

Using Big Data Analysis methods to understand Mesozoic Diversity and Predation

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INTRODUCTION

- Over the last 500 million years there have been numerous extinction events that have led to the diversification of animals. These turnover events are of key importance for understanding biodiversity in the 21stcentury.
- Non tetrapod vertebrates (fishes) do not display the same turnover events as other vertebrate **groups**¹. Evidence suggests that fish underwent multiple turnover events. For example, stem teleosts may have been replaced by radiations of crown teleosts first starting in freshwater in the Jurassic and later in marine reefs in the Late cretaceous.
- It is hypothesized that the 'Big Five' mass extinction events did not have a firsthand effect on fish diversity¹. Trends show that while most large predators (fish) died during the end of the Cretaceous era, but evidence from recent morphospaces indicates an increase in diversity for mid-trophic level fishes over the extinction boundary.
- Fishes and other marine vertebrates may have exhibited mass extinction events unrelated to the 'Big Five' events¹. Evidence suggests there were global and assemblage specific declines in Teleosts over the Cretaceous era and a loss of marine reptile diversity over the Jurassic-Cretaceous boundary.
- Fish diversification is thought to drive the Mesozoic Marine Revolution (MMR)^{1,2} the rapid adaption to shell-crushing and drilling predation in benthic organisms throughout the Mesozoic era, essentially a predator-prey arms race. Cataloguing occurrences of fish species through the Mesozoic era will provide much needed evidence to validate this and many other hypotheses concerning marine evolution.
- The lack of representation of fish in existing fossil compendia is a big confound to our understanding of fish turnover events and marine revolutions.
- The aim of this project is to map the biodiversity of fishes and address these hypotheses by cataloguing the existence of thousands of species in the Cretaceous and Jurassic eras. The databases created here cover two 'Big Five' mass extinction events: the end-Triassic extinction, and the end-Cretaceous.

METHODS

- We created a database by sorting through research papers, books, and museum collections specific to Cretaceous and Jurassic fossil fishes.
- Fossil fish species were cataloged according to occurrences (populations in specific locations) and recognized taxonomic categories. Additional Information about their regional stage, environment and geological formation was included if available.
- The data was further classified by all unique species of fish and all unique genera of fish for analysis.
- For visualization purposes, the data set was cleaned using the following parameters:
 - Repeat entries were removed from the database to make sure only unique entries were analyzed.
 - Species included in between two regional stages were counted separately in both the stages.
 - Species without specified regional stages were excluded from the dataset.
 - Location was normalized by capping specificity to 'country found'
 - Analysis looked at distribution of species by regional stage, distribution of genera by regional stage, global distribution of species in each regional stage and distribution of species by Cretaceous stage (lower or upper).
- The data collected was compared to the Paleobiology Database (PBDB) a publicly available online database of fishes put that has been continuously updated since 1999.
- A detailed search for PBDB Cretaceous fossil fishes resulted in a downloadable excel file that was cleaned up using the same parameters mentioned and then analyzed. The same process was repeated when analyzing the data from the Jurassic era.



Fig 1-3 (from left to right) Saurodon leanus (Cretaceous, Niobara Fm), *Pholidophorus* purbeckensis (Jurassic, England), Luisichthys vinalesensis (Jurassic, Cuba). Pictures by Nobu Tamua

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era data with variables as follows: number of unique species, number of unique genera, regional stage, occurrence by country.

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- apparent in the PBDB data.

- macroevolution in fishes.

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DISCUSSION

• The newly created Jurassic database was 51% larger than the existing PBDB data.

Both the new database created, and the Paleobiology Database had similar patterns in the portion of occurrences found in early and middle stages of the Jurassic. However, the PBDB had significantly fewer occurrences from the Upper Jurassic than the new database.

• The newly created Cretaceous database was 30% larger than the existing PBDB data.

 Preliminary analysis of the new Cretaceous database revealed that it documented 33% more species than the PBDB. The new database also had thirty three percent more genera than the

The Cretaceous database had greater diversity in occurrences, covering species from 76 countries compared to the 54 countries in the PBDB.

• The trends seen in the two databases are similar, however there is a larger, more significant spike in the number of fish genera and species in the Cenomanian and Campanian stages of the Cretaceous

Both the Cretaceous and PBDB databases also displayed more species in the Late Cretaceous compared to the Early Cretaceous, with the new database reporting more entries in both stages.

The data show a huge decline in fish diversity at the end-Jurassic with low diversity in the early Cretaceous, and another huge decline in the Cenomanian-Turonian, none of which was

• In contrast, there's a diversity spike at the Toarcian, which suggests that fishes were not affected by that Ocean Anoxic Event^{1,2} which eliminated some bottom-dwelling invertebrates.

CONCLUSIONS AND FUTURE DIRECTIONS

So far, the data are very promising – **they support the hypothesis that fishes do have** different extinction events when compared to bottom dwelling invertebrates, and are more like marine reptiles, ammonoids and other free-swimming species^{1,2}.

The Jurassic data will help determine the effect of the end-Triassic extinction on fishes and how they recovered while the Cretaceous data will provide an insight into how many fishes died and what ecosystems looked like before.

The data collected so far is preliminary, further steps include collecting more data to finish the databases and resolve inconsistencies in both collections – Cretaceous and Jurassic.

Other members of the Sallan lab are working on identical databases for different geological time periods, thus consolidating the data between all members is an integral next step. The data collected can be used to create faunal lists and find specific details about ecological traits.

This can then be subject to time series analysis as well as novel ecological and phylogenetic comparative methods to reveal new patterns and hypotheses that will further our understanding of

ACKNOWLEDGEMENTS AND REFERENCES

1. Friedman, M. and Sallan, L.C. (2012), Five hundred million years of extinction and recovery: a phanerozoic survey of large-scale diversity patterns in fishes. Paleontology, 55: 707-742.

2. Benson, R.B.J. and Druckenmiller, P.S. (2014), Faunal turnover of marine tetrapods during the Jurassic-Cretaceous transition. Biol Rev. 89: 1-23.