

Responses to reviewers

Editor's comments

The language and the interpretations are still too narrow. The reviewer suggest a more general discussion of what this data set says about the stability of species interactions to cause a co-phylogenetic signal.

We have greatly expanded the discussion, following yours and the reviewers' comments.

I follow the reviewer's comment and suggest additional elements to strengthen the ms. – note that the discussion is too short (only one page!) and it should be expanded at least to another page.

We have expanded the discussion, by adding a paragraph (x) comparing our results to a recent study in mutualistic systems, and by discussing how they fit in the discussion about the turnover of interactions in space and time (x).

There are several ways to expand it. For example, methods used here do not mention a whole branch of tangled trees methods to study potential mechanisms of cospeciation underlying matching phylogenies (Page, D. M., Ed. (2003). Tangled trees. The University of Chicago Press. Chicago.). On pp 42, 6 hypotheses are suggested in the evolution of host-parasite associations (Pure cospeciation, Duplication switching, Cospeciation-duplication, Cospeciation-sorting, Cospeciation-switching, and mixed patterns with cospeciations, duplications and switches) – Can authors discuss a bit more about such (or other) potential hypothesis underlying the observed patterns of co-phylogenetic matching?

We appreciate the suggestion, and have added a paragraph in the discussion (x) to highlight how the addition of time in the phylogenies can rule some of these scenarios apart.

What are the mechanisms decoupling the local and the continental scale patterns of the cophylogenetic signal? Check for example a neutral model that predict strong signal removing completely interaction selection from the underlying processes (Coelho, M. T. P., Rodrigues, J. F. M. and Rangel, T. F. 2016. Neutral biogeography of phylogenetically structured interaction networks. – Ecography doi: 10.1111/ecog.02780).

We have added a discussion of this recent article. We think that some methodological differences between the two articles make them difficult to compare in depth, but we have drawn the reader's attention to the fact that interaction probability (and therefore their contribution to the cophylogenetic signal) should be analysed at the interaction level.

Locally sampled communities rarely showed strong matching despite the fact that the overall system does at the continental scale – How does this connect to the “Parasite Paradox”? (i.e., parasites are generally specialized on a given set of hosts, but host shifts to distantly related hosts may occur frequently, Janz, N. (2011). Ehrlich and Raven revisited: mechanisms underlying codiversification of plants and enemies. *Annual Review of Ecology, Evolution and Systematics*, 42:71-89). Please discuss the potential role of dispersal limitation and host switching as additional processes to the ones driven by the abiotic conditions and species tolerances. Specifically, this should be put in the context of how to fill the big gap between the small-scale biological processes and ecological interactions for predicting large-scale associations between host and parasites as reflected in the phylogenies.

We have added a discussion of these mechanisms in the paragraph on the stability of species interactions (**x**).

Reviewer 2

Poisot and Stouffer have done a nice job revising their manuscript. The revisions improved clarity and I think the manuscript makes a nice contribution. I am not a specialist in this area, so I am trusting the author’s use of appropriate co-phylogenetic methods. I do think that additional text first in the methods (delineation of regions, number of regions) and on the implications of the results would help the non-specialist reader (of which I am one) place the findings into context. Having said that, I have a few minor comments that are aimed to doing this, but overall I think the manuscript is in excellent shape and is well-worthy of publication.

27: birds

Fixed.

54: This would only seem to be true in cases of co-evolution. It seems possible that a keystone species could have powerful interactions that shape the evolution of a number of different taxa.

We have added a discussion of this (**x**), emphasizing that interactions can have different effects.

Line 94: I get that this means 51 local sites. How were regions were delineated?

We have clarified the definition of what we mean by “regional scale” at XX.

203-206: What percentage of the host-parasite interactions in the dataset would be considered co-evolutionary from a phylogenetic perspective (at the continental scale)?

It would be difficult to express this as a percentage – in a sense, the *evolutionary events* could be considered to contribute or not to the coevolutionary dynamics. In the absence of time-resolved trees (see new paragraph in **x**), it is difficult to address this point, and we would rather not speculate about this.

220-223: I had a lot of trouble understanding this. Would this be correct?: ...if some driver acts to maintain the interaction between pairs of species at matching points in the phylogenies the local networks should demonstrate a higher degree of co-phylogenetic matching.

Yes, fixed.

284: from

Fixed.

286:... than they are by potential species interactions (at least relative to regional scales). Hard to say about the relative importance of drivers in an absolute sense.

Fixed.

290: Assuming that the signal of co-phylogenetic signal is considerable in this data at the continental scale (see comment for lines 203-206) I think you could add an even broader statement here speaking to the relationship between macro-evolutionary patterns and ecological communities. Perhaps something along the lines of: “It also draws into question the stability of co-evolutionary interactions over long timescales. We assume these interactions were once strong enough to drive speciation and now they are no longer strong enough to overcome local ecological processes.”

We thank the reviewer for this comment. We have added an explanation at **x**.

295:...at ecologically relevant spatial scales, even in system where phylogenetic structure would be expected to have a profoundly strong role” I think adding something like this to help drive the point home would help.

We agree, and are grateful for the suggestion. Added.

Fig. 3: units on the x-axis could use some explaining in the figure legend (not just main text).

Fixed.