

## ***Interactive comment on “Phylogenetic support for the Tropical Niche Conservatism Hypothesis despite the absence of a clear latitudinal species richness gradient in Yunnan’s woody flora” by G. Tang et al.***

**Anonymous Referee #3**

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The first response is that there have not been many similar analyses. The authors then go on to list a variety of places where a 'few' or more studies have been done. In other words, yes as I stated, there have been many other papers showing this pattern. Whether or not someone has shown this pattern for this exact province in this particular country is not exactly germane. If such a thing was sufficient for publication in a high quality international journal, then one could simply publish patterns of family ages or phylogenetic clustering for every province in China or every country in Africa and suggest it was a major/important breakthrough. In other words, the authors admit that

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similar patterns have been shown essentially in most parts of the world and they have now confirmed all of this work using Yunnan. I simply don't see what that is a major advance.

The other responses worked very hard to say lineage age is not related to things like NRI. Of course these are not the same exact measurement, but they are related no matter how much the authors want to deny it. If one region is occupied by a bunch of very closely related species, then it will have a young mean age. The authors counter with "yeah, but gymnosperms are clustered and an old lineage". This demonstrates a fundamental lack of understanding about phylogenies and phylogenetic diversity analyses. Yes, the root node of gymnosperms is old. Perhaps we can say it is around 400 million years old. This does NOT mean that the gymnosperm species you are looking at in the dataset are 400 myo of course. This is similar to saying that species in *Costus* (a genus less than 10myo) are 'old' because they are angiosperms and the root of the angiosperms is somewhere in the 150-220myo range. Thus, the response and defense using the gymnosperm example is rather weak and indeed completely wrong. If the authors do not understand the fundamental point that a root of a large lineage does not indicate the approximate age of a 'species', then we can't really appreciate their points/arguments as to why NRI is not related to age.

The points made by the other reviewers about using niche models for such an analysis are very well taken and I agree with 100%.

I would also like to ask what alternative hypotheses are rejected or supported? What we have here is a paper showing a pattern (that we already knew existed albeit in other parts of the world) that does not exclusively support one hypothesis and has not rejected any major hypothesis of note. In other words, we have not really progressed. Saying that this has something to do with drought is essentially storytelling without any other evidence. One can look at this pattern and correlation table and come up with a lot of different stories. If the authors continue to strongly disagree, then I would challenge them to clearly articulate all the hypotheses they have firmly rejected and

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why as well as explain why their evidence exclusively supports the niche conservatism hypothesis.

I completely fail to understand how this is biodiversity ecosystem function research. Where is the ecosystem function? The authors state that conceptually they might be talking about traits because things might be conserved because we see a two steps removed phylogenetic pattern in space. Somehow this is then called functional ecology or ecosystem function. To me that seems ridiculous.

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Interactive comment on Biogeosciences Discuss., 11, 7055, 2014.