

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.

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Received and published: 9 June 2014

Thanks for the interesting suggestions! We react a bit late because the corresponding author (that’s me) was on field work in a very nice forest in Brunei.

We hadn’t seen the Zanne et al paper yet, but its a great piece of work. We have already contacted her for possible use of the phylogeny.

We admit that ‘difficult’ may be a bit vague, although in the discussion we do clarify it a bit by linking it to hydraulic properties of woody plants, which was actually one of the

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conclusions of the Zanne et al. paper as well.

‘Difficult’ may also cover the process proposed as alternative to the Tropical Niche Conservatism Hypothesis, namely that extinction is driving the pattern. Indeed, during warmer and wetter periods, many tropical plants could and did venture far into higher latitudes. This has actually happened many times in Earths history, with at some point even extensive Boreal tropical forests. Many of the species found there have subsequently gone extinct when climate deteriorated (cooled and dried down) or survived/migrated in lower latitudes. In our opinion this still supports the Tropical Niche Conservatism Hypothesis because it shows that adaptation to these cooler/drier climates is ‘difficult’ for tropical woody plants. As Zanne et al. also show, most of the woody plants that did establish successfully in cooler climates were already pre-adapted to such conditions while they were still in the tropical biome (narrow conduit vessels), deciduousness. We find it striking that this set of characteristics is very similar to those needed for survival in drier climates, so it may be that these traits were originally developed for coping with dry climates, and then later proved beneficial for survival in cold climates as well.

We still argue that the APGII tree is good enough to detect the main patterns in phylogenetic diversity and clustering as the general patterns in that phylogeny, especially the order in which the different angiosperm lineages included in our analysis emerged, have not changed a lot. The different time callibrations of the newer phylogenies may change the strength of the patterns a bit (making them stronger or weaker), but will not affect the general patterns that we found.

Off course, it would be better to use the most up to date tree, but as said, the responsible student is no longer available, and none of the co-authors has time to redo all the analyses from scratch, so there is a serious risk of the paper never coming out if this was required. Anyway, we leave it to the editor to decide on this matter.