NORTHROP GRUMMAN
ENGINEERING & SCIENCE
STUDENT DESIGN SHOWCASE
FLORIDA TECH

Growing Pains: A Genetic Comparison of Nurse Sharks (*Ginglymostoma cirratum*) with Differing Growth Rates

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Introduction

Nurse sharks, *Ginglymostoma cirratum*, range throughout the tropical and subtropical Atlantic, and are commonly found in coastal ecosystems in Southern Florida and the Keys. Nurse sharks like all Elasmobranchs (sharks, skates, and rays) are slow-growing and long lived, making them susceptible to extinction. Recently listed as vulnerable on the IUCN Red List[1,2], nurse sharks are relatively underrepresented in scientific literature, and much research remains to be done to understand and protect this species.

Growth rates and body size between fish populations of the same species can vary widely. Individuals in the tropics often grow faster and mature at a smaller size compared with individuals in temperate waters, because of the increased productivity of cooler water. But surprisingly, a recent study[6] on nurse sharks in Biscayne Bay, South Florida and Bimini, Bahamas found that the more-temperate Biscayne Bay population showed faster growth and smaller maximum adult size. As data on growth rates is important to conservation, it is vital to understand the source of within-species differences.

Figure 1. Collecting measurements and tissue from a juvenile nurse shark Credit: Shark Research and Conservation Program, University of Miami Rosenstiel School

Materials and Methods

We downloaded DNA sequences from GenBank (Accession numbers JF950288-JF950299 and KU904394) belonging to the cytochrome b gene region of the mitochondrion from nurse shark samples in South Florida and Bimini[7]. This included at least one full mitochondrial genome sequence from Dry Tortugas National Park, Florida[8]. These were aligned using the program MAFFT[9], trimmed, and adapted into a Bayesian phylogenetic tree using the MrBayes plugin for Geneious (Dotomatics).

Results

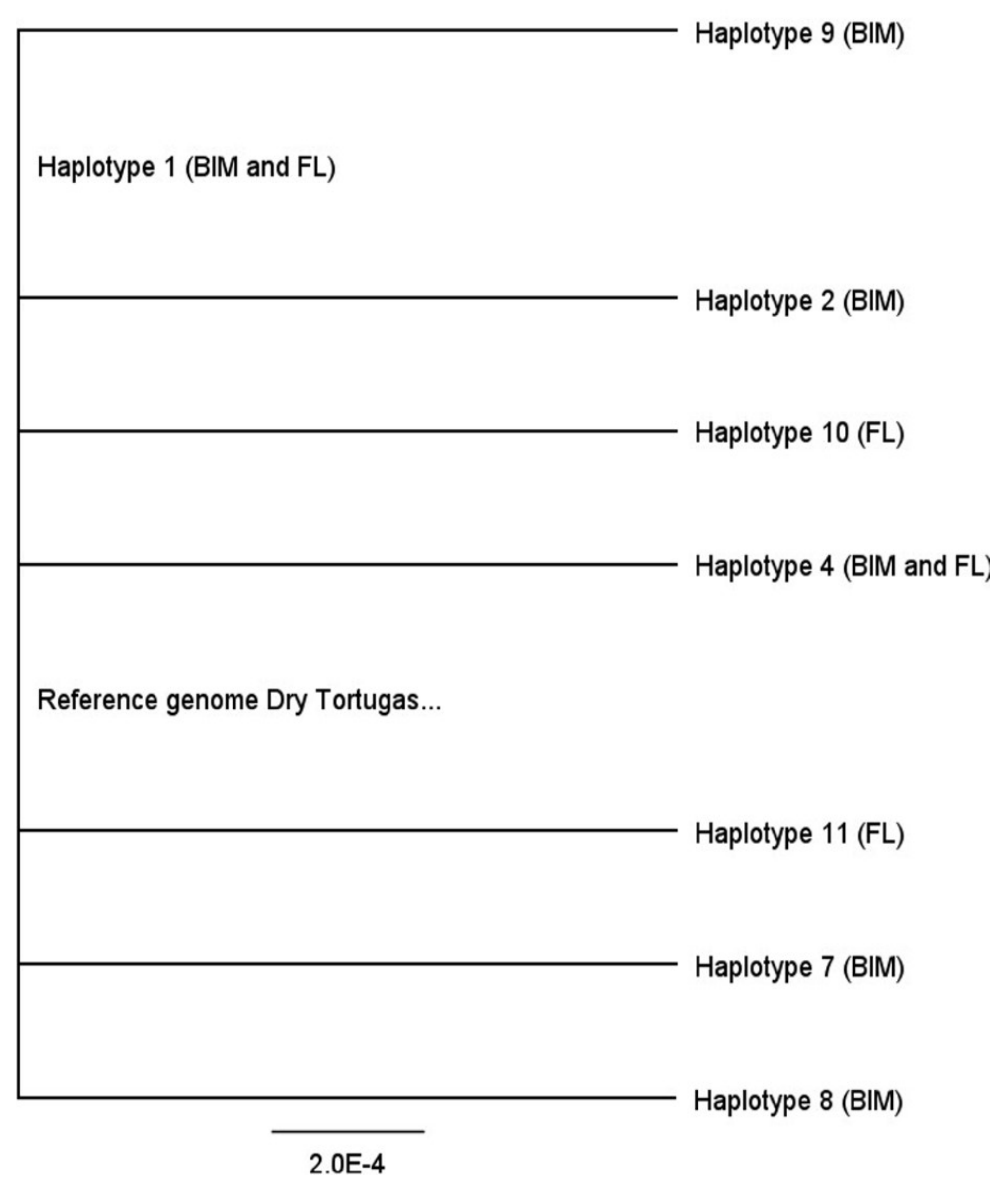
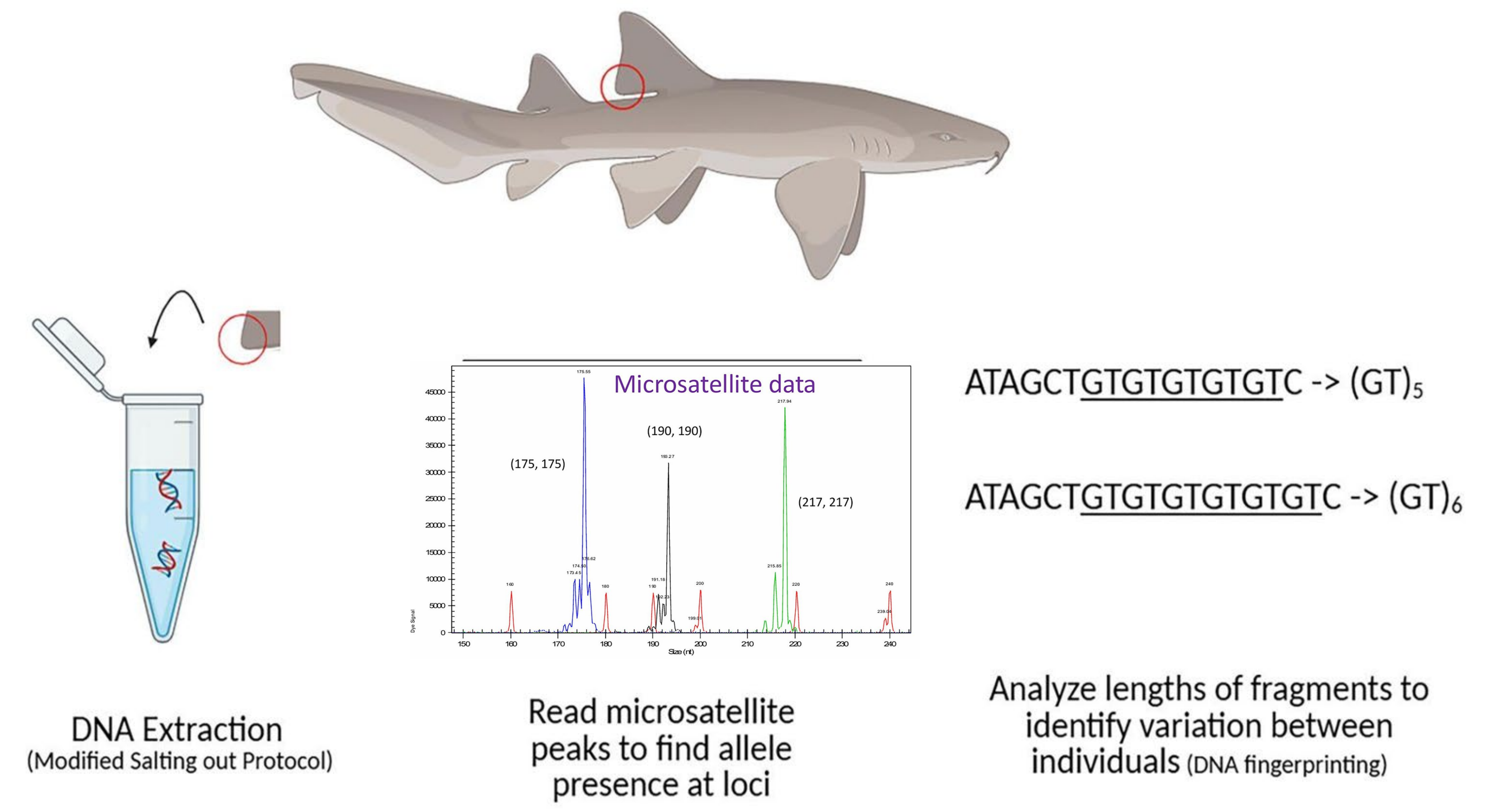


Figure 2. Neighbor-joining tree of the haplotypes found in Bimini (BIM) and Florida (FL) nurse sharks using the cytochrome b gene[7,8] with Dry Tortugas reference.

Conclusions and Future Directions

We found no evidence of genetic differences between the two regions in this study, suggesting a single population. This is not surprising because the two populations are close to one another. Alternatively, it could be a difference in habitat availability or food source, that is causing the difference in growth rates.

The next step to this project is to use a different genetic technique to produce a DNA fingerprint of each individual. By using this level of identification, we can test for more fine-scale disparities between the Biscayne Bay and Bimini populations to pin-point the drivers of their differing growth rates.



ATAGCTGTGTGTGTGTC -> $(GT)_5$

ATAGCTGTGTGTGTGTGTC -> $(GT)_6$

DNA Extraction
(Modified Salting out Protocol)

Read microsatellite peaks to find allele presence at loci

Analyze lengths of fragments to identify variation between individuals (DNA fingerprinting)

Figure 3. Visualization of materials and methods for future research.

Results from this study will give us a better understanding of the differentiation in growth rates among nurse shark populations. Because nurse sharks are threatened by commercial fisheries, climate change, and human development, it is important that natural resource managers have as much information as possible to protect this species[1,2].

Citations:

[1] Bettcher, V. B., Franco, A. C. S., & Dos Santos, L. N. (2023). Habitat-use of the vulnerable Atlantic Nurse Shark: a review. *PeerJ*, *11*, e15540.

[2] Carlson, J. et al. 2021. Ginglymostoma cirratum. The IUCN Red List of Threatened Species 2021: e.T144141186A3095153. https://dx.doi.org/10.2305/IUCN.UK.2021 1.RLTS.T144141186A3095153.en

[3] Castro, J. I. (2000). The biology of the nurse shark, Ginglymostoma cirratum, off the Florida east coast and the Bahama Islands. *Environmental Biology of Fishes*, *58*(1), 1-22.

[4] "Geneious Prime 2026.0.2 ((https://www.geneious.com)" .

[5] Huelsenbeck, J.P., et. al, MRBAYES: Bayesian inference of phylogenetic trees, 2001.

[6] Hlavin, J. F., Yeager, E. A., Martin, C. E., Will, C. J., Perni, N., Pankow, C., & Macdonald, C. C. (2026). Is the seagrass greener on the other side? Faster growth in Biscayne Bay, Florida's nurse sharks (Ginglymostoma cirratum) compared to neighboring conspecifics of Bimini, The Bahamas. *Environmental biology of fishes*, *109*(1), 30.

[7] Karl, S. A., Castro, A. L., & Garla, R. C. (2012). Population genetics of the nurse shark (Ginglymostoma cirratum) in the western Atlantic. Marine Biology, 159(3), 489-498.

[8] Kashiwagi, T., Kingsland, K. M., Pratt, T. C., Pratt, H. L., & Heist, E. J. (2016). Complete mitochondrial genome of the nurse shark Ginglymostoma cirratum. *Mitochondrial DNA Part B*, *1*(1), 464-465.

[9] Katoh, Standley 2013 (Molecular Biology and Evolution30:772-780)