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.

Authors Response: Thank you for your questions. Mature seeds were collected at the start of natural dispersal and dried in a drying room where the relative humidity and temperature were maintained at 15% and 15℃, respectively. Moisture was drawn out of the seeds until water content was the same as that in the air. After drying, 250 seeds were randomly selected to be measured to the nearest 0.1 mg, and repeated four times. In order to protect germplasm resources, each species has more than 1,000 seeds in Germplasm Bank of Wild Species in Southwest China. We will clarify the 1000-seed weight in the Method.

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?

Authors Response: Thank you for your questions. Distribution range size calculated through SDM models are under "ideal" conditions which dispersal ability, time and other important plant traits are not considered as limiting factors. Therefore, this range size is also called potential distribution range size. Usually some potential distribution ranges are not occupied by species, due to the constraint of dispersal ability. While, distribution range determined by species specimens is the species "actual" distribution. Especially, range size estimating on a large number of specimens should be the unbiased estimation of species distribution range size. Using records of species specimens to quantify species distribution range size is more appropriate when having massive amount of specimen data.

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.

Authors Response: Thanks a lot for pointing it. The VIF (variance inflation factor) of the i-th variable is defined as: $VIF_i = 1/(1 - R_i^2)$, where R_i^2 is the goodness-of-fit of the linear model for x_i based on all other predictive variables. Here, we have only two predictive variables and the R^2 values of the two variables are equal. We will clarify in the caption of Table A2.

Specific comments:

P7 L132: "by other models" what kind of "other models" need to be clarified.

Authors Response: Here, "other models" represented autochory, endozoochory and anemochory. We reworded the sentence to make it clear in the revised manuscript.

P9 L180:in our study can be deleted.

Authors Response: Have done.

P10 L194: the distribution of species should be the distributional range size of species.

Authors Response: We have changed accordingly.

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, ..."

Authors Response: We have reworded the sentence accordingly.

In Figure 2, Lambda-value and P-valueneed to be clarified in the caption.

Authors Response: Lambda-value and P-value have been clarified in the caption as "$P< 0.001$ means that the phylogenetic signal of range size is significant, and Lambda-value $= 0.515$ implies that the evolution model of species range size is different from Brownian motion."