

Cytochrome Oxidase I Examined Phylogenetically: Analyzing the Locus to Access the Utility of COI as an Indicator of Biodiversity in Sea Turtles Zachary Lane

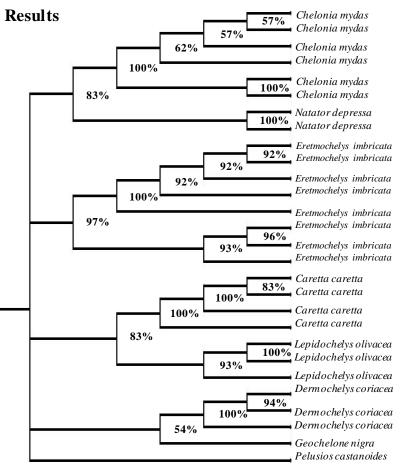


# **Research Question**

- 1. Does the COI gene serve as a accurate locus to identify species like sea turtles to aid in their rescue on a globally threatened level?
- 2. Can the COI gene be used for conservation genetic research within the family Cheloniidae?

#### Introduction

DNA barcoding is one of the most prestigious ideas to look into the inventory of life here on earth. In this study, data is collected from the NCBI website from the COI gene in each of these marine turtle species, along with two out groups. COI serves as a distinctive identifier that can present a needed resolution for differentiating between species, supplying vision into diversification of a species, and understanding evolution molecularly. Using the sequence data from the COI gene will give way to a better understanding of how these different taxonomic species relate to each other on a phylogenetic tree, which can also help design conservation strategies. Sequences were found in a BLAST search and then used to build a tree with strict consensus of the most parsimonious trees with bootstraps for support.



# Acknowledgements

Dr. Cevasco's Phylogenomic (BIOL 397) lab class at Coastal Carolina University. Along with the referenced paper below that I built my analysis off of.

Naro-Maciel, E., Reid, B., Fitzsimmons, N., Le, M., Desalle, R., & Amato, G. (2009, <u>August 20</u>). Dna barcodes for globally threatened marine turtles: A registry approach to documenting biodiversity. Retrieved April 18, 2021, from <u>https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1755-0998.2009.02747.x</u>

# Methods

- 26 different sea turtles
- 6 different species (Green, Flatback, Hawksbill, Loggerhead, Olive Ridley, and Leatherback Sea Turtle.
- 2 out groups (Galapagos Tortoise and the Western African Mud Turtle)
- 593 sequences used from each species. Sequences were aligned using a sequence alignment program (Java) and then trimmed to an even 593 base pairs.

#### Conclusion

I can conclude from the phylogenetic tree that the mitochondrial COI gene can be used to group these taxa in an accurate manner. The only taxa that did not have above 80% support was the Green Sea Turtle. The two out groups at the bottom are also grouped appropriately with less support than the family Cheloniidae, proving they aren't that related. Since COI is an accurate way to group these taxa it can ultimately be used in DNA barcoding for genetic research on a conservation level

