

A Genomic View of *Spisula* Population Structure and Gene Flow

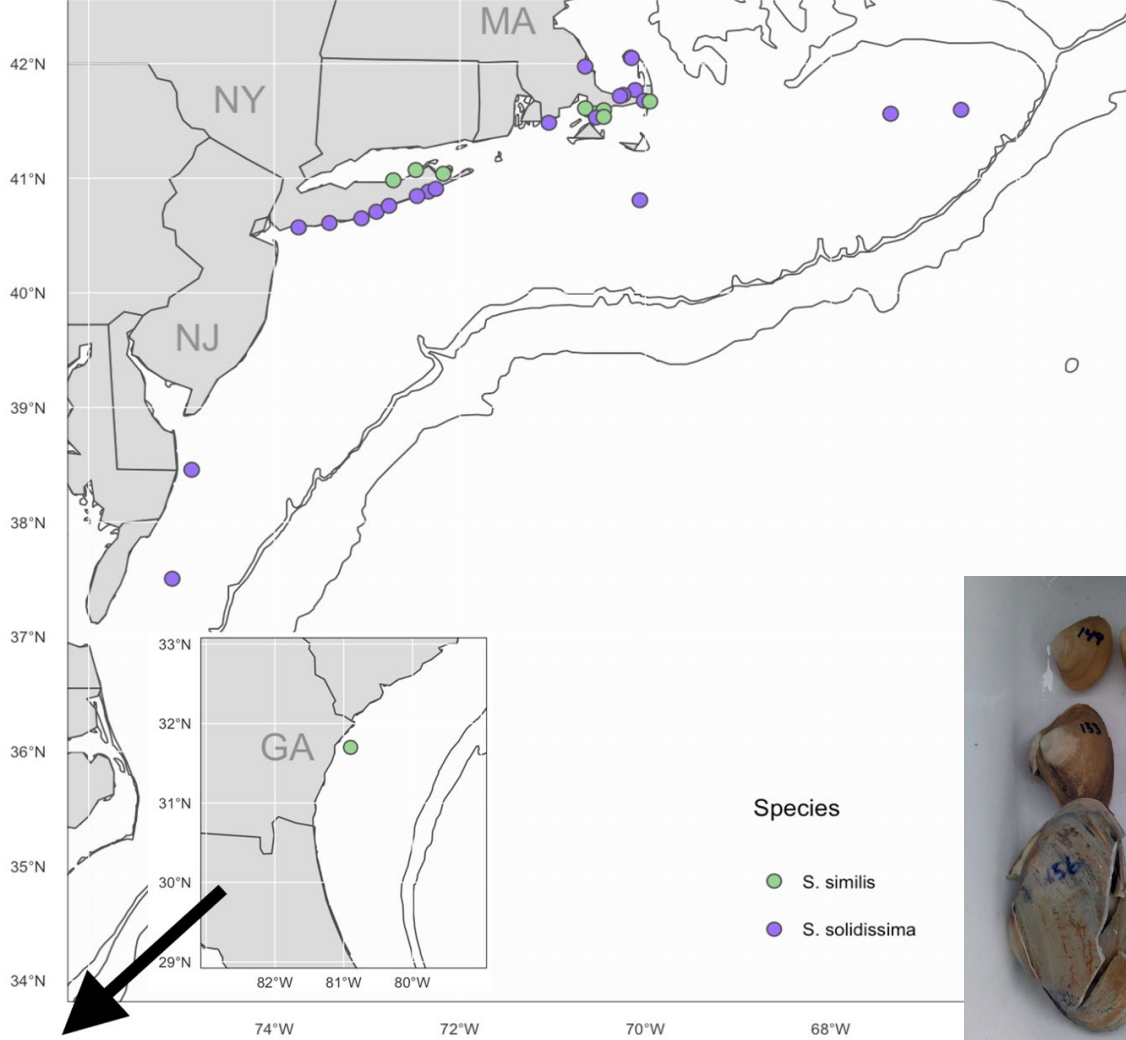
Hannah Hartung, MS candidate
Matthew Hare, Associate Professor

Department of Natural Resources and the
Environment
Cornell University
mph75@cornell.edu

S.s. solidissima

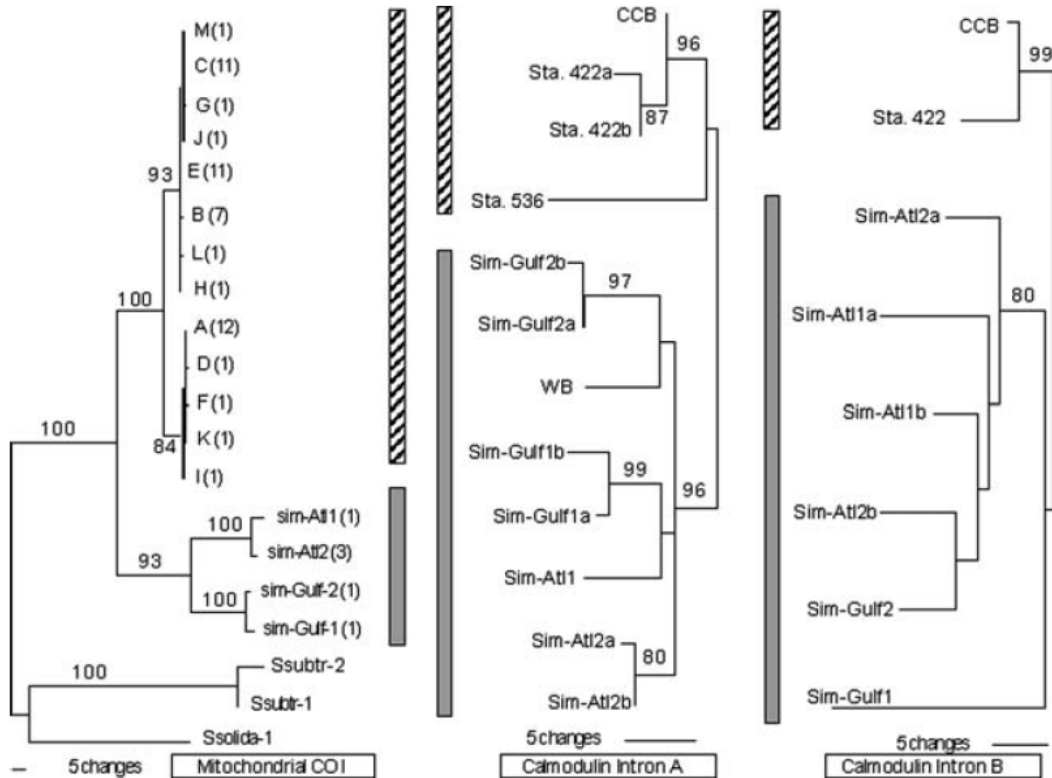


S.s. similis



Genealogical Species Diagnosis

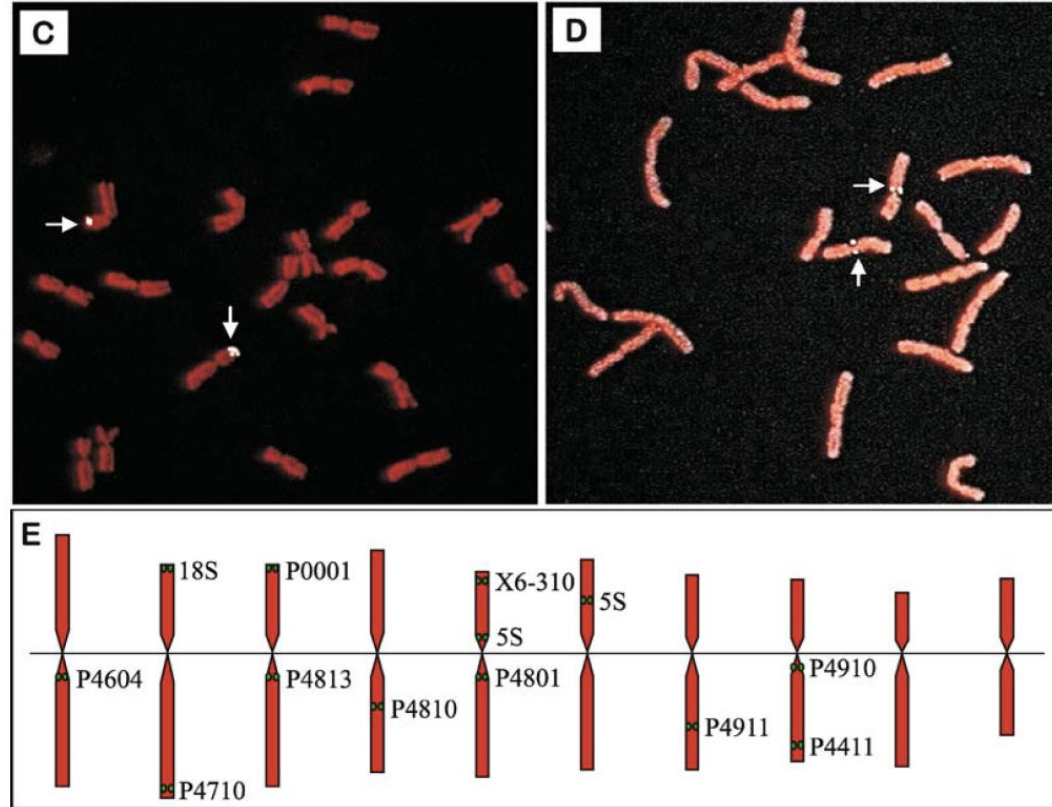
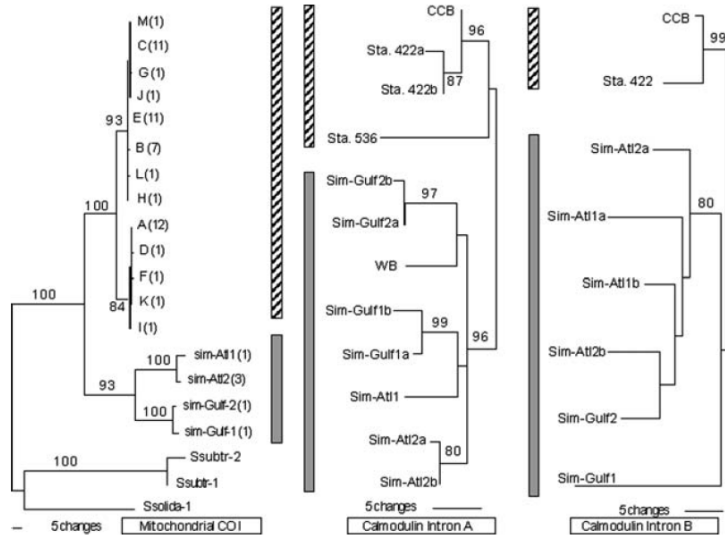
Hare & Weinberg 2005



Genealogical Species Diagnosis

Guo et al. 2008

Hare & Weinberg 2005



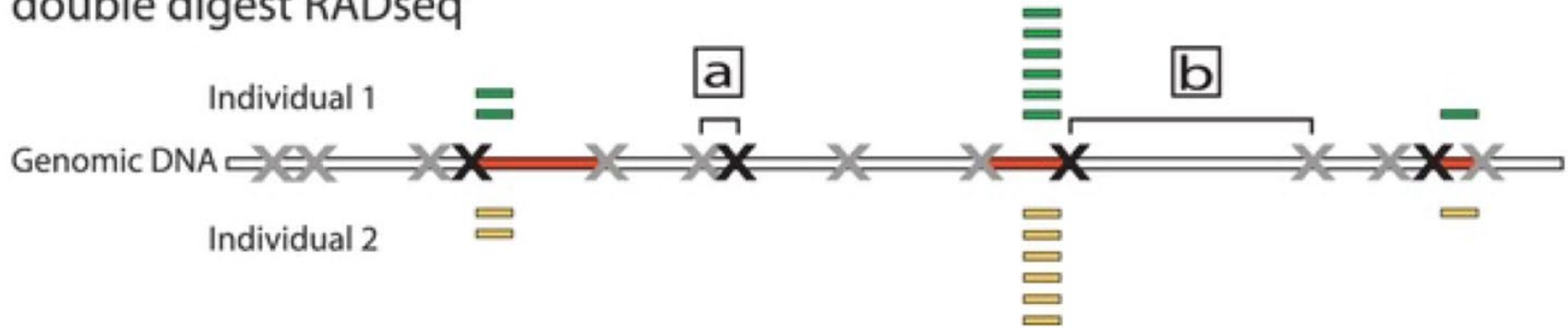
Double digest RADseq genomic sampling schematic

Rare cut restriction enzyme e.g.: CATATG

Common cut restriction enzyme e.g.: GTAC

X Rare cut site **—** Genomic interval present in library
X Common cut site **—** Sequence reads

double digest RADseq

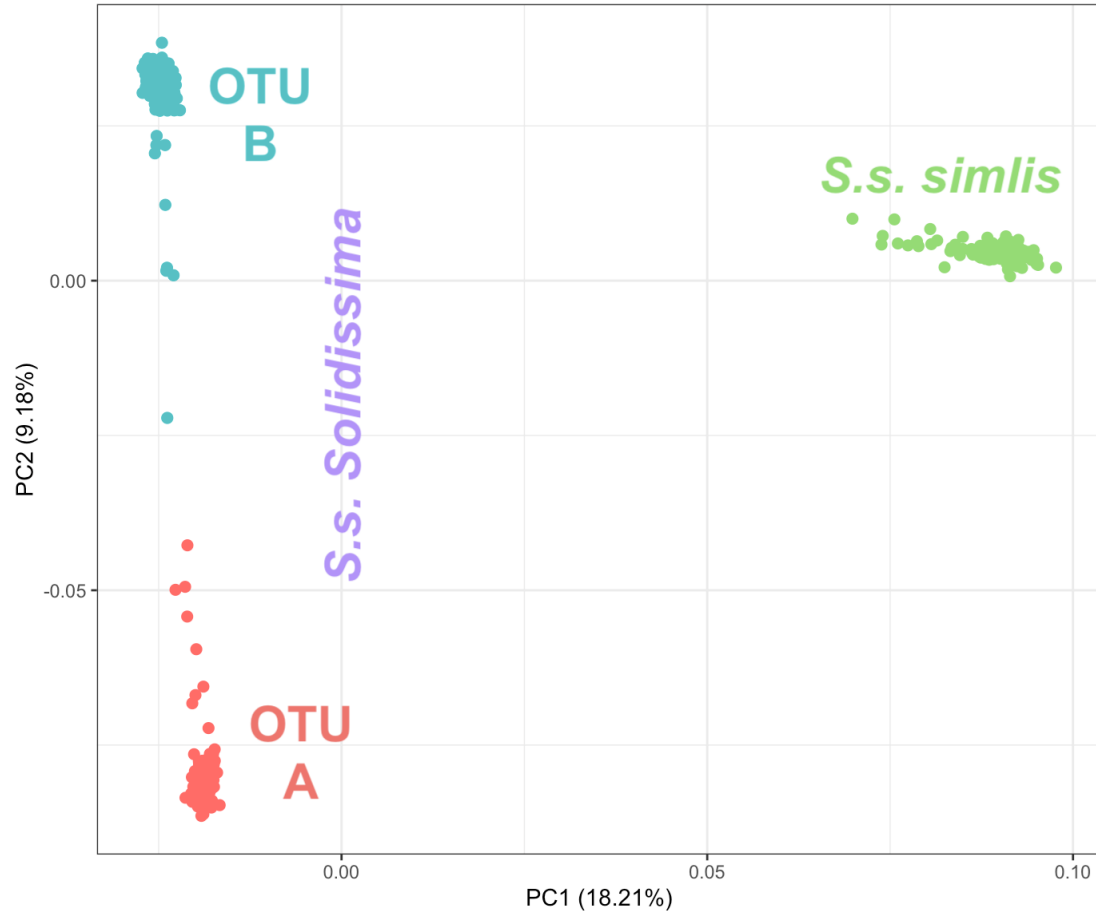


Peterson BK, Weber JN, Kay EH, Fisher HS, Hoekstra HE (2012) Double Digest RADseq: An Inexpensive Method for De Novo SNP Discovery and Genotyping in Model and Non-Model Species. PLOS ONE 7(5): e37135. <https://doi.org/10.1371/journal.pone.0037135>
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0037135>

Single Nucleotide Polymorphisms = SNPs



Principal component analysis of both subspecies; 4.7k SNPs

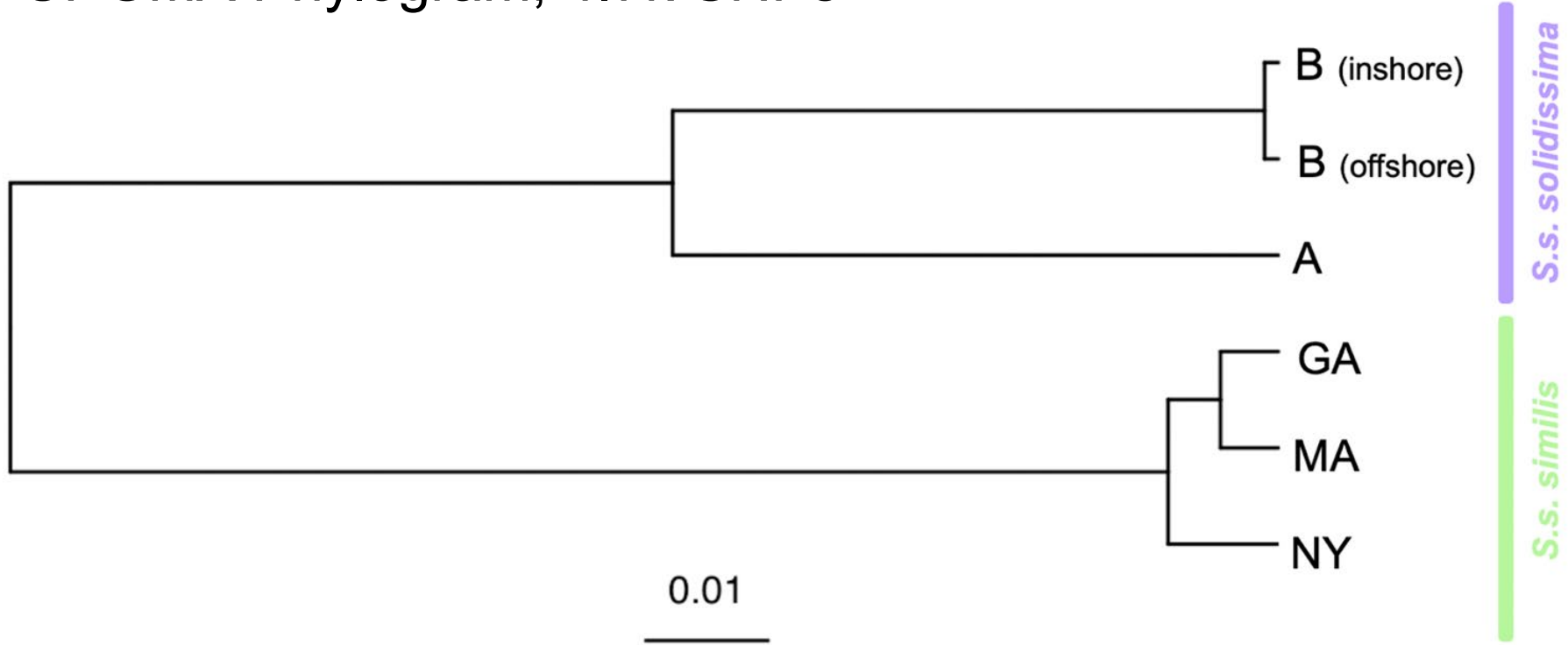


OTU

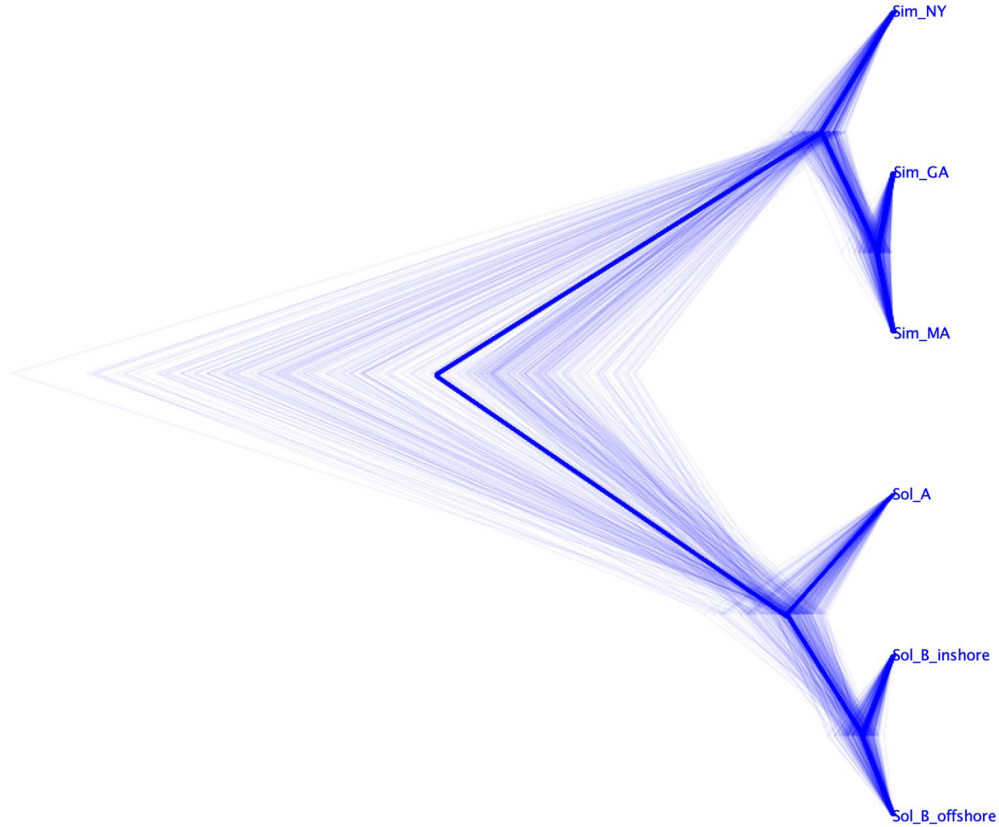
Operational
Taxonomic Unit

an operational
definition to classify
groups of closely
related individuals

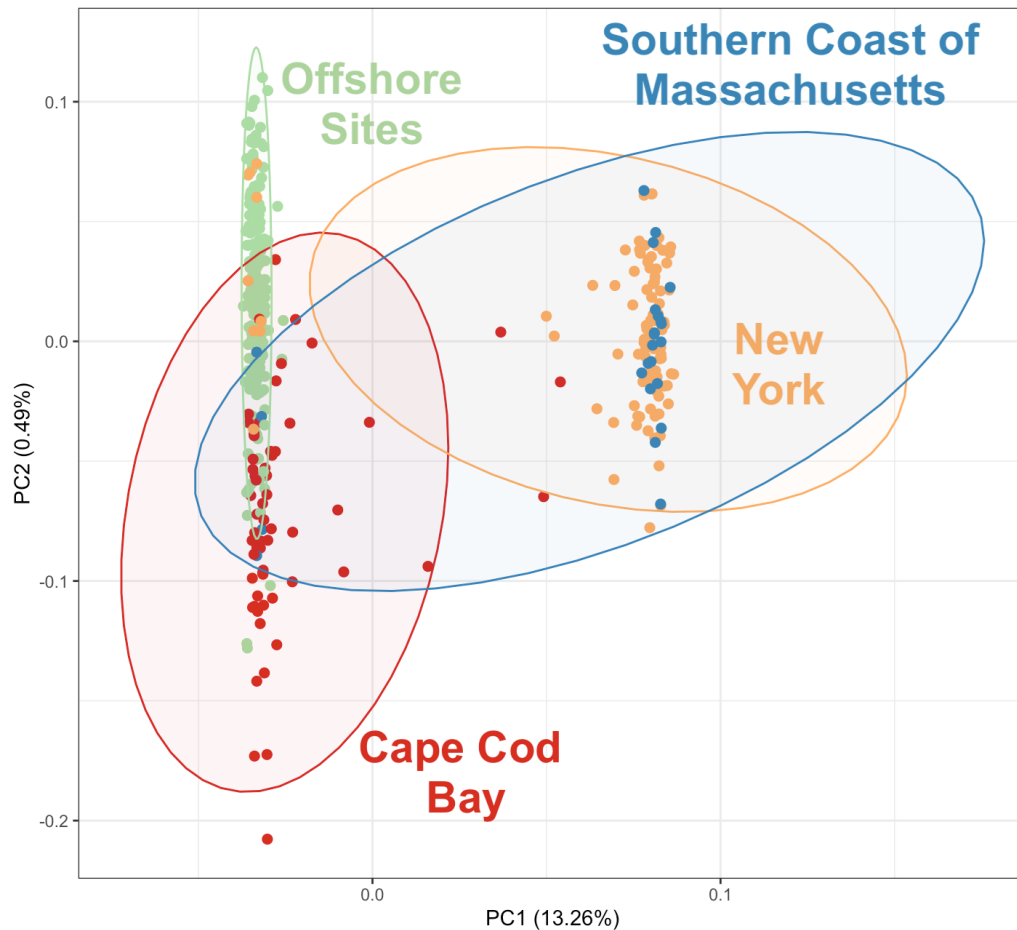
UPGMA Phylogram; 4.7k SNPs



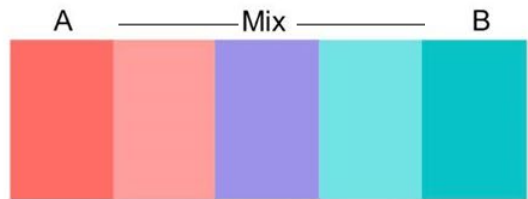
SNAPP Densitree from multispecies coalescent; 4.7k SNPs



PCA of *S.s.solidissima* OTUs A and B; 7.6K SNPs



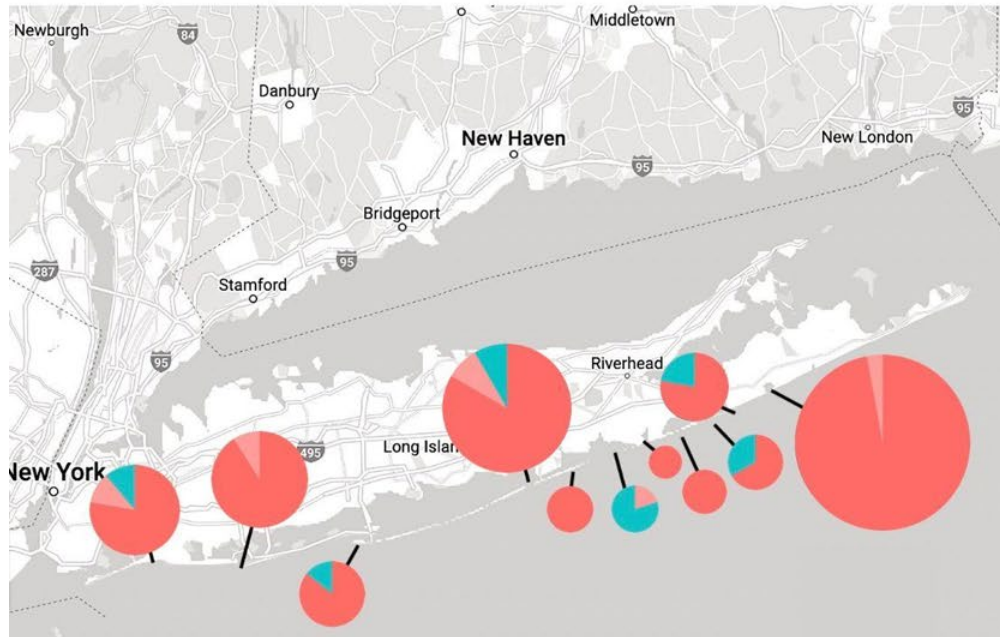
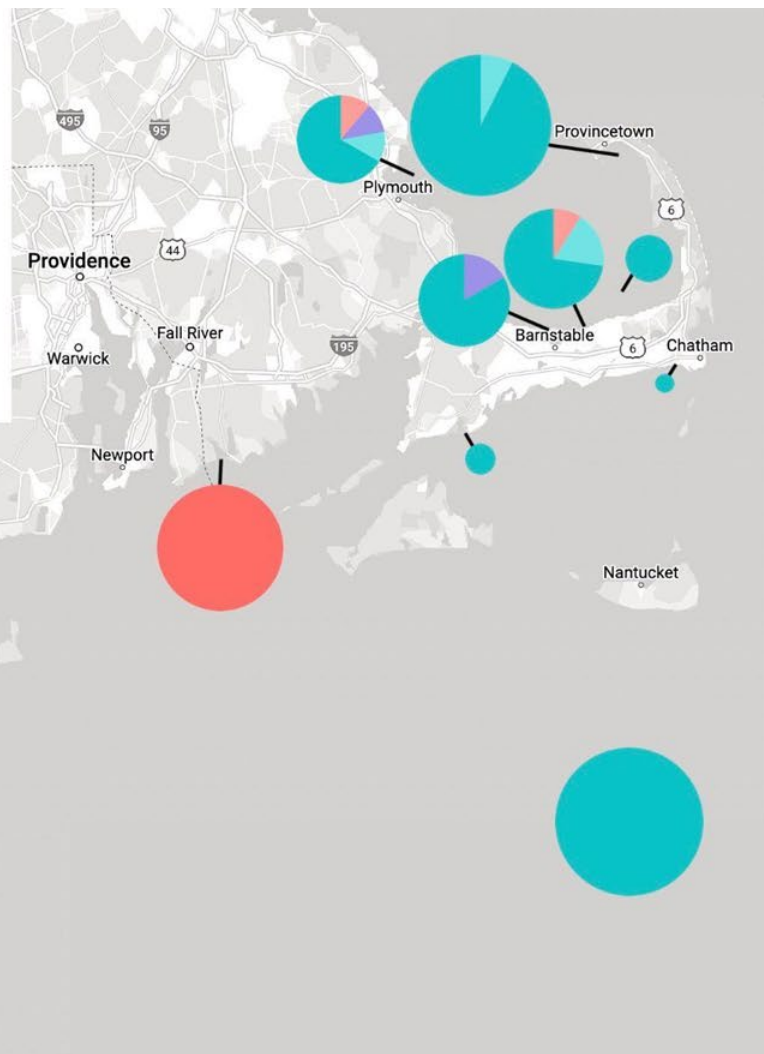
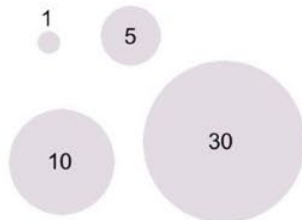
S.s. solidissima Genotypes by Site



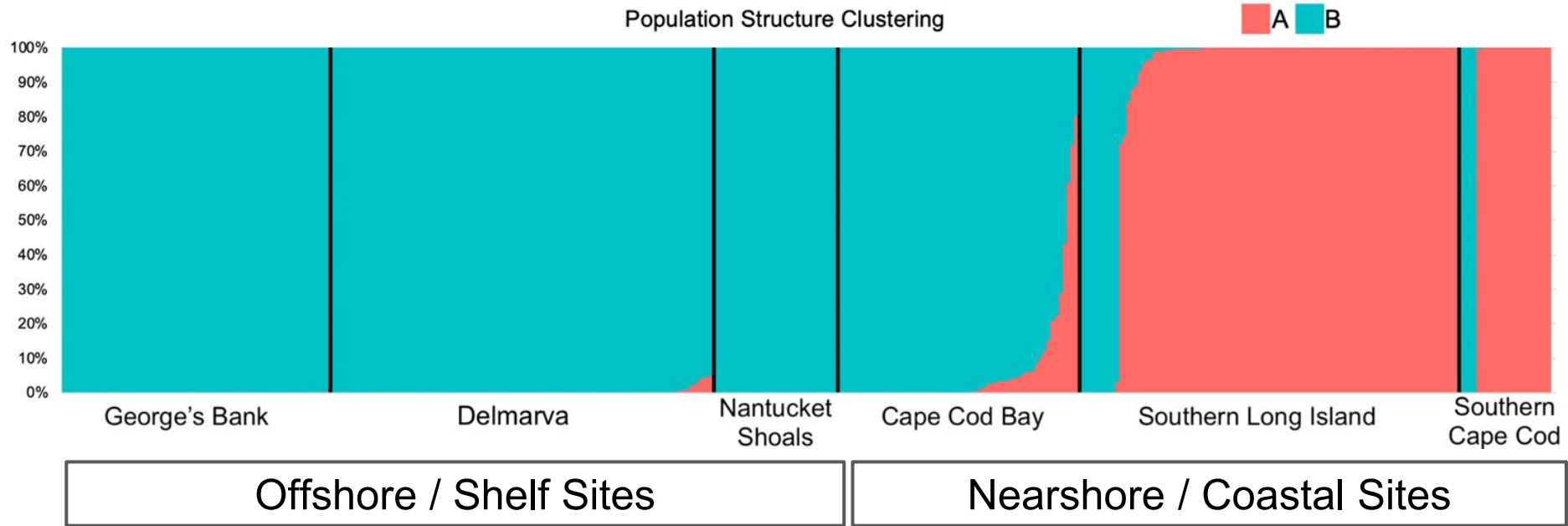
90% 65% 65% 90%

Percent of Loci Clustering with each Genotype

Sample Size



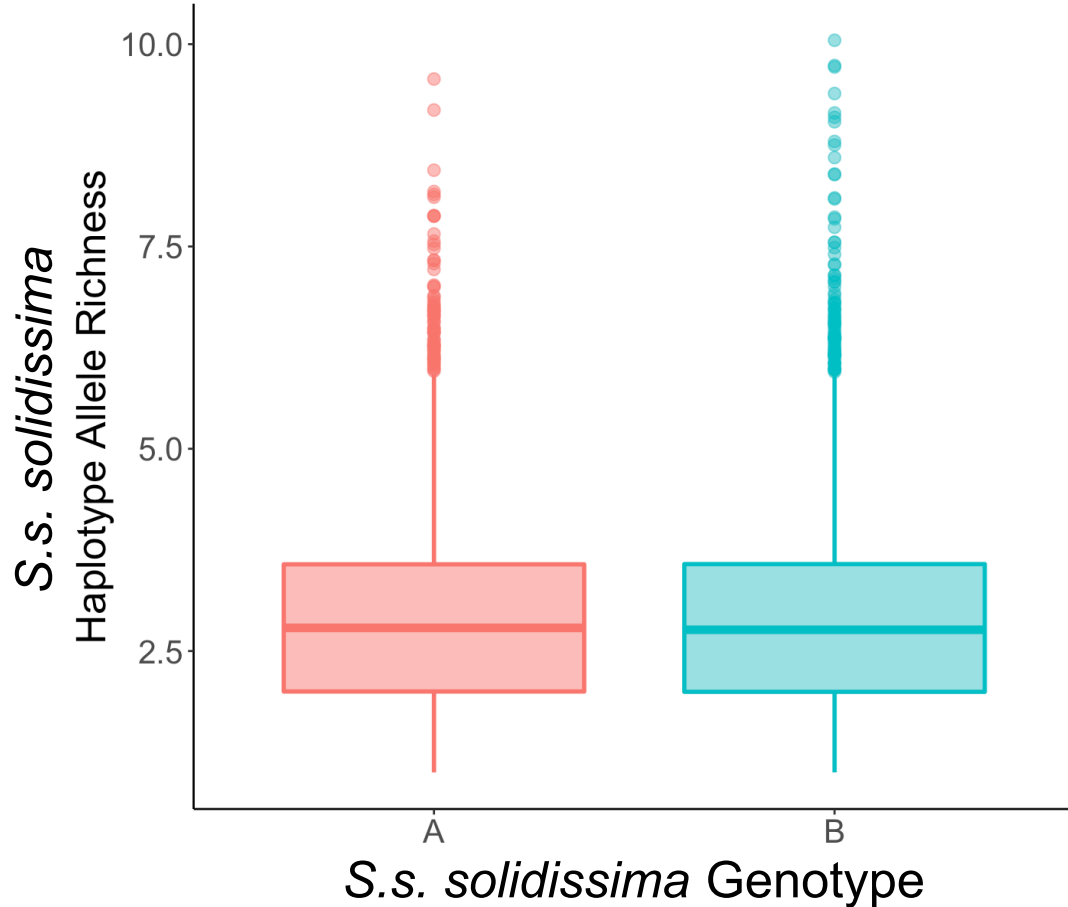
S.s. solidissima admixture analysis, $K = 2$



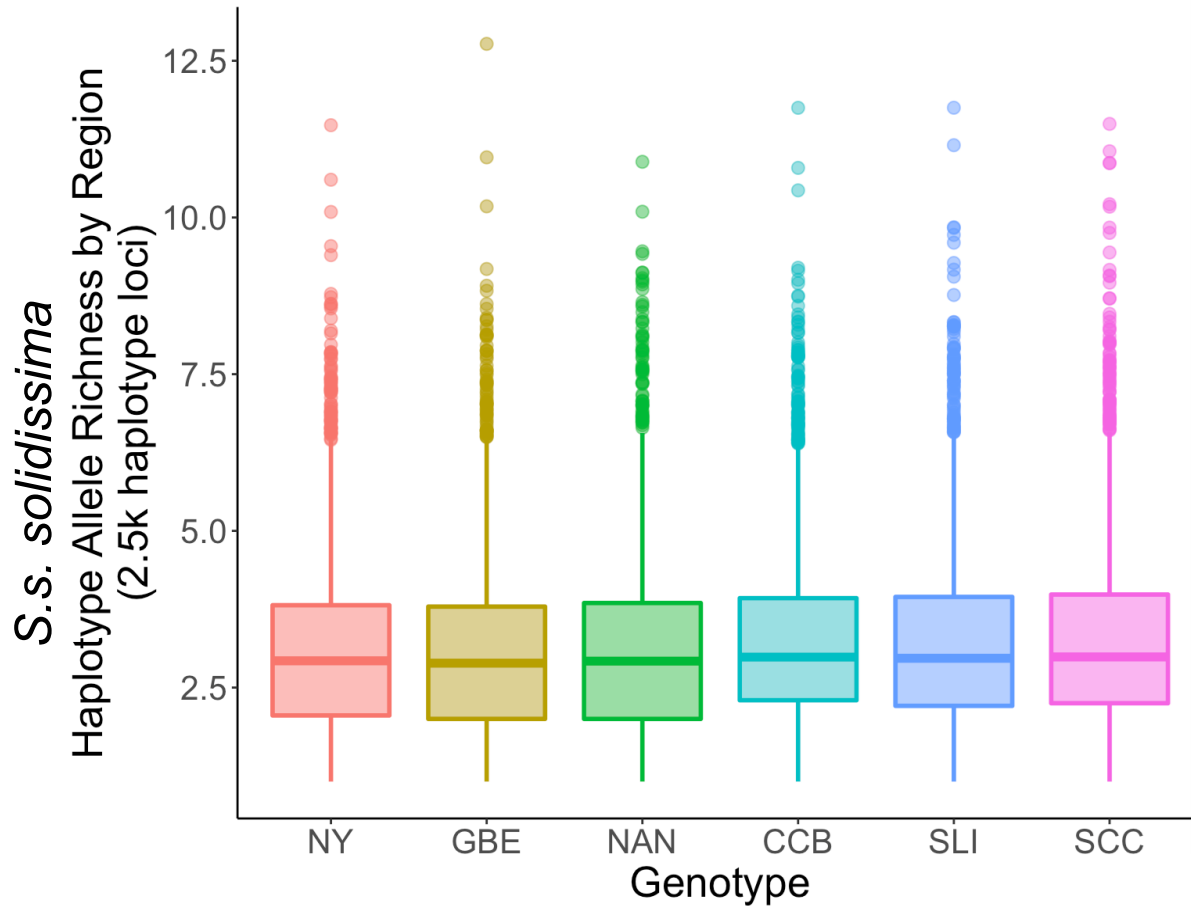
SNPs → Haplotypes

	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6						
Haplotype 1	C	A	G	A	T	C	G	C	T	G	T	1
Haplotype 2	C	A	G	A	T	C	G	T	G	G	A	2
Haplotype 3	C	G	G	A	T	T	G	C	T	G	C	3
Haplotype 4	C	G	G	A	T	T	G	C	A	T	G	4

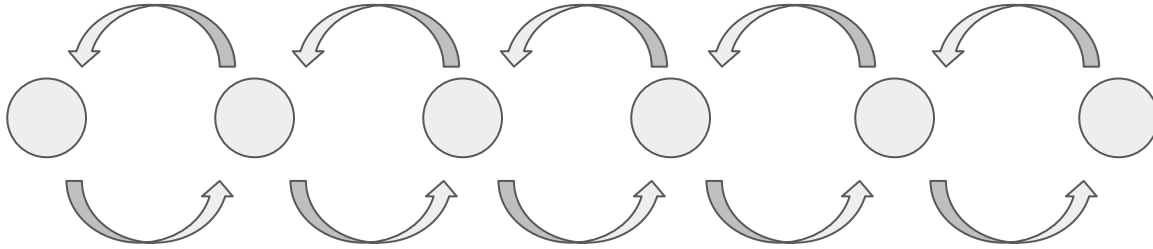
S.s. solidissima Genetic Diversity; 2.5k haplotype loci



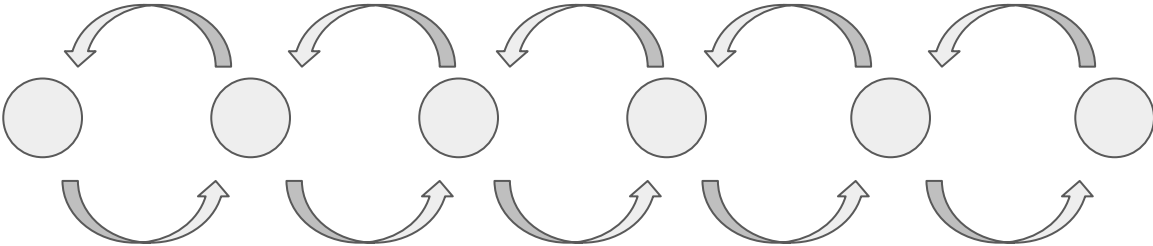
S.s. solidissima Genetic Diversity; 2.5k haplotype loci



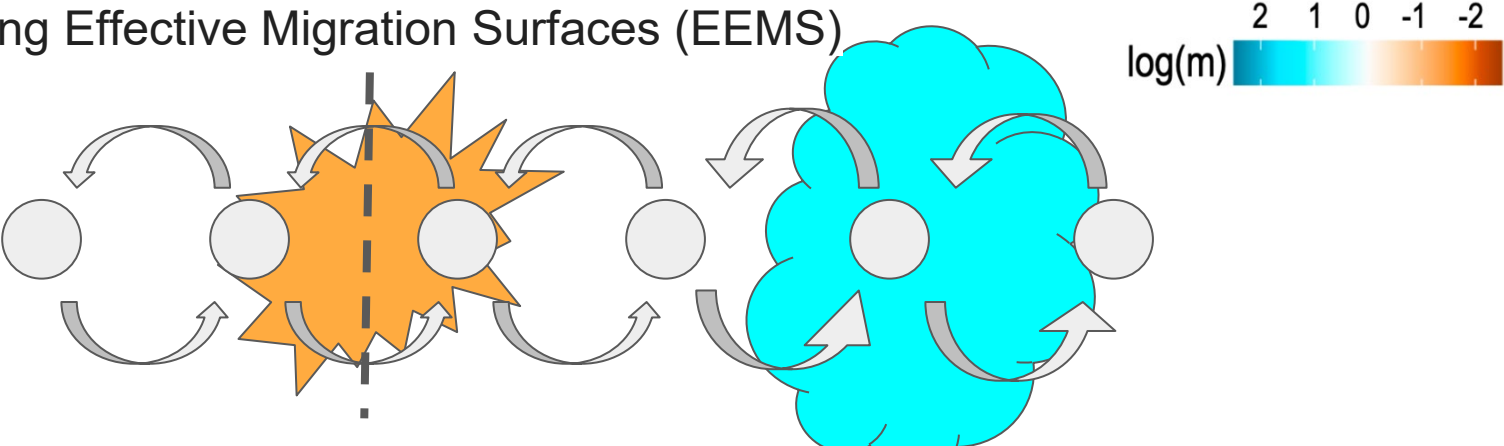
Gene Flow Expectations: Isolation by Distance



Gene Flow Expectations: Isolation by Distance



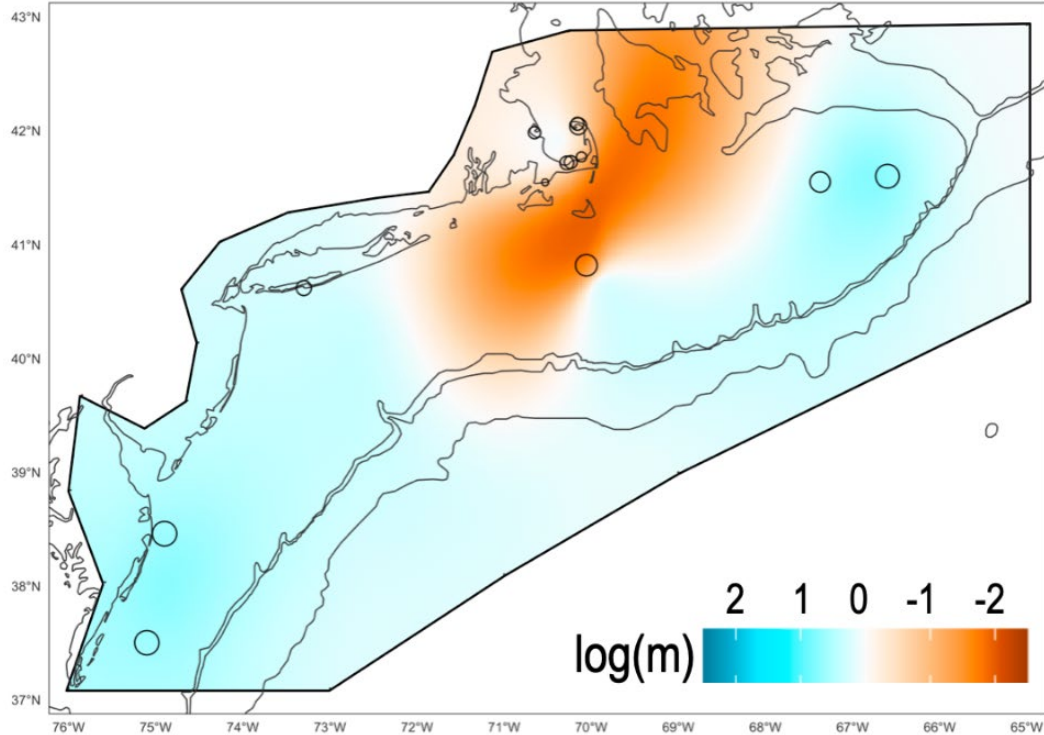
Estimating Effective Migration Surfaces (EEMS)



S.s. solidissima Gene Flow – OTU B

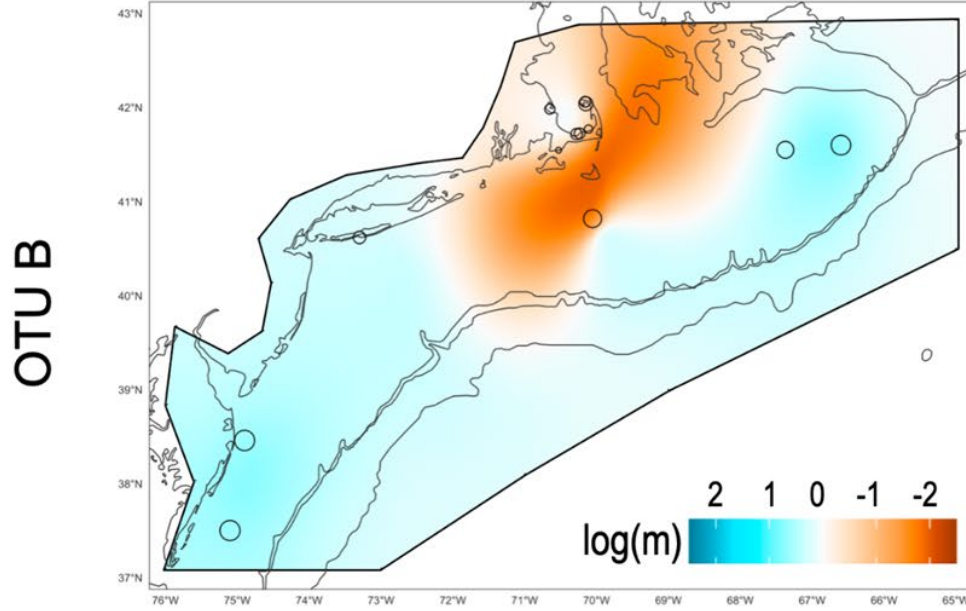
EEMS

OTU B

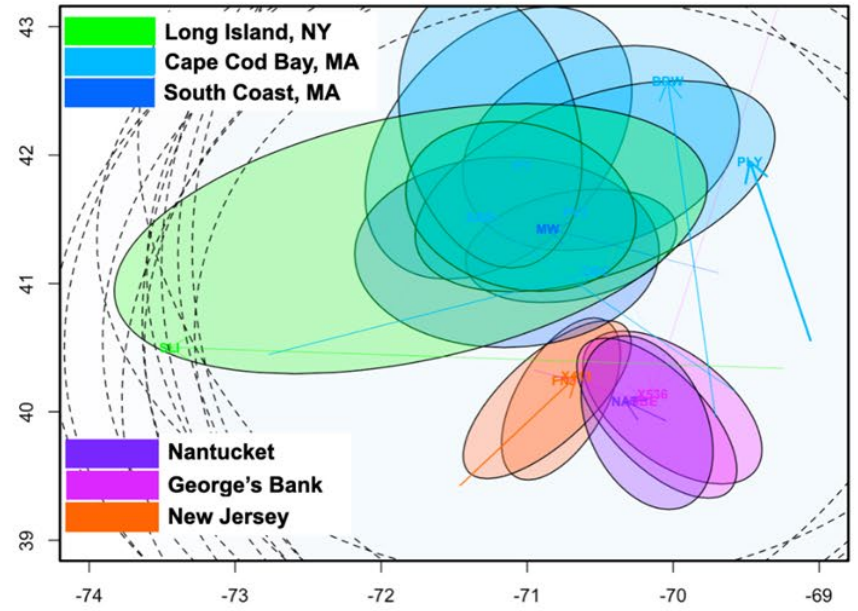


S.s. solidissima OTU B Gene Flow

EEMS

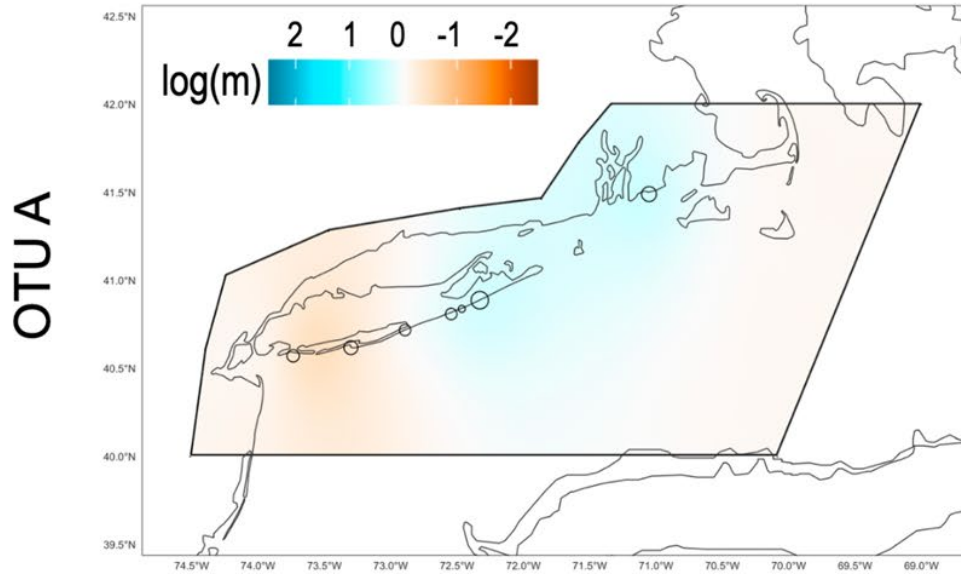


SpaceMix

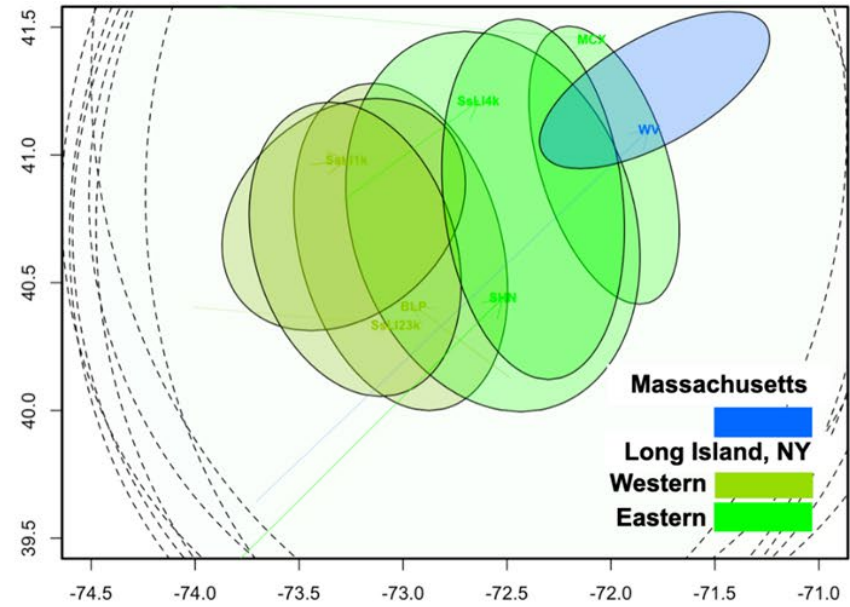


S.s. solidissima OTU A Gene Flow

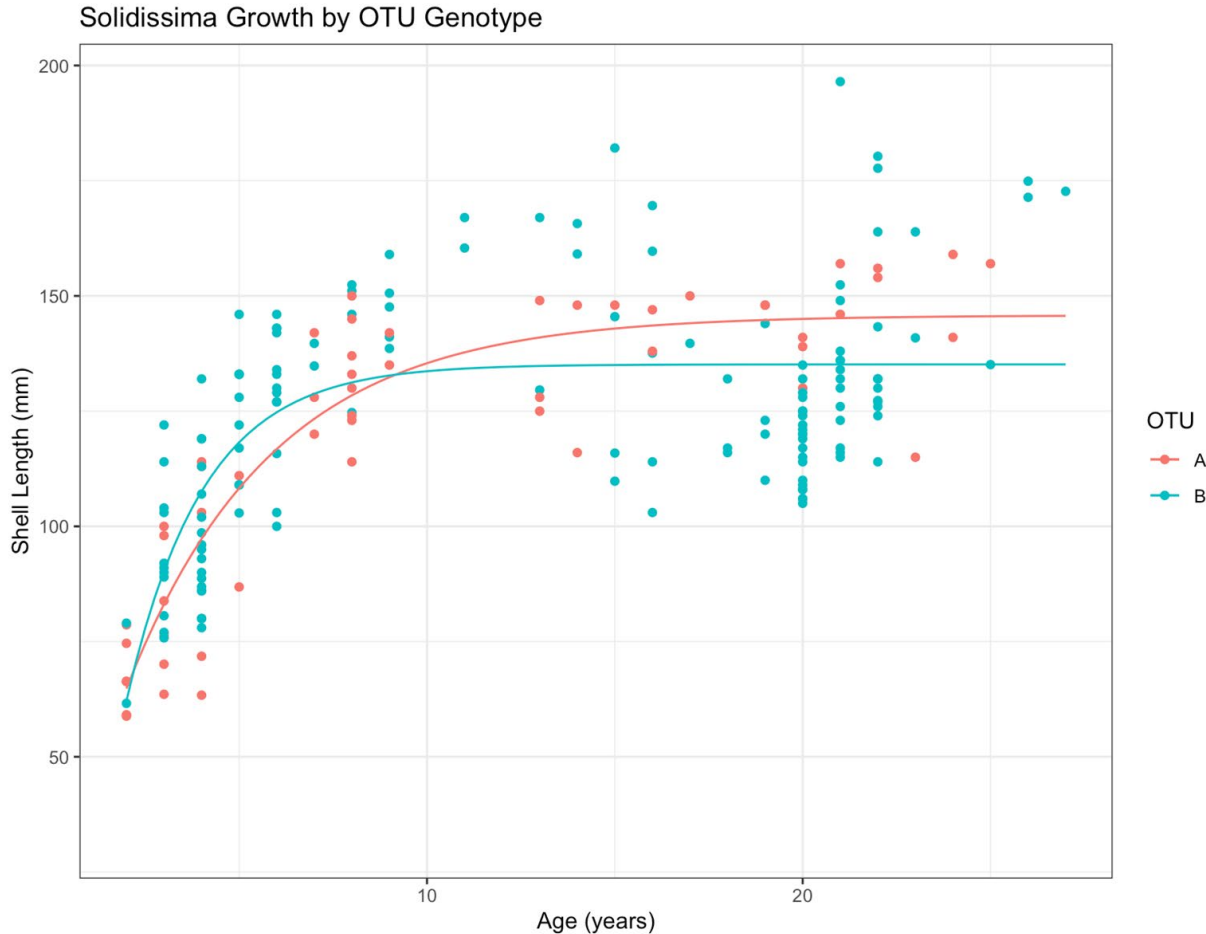
EEMS



SpaceMix



Preliminary von Bertalanffy curve for OTUs **A** and **B**



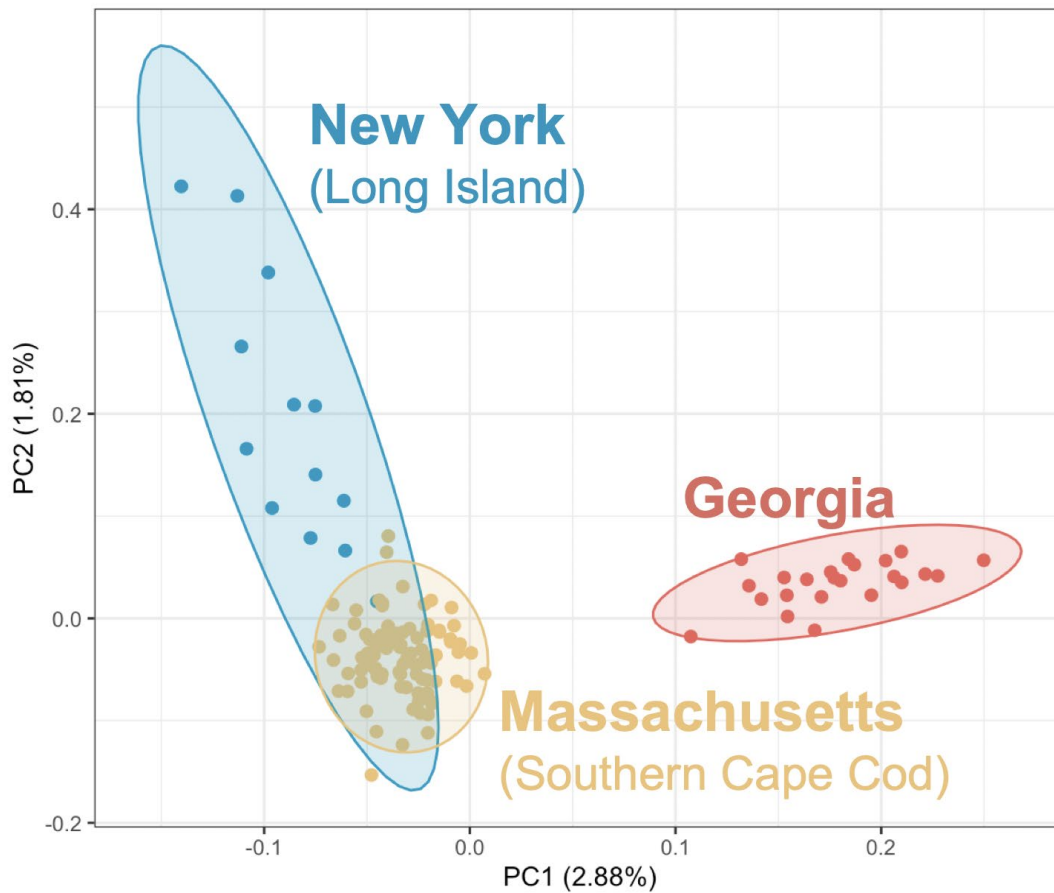
solidissima genotypes A & B
von Bertalanffy preliminary
growth curves

Thanks to Eric Robillard at
NEFSC for working 40 of our shell
specimens into their ageing cue,
and to Dan Hennen (NEFSC) for
helping make this happen!

Genotype B:
Georges Bank
Nantucket Shoals
New Jersey/Delmarva
Cape Cod Bay
Long Island south shore

Genotype A:
Long Island south shore
Southern New England

PCA for *S.s. similis*; 12.7k SNPs



Cluster Analysis using Admixture Model

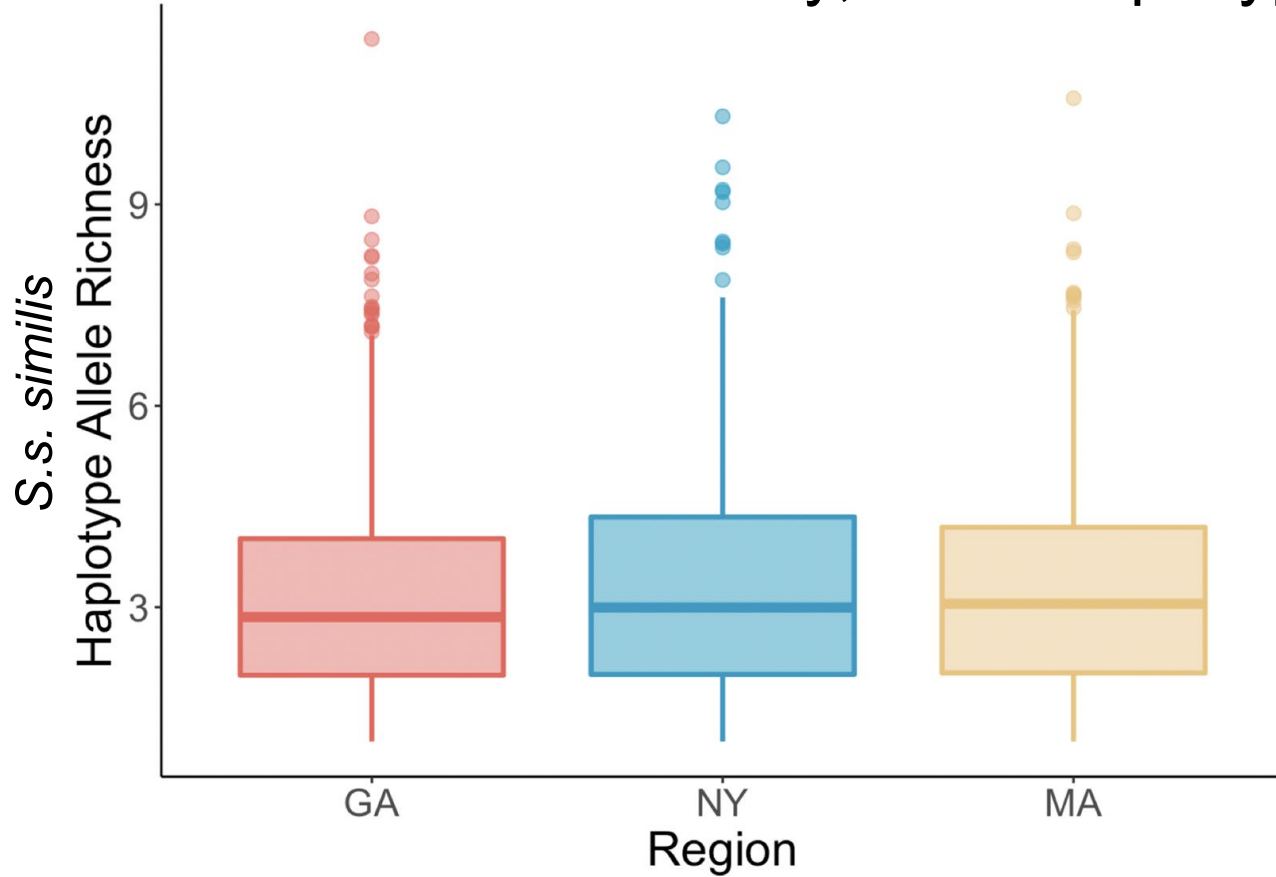
similis haplotypes

1.25k haplotype loci

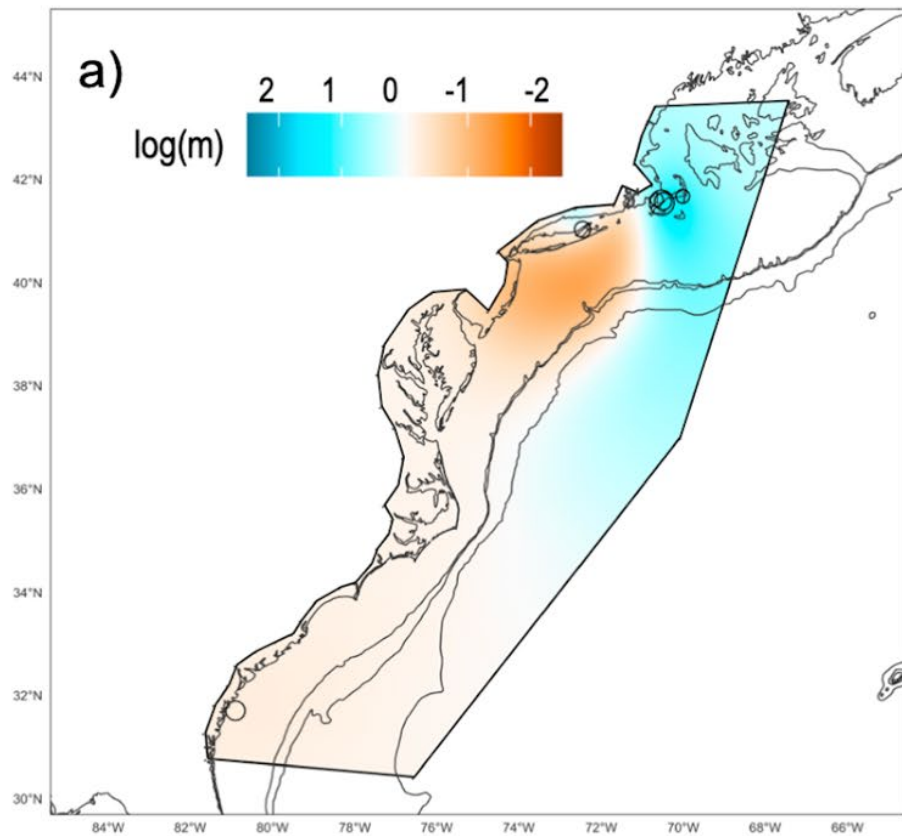
STRUCTURE $K=2$ model best fit



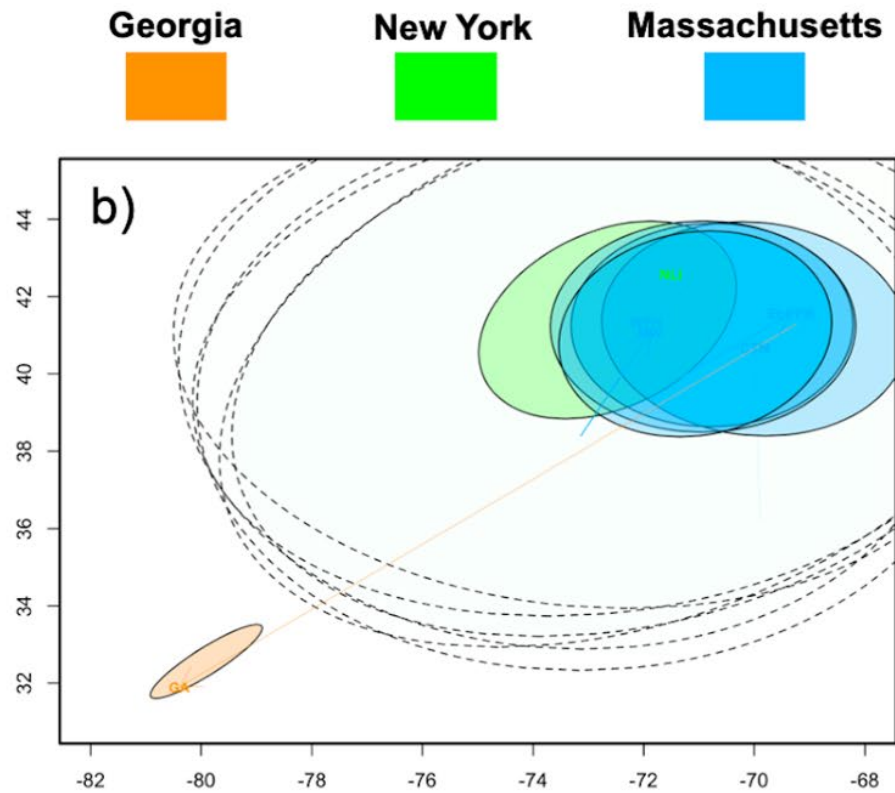
S.s. similis Genetic Diversity; 1.25k haplotype loci



EEMS



SpaceMix



Conclusions

1. *S.s. solidissima* and *S.s. similis* are full species under the biological species concept.
2. *S.s. solidissima* contains two cryptic, partially sympatric OTUs, diverged at the level of subspecies and hybridizing in some nearshore areas.
3. Continental shelf populations of *S.s. solidissima* seem to be entirely OTU B with high gene flow across all fished stocks.
 - a. Cape Cod Bay OTU B *solidissima* is the least connected OTU B population, but still has gene flow connections with shelf populations of OTU B
 - b. Cape Cod Bay OTU B *solidissima* is experiencing hybridization with OTU A at a high rate
4. *S.s. solidissima* OTU A has unknown habitat limits and life history (most sampling for this study was very nearshore).

Acknowledgements

Jessica Coakley, MAFMC

Daniel Hennen, Nicole Charriere,
Nancy Mchugh, Charles Keith -
NOAA/NEFSC

Matt Weeks

Daphne Munroe, Haskin Shellfish
Research Lab, Rutgers

Sam Martin, Atlantic Cape
Fisheries

Contact Information:

mph75@cornell.edu

Open Questions

This project:

- What are the most diagnostic loci for OTUs A and B? How efficiently can they be genotyped?

For future:

- Are there morphometric differences between A and B?
- If A and B can interbreed, what are the important extrinsic repro isolating mechanisms?
- How do A and B differ in phenology, life history, temperature sensitivity, larval behavior?
- What is the proper taxonomy for *S.s. similis*, *S.s. solidissima* A & B?

F_{ST} between *solidissima* genotype A & B

