Black Sea Bass *Centropristis striata* U.S. East Coast Genetic Structure

Results of 2024 Multi-Survey Collection Study

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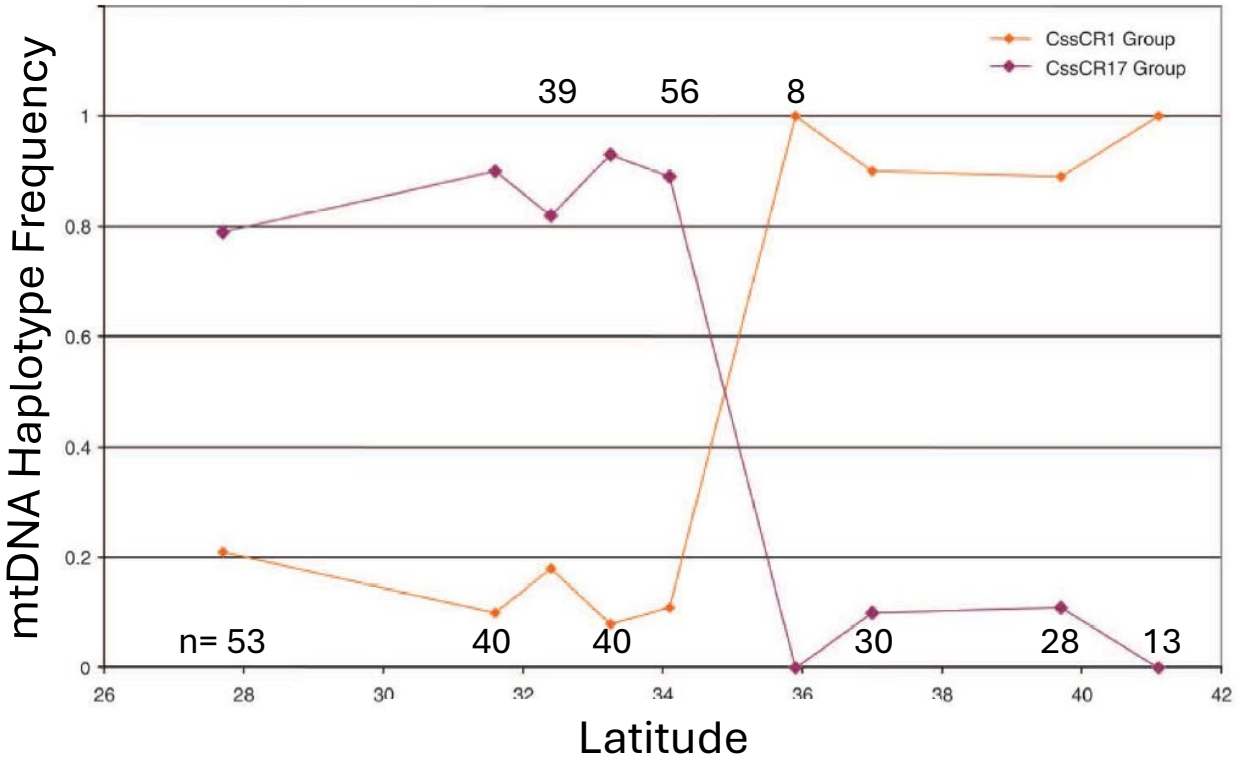
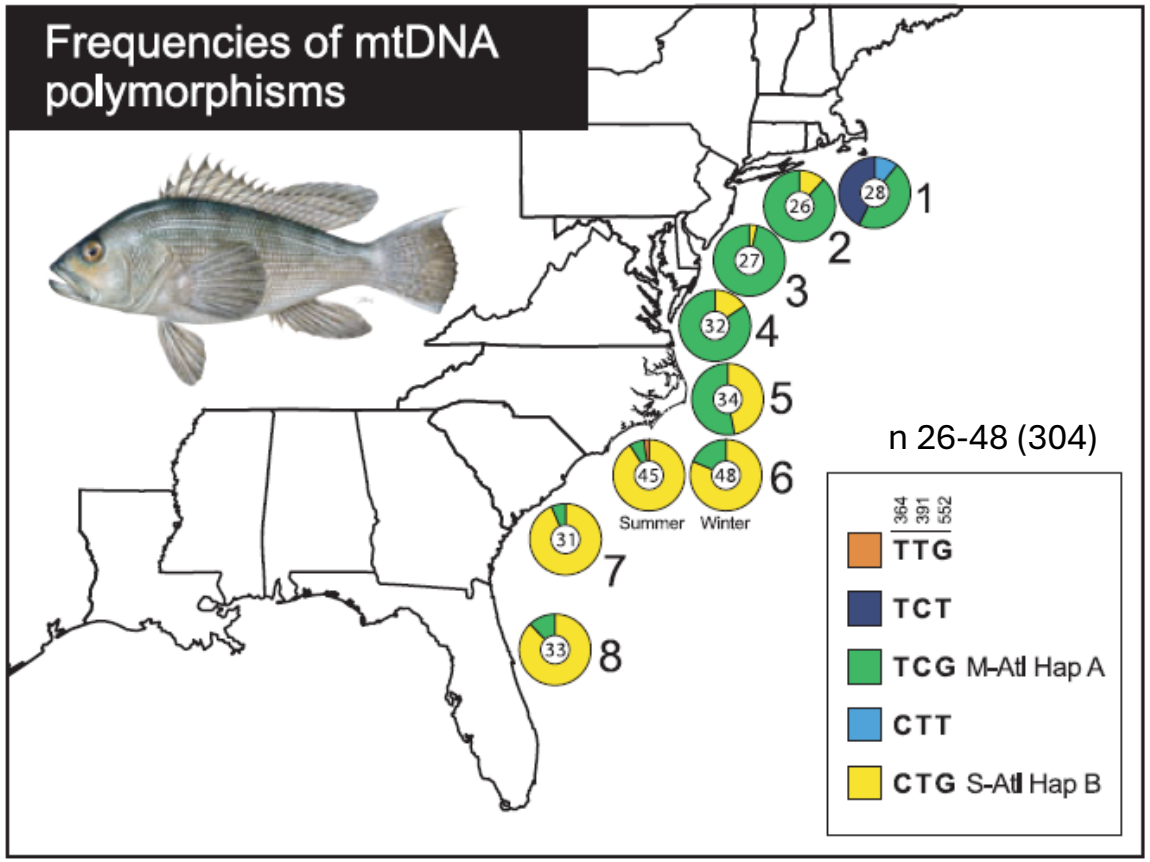
SCDNR MRRI

SSC October 2025

Black Sea Bass (*Centropristis striata*) U.S. Genetics Background

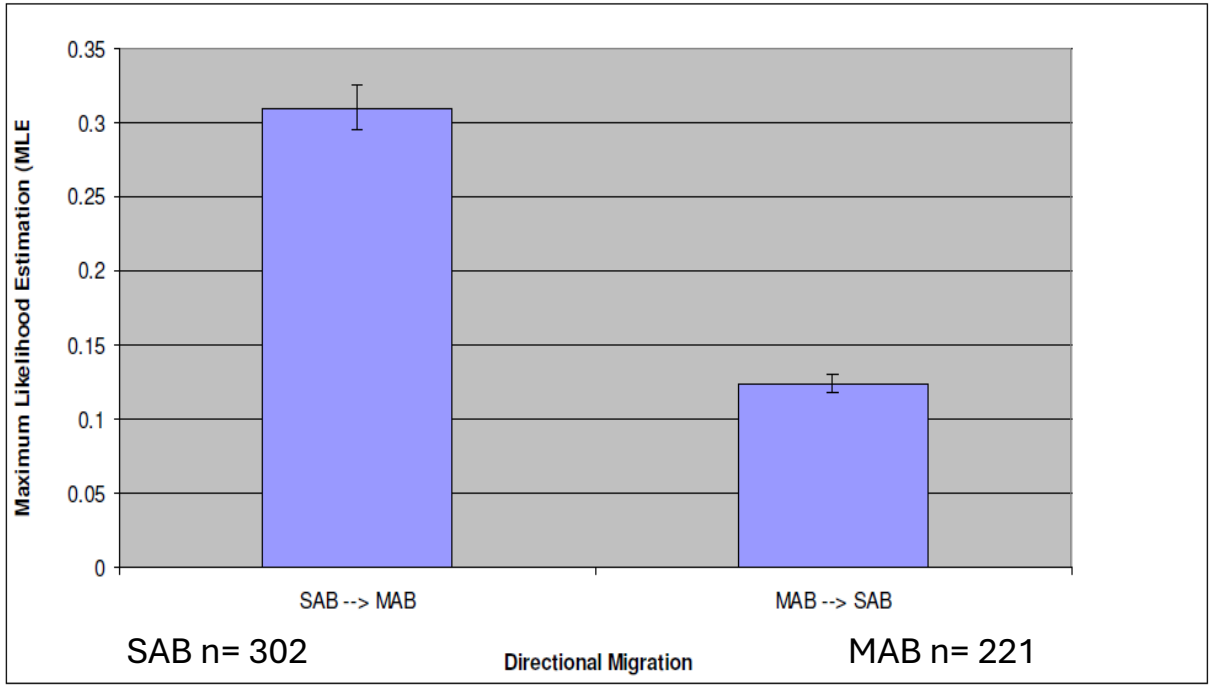


Roy et al. 2012
Mixing, but break @ NC / VA

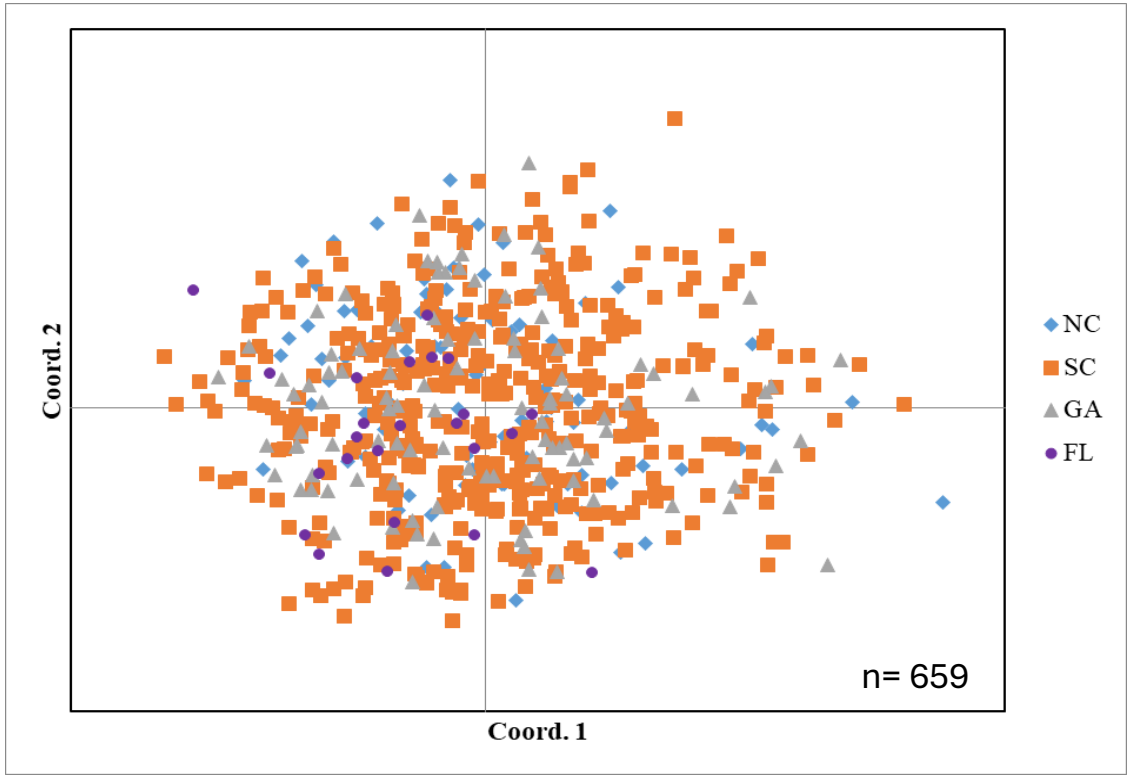


McCartney et al. 2013 (also S25RD42)
Mixing, but break @ NC / VA

Black Sea Bass (*Centropristis striata*) U.S. Genetics Background

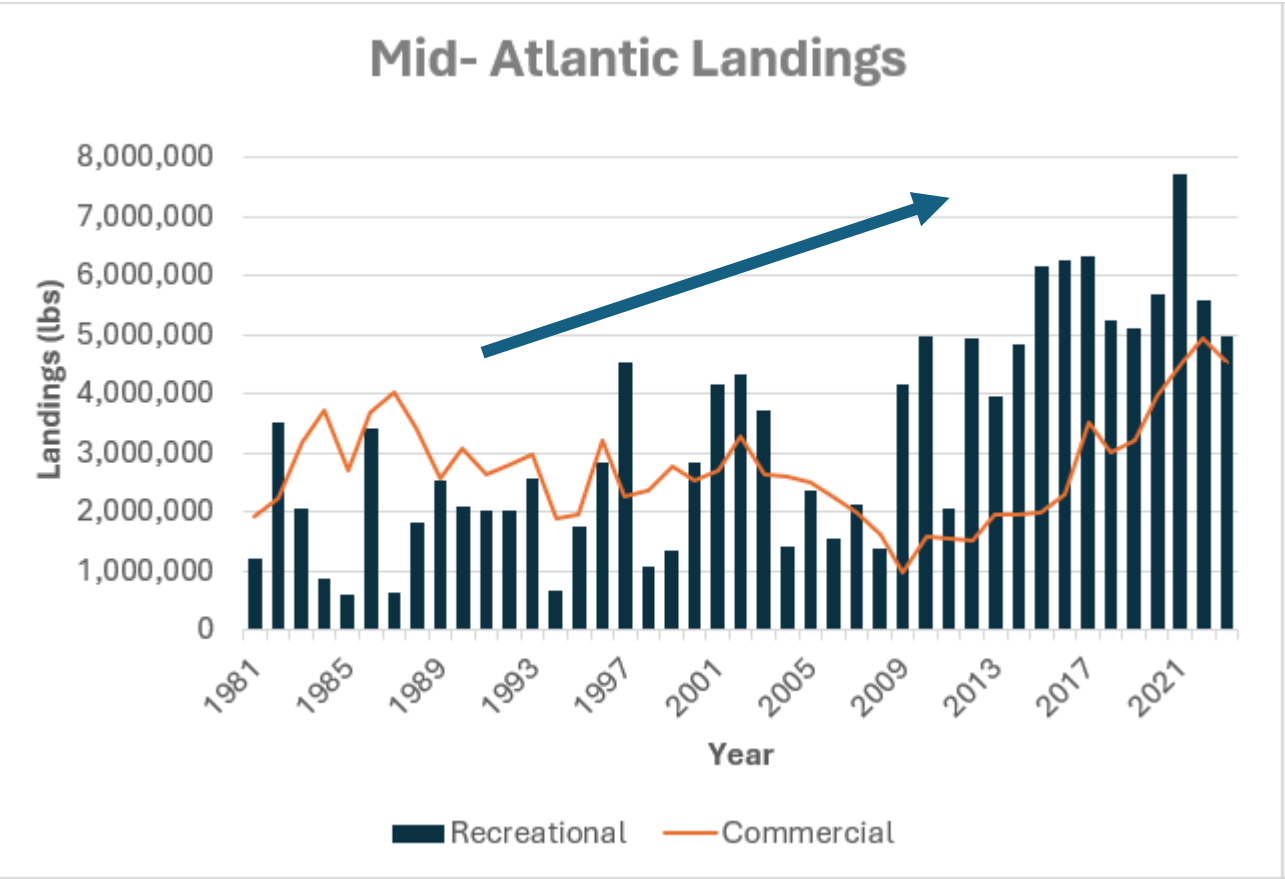


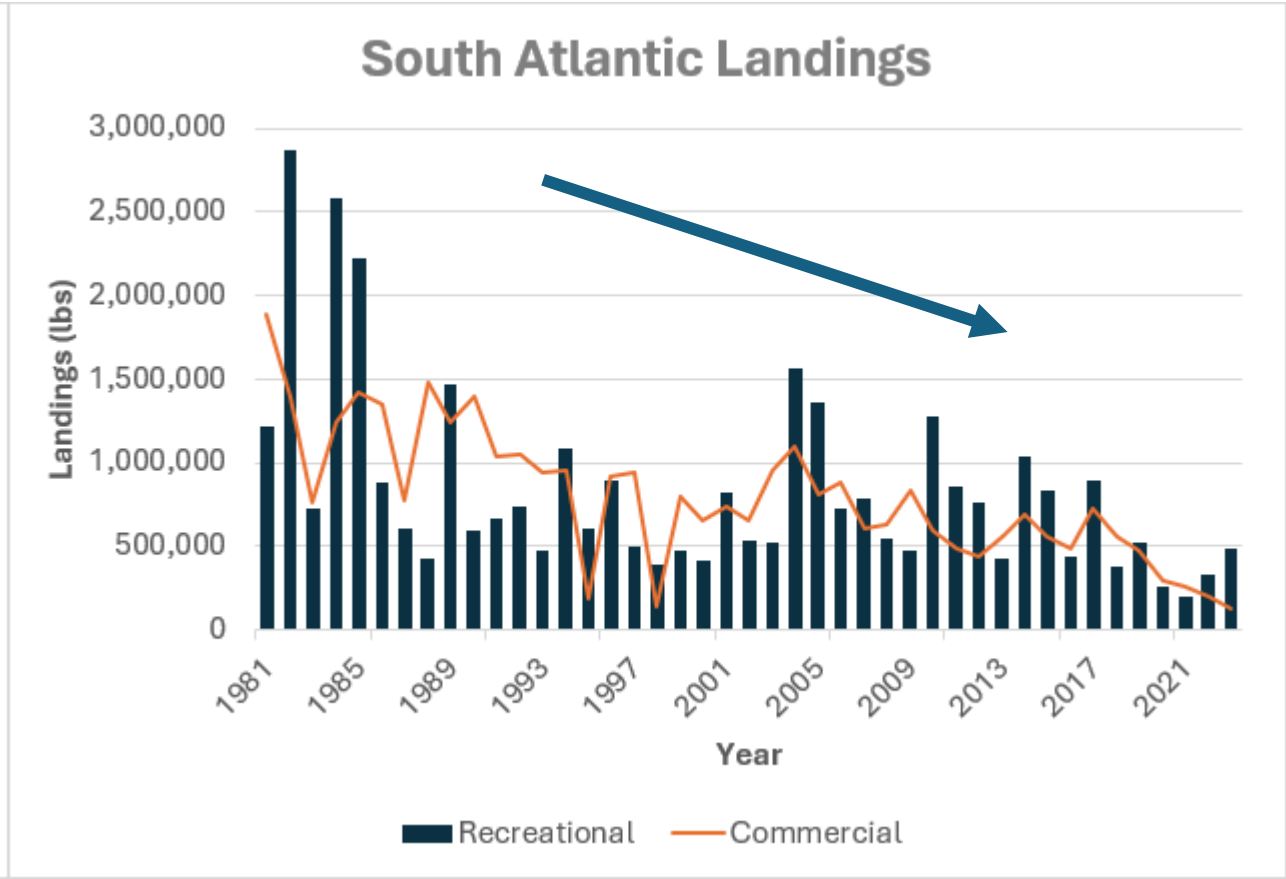
Lewandowski MSc Thesis 2014
nDNA: Mixing, but skewed towards "SAB" signal more prevalent in "MAB"; break at NC / VA



O'Donnell & Darden 2015 SeaGrant Report
Microsatellites, 10-13 loci
Well-mixed within SA "stock"

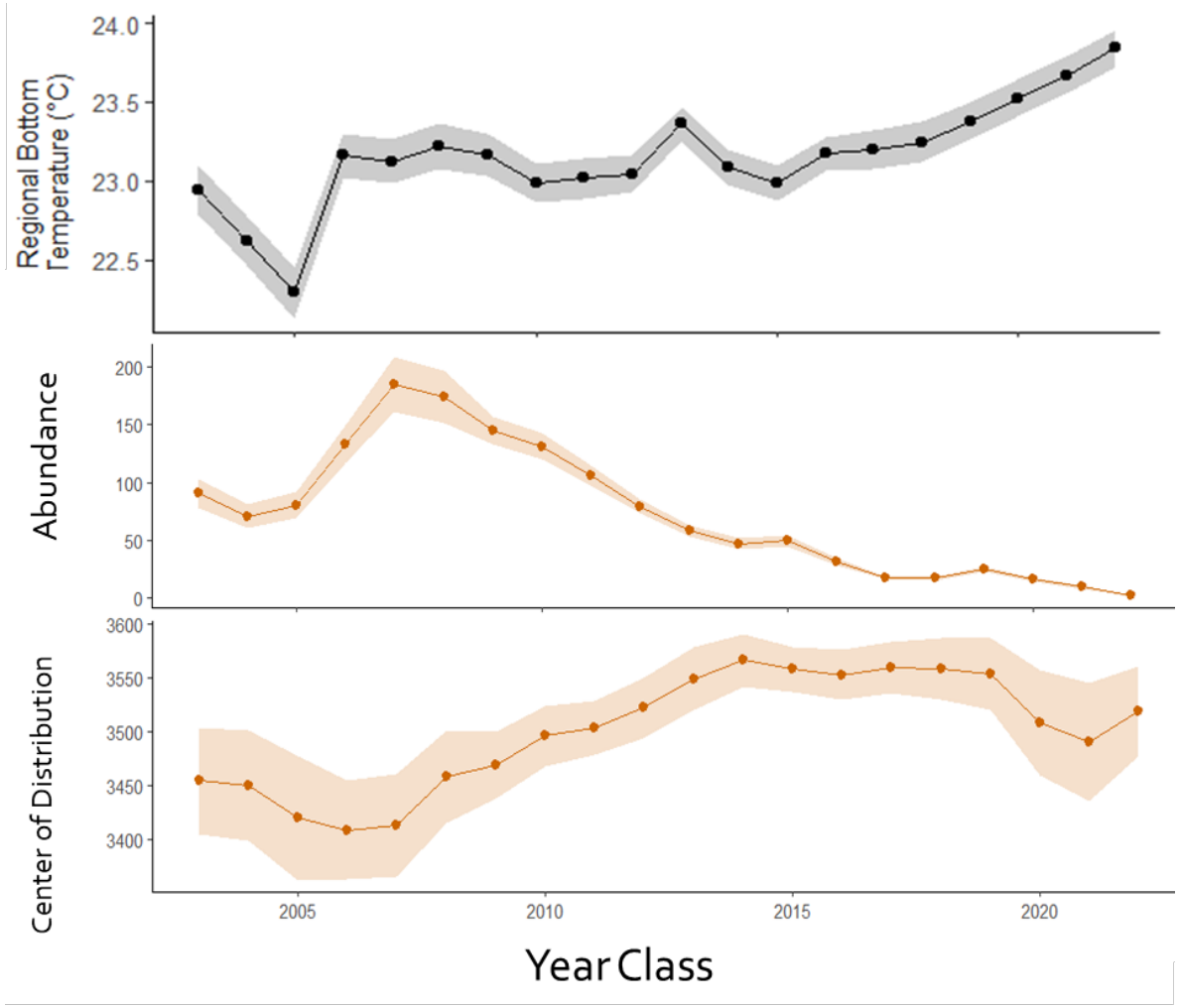
Why look at BSB genetic structure again?

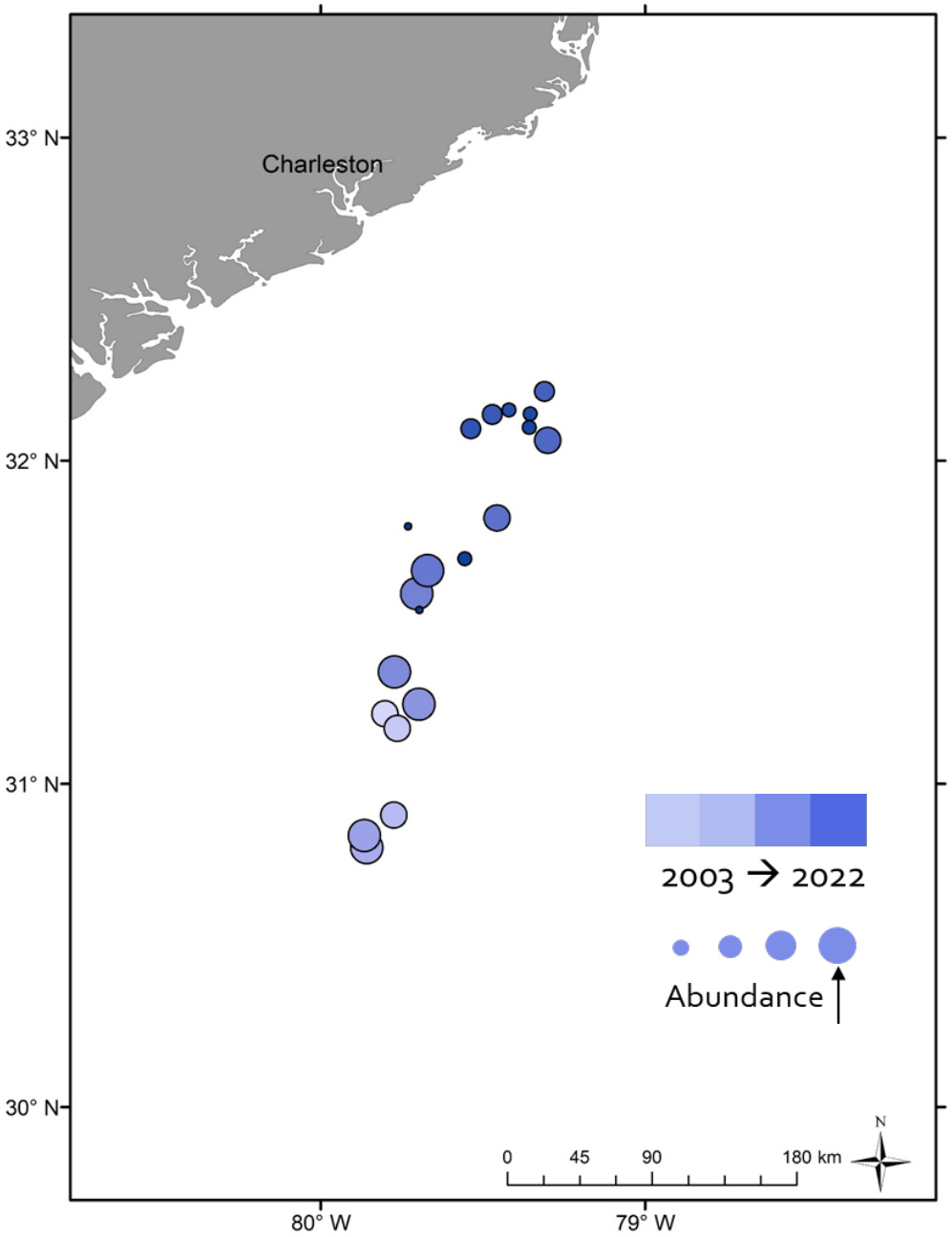




NMFS MRIP and ACCSP

Vecchio et al. 2025

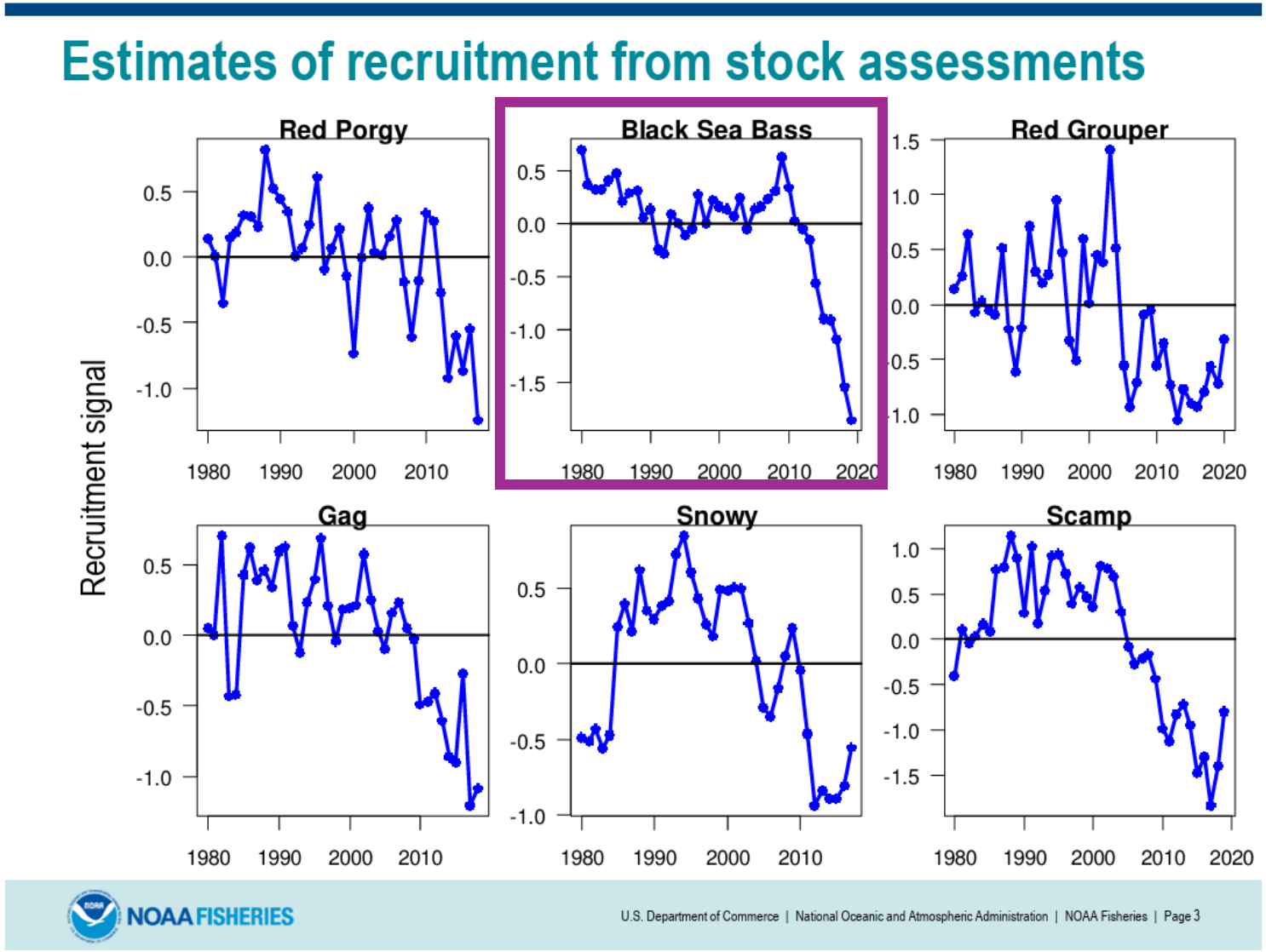




- Compression of the stock or migration of the stock?

Recruitment Winners and Losers?

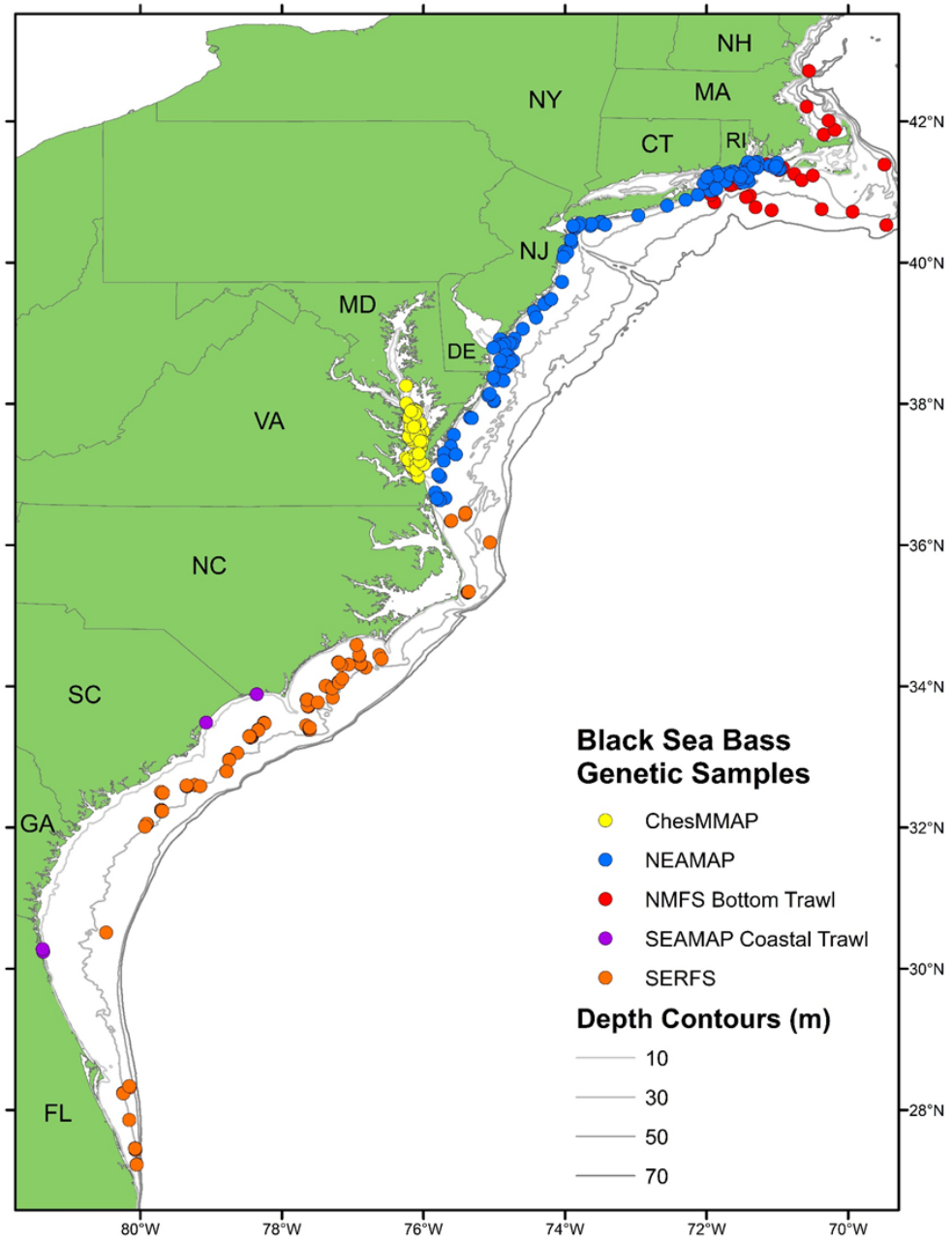
- Shertzer et al. April 2024 SSC presentation



Genetics Assessment Objective:

- **Re-assess population genetic structure along US Atlantic coast**
  - **Southern stock contracting within the south Atlantic?**
  - **Southern stock shifting into the mid Altantic; introgressing with northern stock?**

Field Collections



- **Genetic samples taken during 2024 field season:**

Survey	Samples Collected	Samples Processed
NMFS Bottom Trawl	144	144
NEAMAP	564	293
ChesMMAP	189	147
SEAMAP	6	6
SERFS	202	202
Totals	1,105	792

Genetic Marker Panel

- Samples genotyped at 13 microsatellite loci
  - Previously used in O'Donnell & Darden 2019
- Reduced to 9 loci for analyses
  - Alleles/locus: 14-37
  - Average alleles/locus: 20.8

Glossary of genetic terminology:

- **Locus** (*pl.* loci): a particular location or position in the genome
- **Allele**: one of two or more variants of a single locus

Structure Analysis

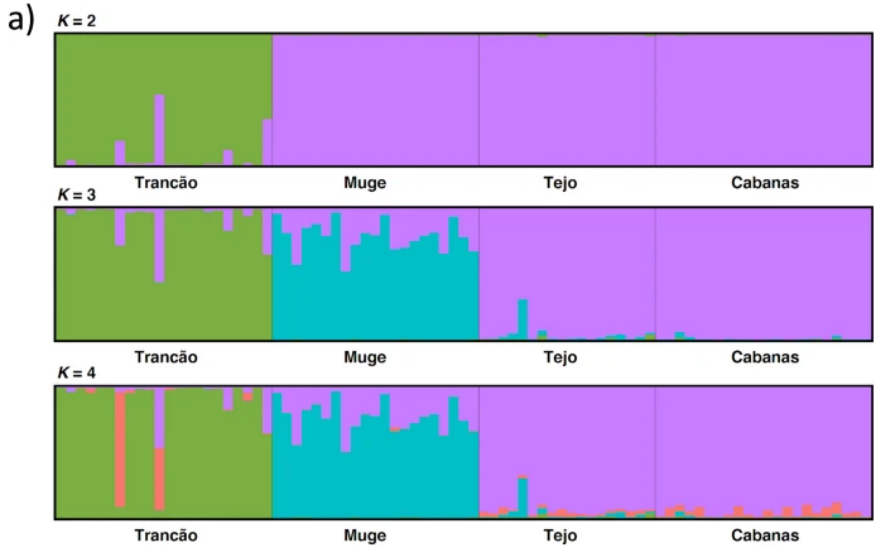
Multi-locus data for individuals

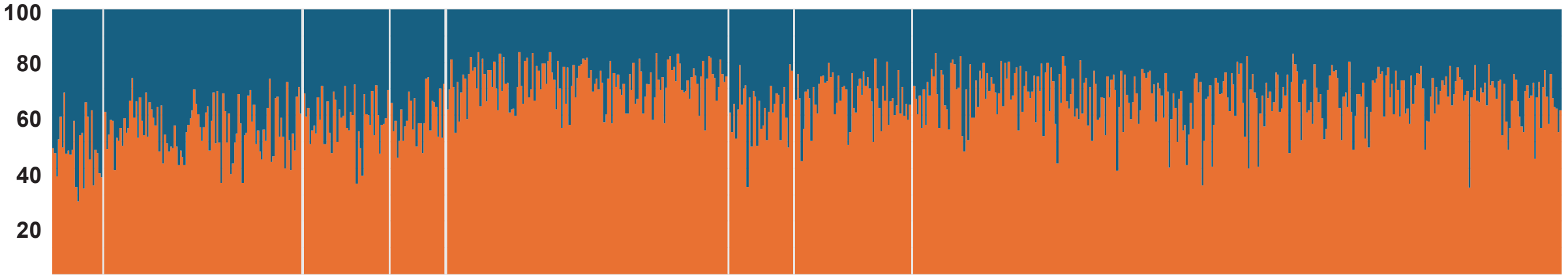
Specify priors, number of populations (*K*) to test

MCMC algorithm to reassign individuals to clusters, improving fit

Calculate overall likelihood, estimate % genetic cluster for each individual

Plot results for each *K*, Compare likelihoods





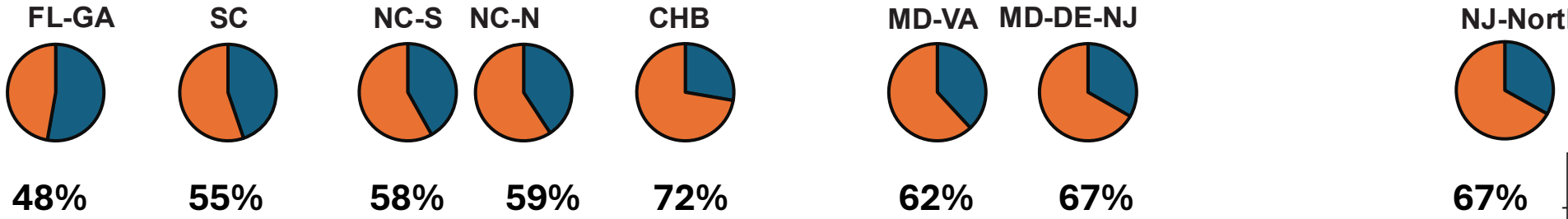
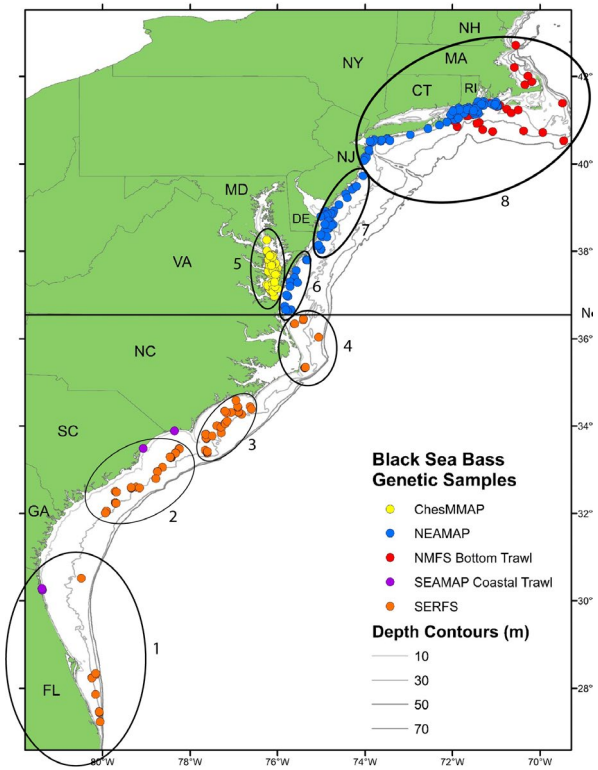
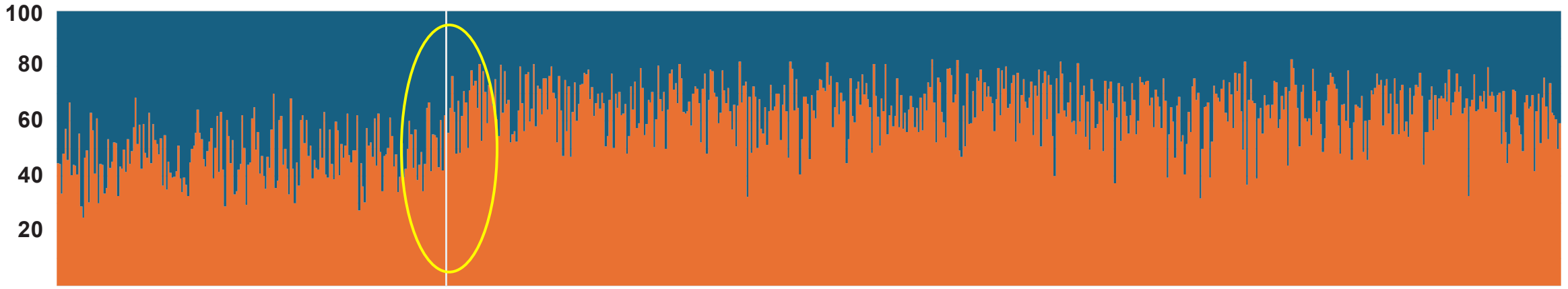


Figure 2

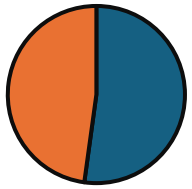
- Complex genetic ancestry
- Shift in composition between southern and northern areas

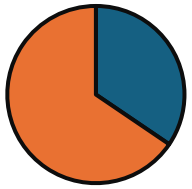




South

North



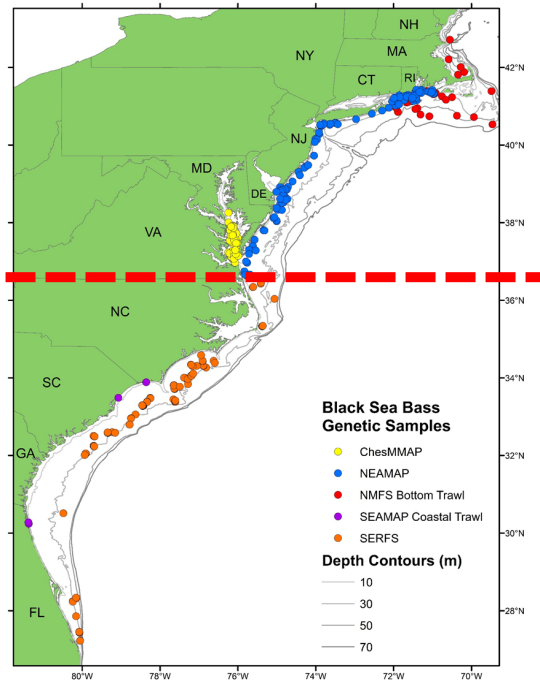


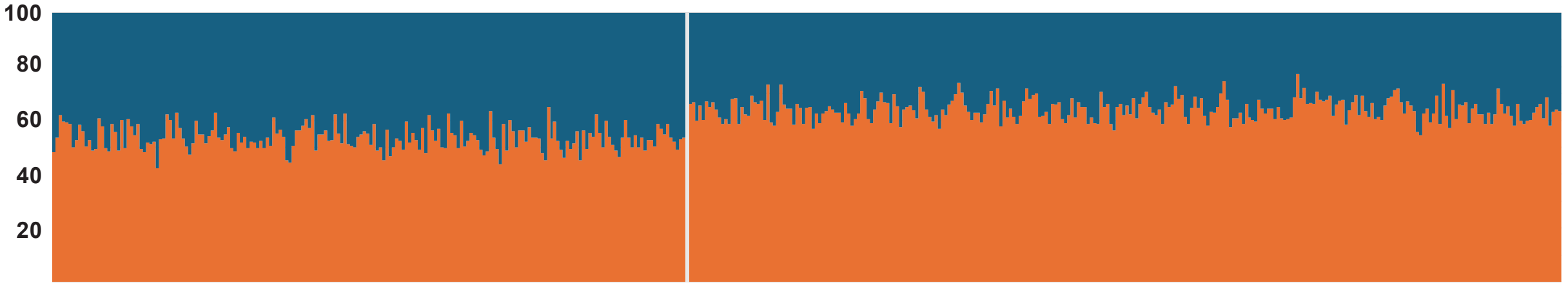
48%

65%

Figure 3

- Distinct genetic compositions between southern and northern areas
- Transition zone apparent





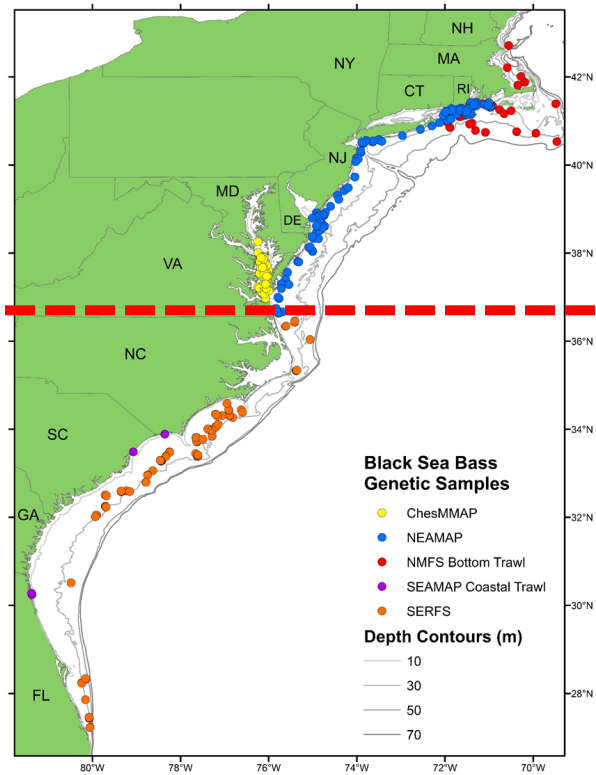
South

46%

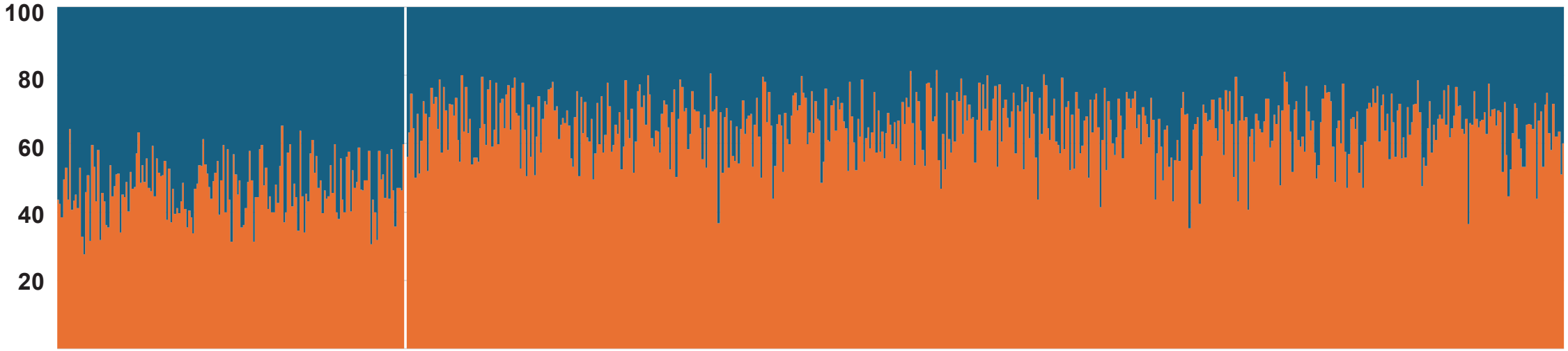
North

64%

Figure 4



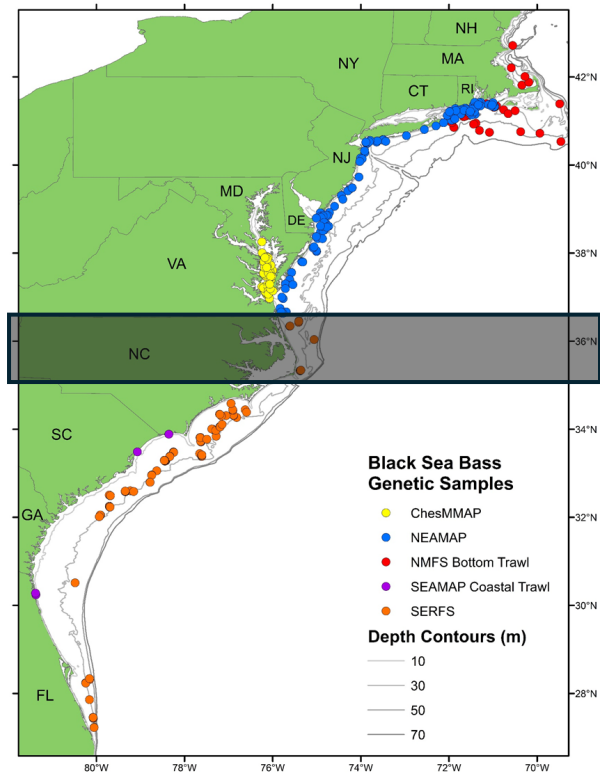
- Age 0-1 fish removed (< 175 mm)
- Distinction between southern and northern areas
- Year class effects not driving pattern



47%

65%

- Transition zone samples removed
- Distinction between southern and northern areas clearer



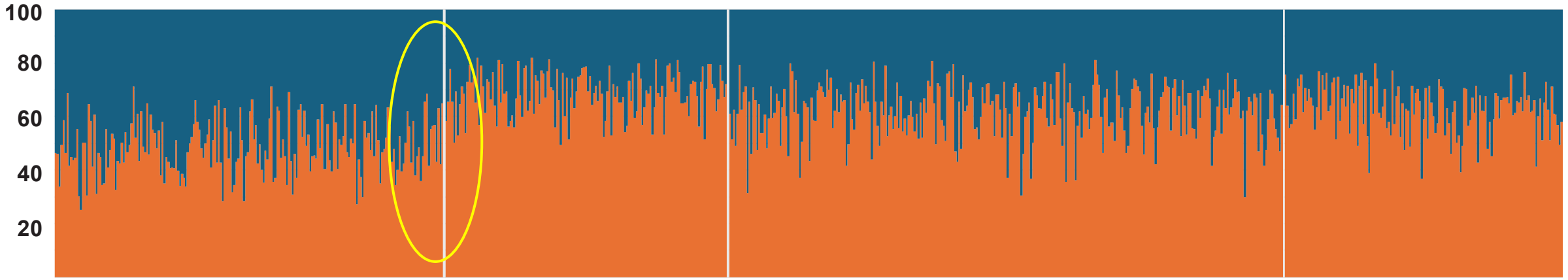


Figure 5

SERFS

49%

ChesMMAP

69%

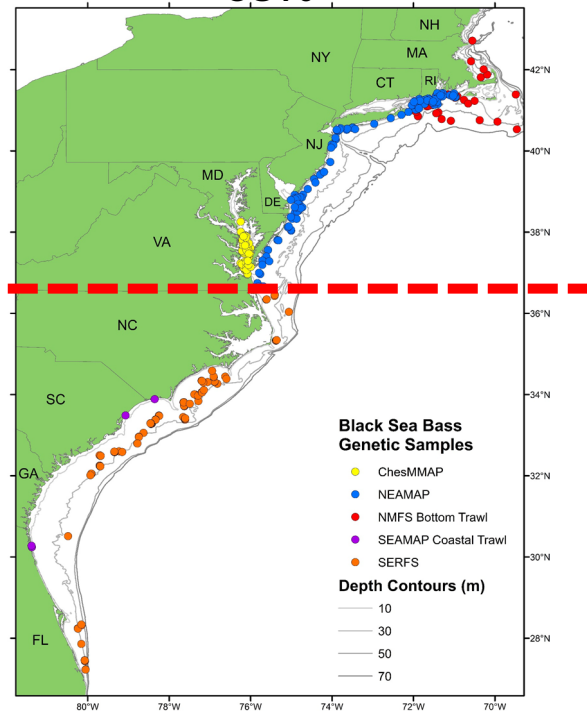
NEAMAP

62%

NEBT

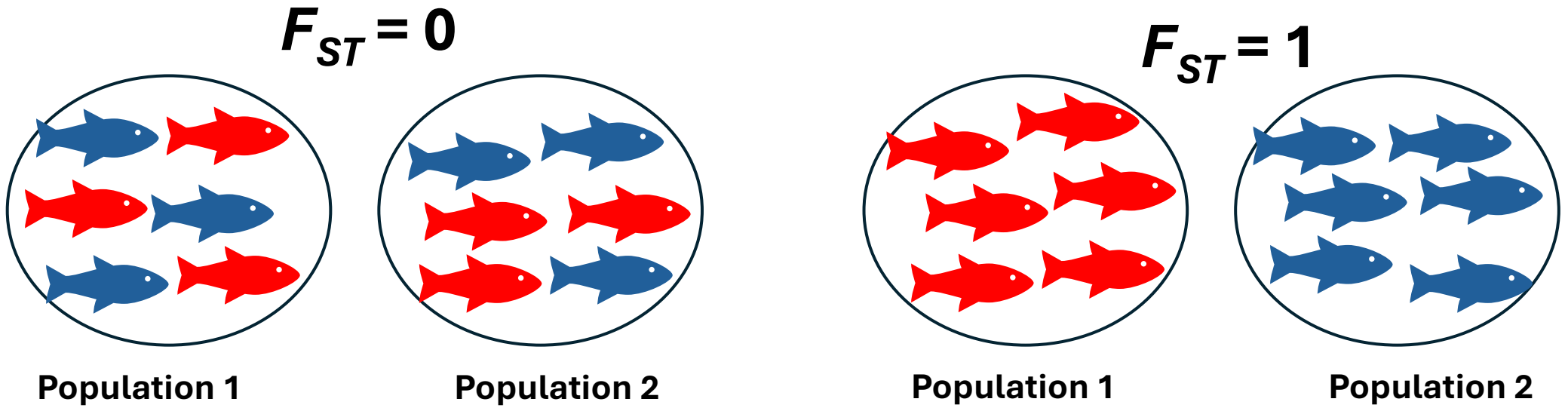
63%

- Distinction between southern and northern surveys
- Transition zone apparent at northern end of SERFS range



F_{ST} The Fixation Index

- Quantifies the amount of differentiation in allele frequencies between populations
  - Ranges from 0 (panmixia) to 1 (complete segregation).



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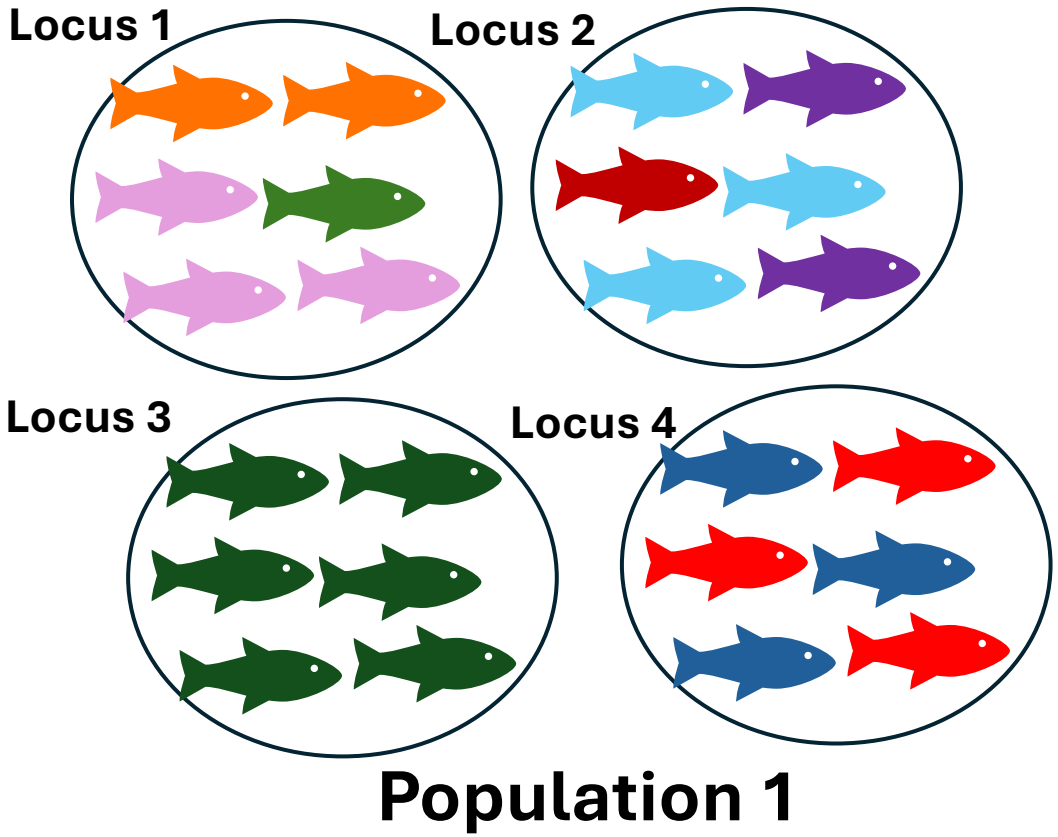
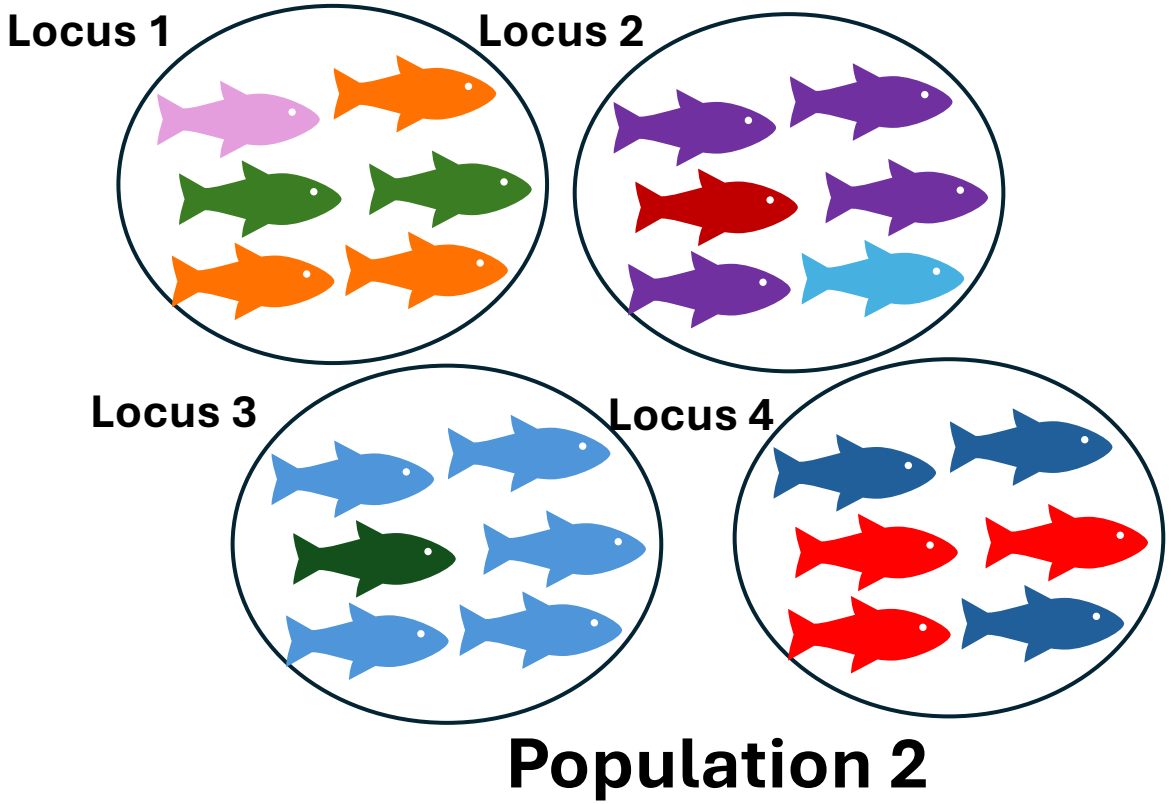
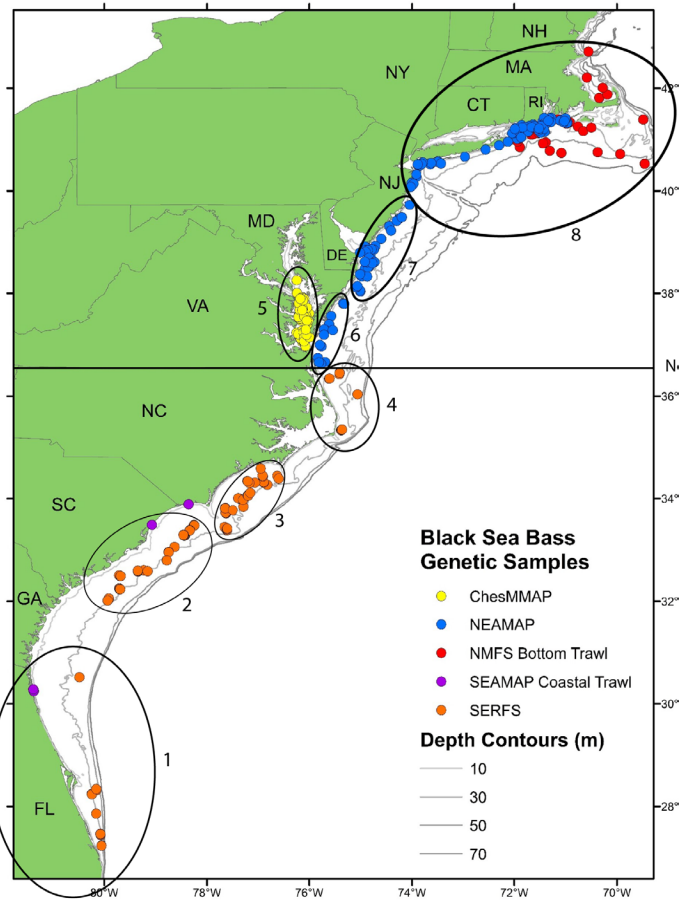




Significant F_{ST} *only between southern and northern areas*

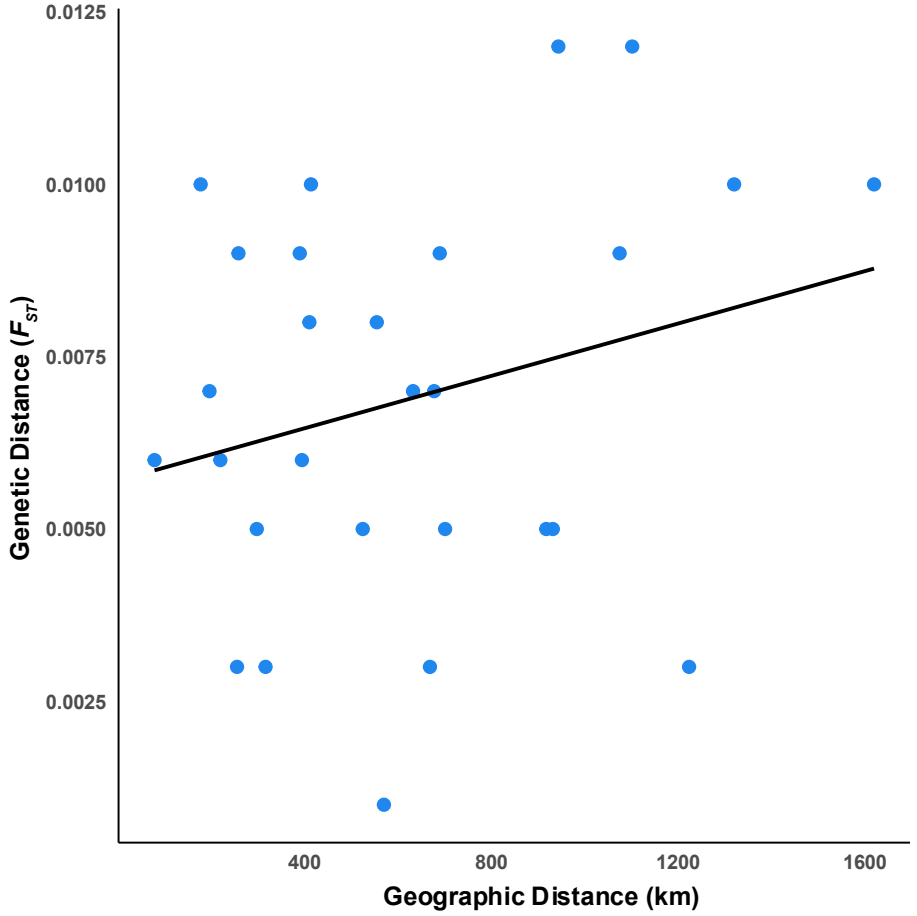
- Pattern supports genetic differences across 2 populations
- Southern vs northern areas: F_{ST} = *0.002*
  - F_{ST} = *0.003* without transition zone samples



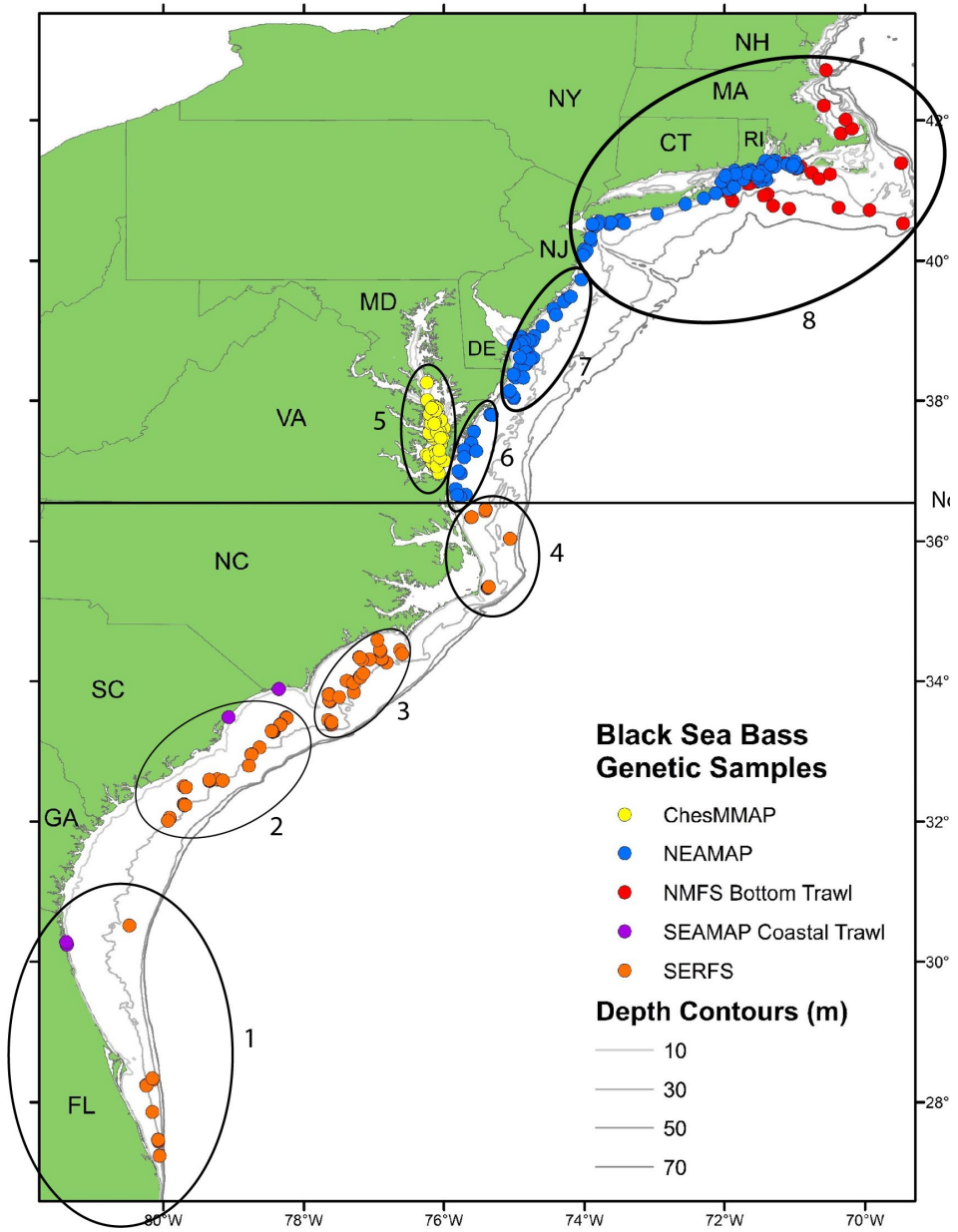
	1. FL_GA	2. SC	3. NC_S	4. NC_N	5. CHB	6. MD_VA_off	7. MD_DE_NJ_Off	8. NJ_North
1. FL_GA		0.192	0.238	0.253	**0.019**	**0.033**	**0.023**	**0.002**
2. SC	0.008		0.440	0.112	**0.042**	0.480	**0.042**	**0.002**
3. NC _S	0.009	0.005		0.230	**0.028**	0.055	0.092	**0.039**
4. NC_N	0.012	0.008	0.009		0.117	0.325	0.078	0.058
5. CHB	**0.009**	**0.003**	**0.006**	0.007		0.265	0.806	0.573
6. MD_VA_Off	**0.012**	0.005	0.010	0.010	0.006		0.522	0.476
7. MD_DE_NJ_Off	**0.010**	**0.005**	0.007	0.009	0.003	0.006		0.511
8. NJ_North	**0.010**	**0.003**	**0.005**	0.007	0.001	0.005	0.003	

No significant Isolation by Distance

- *Consistent with a 2 populations scenario*



Mantel r = 0.255; p-value = 0.175



Migration rate estimates similar to previous studies

Study	Individuals per generation	Source to Destination
Current study	**116**	Directionality not inferred
Roy et al. 2012	**63-163**	Mid-Atlantic to South
McCartney et al. 2013	**179.5**	Mid-Atlantic to North Carolina, north of Cape Hatteras
McCartney et al. 2013	**19.2**	Mid-Atlantic to south of Cape Hatteras

Genetic Health of Populations

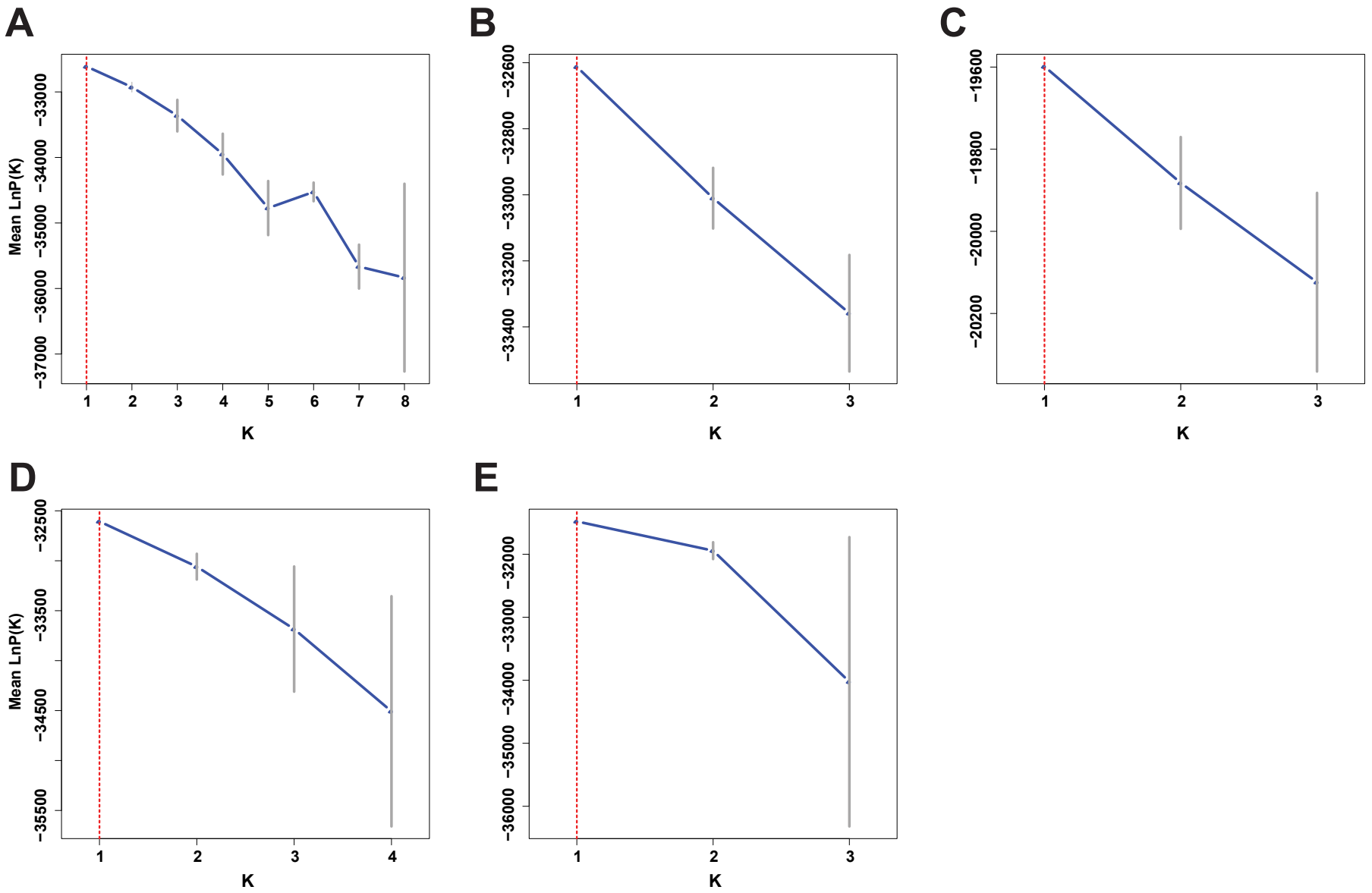
- Similar high genetic diversity in both populations
- Low inbreeding detected in both populations
- Both populations have experienced past bottlenecks
- Effective population sizes both large
  - NOT census size; ratios not static
  - Complex processes

Grouping	N	A_N	A_E	H_O	H_E	F_{IS}	G-W	N_E
South	200	19.56	9.87	0.789	0.860	0.084	0.415	14,571 [3352.6 - ∞]
North	573	22.11	9.77	0.798	0.861	0.074	0.441	15,889 [1291.5 - ∞]
Range-wide	733	20.83	9.82	0.793	0.860	0.078	0.428	

Conclusions

- New data continue to support 2 genetic populations
  - Patterns of allele frequency shifts are consistent with previous studies with a transition zone occurring NC-VA boarder
- Weak differentiation due to effective migration (i.e., gene flow between populations)
  - Rates of exchange are stable across several studies (and time)
- Genetic health of both populations is good
- Therefore, the southern stock is experiencing a constriction of its range
  - No indication of northward range expansion or introgression with northern population

Log likelihood plots from alternative Structure analyses



How Have Stock Boundaries Been Defined?

SEDAR2 set South Atlantic stock boundaries at FL Keys & NC / VA border

Northern

- Movement & Migration
  - Seasonal migration (Musick & Mercer 1977)
- Life History
  - Summer spawning (Musick & Mercer 1977)
- Genetics
  - Single East Coast stock (Bob Chapman SCDNR, pers. comm.)

Southern

- Movement & Migration
  - No seasonal migration (Ansley & Harris 1981, Collins et al. 1996)
- Life History
  - Winter/Spring spawning (McGovern et al. 2002)
- Genetics
  - Single East Coast stock (Bob Chapman SCDNR, pers. comm.

Stock ID from SEDAR25, 56, 76

- SEDAR25 Benchmark
  - Maintained splits at FL Keys and NC/VA
  - McCartney & Burton S25RD42: Genetics= Gulf, SA, MA/NE, mixing NC/VA
  - Schaffler, J. (ODU, pers. comm.): otolith microchemisty matched source waters (SC/NC vs VA/DE)
  - Rudershausen et al. (2010): minimal movement off NC
- SEDAR56 Standard
  - No TOR for stock boundaries
- SEDAR76 Operational
  - No TOR for stock boundaries

What to do with this?

- Genetics not the only input to setting a stock boundary
  - New genetics data
  - New movement data by region
  - New LH data by region

New Movement Information

Mid-Atlantic / Northeast

- Moser & Shepherd 2009
- Provost et al. 2017
- Zavell et al. 2023
- Patel et al. 2024
- Santos et al. 2025

South Atlantic

- Edwards et al. 2008

New Life History Information

Mid-Atlantic / Northeast

- Berlinsky et al. 2000, 2004
- Colburn et al. 2009
- Hales & Able 2001
- Miller et al. 2016
- Provost et al. 2017
- McBride et al. 2018
- Slesinger et al. 2019, 2022
- Younes et al. 2020
- McMahan et al. 2020
- Meseck et al. 2022

South Atlantic