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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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AGAIN ANSWERS IN CAPS

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. WE MENTIONED THREE OTHER STUDIES, ALL USING DIFFERENT METHODS AND APPROACHES THAN OURS. WE WOULDN'T JUST CALL THIS 'MANY STUDIES' DOING THE SAME THING.

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 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. AS SAID BEFORE, WE DO NOT SIMPLY REPLICATE OTHER STUDIES AND WE HAVE ADDED A SIGNIFICANT NEW POSSIBLE EXPLANATION FOR THE OBSERVED LATITUDINAL DIVERSITY GRADIENT. WE DON'T REALLY UNDERSTAND WHY THIS REVIEWER KEEPS SAYING THAT THESE PHYLOGENETIC DIVERSITY PATTERNS ARE ALL LONG AND WELL ESTABLISHED. THEY ARE NOT.

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 cos- tus (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. THIS

IS NOT TRUE. JUST LOOK AT HOW PHYLOGENEIC DIVERSITY IS CALCULATED. THERE MAY BE TEN GYMNOSPERMS IN A COMMUNITY WHICH MAY INDEED BE YOUNG AND HAVE LOW PHYLOGENETIC DIVERSITY. HOWEVER, ADDITION OF JUST ONE ANGIOSPERM WOULD TREMENDOUSLY INCREASE PHYLOGENETIC DIVERSITY OF THE SITE PRECISELY BECAUSE PHYLOGENETIC DIVERSITY WOULD INCLUDE THE WHOLE DISTANCE TO THE ROOT! THE ANGIOSPERM SPECIES MAY BE YOUNG, THE GYMNOSPERM SPECIES MAY ALL BE YOUNG, STILL THE PHYLOGENETIC DIVERSITY WOULD BE VERY HIGH BECAUSE IT IS CALCULATED AS BRANCH LENGTH CONNECTING THE TERMINAL POINTS, I.E. IN THIS CASE ALL THE WAY BACK TO THE SPLIT OF GYMNOSPERMS AND ANGIOSPERMS. PHYLOGENETIC CLUSTERING CAN INDICATE YOUNG AGE, AS WE STATED IN OUR EARLIER RESPONSE, BUT, AS WE HOPED TO MAKE CLEAR IN OUR PREVIOUS REPLY, IN MOST CASES IT DOESN'T HAVE TO! IN PRINCIPLE IT JUST INDICATES THAT CERTAIN CLADES THAT ARE CLOSELY RELATED ARE FOUND DISPROPORTIONATELY IN A CERTAIN AREA COMPARED TO WHAT MIGHT HAVE BEEN EXPECTED. IN OUR VIEW PHYLOGENETIC CLUSTERING DOES NOT INDICATE THAT ALL SPECIES IN SUCH CLUSTERED AREAS ARE YOUNG (ONE CAN ASSUME THAT ALL SPECIES ARE ON AVERAGE OF EQUAL AGE), BUT THAT ONLY CERTAIN LINEAGES WITH SPECIFIC TRAITS (ASSUMING CLOSE RELATIONSHIP MEANS SIMILAR TRAITS, WHICH IS GENERALLY A FAIR ASSUMPTION) HAVE BEEN ABLE TO OCCUPY THAT AREA, I.E. THE PATTERN IS ENVIRONMENTALLY DRIVEN, NOT SPECIES AGE DRIVEN.

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 do to 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 why as well as explain why their evidence exclusively supports the niche conservatism hypothesis. AN ALTERNATIVE HYPOTHESIS WOULD BE THAT THERE IS NO LATITUDINAL GRADIENT, IN WHICH CASE THE TROPICAL NICHE CONSERVATISM HYPOTHESIS WOULD NOT BE SUPPORTED. AS SAID, WE DO NOT PROVIDE PROOF OF THE TROPICAL NICHE CONSERVATISM HYPOTHESIS, WE FIND SUPPORT FOR IT AND PROVIDE A POSSIBLE MECHANISM OF HOW IT MAY COME ABOUT. TO PROOF IT, EXPERIMENTAL WORK WOULD BE REQUIRED. THAT WOULD BE A DIFFERENT STUDY.

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. WE ARE NOT GOING INTO THIS ARGUMENT AGAIN. APPARENTLY THE EDITOR AGREED WITH US THAT THE PAPER FITS THE JOURNAL, SO WE PASSED THAT STEP ALREADY.

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