**TITLE:** No evidence, indeed: a critique of Thompson and Ramirez-Barahona (2023)

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**Abstract**

The

**Introduction**

Since the introduction of molecular phylogenies and the comparative methods that employ them, practitioners have defied expectations of what was thought possible. For example, when Felsenstein (1985) famously introduced phylogenetic independent contrasts, reviewers were skeptical that there would ever be sufficient robust phylogenies for the method to prove useful (Huey et al. 2019). Many would argue that another example of this is estimation of extinction rates from phylogenies that are entirely extant; however, this issue is much stickier. Nee et al. (1994) demonstrated that extinction rates can be estimated, and mass extinction events can be inferred, from lineage-through-time (LTT) plots that only contain information about lineage “births.” However, estimation of extinction rates from phylogenies of extant taxa has proven controversial: Rabosky (2010) went so far as to argue that extinction rates should not even be estimated from molecular phylogenies, while others, such as Beaulieu and O’Meara (2015), have argued that reliable extinction estimates can be gleaned from phylogenies that are sufficiently large using sophisticated methods that incorporate things like rate heterogeneity. Most recently, Louca and Pennell (2020) demonstrated that evolutionary rates cannot be reliably inferred from LTTs, inspiring widespread doubt in the degree to which inferences from phylogenies are stretched.

However, optimism remains – perhaps too much optimism. Recently, Thompson and Ramírez-Barahona (2023) attempted to detect a signature of the Cretaceous-Paleogene mass extinction on two very large phylogenies of flowering plants. They failed to do so, arguing that this demonstrated the resilience of angiosperms, likely due to their rich adaptations.

-This disagrees with fossil evidence

-Other problems

-Losos address (2011)

**Lack of Information**

The

* Nee 1994 and LTTs
* How much information in Smith & Brown tree at time period of interest? (O’Meara and Beaulieu 2021)
* Only about 0.7% of all evolutionary events (speciations) in the Smith & Brown tree occur at or before 65 mya
  + Examined in another way, there are only 548 lineages present at the 65 mya timeslice, compared to about 77,000 tips in the Smith & Brown tree.
  + We are attempting to study something deep in the past “from a study of their weird, few surviving lineages” (O’Meara and Beaulieu 2021).
* There’s also uncertainty in the form of information loss (Boyko and Beaulieu 2021)

**TESS Issues**

The

-High Type II error rate (Chang et al. 2020)

-Our own analysis

\*Generate trees with various issues to stress-test

\*Models we run TESS with are constant BD, episodic BD, and mass ext

\*Extinct\_removed: Episodic supported over constant or mass ext

\*Mass ext sim tree: Episodic supported over constant or mass ext

**How Many Fossils Do We Need?**

The

-Diversitree stress-testing

**Conclusions**

The

-O’Meara and Beaulieu implore comparative biologists that “it is important to recognize that our methods are better suited for using the past to learn about the present survivors, not using the present survivors to learn about the past.”

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