

A phylogenetic comparative analysis of Coelacanthiform environmental distributions through the fossil record.

Abstract

A preliminary evaluation of evolutionary changes in the environmental preferences of Coelacanthiformes is performed, beginning with the included family Latimeriidae, that includes the extant coelacanth *Latimeria*. Coelacanthiformes also includes Whiteiidae, a family of extinct coelacanths from the Triassic, and Mawsoniidae, a family of extinct coelacanths from the Triassic to the Cretaceous, as well as a few genera that will be considered in the fall semester. A database created with resources located with the Paleobiology Database is utilized to reconstruct the evolutionary changes in habitat preferences revealed by changes in depositional environment along Latimeriid lineages, with a focus on the lineage leading to *Latimeria*. In order to assess these changes, the algorithm BayesTraitsV2 is used to reconstruct the evolutionary preferences at internal nodes of the Latimeriid phylogeny using maximum-likelihood methods. The results of this preliminary evaluation indicate a shift to deep water preferences in the clade containing *Macropoma*, *Swenzia*, and *Latimeria*.



Introduction

Coelacanths are part of Sarcopterygii, the lobe-finned fish, a group that also includes Tetrapoda, the land vertebrates. They were thought to have gone extinct at the Cretaceous-Paleogene boundary until 1938, when *Latimeria chalumnae* was discovered off the coast of South Africa. Subsequently another species was discovered off the coasts of some Indonesian islands in 1997 and was determined to be a different species through genetic testing (Nikaido et al. 2011).

Fossil coelacanth species have been known since the mid-1800s and some have been preserved in great detail. Yet, the morphologies of the fossil species and the environments in which they are discovered vary greatly, including both freshwater and saltwater habitats. In contrast, the two living species of *Latimeria* dwell in deep sea caves at depths of around 200 meters during the day, and around 50 to 150 meters during the night, on opposite ends of the Indian Ocean (Fricke 1988). This study is an attempt to examine the evolutionary trends resulting in this habitat preference are unknown. This study examines the trends within the coelacanth group Latimeriidae, which includes the living species and their closest relatives.

H_0 = Reconstructed habitat preferences of common ancestors of known Latimeriidae taxa reveal no particular trend in habitat preference.

H_1 = Reconstructed habitat preferences of common ancestors of known Latimeriidae taxa reveal an evolutionary trend(s) in habitat preference.

Materials and Methods

- The database of species, their stratigraphic occurrence, and the inferred environment of deposition was collected.
- For genera with multiple species, the most common environments were used to represent each genus.
- BayesTraitsV2 (Pagel et al. 2004) was used to infer the ancestral states at each node of the cladogram.
- The Multistate method was used as the variable "environment of deposition" has more than two discrete states.
- The Maximum-Likelihood protocol was used to determine the relative probability of the different character states at each node, given the observed character states of the rest of the phylogeny.
- Each analysis was one with 1000 simulations.
- The data BayesTraitsV2 returns is in percentages, considering the possibility of each state of habitat preference at the ancestral nodes.
- This data was then modeled in pie-charts to better evaluate the data for a trend in habitat preference along the lineage to *Latimeria* within Latimeriidae.

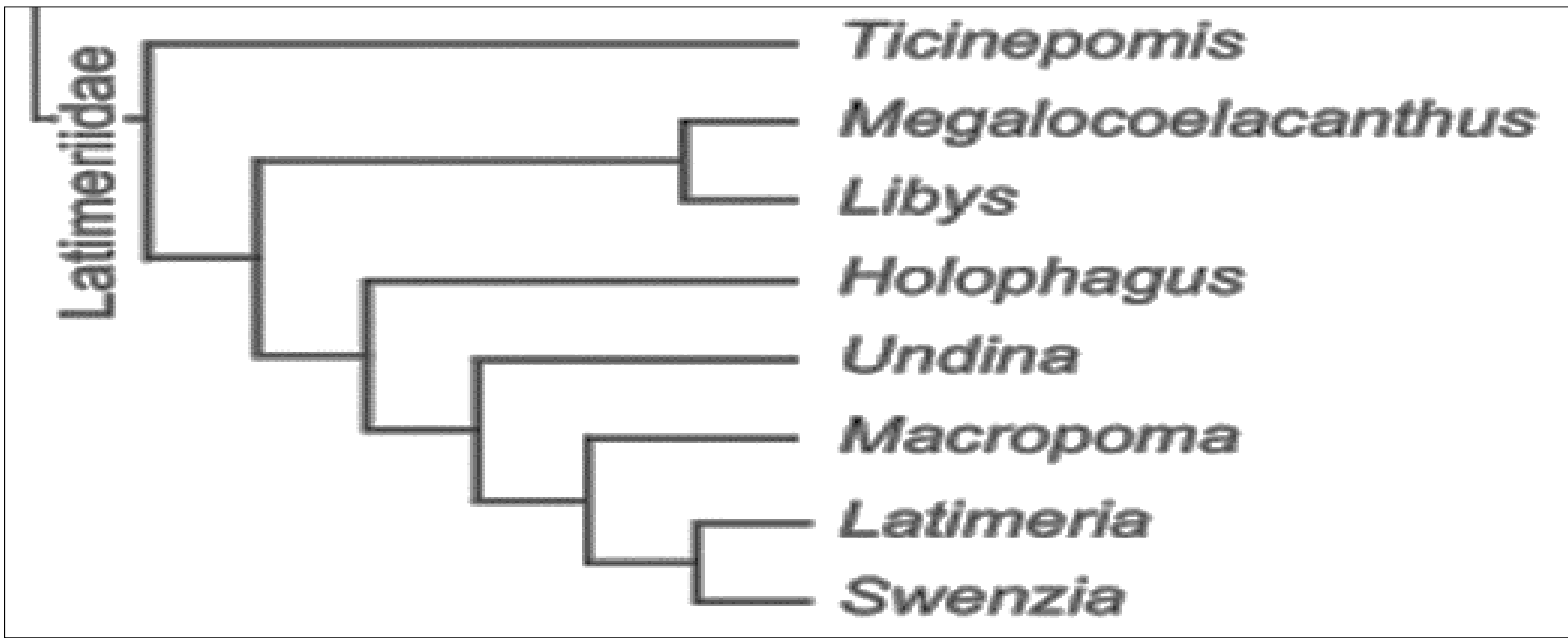
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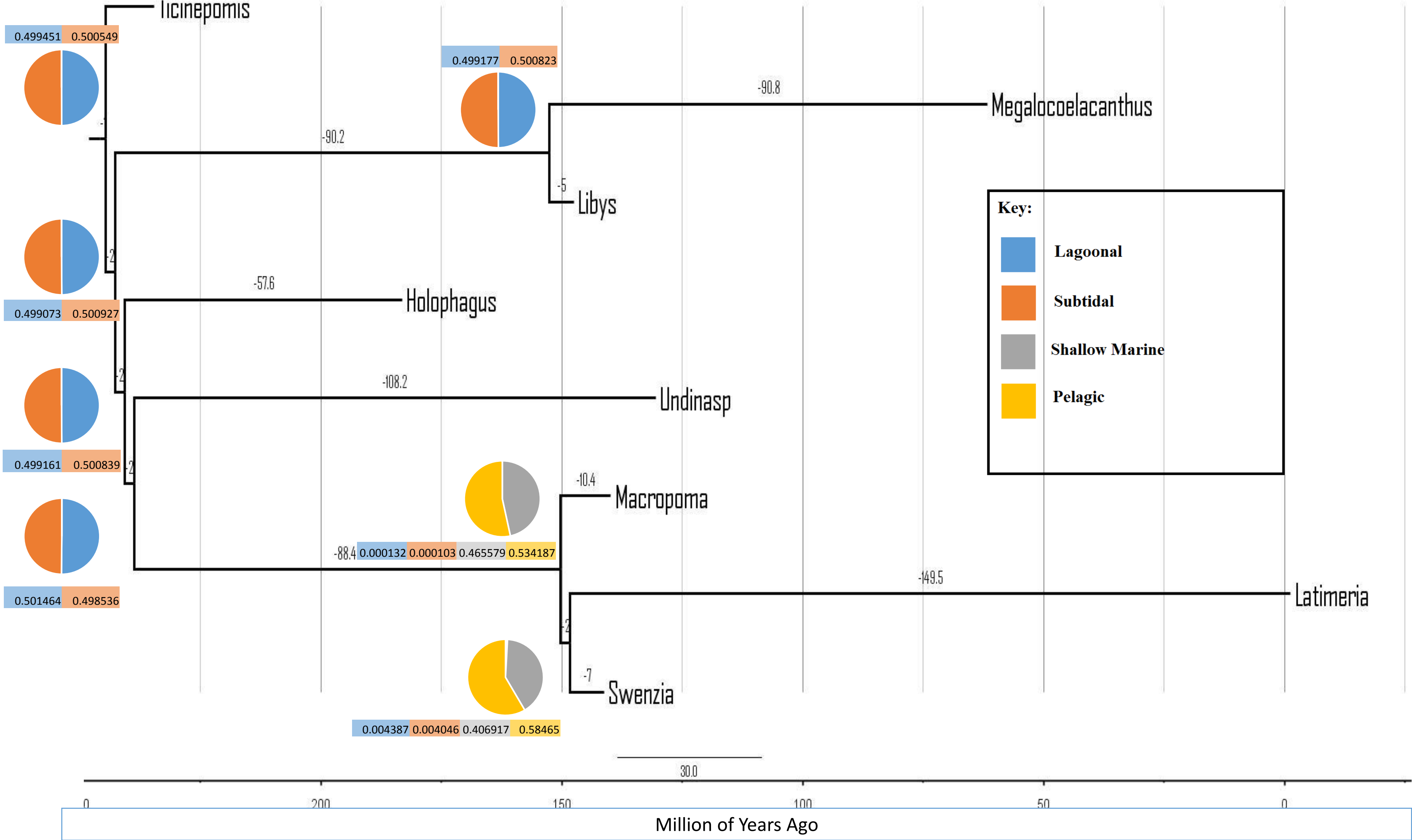
Database

Genus	Species	Depositional Environment	Salinity	Reference
Ticinepomis	peyeri n. gen. n. sp.	Lagoonal	Saline	T. Bürgin. 1992.
Ticinepomis	cf. peyeri	Lagoonal	Hyper/Saline	L. Cavin, H. Furrer, and C. Obrist. 2013.
Ticinepomis	cf. peyeri	Lagoonal	Hyper/Saline	L. Cavin, H. Furrer, and C. Obrist. 2013.
Megalocoelacanthus	dobiei	Pelagic	Saline	W. B. Gallagher, D. C. Parris, and E. E. Spamer. 1986.
Megalocoelacanthus	dobiei	Shallow Marine/Pelagic	Saline	D. R. Schwimmer. 1986
Megalocoelacanthus	dobiei	Subtidal	Saline	D. R. Schwimmer, J. D. Steward, and G. D. Williams. 1994.
Megalocoelacanthus	dobiei n. gen., n. sp.	Subtidal	Saline	D. R. Schwimmer, J. D. Steward, and G. D. Williams. 1994.
Libys	superbus	Lagoonal	Hyper/Saline	K. A. Zittel. 1887.
Libys	polypterus	Lagoonal	Hyper/Saline	G. Münster. 1842.
Holophagus	gulo	Pelagic	Saline	P. M. G. Egerton. 1861.
Holophagus	gulo	Pelagic	Saline	P. M. G. Egerton. 1858.
Holophagus	gulo	Pelagic	Saline	P. Egerton. 1854.
Holophagus	picens	Lagoonal	Saline	F. Bassani. 1895.
Holophagus	picens	Lagoonal	Saline	O. Rieppel. 1985.
Holophagus	picens	Lagoonal	Saline	O. Rieppel. 1985.
Undina	sp.	Pelagic	Saline	E. Andersson. 1916.
Undina	sp.	Lagoonal, Subtidal	Saline	F. Bassani. 1895
Undina	sp.	Lagoonal	Saline	A. Bidar, L. Demay, and G. Thomel. 1972.
Undina	barroviensis	Shallow Marine	Saline	A. S. Woodward. 1890.
Undina	barroviensis	Shallow Marine	Saline	A. S. Woodward. 1890.
Undina	barroviensis	?	?	A. S. Woodward. 1891.
Undina	barroviensis	Pelagic	Saline	A. S. Woodward. 1895.
Undina	penicillata	Lagoonal, Subtidal	Saline	G. Arratia. 2000.
Undina	penicillata	?	?	G. Dietl and G. Schweigert. 2011.
Undina	penicillata	Pelagic	Saline	G. Dietl and G. Schweigert. 2011.
Undina	cf. purbeckensis	Lagoonal	Hyper/Saline	P. L. Forey, O. Monod, and C. Patterson. 1985.
Undina	cf. purbeckensis	Lagoonal	Hyper/Saline	A. S. Woodward. 1916.
Macropoma	sp.	Shallow Marine/Pelagic	Saline	W. J. Kennedy. 1969.
Macropoma	mantelli	Pelagic	Saline	M. Waldman. 1965.
Swenzia	latimerae	Shallow Marine/Pelagic	Saline	G. Clement. 2005.
Latimeria	chalumnae	Shallow Marine	Saline	
Latimeria	menandonesis	Shallow Marine	Saline	



Analysis

- The data collected is simplified into a database with simplified traits to be evaluated.
- Several species were evaluated, and then the most common environments were used to represent each genus.
- BayesTraitsV2 can be used to algorithmically analyze missing traits or characteristics on an ancestral node in the phylogeny.
 - The Multistate method is used as it allows for a finite number of discrete states to be evaluated and reconstructed.
 - The Maximum-Likelihood analysis is used to determine the probability of the character state at each most recent common ancestor node, given the character states of the rest of the phylogeny.
- Environmental habitat preferences were input instead of evaluating physical traits.
- BayesTraitsV2 is given the database information in a format that it could read, and told to run this information 1000 times.
- The data BayesTraitsV2 returns is in percentages, considering the possibility of each state of habitat preference at the missing nodes.
- This data is then modeled in pie-charts to better evaluate the data for a trend in habitat preference along the lineage to *Latimeria* within Latimeriidae.



Results & Future Work

This preliminary analysis indicated a noticeable shift in environmental preference within the lineage leading to *Latimeria*. The preferences evaluated by BayesTraitsV2 revealed an almost 50/50 ratio of lagoonal to subtidal environments within Latimeriidae until the most recent common ancestor of *Latimeria*, *Swenzia*, and *Macropoma*. At this node, there is a complete shift to a ratio between shallow marine and pelagic environments. This shift, although seemingly abrupt at this scale, reveals there is a trend along the lineage to *Latimeria* within Latimeriidae towards a more deep sea environment.

With this data showing a trend from lagoonal and subtidal to shallow marine and pelagic environments, there is a possibility that this trend extends throughout Coelacanthiformes. Taking this into consideration, I await the evidence of this trend to continue in Coelacanthiformes during the continuation of thesis.

In the future, data collection will continue and eventually include all of the genus and taxa within Coelacanthiformes that have been reported with the appropriate information. The database will then be expanded to include additional clades within Coelacanthiformes. Along with this new information, a more in-depth look at the environmental preferences for each genus will be determined to better evaluate the probabilities at each missing node. To better determine the environmental preferences, salinity conditions will also be determined in the future as well as possibly looking at the tailfins of the different species to determine eating habits and energy. Additionally, the data will be tested to evaluate if any shifts in environmental habitats are associated with Earth system events, such as mass extinctions.

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