



EGUsphere, author comment AC3
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Reply on RC3

Deming Yang and Gabriel J. Bowen

Author comment on "Integrating plant wax abundance and isotopes for paleo-vegetation and paleoclimate reconstructions: a multi-source mixing model using a Bayesian framework" by Deming Yang and Gabriel J. Bowen, EGU sphere,
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We thank the reviewer for the follow-up questions and thoughts.

The reviewer asked about the treatment of Characeae (genus Chara) in our data sheet shared on GitHub. The genus Chara is treated as algae while we did not specify whether it is micro or macro algae. This treatment is following Aichner et al., 2010 and Liu & Liu, 2016. When we were putting the data together, we observed that the genus Chara display much lower $\delta^{13}\text{C}$ values than macrophytes as reported by Aichner et al., 2010. This further justifies the reason why Chara is not grouped with macrophytes, which display higher and more variable $\delta^{13}\text{C}$ values according to Aichner et al., 2010. We can certainly elaborate on this decision in the revised manuscript.

The reviewer also asked about how to make this approach more accessible to a broad range of researchers, as the approach may seem rather complicated. We would like to add to this question by emphasizing the main benefits of using such a Bayesian approach, which are 1) getting the most out of compound-specific isotope analysis by offering mixing solutions of multiple sources, and 2) straightforward handling of uncertainty in the analysis. It is intuitive that researchers would only choose to use this approach if the benefits outweigh the "costs". We would like to start with the notion that there are potentially huge benefits in using this approach, some of which are outlined in section 4.2. Case study 3 will specifically demonstrate the benefits of handling uncertainty and add to what is already in section 4.2. We really hope that this publication can increase the awareness on the benefits that this approach may bring to the community.

In terms of lowering the hurdle (cost), there are several things that can be done. One is to develop more user-friendly versions of the code into perhaps an R package and distribute it with a detailed tutorial. Our longer-term plan is to do this, combining the work presented here with other proxy system models under development and providing a common interface and framework for proxy data interpretation. Such a development is premature at this point, however, and one of our short-term goals is to receive community feedback on the approach and how it is/may be useful to the research community through this and other publications. Another way to lower the 'bar to entry' is to organize workshops online or at conferences for the technical details of this approach if there is enough interest. Again, community feedback is key. We are also open to inquiries and potential collaborations if necessary.

The reviewer also asked about the handling of prior distributions with examples of whether to use regional compilations or global averages. The model itself is flexible enough to accommodate either choice, so it ultimately depends on the user and the reasons to justify it. We chose to use regional compilations in case studies 1 and 2 because we think that this is more consistent with what we know about the production, transport and mixing processes of plant wax lipids in lake sediments. If using global averages can be justified in certain situations, we see no reason why they cannot be used. Related to this and the reviewer's last comment, we think that having a centralized lipid database is important because it can make this model approach much easier to use from a user's perspective, whether the need is for a regional compilation as demonstrated, or a global one.