

Madrid 21st of November 2023

Dear Dr. Berenbaum
Editor-in-Chief, *Proceedings of the National Academy of Sciences*

We are excited to submit our manuscript titled “**Geographic patterns of living tetrapod diversity reveal the signature of global diversification dynamics**”, for consideration as an Article in *PNAS*.

The study of patterns of biodiversity constitutes the core of macroevolutionary research. Species richness patterns of many groups of the tree of life have been widely reported for decades, but in recent years we have seen an increasing interest in the phylogenetic component of those patterns (phylogenetic diversity), given the importance of knowing the species relatedness to decipher the evolutionary processes that have shaped today’s biodiversity. Furthermore, the phylogenetic dimension of diversity patterns has crucial implications for conservation studies, since preserving the evolutionary history (and not only richness hotspots) has become a priority to face the challenges imposed by the ongoing loss of biodiversity at a global scale.

In this work, we report patterns of a richness-corrected phylogenetic diversity metric (residual PD) for amphibians, squamates, birds, and mammals. Although these have been independently studied in the past, here we use recently published global distribution and phylogenetic data and, importantly, we interpret them in a common and comparative framework. This allows us to uncover particular regions and continents where patterns are congruent or different across tetrapod clades. This, in turn, enables a comprehensive search for the evolutionary and ecological causes underlying the patterns observed. We explicitly explore the relationship between residual PD levels and multiple factors: recent speciation rates, evolutionary time, and different climatic and environmental variables in the regions identified as extreme in residual PD. Our results reveal an important effect of recent speciation rates in the patterns we report, and further suggest that other factors, such as extinction dynamics and life history traits, might have also played a determinant role in shaping the distribution of species relatedness across the globe. Therefore, we consider our work as the basis of future research in this direction.

We are confident that the results of this paper, as well as its methodological and conceptual perspectives, are of great relevance to the community of evolutionary biologists and macroecologists. Moreover, the implications of this work go beyond the study of evolutionary processes, reaching a special interest for those dedicated to studying and designing conservation strategies. In summary, we believe our work is a perfect fit for *PNAS*.

All authors have agreed to the content of the manuscript and its conclusions, and the paper is not under consideration elsewhere (please note that it has been recently posted in the preprint server *bioRxiv*: <https://doi.org/10.1101/2023.11.03.565445>).

Sincerely,



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