
In this article the authors empirically address the distinction between vicariance and isolation by distance. To accomplish this, they carried out thorough molecular sampling in a lizard system and phylogeographic approaches to characterize population units, and statistically test whether these lineages correspond to vicariant units or are the result of IBD alone. Their results point to a mix of vicariance and IBD in explaining the genetic diversity of the study group, and also highlight that overreliance on mitochondrial markers could bias conclusions about the causes behind genetic differentiation.

I believe that the paper is a great contribution to the phylogeographic literature given that it explicitly address the causes behind genetic structure, being applicable to several study systems. The data and methodological approaches are appropriate to the research question, and the results support their conclusions. In particular, I found exemplary the use of MCA to define phylogeographic units with nuclear data. Overall, the paper is very well written, clearly stating the knowledge gaps and the objectives of the study; also, the figures are well crafted. However, I consider that some minor issues should be addressed:

1. Title and Abstract

- Ln 53: I found some trouble with the word “safely”; is there any synonym?

2. Introduction

- Lns 104-106: ... and ILS.
- Ln 169: change “could results” to “could result”.

3. Materials and methods

- Ln 186: State here that your are using a subset of those 392 sequences, not all of them. i.e. 296 samples, or 306 including outgroups.
- Ln 221: Why not to use the multilocus dataset to calibrate the phylogeny? (e.g. with starBeast).
- Ln 218: Why didn't you also estimate branch supports with ultrafast bootstrap?

- Ln 239: How did you know that only exons were included in the nuclear dataset?
- Lns 275-276: To ease the reading with figure 1, state which subgroups are included in each phylogeographic unit, e.g. Rif includes N-Rif and S-Rif, Mid-Atl includes Mid-Atl1 and Mid-Atl2, etc.
- Ln 284: You missed an “r” in the web link.
- Ln 292: “two-step approach”, remove “s”.
- Lns 306-307: Please clarify that you are including adjacent Atlantic lineages to test for IBD in Inland lineages. Also state that O-Gha is included in S-Atl, because it does not appear in the map.

4. Results

- Lns 350-351: You could add the branch leading to the IM clade in the figure.
- Lns 352-360 and Figure 1: The 11 lineage names could be added to the phylogenetic trees to ease the reading of the text and the map.
- Ln 361: instead of “lineages 3 and 6” use the name of these groups.
- Ln 400: Add “the” before “latter”.

5. Discussion and Conclusions

- Ln 550: “extent” instead of “extant”.
- Figure 5: You could use a different color for each contour, to ease interpretation.