## Recommendation

# Remarkable insights into processes shaping African tropical tree diversity

Michael David Pirie based on reviews by Lars Chatrou, Miguel Navascués and Oscar Vargas

A recommendation of:

Andrew J. Helmstetter, Biowa E. N. Amoussou, Kevin Bethune, Narcisse G. Kandem, Romain Glèlè Kakaï, Bonaventure Sonké, Thomas L. P. Couvreur. **Phylogenomic approaches reveal how a climatic inversion and glacial refugia shape patterns of diversity in an African rain forest tree species** *(2020), bioRxiv, 807727, ver. 3 peer-reviewed and recommended by Peer Community in Evolutionary Biology.* 10.1101/807727 (https://doi.org/10.1101/807727)

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Tropical biodiversity is immense, under enormous threat, and yet still poorly understood. Global climatic breakdown and habitat destruction are impacting on and removing this diversity before we can understand how the biota responds to such changes, or even fully appreciate what we are losing [1]. This is particularly the case for woody shrubs and trees [2] and for the flora of tropical Africa [3].

Helmstetter et al. [4] have taken a significant step to improve our understanding of African tropical tree diversity in the context of past climatic change. They have done so by means of a remarkably in-depth analysis of one species of the tropical plant family Annonaceae: *Annickia affinis* [5]. *A. affinis* shows a distribution pattern in Africa found in various plant (but interestingly not animal) groups: a discontinuity between north and south of the equator [6]. There is no obvious physical barrier to cause this discontinuity, but it does correspond with present day distinct northern and southern rainy seasons. Various explanations have been proposed for this discontinuity, set out as hypotheses to be tested in this paper: climatic fluctuations resulting in changes in plant distributions in the Pleistocene, or differences in flowering times or in ecological niche between northerly and southerly populations. These explanations are not mutually exclusive, but they can be tested using phylogenetic inference – if you can sample variable enough sequence data from enough individuals – complemented with analysis of ecological niches and traits.

Using targeted sequence capture, the authors amassed a dataset representing 351 nuclear markers for 112 individuals of *A. affinis*. This dataset is impressive for a number of reasons: First, sampling such a species across such a wide range in tropical Africa presents numerous challenges of itself. Second, the technical achievement of using this still relatively new sequencing technique with a custom set of baits designed specifically for this plant family [7] is also considerable. The result is a volume of data that just a few years ago would not have been feasible to collect, and which now offers the possibility to meaningfully analyse DNA sequence variation within a species across numerous independent loci of the nuclear genome. This is the future of our research field, and the authors have ably demonstrated some of its possibilities.

Using this data, they performed on the one hand different population genetic clustering approaches, and on the other, different phylogenetic inference methods. I would draw attention to their use and comparison of coalescence and network-based approaches, which can account for the differences between gene trees that might be expected between populations of a single species. The results revealed four clades and a consistent sequence of divergences between them. The authors inferred past shifts in geographic range (using a continuous state phylogeographic model), depicting a biogeographic scenario involving a dispersal north over the north/south discontinuity; and demographic history, inferring in some (but not all) lineages increases in effective population size around the time of the last glacial maximum, suggestive of expansion from refugia. Using georeferenced specimen data, they compared ecological niches between populations, discovering that overlap was indeed smallest comparing north to south. Just the phenology results were effectively inconclusive: far better data on flowering times is needed than can currently be harvested from digitised herbarium specimens.

Overall, the results add to the body of evidence for the impact of Pleistocene climatic changes on population structure, and for niche differences contributing to the present day north/south discontinuity. However, they also paint a complex picture of idiosyncratic lineage-specific responses, even within a single species. With the increasing accessibility of the techniques used here we can look forward to more such detailed analyses of independent clades necessary to test and to expand on these conclusions, better to understand the nature of our tropical plant diversity while there is still opportunity to preserve it for future generations.

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