Molecular Phylogenetics

Jordan Lillard

April 18, 2019

**Introduction**

With the earliest known turtle species dating back to over 220 million years ago, turtles are one of the oldest reptile groups in the world. They are more ancient than both snakes and crocodiles. Being such an ancient species, I am very curious to see how the different species of turtles evolved.

Turtles belong to the order Testudines, an order of reptiles. As the only living anapsid amniotes, their phylogenetic history is critical in determining basal condition and early transformations of many amniote characters (Gaffney, 1979). Prior to genome analyses, phylogenetic hypotheses were based on cladistic analyses of morphological data (Gaffney and Meylan, 1988). With new methods and technology to analyze molecular sequences, there have been many discrepancies found with the morphological phylogenetic hypotheses (Crawford, 2014).

Turtles are divided into two extant suborders: Cryptodira and Pleurodira. These two suborders differ morphologically. The Cryptodira is the larger of the two groups and includes all the marine turtles, the terrestrial tortoises, and many of the freshwater turtles. The Pleurodira are known as the side-necked turtles and consists primarily of various freshwater turtles. The suborders are further divided in 13 different families. H. Bradley Shaffer conducted a study in which he used the molecular, morphological, and paleontological approaches to hypothesize turtle phylogeny. Using his data as a reference, I will present the molecular phylogenetic analyses for 23 different turtle taxa, including representatives of all living families and subfamilies. Using molecular sequences from cytochrome b, I will be perform three different analyses (Maximum Parsimony, Distance Analysis, and Maximum Likelihood) to construct phylogenetic trees for the 23 taxa.

**Methods**

*Data Collection*

All GenBank accession numbers were acquired from the literature. Using <https://www.ncbi.nlm.nih.gov/>, the cytochrome b sequence (892 bp) was acquired for all 23 taxa. The retrieved sequences were aligned with MAFFT and exported in fasta, nexus and phylip format.

*Parsimony Bootstrap Analysis*

The parsimony bootstrap analysis was conducted using PAUP\*. 1000 replications were done using a heuristic search to find the maximum parsimony tree. All trees were retained after the search. The 50% Majority Rule Consensus tree was found and reconstructed with FigTree.

*Distance Analysis*

Using PAUP\* again, pairwise distances were used to estimate a phylogenetic tree with the neighbor-joining clustering algorithm. The distance matrix was calculated from the nucleotides, under Jukes-Cantor model of sequence evolution.

*Maximum Likelihood*

Likelihood analysis was performed with RAxML-MG.

**Results & Discussion**

**Conclusion**

**References**

<https://www.researchgate.net/profile/Minh_Le8/publication/23226684_Evolutionary_relationships_of_marine_turtles_A_molecular_phylogeny_based_on_nuclear_and_mitochondrial_genes/links/59df672ca6fdccfcfda3586e/Evolutionary-relationships-of-marine-turtles-A-molecular-phylogeny-based-on-nuclear-and-mitochondrial-genes.pdf>