**01-May-2024  
  
Dear Dr. Tejero-Cicuéndez  
  
RE: Geographic patterns of living tetrapod diversity reveal the signature of global diversification dynamics  
Ref.: GEB-2024-0025  
  
We have now completed the review process on your manuscript. We regret to inform you that we have decided to decline publication of this manuscript in Global Ecology and Biogeography. This decision is based on the assessment of two members of the Editor in Chief team, the recommendation of the handling editor, Dr. Jonathan Davies, and the reviewers' reports (if applicable).  You will find the reports appended below, and we hope these will be useful in improving your manuscript for submission elsewhere.  
  
We are sorry not to bring a happier decision about the present manuscript. Global Ecology and Biogeography receives far more papers than we can publish.  Consequently, we often have to turn down manuscripts that have the potential to be significant contributions to the scientific literature, as we try to select the manuscripts we believe best match the Journal scope.  
  
Thank you for your submission. We hope that you will continue to consider Global Ecology and Biogeography for your future submissions.  
  
Yours sincerely  
Amanda Bates, Maria Dornelas and Richard Field  
Editors-in-Chief, Global Ecology and Biogeography  
  
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EDITOR'S COMMENTS TO AUTHOR  
Editor: Davies, Jonathan  
Comments to the Author:  
While both reviewers saw value in the analyses presented, they identified a number of potential weaknesses, not least the complex interrelationship between the processes of speciation and extinction that mean different evolutionary histories can generate similar patterns of phylogenetic diversity and LTT. Echoing comments from the reviewers, I was also concerned that patterns of residual PD were perhaps over-interpreted while alternative drivers were not fully considered. I also wondered whether a measure of the standard effect size (SES) of PD (see**[**https://www.rdocumentation.org/packages/picante/versions/1.8.2/topics/ses.pd**](https://www.rdocumentation.org/packages/picante/versions/1.8.2/topics/ses.pd)**) might have been a more robust measure than residual PD. A possibly more pernicious concern is the inherent non-independence between DR and PD. While I am unable to recommend this submission for publication in GEB, I believe a reframed manuscript would be suitable for publication elsewhere.**See my comments on specific sentences and my thoughts on the reviewers’ comments below. I don’t really see a justified rejection of the paper honestly.

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REVIEWER COMMENTS TO AUTHOR  
  
Referee: 1  
  
Comments to the Author**

They don’t provide a general assessment about the paper, which would be helpful.

**Line 90: would reduced extinction of younger lineages not also be a “cradle?”**I would say that the original definition of cradle is an area of high speciation and extinction at the present time (high turnover), with the “high speciation” component being perhaps more relevant in works using extant phylogenies. So, reduced extinction of younger lineages would not be a cradle according to the definition of cradle.

**-The authors cite the Vasconcelos et al. 2022 paper “retiring” these notions, but still place a a great deal of emphasis on them in the Introduction. They also don’t mention salient aspects from that paper, such as the influence of traits.**I would not say that we place a great deal of emphasis on these terms (we mention them in one paragraph in the Introduction). And when we talk about them we do it to explicitly show the problems of using them due to the simplification of the evolutionary processes that cause certain patterns.

**-The Introduction doesn’t contain a clear statement and justification of the hypotheses to be tested.**We could include some explicit hypotheses in the Intro and/or the Methods (e.g., we expect higher recent speciation rates in places with low residual PD).

**-For PD and DR, is “mean” the best summary compared to “median” or even “geometric” mean for the rate statistics?**We could get the results and figures with the median for comparison.

**-Given the extreme identifiability problems associated with LTT plots identified by Louca and Pennell (2020), is this spatial analysis fully justified?**This is like saying that BAMM analyses are not justified, but in my opinion it’s not that they are not justified, it’s just that the interpretation of results (if they are clearly interpretable) should be carried out with caution. In our case we don’t have clearly interpretable results. We are just showing that there are no clear patterns in LTTs, which is not entirely unexpected but it wouldn’t have to be that way necessarily.

**-With the environmental variables analysis, how do the authors justify a time-zero (last 50 years) approach to a question that reaches back to the Devonian? On what ways will present-day relationships between climate and PD/DR inform us about historical macroevolutionary and macroecological processes?**We could use data on environmental variables reaching further back (I am not sure the availability of such data, how far back we can get).

**-The authors seem to overlook how the various “biodiversity shortfalls” – especially the Wallace and Linnaean – might be impacting their results. Is the result for residual squamate PD in tropical Africa real, or an artifact of poor alpha taxonomy and distribution mapping in this region?**We could acknowledge that this might be a problem in the Discussion.

**-The mathematical identity of PD/FP/DR and similar metrics makes their comparison of residual PD and DR somewhat problematic; was this accounted for at all? Both are heavily influenced by the lengths of the pendant edges, so strong correlations between them are expected. How are deviations from this model assessed?**What do they mean with “mathematical identity” of PD and DR? They are not the same, and the pool of species used to get DR (whole phylogeny) and PD (regional assemblages) are different.

**-The description of the environmental variables again seems lacking; what were the expectations and hypotheses here?**I don’t think we really have hypotheses about the relationship of environmental variables and residual PD. We could search for the expected potential effect of mainly temperature and precipitation (and temperature variability and precipitation variability) on speciation and extinction rates. The hypotheses would be about the effect of the environment on residual PD through diversification, I guess.

**-In the Discussion, the authors say “Our results show that the integration of phylogenetic metrics with analyses of global geographic patterns of diversity among terrestrial vertebrates facilitates a more holistic approach to exploring the evolutionary and ecological processes underlying current spatial patterns of biodiversity” but it is not clear that this is true. How have any ecological processes been addressed by these analyses? What mechanisms were tested?**I think we have focused on speciation, which could be considered an evolutionary process, while ecological processes should be investigated at smaller scales (competition and other biotic interactions). Although the exploration of the effect of environmental variables on these patterns could be considered also an exploration of ecological processes.

**-They also say “We found that both American continents are regions of consistently low residual PD, meaning that regional assemblages are composed of species that are more closely related We found that both American continents are regions of consistently low residual PD, than expected by their richness. This applies to all the studied clades, with the exception of amphibians in North America and mammals in Eastern North America.”  
Those are big exceptions! North America is a major global hotspot of amphibian (especially salamander) diversity, with numerous ancient lineages. What does this analysis purport to test and demonstrate about these patterns? In Figure 2, why are some areas circled and not others? For example, Northwestern North America for having high residual PD in amphibians.**Those might be big exceptions but they are only two cases out of eight. Which ones wouldn’t be “big exceptions”?

This analysis aims to 1) identify regions of particularly high and low residual PD and compare them across tetrapod clades, and 2) search for factors that could be related to those patterns, especially recent speciation rates.

I agree with the reviewer in asking what are the reasons for choosing some areas and not others, I am not sure how we could define the regions of interest… They are in general areas with a large extension of contiguous cells with extremely high or low residual PD, but there is no formal definition.

**The extensive speculation in the Discussion about the specific idiosyncratic routes each group may have taken to achieve diversity in each region seem unfounded, and don’t comprehensively review the possible mechanisms responsible for the observed patterns.**We could simplify things to reduce the Discussion, just commenting on the results and maybe put all the speculation in one paragraph.

**They conclude by saying they have introduced a “methodology to quantify spatial phylogenetic diversity,” but I don’t see where this has been codified? Without a way to incorporate extinction and historical diversification processes, Fig. 1 is overdetermined.**I don’t know what they mean with “codified”. Does it need to be an R package for it to be a methodology? I don’t really understand. The methodology is to map the residuals of PD and SR.

**They then switch to talking about conservation priorities, but this is not addressed elsewhere in the MS, and doesn’t seem to be supported by their analyses.**

What do we say about conservation that is not supported by the analyses? We just say that this way of mapping biodiversity could help to identify conservation priorities. I don’t understand the big trouble of mentioning the benefits that this may have for conservation even though our manuscript is not about conservation, but many people seem to have problems with that.

**I think some more focus in defining the aims and goals of the MS in the Introduction, with some explicit hypotheses set up to be tested, would improve things dramatically.**We can add explicit hypotheses to be tested. If this is the main conclusion of the review, it doesn’t seem to be so negative to me even though they didn’t say a single positive thing.   
 **Referee: 2  
  
Comments to the Author  
  
The study investigates geographic patterns in phylogenetic diversity (PD). Tetrapod vertebrates (amphibians, reptiles, birds and mammals) serve as the study system. The authors identify regions that harbor higher and lower phylogenetic diversity than expected, given species diversity. Deviations from the expected PD are studied in relation to regional speciation rates, lineage through time plots, and environmental conditions (climate, topography, environmental productivity). The authors conclude that different factors govern the uncovered geographic patterns across regions and taxa. They also highlight that their results could advance biodiversity conservation by focusing on areas that harbor more phylogenetic history than expected, given their species diversity.**Focusing not only on areas with more phylogenetic history than expected, also with less because they could be regions where diversity is currently originating.

**The study contains an impressive amount of well-executed analyses. The results are detailed and discussed within the context of the natural history of the studied clades, and the language and the structure of the text are clear. However, the conceptual framing of the study, its introduction and discussion often drift away from the results themselves. There is some mismatch between the stated objectives of the study and its actual analyses. More detailed comments are given below.**Some positives at last!

**1. Study subject. The authors frame their study in terms of diversification dynamics (the title), but the introduction refers explicitly to species richness (lines 40-47) and conclusions to diversity dynamics (lines 429-430). This framing somewhat obscures the actual study subject. All the analyses involve phylogenetic diversity (PD); in particular, the residuals in PD after PD was regressed against regional species diversity. This metric could be interpreted in terms of diversity cradles (lower PD than expected) and museums (higher PD than expected), as the authors mention in the text. However, there is no clear connection to biodiversity patterns, species richness, or diversity dynamics.**See comment about the first paragraph alone not constituting the framing of the paper in my opinion.

We do mention that the residual PD could be interpreted in terms of cradles and museums, but we state the problems of doing so.

I don’t understand when they say “there is no clear connection to biodiversity patterns, species richness, or diversity dynamics”. OK, not to species richness, but this is just that what they think is the framing of the paper (first paragraph of the intro) is not really our framing of the paper. But connection to biodiversity patterns (for me, this could be just the geographic distribution of residual PD) and diversity dynamics (speciation and extinction), I think this is explicitly in the paper.

**PD represents a very interesting topic that might constitute a compelling paper. However, the focus on PD needs to be explicitly stated, and this study subject properly developed. For example, there are many classic as well as new scientific studies that have compared phylogenetic and species diversity, and mapped out the corresponding residuals to identify regions with higher or lower than expected phylogenetic diversity. The authors could frame their study specifically in terms of studying the cradles and the museums, with implications for conservation, while referring in more depth to previous work which has been concerned with this topic (e.g. Safi et al. 2011, Robuchon et al. 2021).**I didn’t know about these papers, they seem interesting! But what hasn’t been done (to the best of my knowledge) is comparing these patterns across tetrapod clades and explicitly testing the relationship with speciation.

**2. Hypotheses and results. The authors test three factors that might explain the geographic patterns in residual PD: speciation rates, time measured in terms of the lineage through time plots, and environmental conditions. While these are generally relevant factors, their links to PD are not sufficiently explained. For example, why should some environments act as diversity cradles and others as diversity museums? Is it possible that both the cradles and the museums co-occur in the same environment (e.g. tropical mountains)? The mechanisms linking environmental conditions and PD might need to be better developed. The effects of time might also need to be somewhat clarified, as they are measured using lineage through time plots (LTT plots) that capture how lineages accumulate along the phylogeny, which was constructed for species occurring within a given region. This metric is hard to interpret, however, especially since the authors’ primary focus is on the shape of the LTT plot (which reflects changes in the rate at which species accumulate along the regional phylogeny) rather than the time itself. Perhaps for these reasons it is not surprising that the effects of environmental conditions and time do not show any consistent effects on PD residuals. The only clear effect is that of present-day speciation rates. However, this result largely follows from the definition of the examined metrics. Namely, both speciation rates (DR) and PD are calculated from the regional phylogenies. Regions with lower-than-expected PD (i.e. resident species are closely related and show fast branching) are expected to have generally high DR. My impression is that the stated hypotheses (time, speciation rates, environmental conditions) have originally been defined to explain species diversity (e.g. Mittlebach et al. 2007), but the authors use them to explain PD. While the hypotheses might be transferable to some extent, this needs to be explained and justified in the text. This is currently largely lacking and presumably produces a mismatch between the predicted variable and its predictors, which might explain why the authors did not receive very robust findings.**A tighter link or a more explicit explanation of the hypotheses could be made, I agree, maybe comparing the effect of those factors on richness and on PD or residual PD.

**My recommendation would to be focus on those factors that can be convincingly linked to PD, cradles and museums. For example, the authors discuss the effects of mountains (topography) that have been long hypothesized to facilitate speciation (low residual PD) and suppress extinction (high residual PD). Mountains might presumably act both as museums and cradles, but it is possible that these roles vary depending on whether the mountains are tropical, temperate, etc. Similarly, the authors mention deserts as possible sinks of diversity, showing limited diversification. The maps identifying diversity museums and cradles are also impressive and interesting in their own right. I feel this could be one element of the manuscript (e.g. lines 393-403) that could be elaborated with strong connections to PD.**We could give more importance to mountains and deserts and maybe explicitly test something about them. I don’t know, for instance, having the polygons of mountain systems and deserts, see if they are regions of low or high resPD in general, or if there are latitudinal differences as the referee suggests… **Altogether, I was very impressed by the amount of well-executed analyses and results. However, the study could perhaps benefit from better conceptual framing, both in terms of the predicted variable and its predictors. By stating explicitly that the study is concerned with PD and formulating hypotheses to specifically explain PD, the authors could attain a more compelling manuscript that could constitute a valuable contribution to a significant topic, with longstanding tradition in the field. I am sorry I could not be more encouraging this time, and I also apologize for the delayed submission of my review. However, I sincerely hope that some of the comments above might be useful to further improve and strengthen this study, given the impressive amount of work that it includes.**This review doesn’t seem that bad either, it is more positive than the first one and the main concern is the framing of the paper (for instance start talking about PD earlier in the introduction) and stating explicit hypotheses.

**Mittelbach G.G., Schemske D.W., Cornell H.V., Allen A.P., Brown J.M., Bush M.B., Harrison S.P., Hurlbert A.H., Knowlton N., Lessios H.A., McCain C.M., McCune A.R., McDade L.A., McPeek M.A., Near T.J., Price T.D., Ricklefs R.E., Roy K., Sax D.F., Schluter D., Sobel J.M., Turelli M. 2007. Evolution and the latitudinal diversity gradient: speciation, extinction and biogeography. Ecol. Lett. 10:315–331.  
Robuchon M., Pavoine S., Véron S., Delli G., Faith D.P., Mandrici A., Pellens R., Dubois G., Leroy B. 2021. Revisiting species and areas of interest for conserving global mammalian phylogenetic diversity. Nat. Commun. 12:3694.  
Safi K., Cianciaruso M.V., Loyola R.D., Brito D., Armour-Marshall K., Diniz-Filho J.A.F. 2011. Understanding global patterns of mammalian functional and phylogenetic diversity. Philos. Trans. R. Soc. Lond. B. Biol. Sci. 366:2536–2544.  
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If there are no comments above, the reviewer may have chosen to upload a file. Please check ScholarOne Manuscripts for any attached files, which may be found at the end of the decision letter in your author centre under 'Manuscripts with decisions'.**