

Dear Dr Pirie,

your "further comments" illustrate finely your philosophy regarding what phylogenetic trees show and should show. A philosophy that may be (still) mainstream (but see e.g. the blog and works of David Morrison, obviously you have the opinion my works on this topic are irrelevant, which comes to no surprise to me), but nevertheless has resulted in many hypotheses about evolution that were made for the bin. I may quote one of my later reviewers saying that it was refreshing to see a paper like ours passing through the editor-driven publication system (the paper being Bomfleur et al., *BMC Evol. Biol.*, 2015; the journal that rejected it - following a similar editorial viewpoint than yours, was *Bot. J. Linn. Soc.*) I find your critique regarding that we report and show also low values (in fact this is something missing in many studies and could have avoided many errors in the last 20 years done in molecular phylogenetics) and Figure 3 being a "detriment" unacceptable.

Our analyses are well done and – I may add – more comprehensive than in most studies (including such frequently published in *TAXON*). We not only show the low support along the trees, but also what alternatives there may be competing with them (Fig. 3; supplement files). Obviously, this provides more information than just showing a number of unresolved single-gene trees, majority consensus trees or a single tree where all values below a certain (entirely arbitrary, please refer e.g. to Felsenstein's book) threshold are just *not* reported. Just a recent quote on the topic: "*The predominant worry of users is that their support values are "too low." Instead of striving to somehow increase them, it might be better to publish them as they are but conduct an in-depth analysis as to why this is the case*" (Stamatakis, *Curr. Protoc. Bioinform.*, 2015).

In fact, it would be much more important that people document their support analyses results (like we did already in the original submission) rather than just their preferred and single-gene trees as you suggested in your recent tutorial. A colleague and I just browsed TreeBASE for useable datasets to conduct an in-depth analysis comparing best-supported branches with networks (you'd be surprised how often they fit, particular when it comes to "low" support). About 75% of the entries I looked at were useless, many showing single-gene trees, but no tree with support values on it. You may want to add that in your next editorial [Info to the reader: Pirie wrote an editorial outlining how he figures a good phylogenetic study should look like and be documented, which, from my perspective, would just fulfil minimum standard].

Consensus networks, massively underused as they are, are the only means to visualise all signals in e.g. a bootstrap sample (or any tree sample, by the way). You may not like it, which is your right, and you can take comfort from the fact that many systematic botanists would side with

you (well, many systematic botanists have also published trees that were obsolete after the next sequenced gene region...). But it's not your right to prevent the publication of this paper based on your beliefs and to force authors into a line that you believe is the only possible one. You misuse your power as an editor.

If you think our data shows something else than we wrote...well you have had access to it since months. Please feel free to make a better inference that recovers all our dirt under our carpet. You may even want to write a comment to Khanum et al.

I will not participate in any further streamlining of the results to fit your liking. To allow publication of the paper fitting to the particular quality standards of TAXON enforced so passionately by the editorial board, I hereby step down as a co-author of the paper. I am sure, in case it's needed, you'll be more than qualified to fill my role, advising further my poor coauthors (so misguided by me) how to properly do the analysis of their data. May it be deemed to be presentable by the High Editors.

Cheers, Guido