Phylogenomic Relationships of Ephemeroptera

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Introduction

Turtle's origins trace back over 210 million years to the Late Triassic (1). Their evolutionary history has been molded by continental drift, climate change, and extinctions, leading to the diversity of species we see today. Around 208 million years ago, turtles diverged into two major groups: Cryptodira (hidden-necked turtles) and Pleurodira (side-necked turtles), each characterized by unique anatomical adaptations (1). During the Jurassic period (~180–145 million years ago), continental shifts influenced turtle distribution, with Cryptodira primarily evolving in northern continents (Laurasia) and Pleurodira thriving in southern landmasses (Gondwana) (6). Despite the Cretaceous-Paleogene mass extinction (~66 million years ago), turtles demonstrated resilience, adapting to new environments during the Paleogene (~66–23 million years ago) (4). Genetic studies confirm that turtles are more closely related to birds and crocodiles (archosaurs) than to lizards and snakes, revising traditional taxonomic classifications (3).A significant climate shift occurred during the Eocene-Oligocene transition (~34 million years ago), as global cooling led to sea-level decline and the emergence of new coastal habitats, fostering turtle diversification (1;7). As illustrated in (7) - Figure 1, this period increased diversification along continental margins. While some species dependent on wetland ecosystems in regions like Western North America faced extinction due to increasing arid conditions (7), molecular data indicate that turtles in other regions successfully adapted, evolving into new lineages (7). Marine turtles developed slow genetic mutation rates and specialized diets, enabling them to thrive in oceanic environments (4). As climate change continues to reshape our ecosystems, understanding turtle evolution is crucial for modern conservation strategies, ensuring the protection and potential relocation of endangered species to prevent further declines (3;7).
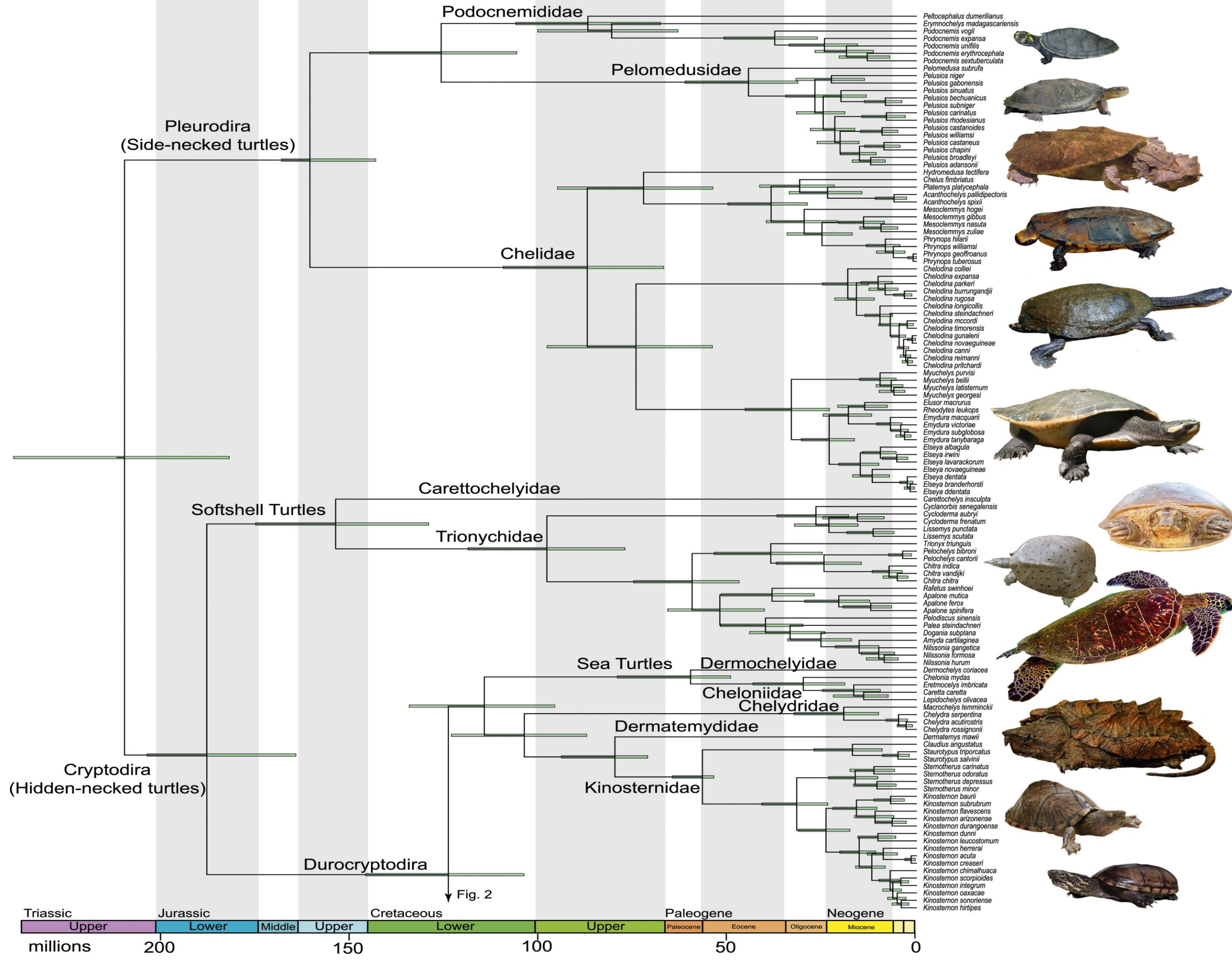

Figure 1.
Phylogenetic relationships of turtles and evolution change (Thomson et al., 2021.

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Methods

• Dataset: # 591 Taxa and 15 Genes
  o Get Turtle Data – Downloaded CSV file from a published study containing turtle species information.
  o Retrieve DNA Sequences – Used Entrez Batch to find genetic sequences based on accession codes.
  o Rename Files – Renamed each file to match specific genes correctly.
  o Align Sequences – Used MAFFT and BMGE to clean and align the data for analysis.
  o Combine Data – Merged all 15 gene files into one dataset using FASconCAT.
• Tree Reconstruction: IQTREE & Bootstrap values
  o Collapsed select branches (From 500 to 281)
• Used FigTree to visualize the phylogenetic tree and compare findings to the original research.
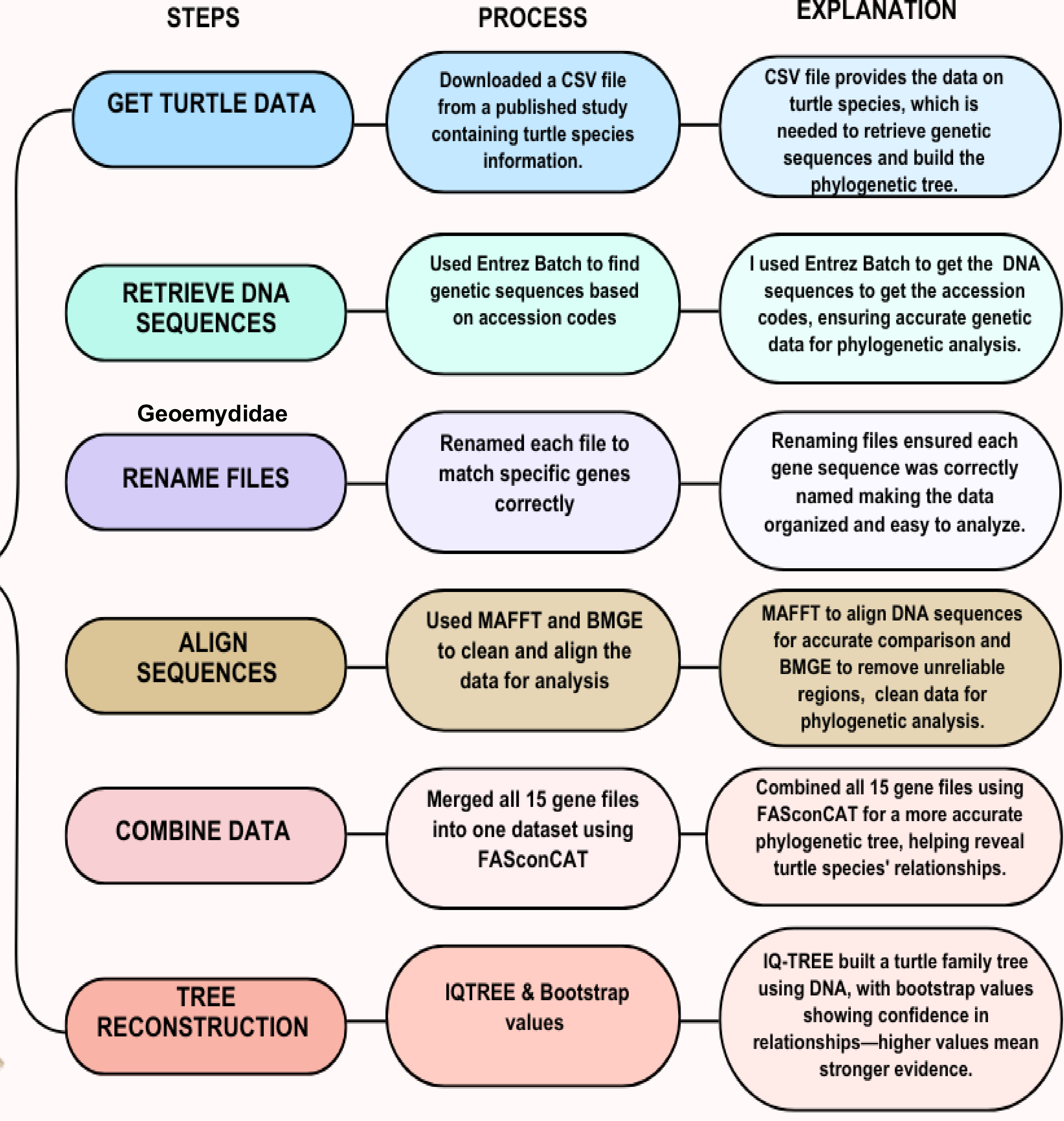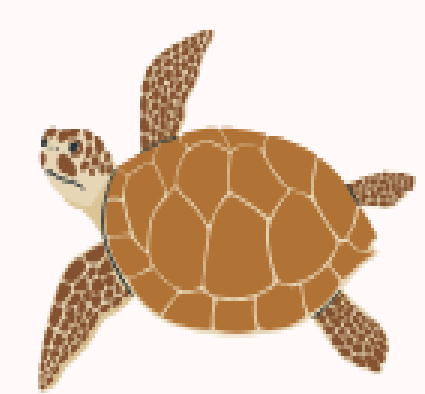

STEPS	PROCESS	EXPLANATION
GET TURTLE DATA	Downloaded a CSV file from a published study containing turtle species information.	CSV file provides the data on turtle species, which is needed to retrieve genetic sequences and build the phylogenetic tree.
RETRIEVE DNA SEQUENCES	Used Entrez Batch to find genetic sequences based on accession codes	I used Entrez Batch to get the DNA sequences to get the accession codes, ensuring accurate genetic data for phylogenetic analysis.
RENAME FILES	Renamed each file to match specific genes correctly	Renaming files ensured each gene sequence was correctly named making the data organized and easy to analyze.
ALIGN SEQUENCES	Used MAFFT and BMGE to clean and align the data for analysis	MAFFT to align DNA sequences for accurate comparison and BMGE to remove unreliable regions, clean data for phylogenetic analysis.
COMBINE DATA	Merged all 15 gene files into one dataset using FASconCAT	Combined all 15 gene files using FASconCAT for a more accurate phylogenetic tree, helping reveal turtle species' relationships.
TREE RECONSTRUCTION	IQTREE & Bootstrap values	IQ-TREE built a turtle family tree using DNA, with bootstrap values showing confidence in relationships—higher values mean stronger evidence.

DATASET: # 591 TAXA AND 15 GENES

Fig. 2. Flowchart of the methods for this project created on Canva.

Results & Conclusions

• Monophyletic groups:
  ▪ Cheloniidae (sea turtles), Kinosternidae, Testudinidae and Trachemys with high bootstrap values.
• There was an unclear relationship with Kinosternon since some of the values for the bootstrap were ranging from 60 to 80).
• In the Phylogenetic tree Kinosternon and Crytochelys had a variation of turtle species.
• Carettochelyidae was the only species left of its kind.

Fig 3. ML Phylogeny using IQ-TREE. Collapsed lineages are represented by tiengles on tips.
Explanation: Branch lengths (scale bar) indicate genetic divergence, with longer branches showing greater evolutionary change.