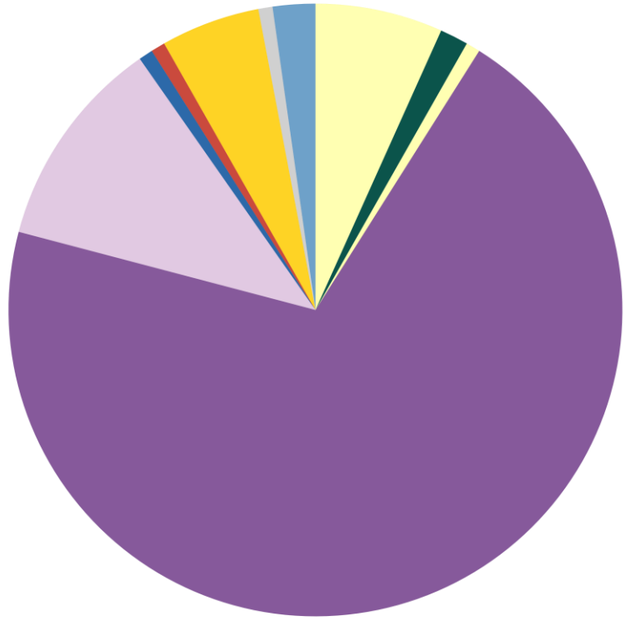
eDNA



75 haplotypes

N= 34,504 reads

Tissue



10 haplotypes

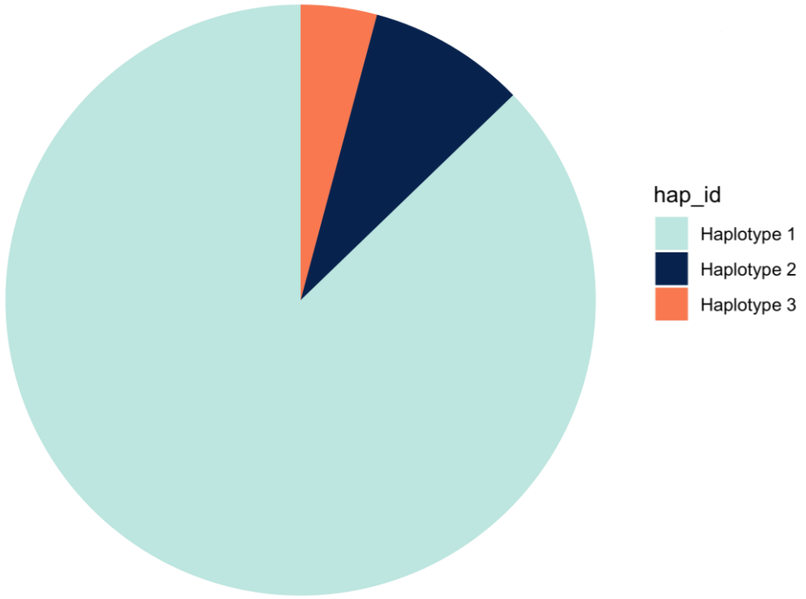
N= 133 individuals

Detected in 197 water samples

Haplotype Frequencies

Chaetodon miliaris

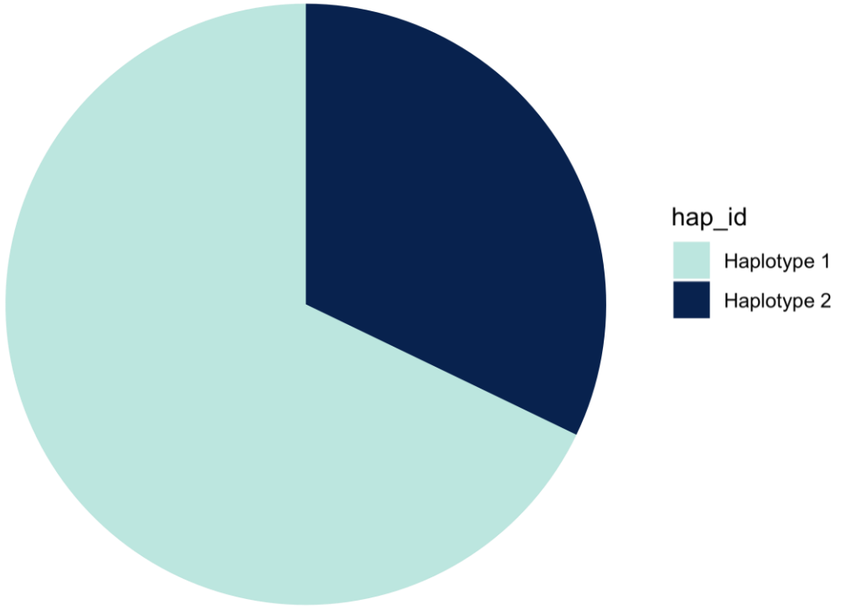
eDNA



N= 336 reads

Detected in 5 water samples

Tissue

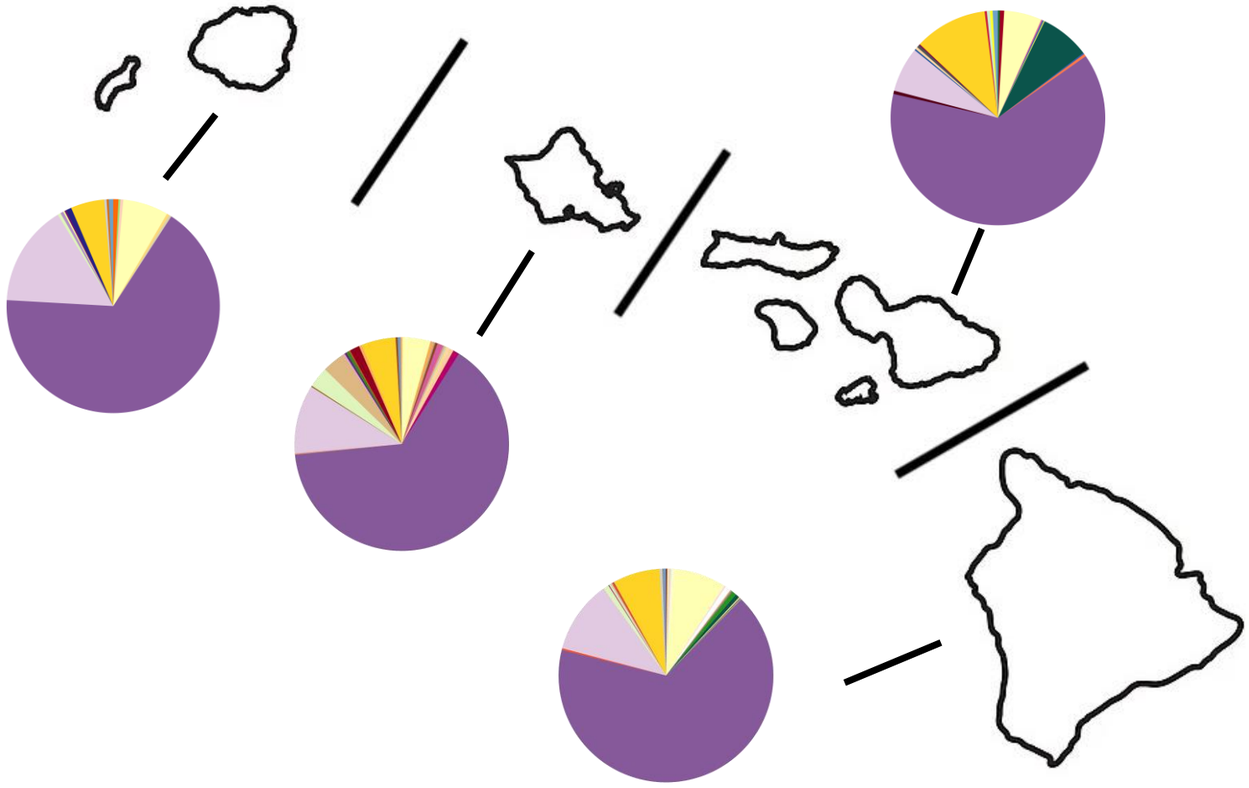


N= 28 individuals

Haplotype Frequencies

Acanthurus nigrofuscus

eDNA

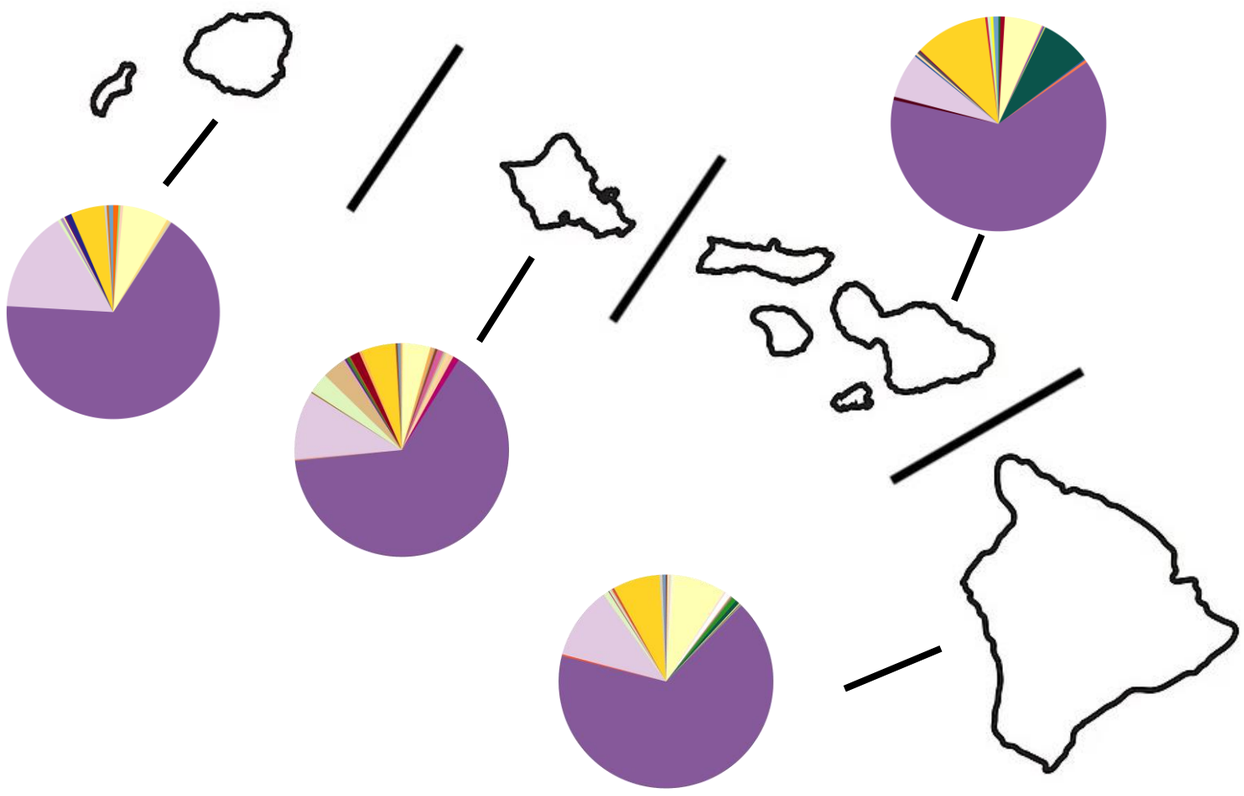


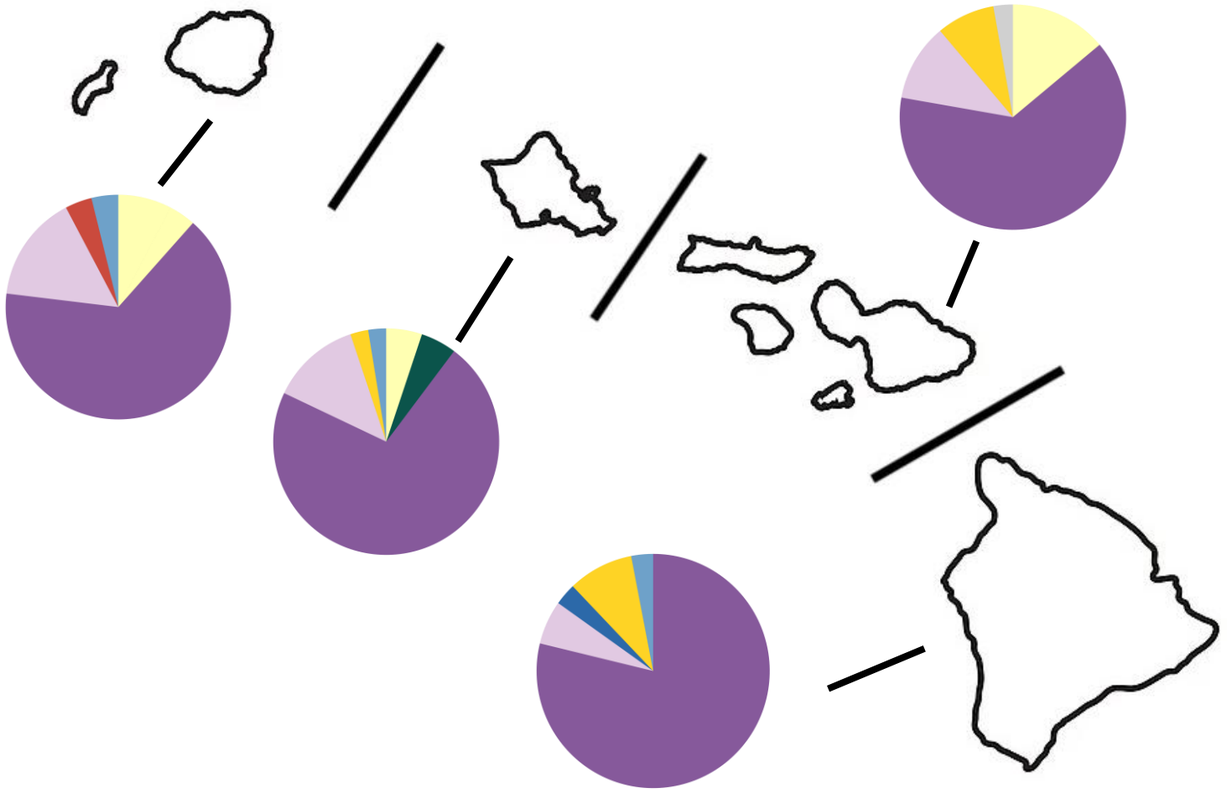
Haplotype Frequencies

Acanthurus nigrofuscus

eDNA

Tissue





Haplotype Frequencies

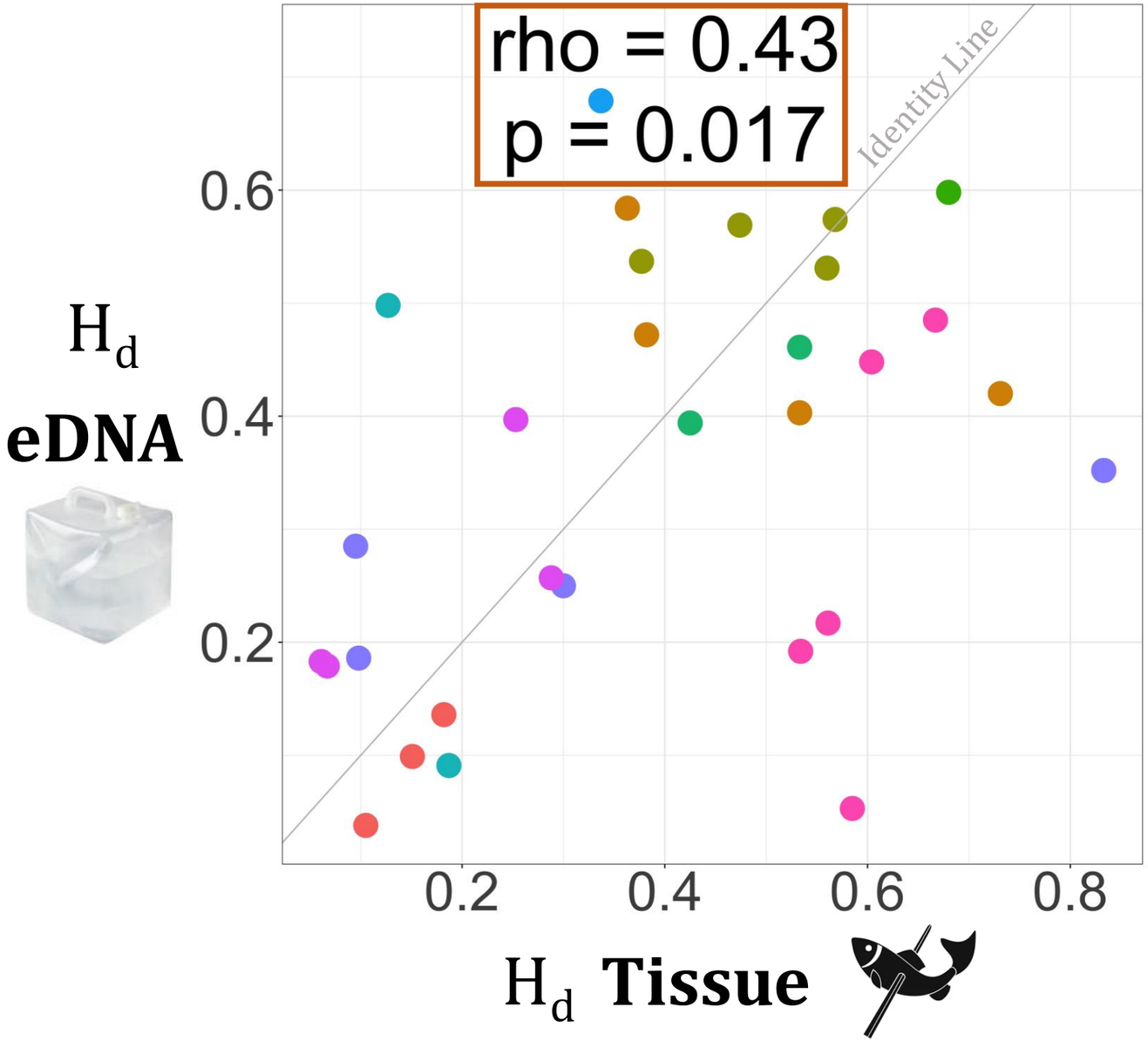
Acanthurus nigrofuscus

eDNA

Tissue

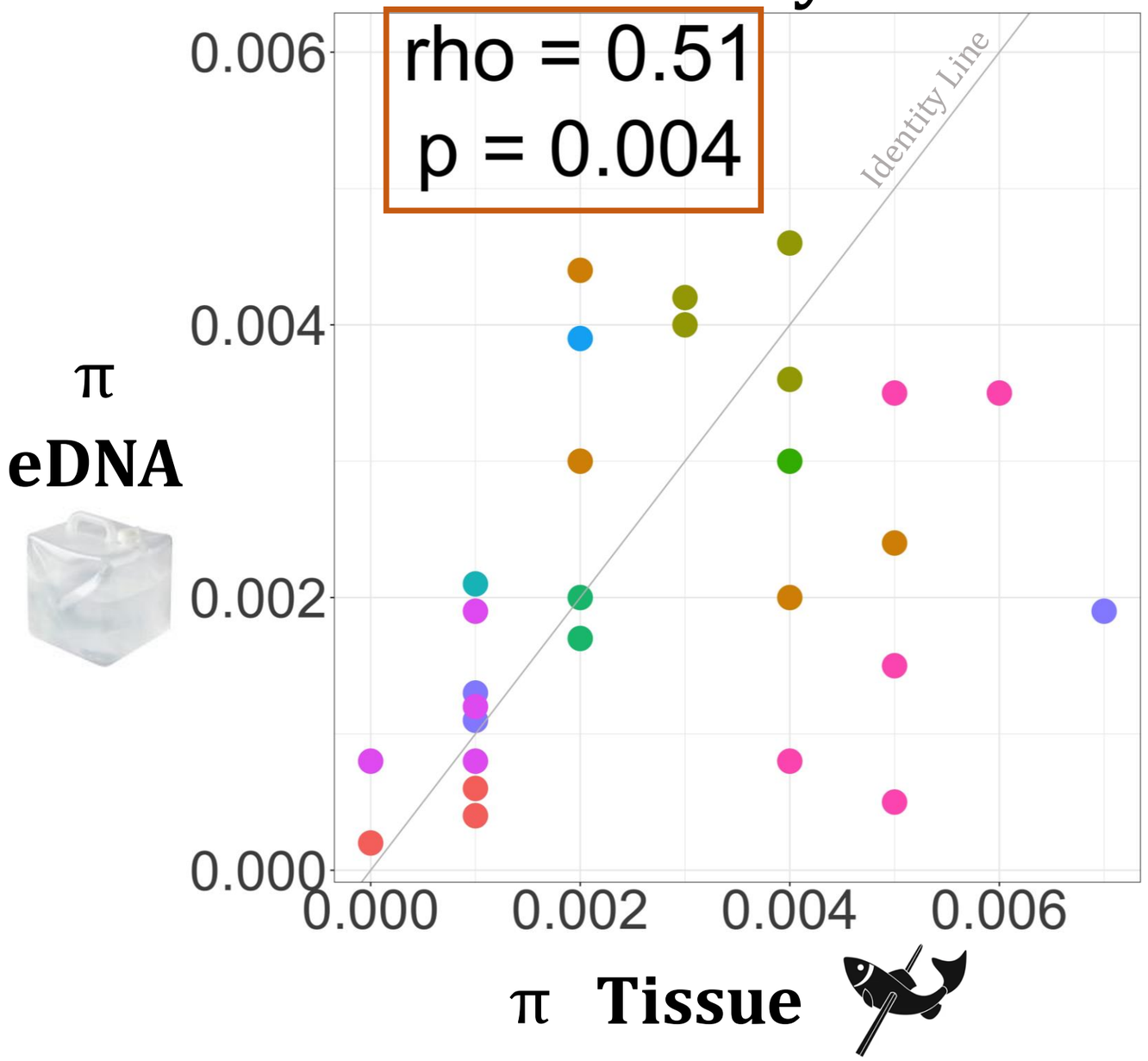
11 species:
36/37 island populations had the same dominant haplotype

Haplotype Diversity is correlated



N = 37 populations
from 11 species

Nucleotide Diversity is correlated



N = 37 populations
from 11 species

Significant genetic breaks (Φ_{ST}) increased with eDNA

eDNA

14/14

9/11

9/11

N = 208,403 reads

Tissue

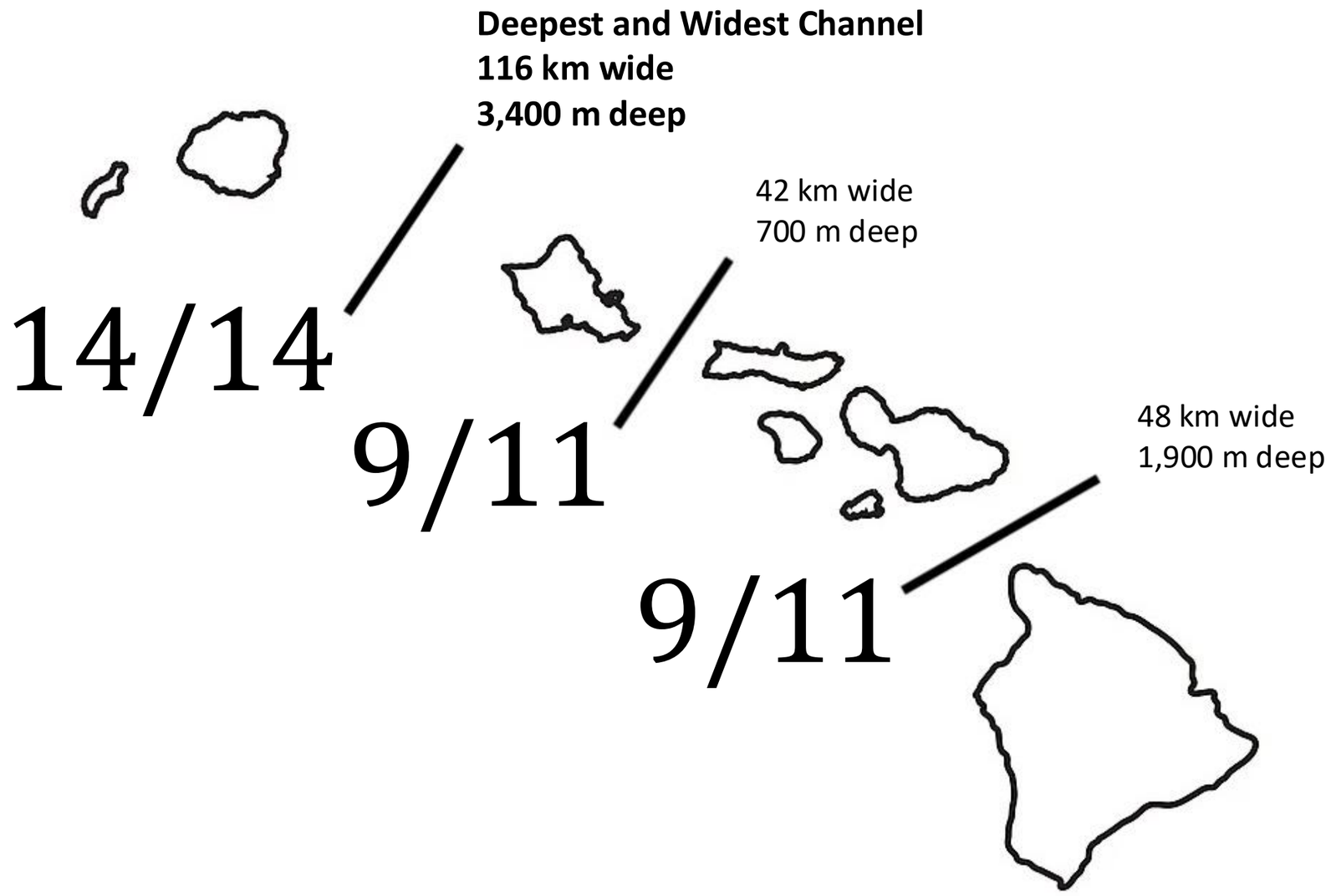
1/14

1/11

1/11

N = 1,727

Significant genetic breaks (Φ_{ST}) increased with eDNA



eDNA

Significant genetic breaks (Φ_{ST}) increased with eDNA

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

42 km wide
700 m deep

48 km wide
1,900 m deep

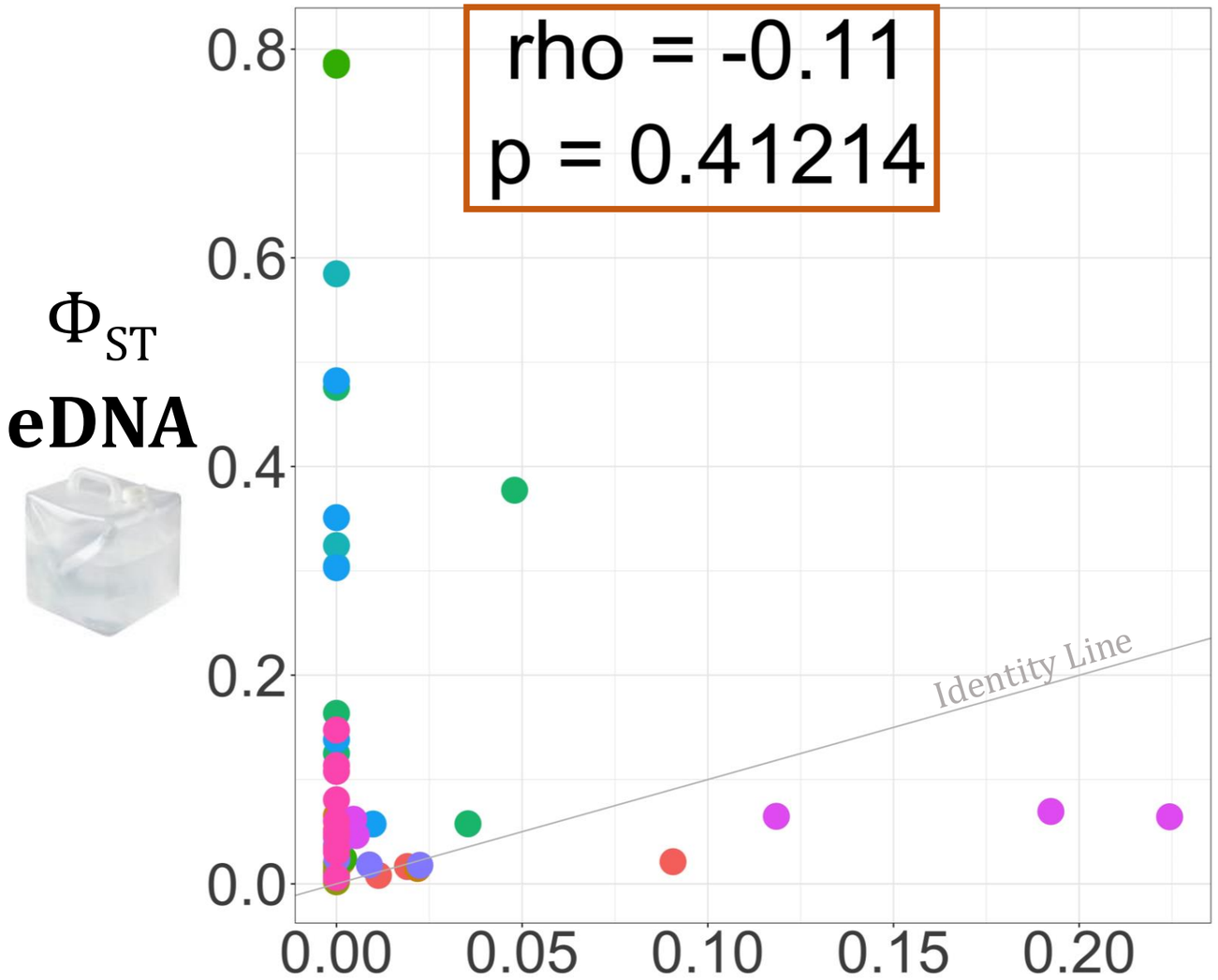
14/14

9/11

9/11

eDNA

Φ_{ST} not correlated with all data



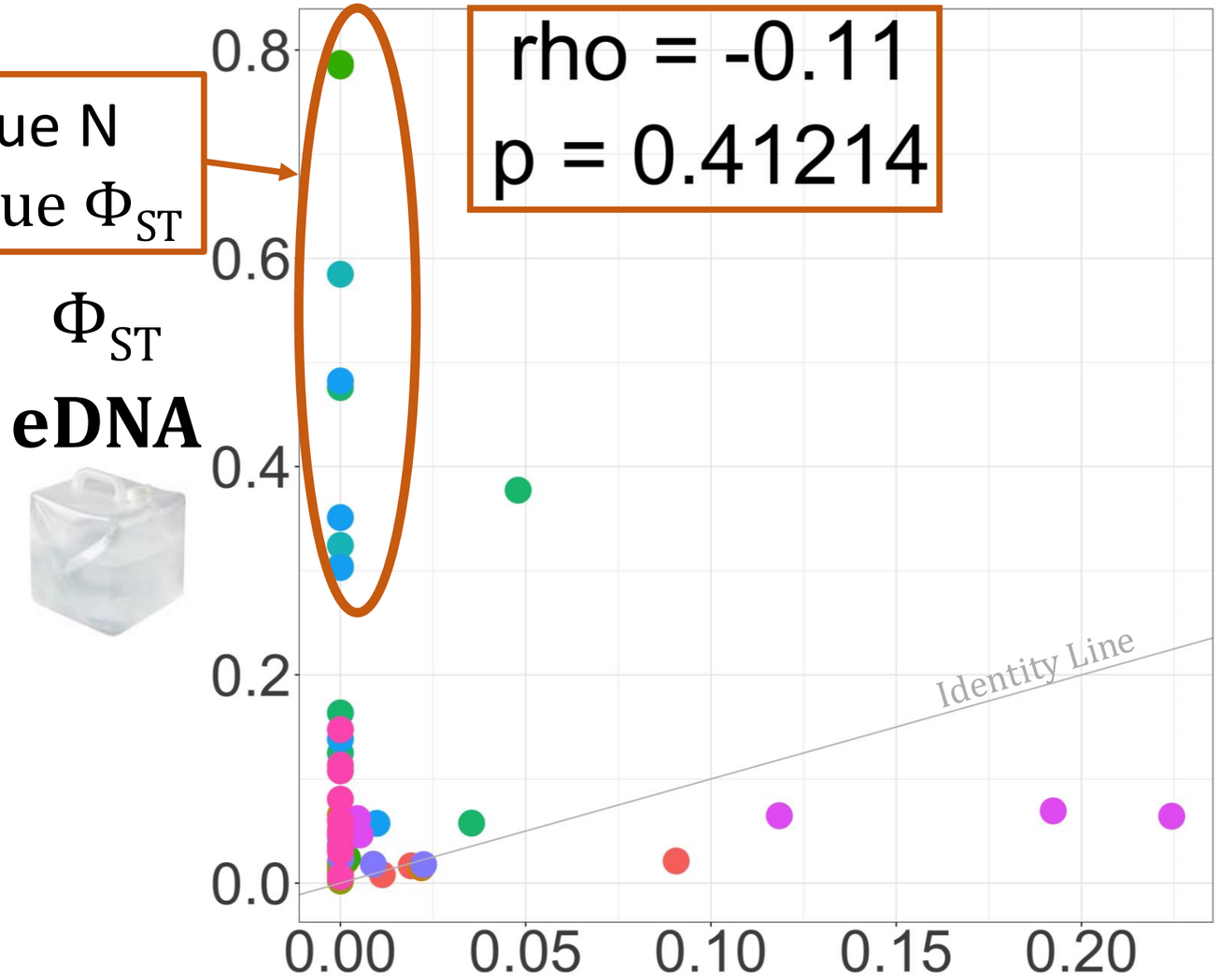
Φ_{ST} **eDNA**

Φ_{ST} **Tissue**

N = 78 pairwise population comparisons from 16 species

Φ_{ST} not correlated with all data

eDNA N << tissue N
eDNA Φ_{ST} >> tissue Φ_{ST}



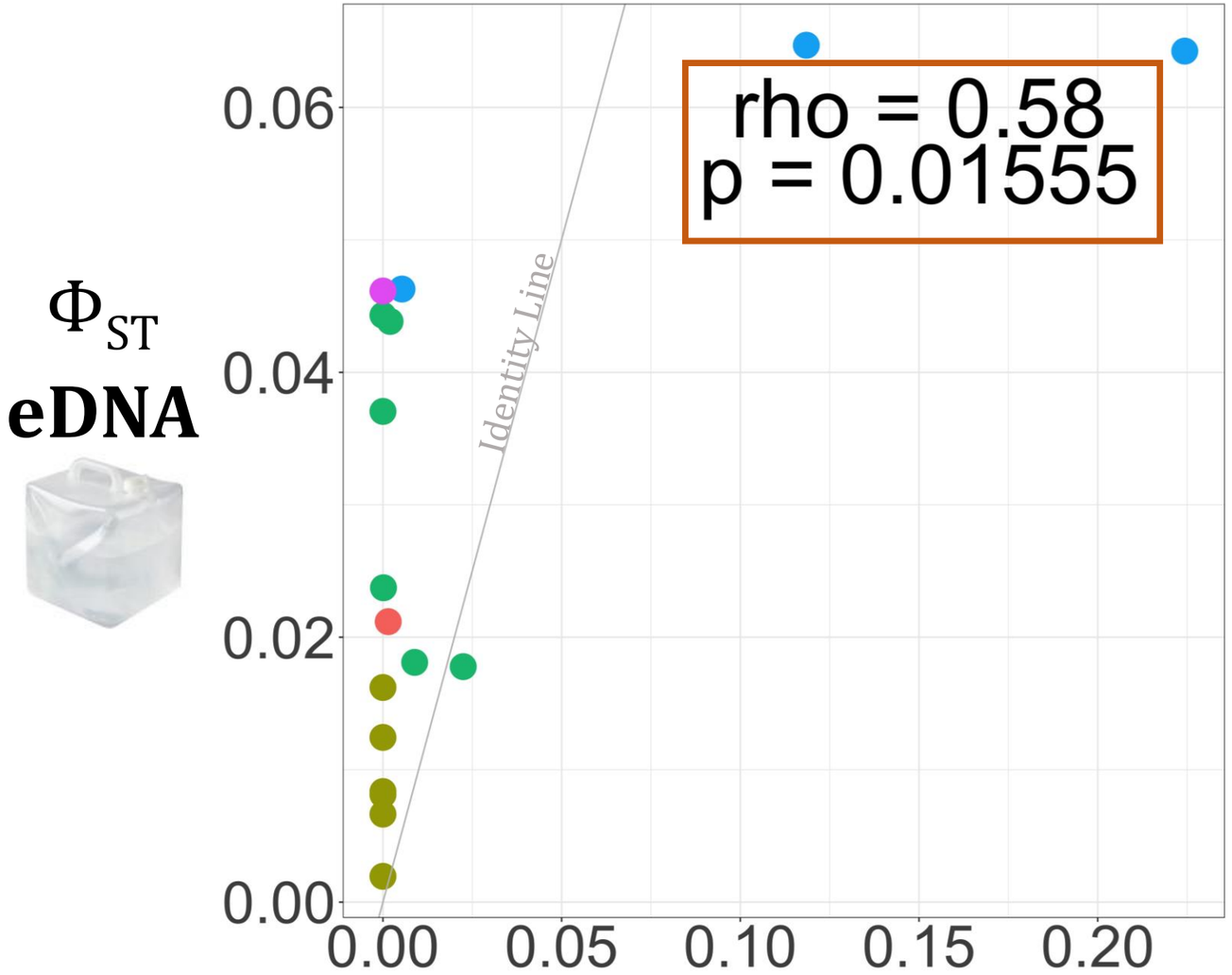
Φ_{ST}

eDNA

Φ_{ST} **Tissue**

N = 78 pairwise population comparisons from 16 species

Φ_{ST} correlation is sensitive to low sample size

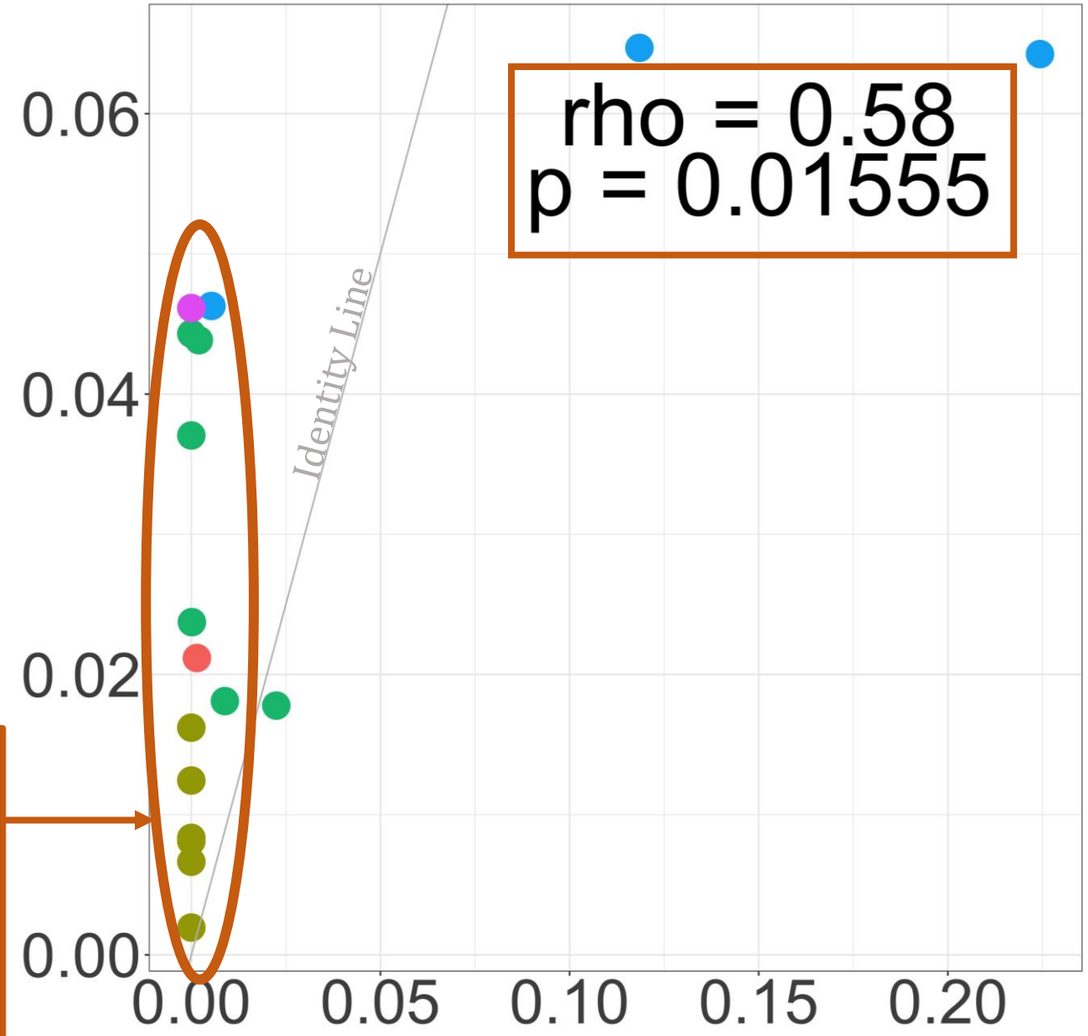


Φ_{ST} **eDNA**

Φ_{ST} **Tissue**

N = 17 pairwise population comparisons from 5 species

Φ_{ST} correlation is sensitive to low sample size



Φ_{ST} **eDNA**

Φ_{ST} **Tissue**

many tissue $\Phi_{ST} = 0$, eDNA N > tissue N, error is very large with small Φ_{ST} values

N = 17 pairwise population comparisons from 5 species

eDNA is informative for pop gen

1. Haplotypes

   ↳ The data are very similar

2. Significant population structure

   ↳ eDNA has more power

3. Φ_{ST}

   ↳ Correlation rank significant
   Sensitive to low sampling

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Questions?

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