Biogeosciences

Discussions

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Interactive comment on "Seed traits and phylogeny explain plant distribution at large geographic scale" *by* Kai Chen et al.

Anonymous Referee #1

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Chen et al.' MS entitled "Seed traits and phylogeny explain plant distribution at large geographic scale" addresses how seed mass, seed dispersal mode and phylogeny jointly affect species distribution based on a fascinating dataset of seed traits from 1616 seed plant species mainly from China. The authors quantify the effects of seed mass, seed dispersal mode and phylogeny on species distribution, and observe that species range size is constrained by seed dispersal mode and phylogeny. The results of the study provide the direct evidence that seed mass, seed dispersal modes and phylogeny explain species distribution variation on a large geographic scale, which is very important for understanding the seed plant biogeographic pattern and predicting the response of plant geographic distribution to climate change.

In general, the text is well written, although some clarifications are needed in some

places. The language is appropriate. The discussion and conclusions seem to be fairly well supported by the results. However, I have a few minor concerns about the methods and results on improving the manuscript. Once these concerns are resolved I think the manuscript would potentially deserve to be published.

The presentation of the 1000 seeds per species of seed mass in the Materials and methods section is not clear. How the 1000 seeds per species were selected? Did all the species have at least 1000 seeds used for measurement? Please clarify.

The authors used records of species specimens to quantify species distribution range size, while some other related studies adopt SDM models to estimate species distribution. Why do the authors use specimen records to quantify species distribution range size rather than using SDM models? Which method is more appropriate? Why?

The authors mentioned that they tested the models based on a variance inflation factor (VIF) in the methods (L122). It is remarkable that the VIF values are same for different predictors (see Table A2), which needs to be clarified in the results and discussion respectively.

Specific comments:

P7 L132: "by other models" what kind of "other models" need to be clarified. P9 L180: in our study can be deleted. P10 L194: the distribution of species should be the distributional range size of species. P10 L201: Change "Seed traits and phylogeny jointly affect species distribution in our study" to "Our results here demonstrated that seed traits and phylogeny jointly affect the species distribution, ..." P10 L201: Seed traits and phylogeny jointly affect species distribution In Figure 2, Lambda-value and P-value need to be clarified in the caption.