

# Assessing the population structure and demographic dynamics of the North Atlantic Bonnethead, *Sphyrna tiburo*, as a potential response to ocean warming



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## INTRODUCTION

*Sphyrna tiburo*, commonly known as the bonnethead shark, is a small coastal shark distributed in subtropical and tropical waters. In the western north Atlantic, three genetically distinct populations are present, one being the southeastern US Atlantic coast population<sup>[1]</sup>.

### Significance

- Bonnetheads are identified as a globally endangered species by the IUCN<sup>[2]</sup> and are among other small coastal sharks vulnerable to recreational and commercial fisheries<sup>[3]</sup>.
- Assessing the genetic diversity and connectivity within and between populations in sharks is relevant for understanding their biology and delineating conservation plans.
- Genetic data also allow for the temporal analysis of genetic diversity and demographic trends that can reflect population declines or expansions. Recently, population expansions (e.g., in tiger sharks) have been associated with ocean warming<sup>[4]</sup>

### Objectives & Hypotheses

- Assessing the genetic diversity and population connectivity of the bonnethead from locations in the south-eastern US Atlantic coast:** We hypothesized that North Carolina samples belong to the same population as those samples from other southern localities (South Carolina, Georgia, Central Florida, North Florida), given known migratory patterns and the lack of biogeographic barriers to gene flow for coastal species in the South Atlantic Bight.
- Estimating contemporary effective population size in the eastern US Atlantic coast, and assessing changes of effective population size across time in this population.** Given the biology and distribution of the species, we hypothesized that we would find signals of recent population expansion in the eastern US Atlantic coast population as consequence of ocean warming.

## MATERIALS & METHODS

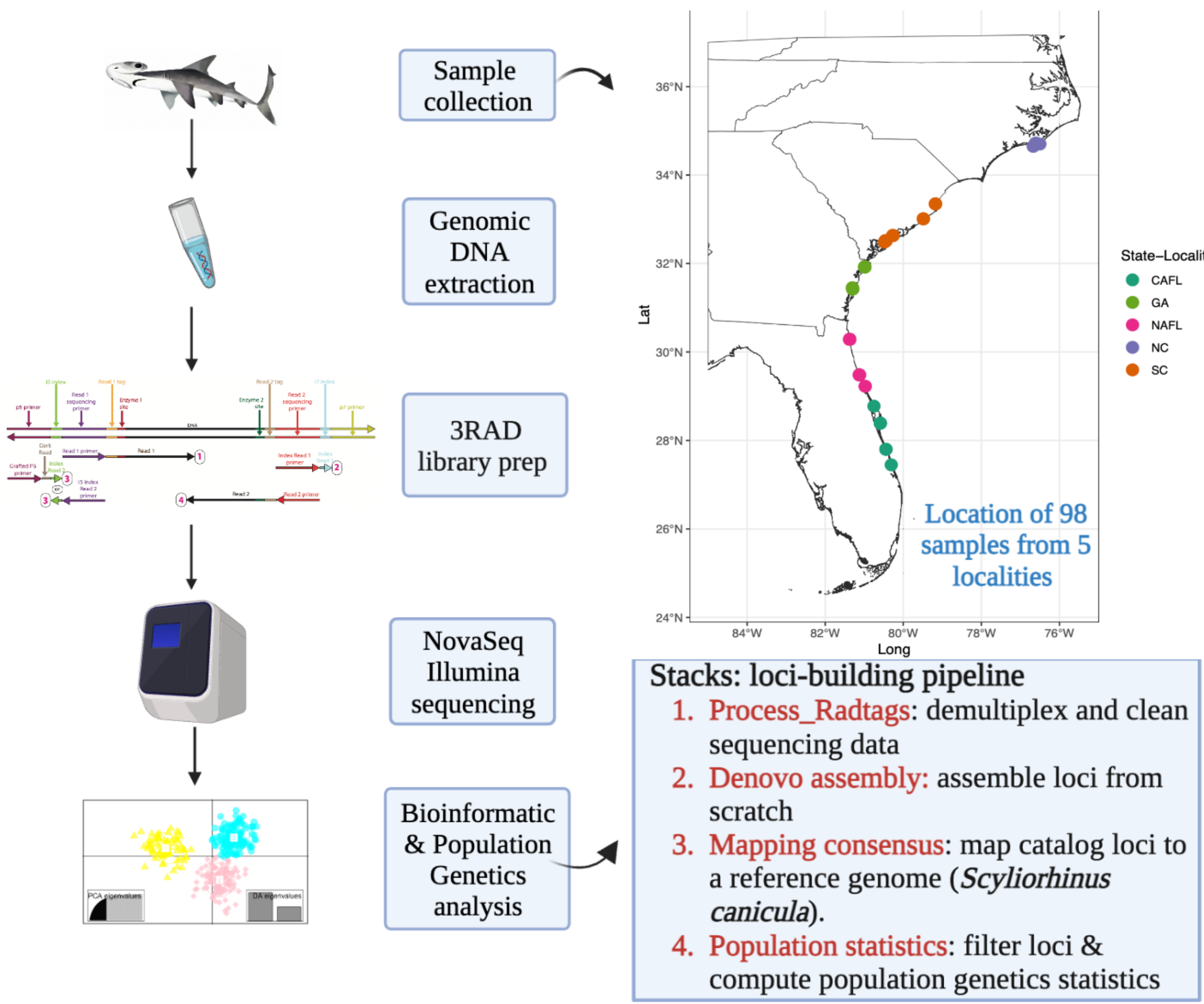


Figure 1. Workflow for the generation and analysis of genomic data from the 98 bonnethead sharks (*Sphyrna tiburo*) from samples collected in the eastern US Atlantic coast.

## RESULTS

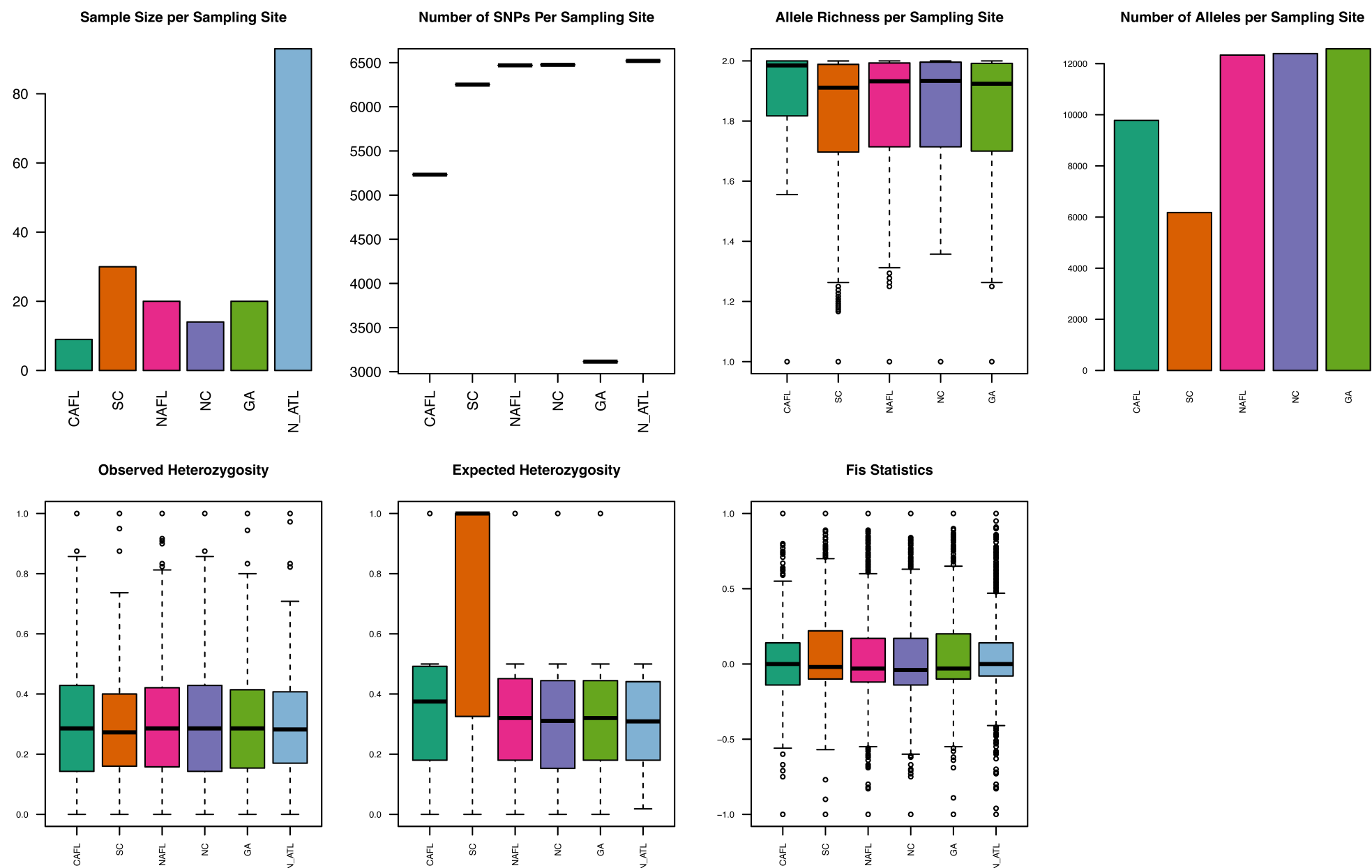


Figure 2: Genetic diversity indexes for 93 bonnethead sharks from five localities from the eastern US Atlantic coast using 3RAD data. Number of samples, number of SNPs (Single Nucleotide Polymorphisms), number of alleles, allele richness, observed and expected heterozygosity per sampling site and all sites combined are presented. Note that N\_ATL (North Atlantic) refers to all sampling sites combined. This database contains 31.95% missing data among individuals and SNPs. No major differences between localities in terms of genetic diversity are observed.

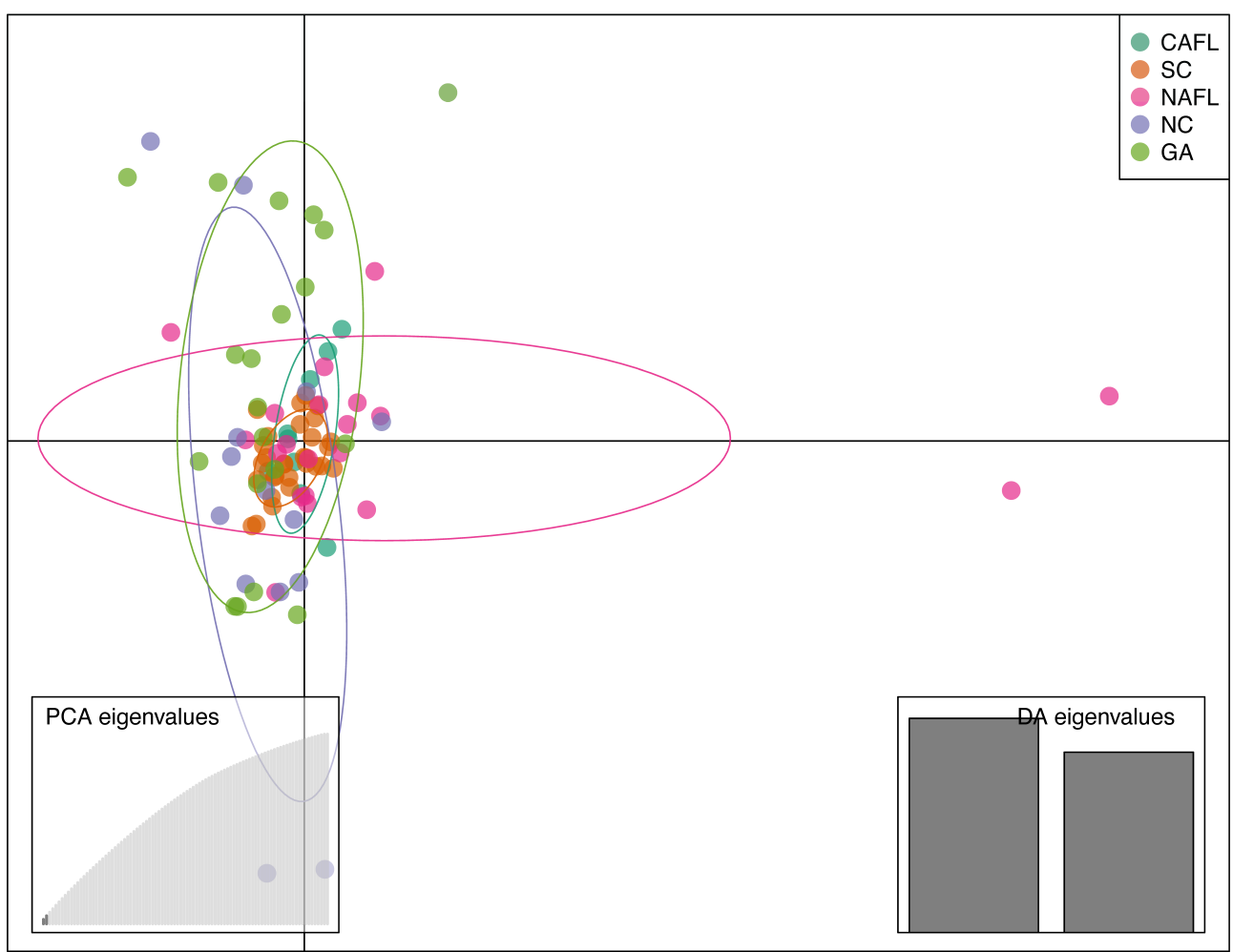


Figure 3. Discriminant Analysis of Principal Components (DAPC) of 3RAD data from 93 bonnethead sharks from the eastern US Atlantic coast. Using the first two principal components from a database of 6,520 SNPs. Samples from the five localities cluster together suggesting one panmictic population.

	CAFL	SC	NAFL	NC	GA
CAFL		0.006	0.001	0.007	0.006
SC	0.003		0.009	0.009	0.010
NAFL	0.000	0.004		0.008	0.008
NC	0.006	0.004	0.007		0.002
GA	0.005	0.004	0.007	0.002	

Table 1: Pairwise  $F_{st}$  estimates between bonnethead sharks from five localities from the eastern US Atlantic coast using 6,520 SNPs. Above the diagonal is pairwise Nei's  $F_{st}$ , and below the diagonal is Weir & Cockerham  $F_{st}$ . Overall  $F_{st}$  values suggest no genetic differentiation between localities.

Lowest Allele Frequency	# Independent Alleles	$N_e$	95% CIs for $N_e$			
			Parametric		Jackknife	
0.1	11431734	841.9	823.5	861.1	231.7	Infinite
0.05	19433439	586.7	579.8	593.9	200.6	Infinite
0.02	20576781	509	503.8	514.3	193.6	Infinite
0	20699691	503.9	498.8	509	192.7	Infinite

Table 2: Estimations of contemporary effective population size ( $N_e$ ) using the linkage-disequilibrium (LDNE) method implemented in NEESTIMATOR2. The estimations are presented for different criteria values of lowest allele frequency (i.e., 0.1, 0.05, 0.02 and 0), as well as for the two methods implemented, parametric and jackknife, for which 95% confidence intervals are provided. The  $N_e$  column represents the mean  $N_e$  under the parametric method. Contemporary population size range between 504 and 842 individuals. These values are similar to those reported for other populations of sharks such as grey reef<sup>[6]</sup>.

## RESULTS (CONTINUED)

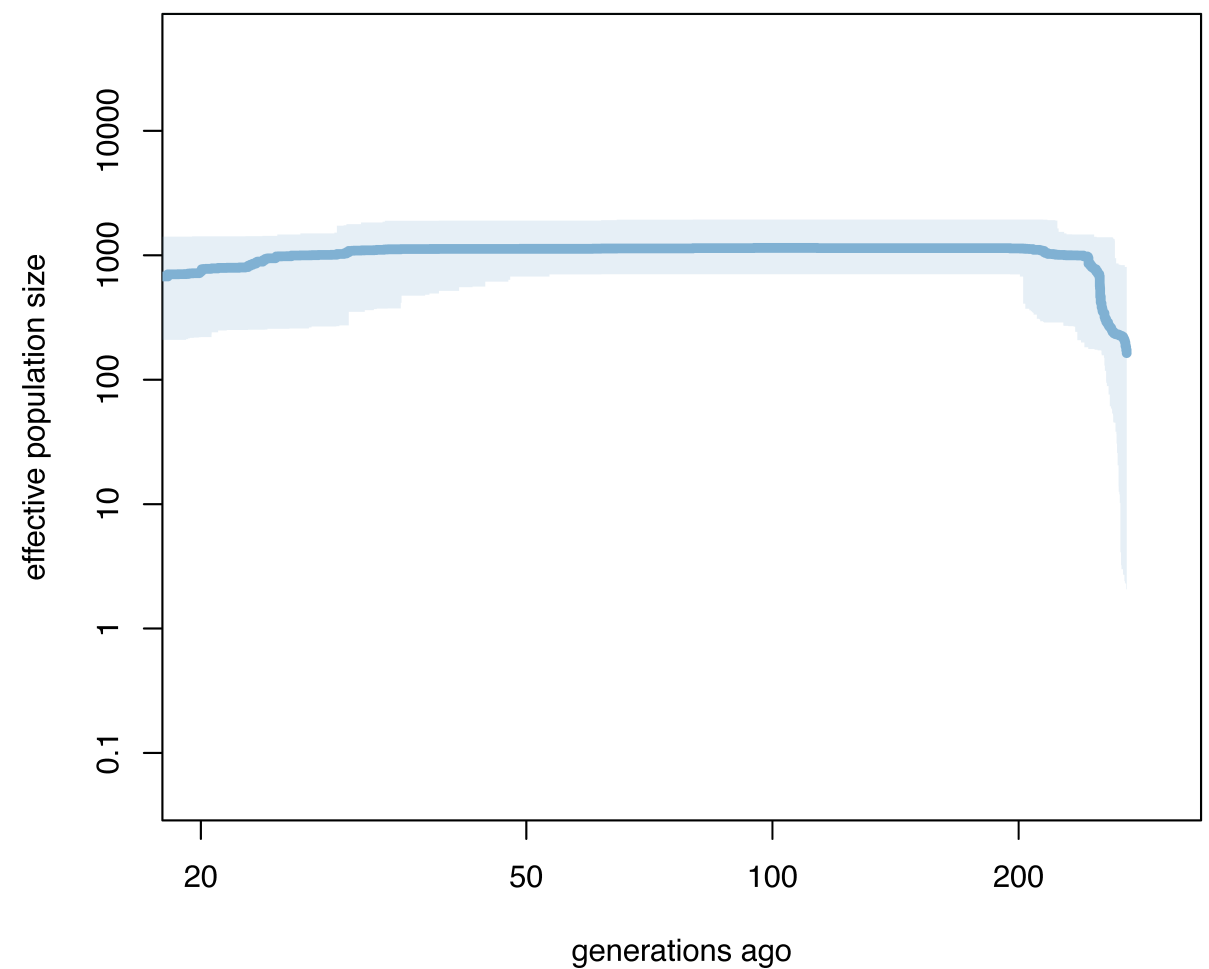


Figure 4: Historical population size changes in bonnethead sharks from the eastern US Atlantic coast. Variation of the effective population size ( $N_e$ ) through time/generations and its 95% confidence interval estimated by stairwayplot2 for the North Atlantic population of *Sphyrna tiburo*. The stairwayplot was computed using the folded site frequency spectrum from 56 individuals, 4,515 segregating sites, and a mutation rate  $\mu=1.93e-08$  per site per generation<sup>[5]</sup>. An ancestral expansion followed by a constant phase and slight decrease in recent times is observed.

## CONCLUSIONS

- Genetic diversity estimates, such as observed and expected heterozygosities, are similar across localities (Fig.2).
- We support our hypothesis that bonnethead shark samples from five localities from the eastern US Atlantic coast—Central Florida, North Florida, Georgia, South Carolina, and North Carolina—belong to one panmictic population (Table 1, Fig. 3).
- Estimated contemporary effective population size ranges from 500 to 800 individuals when using the linkage disequilibrium method implemented in Neestimator2 (Table 2).
- Reconstruction of historical population demography reveals a recent slight decrease in effective population size, rather than population expansion as it was expected under the hypothesis of population expansion facilitated by ocean warming (Fig. 4).

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## ACKNOWLEDGEMENTS

Thanks to Dr. Alfred Farris and OCIT team for their support with the HPC cluster at Oxford College. To Travis Glenn and Mandy Howard for their support with sequencing. To Dr. Taliaferro-Smith for support in the research laboratory space. To Joel Fodrie (UNC) and Jeff Plumlee for shark samples from NC and GA. And to FWC-FWRI and SCDNR for support with shark collections. And to Todd Pierson for support with data analyses.