**Responses to #Reviewer 1**

This is a well-prepared manuscript. The authors focused on mapping several key plant functional traits in China by integrating three kinds of machine learning algorithms and climate, soil, and vegetation variables. Comprehensive experiments were implemented and all necessary technical details were properly introduced. It could be of great interest to those who are interested in trait ecology, and global vegetation modeling. However, at present, some technical details need to be added and the language of the paper needs to be further improved. In its current form, major revisions are needed before this manuscript could be accepted, thereby further improving the quality and legibility of this manuscript. The main comments are as follows:

**[Response]:** Thanks for your positive comments and constructive suggestions for our manuscript. We have carefully addressed the comments and suggestions in the revision, and detailed revisions and responses are listed below. In addition, the language of this manuscript has been professionally revised, and we have used tracks to highlight the revisions in the revised manuscript.

1. We are aware that the plant functional traits have strong seasonal variability. However, it seems that the issue of seasonality was not taken into account in the synthesized plant functional traits database by the authors. As a result, I don't know which time period of these estimated plant functional trait maps. Could you please provide some additional explanations regarding the temporal information associated with these plant trait maps?

**[Response]:** Thanks for your suggestions. In literature and public databases that provided the sampling time used in our study, the sampling time mostly focused on the growing season of a year (i.e., May-October), thus the effect of seasonality is relative minor. In addition, we collected trait data that must meet this criterion: plant trait observations must be made on mature plant individuals, so some specific leaf and plant growth stages (e.g., seedlings, leaf expanding stage or senescent leaves) were excluded to minimize the effect of seasonality. We added the above-mentioned explanation in the section 2.2 in Materials and Methods (see Lines 163–165 in the revised manuscript). And the sampling time of plant functional traits was shown in the dataset used in this study at the figshare link: https://figshare.com/s/c527c12d310cb8156ed2.

2. It is really good you compiled a large plant trait database with more than 50 thousand samples, spanning large geographic regions and species, please present the number of samples for each selected plant functional trait. And how many samples are for model calibration and validation?

**[Response]:** Thanks for your suggestion. We have added the number of samples for each plant functional trait and the number of samples used for model training and validation in the Table B3 in Appendix B as follows.

**Table B3** The number of samples of eight plant functional trait used for model training (80%) and validation (20%).

| Traits | No. of samples | No. of samples used for model training | No. of samples used for model validation |
|--------|----------------|----------------------------------------|------------------------------------------|
| SLA    | 9195           | 7356                                   | 1839                                     |
| LDMC   | 3957           | 3166                                   | 791                                      |
| LNC    | 7407           | 5926                                   | 1481                                     |
| LPC    | 6266           | 5013                                   | 1253                                     |
| LA     | 5976           | 4781                                   | 1195                                     |
| WD     | 1787           | 1430                                   | 357                                      |

3. There are many choices of climate variable products and each product carries varying levels of uncertainty. Why did you choose the WorldClim dataset and did you assess the uncertainties of these datasets?

**[Response]:** We selected the Worldclim dataset mainly based on two reasons as follows. First, Worldclim version 2.1 dataset includes 19 bioclimatic variables, covering minimum, mean, and maximum temperature, precipitation, solar radiation and total precipitation. When we selected climate datasets in the stage of data processing, we compared Worldclim version 2.1 with some datasets (e.g., CRU v4.0, ERA5-land and China Meteorological Forcing Dataset) from the comprehensiveness of variables, spatial resolution and time period. We used the Worldclim version 2.1 dataset for this study instead of the other three datasets as the latter does not have high resolution and include multiple aspects of climate variables needed in this study. Second, our previous study has proved that climate variability and seasonality variables, in particular, mean temperature of the warmest and coldest seasons of a year and mean precipitation in the wettest and driest seasons of a year, were more important drivers of leaf trait variation than mean annual temperature and mean annual precipitation (An et al., 2021). Therefore, given that Worldclim version 2.1 includes these above-mentioned indicators, we selected it.

Indeed, although WorldClim dataset has been widely applied in different biogeographical applications in the global and regional studies (Loozen et al., 2020; Huang et al., 2021; Liu et al., 2022), and it is classical and recognized by the researchers, we have to admit that climate dataset has certain limitation and uncertainties. We have added the corresponding description about the uncertainties as "*In addition, although Worldclim version 2.1 product has high spatial resolution and includes various aspects of climatic parameters, there exists certain limitation and uncertainty in predicting trait maps. Therefore, integrating satellite remote sensing monitoring methods with in in-situ trait data collection can also provide an effective way to estimate and assess the species diversity at a large scale (Cavender-Bares et al., 2022).*" in the Discussion section (see Lines 625–629 in the revised manuscript).

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4. I found that the time period for bioclimate variables and RAD is from 1970 to 2000, while the AI data is from 1950 to 2000 and the vegetation indices are 2000-2018 & 2002-2011, please explain why the time period of different input variables are not consistent.

[Response]: The bioclimate variables and RAD were extracted from the Worldclim version 2.1 for the period from 1970 to 2000, because this dataset has a high spatial resolution and the comprehensiveness of indicators that are related to plant functional trait variation. There was a mistake in the text, the AI data was from 1970 to 2000 instead of 1950-2000. We have corrected it in the revised manuscript. The AI data was calculated based on WorldClim 2.1 and implementation of a Penman Montieth Reference Evapotranspiration (ET0) equation, and the spatial resolution is 1 km (Trabucco and Zomer, 2018). In addition, vegetation indices included

enhanced vegetation index (EVI) and the MERIS terrestrial chlorophyll index (MTCI) in our study. The EVI data was extracted from the MOD13A3 V006 product, ranging from April 1998 to December 2018 when we began to conduct this study. Due to the incompleteness of January to March in 1998, so we calculated the monthly EVI data from 2000 to 2018. The monthly MTCI data was extracted from MERIS Level 3 MTCI products that only provided the time period for 2002-2011. Given of the data availability and high spatial resolution, the climate and vegetation datasets with different time periods is unavoidable in spatial mapping and biogeographical studies so far (Crowther et al., 2015; Moreno-Martínez et al., 2018; Loozen et al., 2020; Huang et al., 2021; Ma et al., 2021). Indeed, we must admit that the inconsistency in the time period could lead to predictive uncertainty, thus we have added the corresponding content to discuss the possible uncertainties as "*The lack of consistent time period and spatial resolution of predictors due to limitation of data availability is another key challenges in the spatial mapping of plant functional traits.*" in the Discussion section (see Lines 623–625 in the revised manuscript).

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5. The authors used the nearest neighborhood method to resample all the input data to a consistent spatial resolution of 1 km. It is fine for the original resolution of the data below 1 km to upscale to 1km. However, Downscaling data to 1km resolution using this method is not meant for datasets with spatial resolutions greater than 1km such as MTCI with 4.63 km spatial resolution.

**[Response]:** MTCI is an important factor that is closely related to plant functional traits (Loozen et al., 2020). However, MTCI dataset currently available is just 4.63 km in spatial resolution. Although the downscaling data is a common resolution used in spatial mapping studies (Moreno-Martínez et al., 2018; Huang et al., 2021) and a good compromise, we must admit that downscaling data from low spatial resolution may generate the uncertainty. So we have added the relevant contents to discuss this uncertainty as "*The lack of consistent time period and spatial resolution of predictors due to limitation of data availability is another key challenges in the spatial mapping of plant functional traits.*" in the Discussion section (see Lines 623–625 in the revised manuscript).

6. Did you build separate models for each plant trait, or estimated these traits simultaneously? How did you consider the covariance of these traits when you were modeling?

**[Response]:** We built separate models for each plant trait, so trait covariance need not be considered in the manuscript. To avoid the misleading information in the predictive methods for plant functional traits, we have corrected the relevant content to describe the model predictions more clearly (see Line 286 in the revised manuscript).

7. For the calculations of community-weighted mean values, you first build the relationships between the observed trait values and the input variables with 1km spatial resolution. I think your predicted values of traits present the values of 1km grid cells, so my question is how you applied CWM using the abundance of each PFT in each 1km grid cell.

**[Response]:** Thanks. We generated the plant functional trait maps in four steps as follows. First, we associated each species with a corresponding PFT based on plant growth form (tree, shrub and grass), leaf type (broadleaf and needleleaf) and leaf phenology (deciduous and evergreen). For example, the information on *Salix matsudana* is: tree, deciduous and broadleaf, thus, we were able to associate the PFT of deciduous broadleaf forest (DBF) to this species (see Lines 177–187). The species that did not correspond to any PFT were discarded. Second, we predicted the trait values for six PFTs separately by building the machine learning models using the field measurement data and predictors at a 1 km spatial resolution. Then, we obtained six prediction layers for each plant functional trait. Third, the classification of natural PFT types includes evergreen needleleaf forest (ENF), evergreen broadleaf forest (EBF), deciduous needleleaf forest (DNF), deciduous broadleaf forest (DBF), shrubland (SHL), grassland (GRL). We

calculated the abundance of individual PFT within 1 km grid cell using a land cover map with a spatial high-resolution of 100 m. Forth, the final community weighted mean trait values were calculated according to the predicted trait values (the second step) and corresponding abundance of each PFT (the third step) refer to the equation of CWM calculation in the community as Eq. (1) (Garnier et al., 2004). As we all know, we cannot obtain the data surrounding species co-occurrence and their relative cover or abundance in ecological communities, which is a key challenges in how scales up from the species to the community levels. The abundance of each PFT can be considered as an alternative way (Moreno-Martínez et al., 2018; Dong et al., 2023) relative to unweighted or equal weight community means methods, in order to scale-up plant trait observations and matching the spatial scales of the local trait observations and environment and vegetation data.

$$CWM = \sum_{i=1}^{n} W_i X_i \tag{1}$$

where $n$ is the total number of PFT in a given grid, $W_i$ is the relative abundance of the $i$th PFT, and $X_i$ is the predicted trait value of the $i$th PFT.

We have revised the relevant content in the sections 2.2 and 2.5 in Materials and Methods (see Lines 177–187, 249–258, 314–322 in the revised manuscript).

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8. What is the ensemble model mean? how to merge the results of RF and boosted regression trees as you presented in line 263. Could you please present more details of the ensemble model?

**[Response]:** Previous studies have been proved to have differences and uncertainties among different single technique in their modelling performance. Therefore, the ensemble models have the advantages in overcoming the problem of variability in predictions and constructing a more stable and accurate model (Thuiller et al., 2003; 2005). Ensemble models are based on combinative algorithms of the predictions provided by different single-models, and they show

promise for different biogeographical and conservation biological applications (Marmion et al., 2009; Boonman et al., 2020). The most commonly used techniques of ensemble methods include Weighted Average, Mean (All), Median (All), Median (PCA) and Best (Marmion et al., 2009). Previous studies have reported that Weighted Average methods provided significantly more robust predictions than all the single-models and the other consensus methods (Marmion et al., 2009; Bourel et al., 2018).

In this manuscript, we used Weighted Average methods based on the $R^2$ values of random forest and boosted regression trees to obtain the predictive performance of the ensemble models. First, we calculated the predictive values of ensemble model, in a given grid cell, based on predictive values and the cross-validated $R^2$ values of random forest and boosted regression trees as described by the following equation (Marmion et al., 2009; Boonman et al., 2020).

$$Pred\_EM_t = \frac{\sum_{m=1}^{2}(pred_{m,t} \times r_{m,t}^2)}{\sum_{m=1}^{2} r_{m,t}^2}$$

where $Pred\_EM_t$ is the predictive values of $t$ trait in ensemble model, $pred_{m,t}$ is the predictive values of $t$ trait in $m$ model, $r_{m,t}^2$ is the cross-validated $R^2$ of $t$ trait in $m$ model.

Second, the accuracy of the ensemble model was calculated by regressing the predictive values of ensemble model based on the equation above against the observed trait values.

We have added more detailed information of the ensemble model in the section 2.5 in the Materials and Methods (see Lines 326–336 in the revised manuscript).

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9. You just build the models between the 1km spatial resolution data and the filed measurement data. Do you think that is there any spatial mismatch between them?

**[Response]:** Yes, we have considered this issue when we extracted the predictive variables of sampling sites from the 1 km spatial resolution data. However, it is not avoidable in a meta-analysis at the large scale. It may be mainly attributed into two reasons. First, our study was conducted at a large scale, and was obtained plant functional traits from previous studies on field survey. Given that each study where we collected data focused on different aims and experimental designs, so it is impossible to provide comprehensive auxiliary data such as climate, soil and topography in the original literature and public databases. Indeed, when we extracted the plant functional trait data from literature and public databases, several auxiliary data are always missing. Due to the deficits of original auxiliary data, we have to extract the auxiliary data (i.e., environmental variables and vegetation indices) from public datasets with high spatial resolution to ensure their data match as far as possible. Second, we used environmental variables and vegetation indices with high resolution as much as possible to match field measurement data, in order to minimize the difference between them. In addition, we have found that the MAT and MAP from the original literature agreed well with the values in the dataset ($R^2$ values were 0.96 and 0.89, $p < 0.05$) in our previous study. Although this method is a most common resolution and accepted practice in similar studies such as large-scale spatial mapping and biogeography based on collected field measurement data (Valverde-Barrantes et al., 2018; Boonman et al., 2020; Ma et al., 2021). We must admit that there exist uncertainties of the spatial mismatch between them, thus we have added the corresponding discussion as "*The environmental information of sampling sites was not always obtained from original literature, thus using the public environmental products is a common resolution used in large-scale plant trait studies (Boonman et al., 2020; Vallicrosa et al., 2022). Such mismatch between in-situ trait measurements and predictors should be resolved in further work.*" in the Discussion section (see Lines 613–616 in the revised manuscript).

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10. Please add the units of these traits in Table 2 although you present them in your supplementary table. And I suggest that it is better to use nRMSE in the realm of leaf functional trait estimation (nRMSE = RMSE/range of estimated plant traits).

**[Response]:** Thanks for your constructive suggestions. We have added the units of these traits in Table 2, and we have also calculated nRMSE to place of RMSE in the revised manuscript (see Line 297, 363–366 and Table 2).

11. When analyzing the spatial patterns of plant functional traits, it is better to have a map to show the readers where the locations you mentioned in the manuscript like Yunnan, Loes Plateau, etc. are.

**[Response]:** Thanks for your nice suggestion. We have added corresponding locations in the Figs. 3, 4 and 6 according to the result description in the revised manuscript as follows.
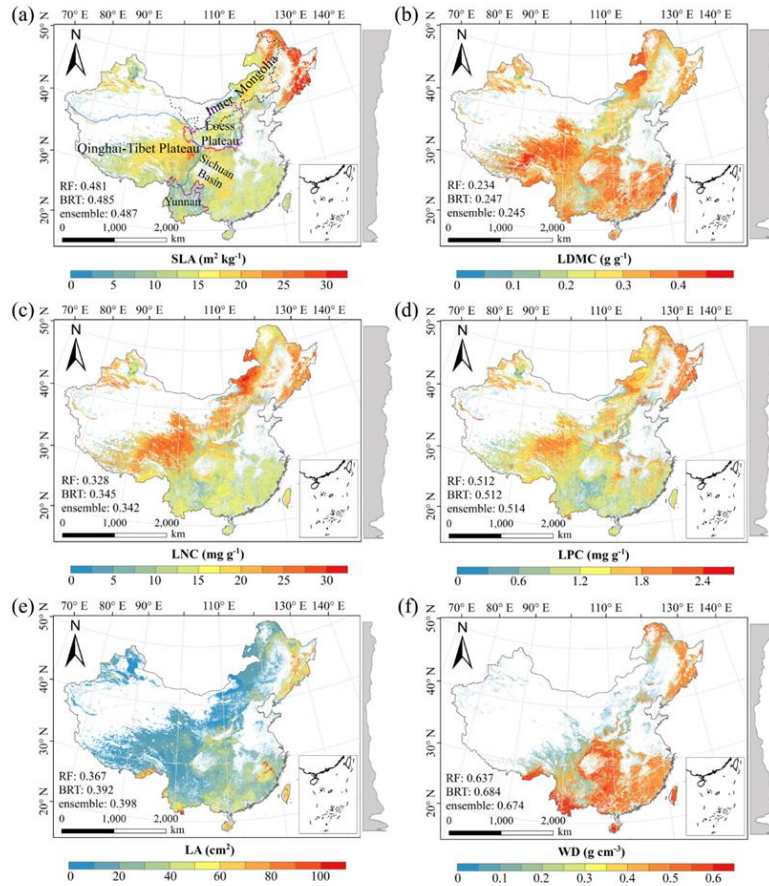
**Figure 3.** Spatial patterns of predicted plant functional traits in China based on the ensemble model. The grey curves to the right of the maps display trait distribution along with latitude. RF, random forest; BRT, boosted regression trees; ensemble, ensemble model; SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.
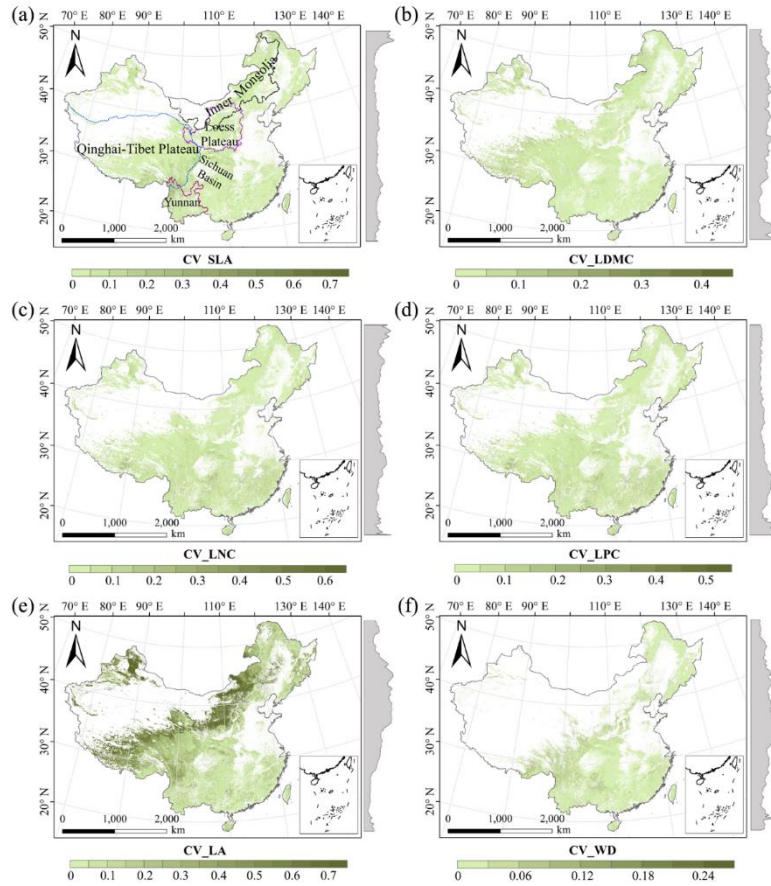
**Figure 4.** The variability in plant functional trait predictions among random forest, boosted regression trees and ensemble model. The grey curves to the right of the maps display coefficient of variation along with latitude. SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.
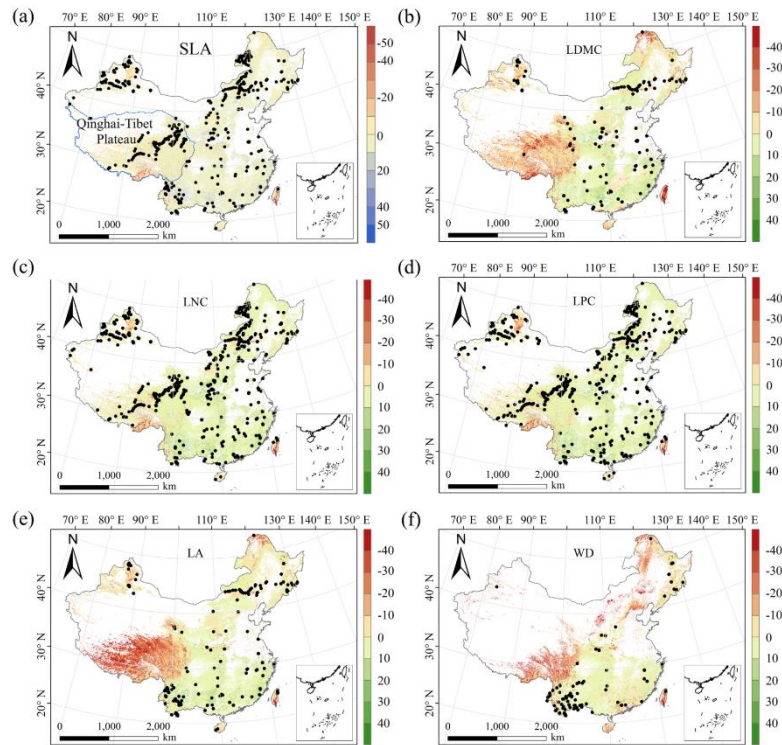
**Figure 6.** Multivariate environmental similarity surface (MESS) assessments for the six plant functional traits. The black dots represented the locations of trait observations. More intense shades indicate greater similarity (blue) or difference (red) in environmental conditions of the location compared to the predictive factors covered by the training dataset. SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.

12. For the accuracy of these estimated plant functional traits. The sampling of WD, LPC and SLA is dense, it's reasonable that these three traits have relatively high performance. But LNC and LA also show relatively dense sampling across China as shown in Fig. 5, Could you please tell me why LNC and LA show relatively poor performance?

**[Response]:** This is a good question. Indeed, LNC and LA had relatively dense sampling across China, whereas they showed relatively poor performance. The main reason is that the environmental variables and vegetation indices were not the primary influencing factors of LNC and LA variations. Our previous study on leaf trait variation has showed that relative to SLA and LPC, LNC and LA were more influenced by phylogeny than environmental variables in China (An et al., 2021). Similar results have been found in other studies. For example, Yang et al. (2016) have reported that LNC and LPC were phylogenetically conserved, but LPC were less conserved than LNC. In addition, Valverde-Barrantes et al. (2017) have suggested that LNC were more influenced by phylogenetic effect rather than climate, while SLA were more controlled by climate. Yang et al. (2017) have also reported that LA and LNC were more

effected by phylogeny than site or climate in China. Therefore, LNC and LA showed relatively poor performance. We have added the relevant discussion as "*However, LNC and LA showed relatively poor performance, which may be related to the reason that these two traits were more influenced by phylogeny than environmental variables (Yang et al., 2017; An et al., 2021).*" in the Discussion section (see Lines 465–468 in the revised manuscript).

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13. I suggest that the authors may consider excluding the plant trait of SM and Height, despite their significance in many terrestrial ecosystem processes. The sampling for these traits seems too sparse to accurately represent the trait variability across the entire region of China. As a result, it becomes difficult for me to place trust in the obtained results.

**[Response]:** Thanks for your suggestion. We have removed the maps of SM and plant height and their relevant content in the revised manuscript.